Investigations into *O*-GlcNAcylation through analytical mass spectrometry

by

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Abstract

The modification of proteins with O-linked N-acetylglucosamine residues (O-GlcNAc) is found on many proteins in the nucleus and cytoplasm. O-GlcNAc has been implicated in many physiological processes but much remains to be learned about the effects of this modification on protein function. In this thesis I detail two studies aimed to improve our understanding of protein modification by O-GlcNAc.

First, I describe a bioinformatics study focused on uncovering the protein structural features that favour O-GlcNAcylation by the enzyme O-GlcNAc transferase. The search for a sequence or structural motif to be found amongst the many substrates O-GlcNAcylated by OGT is a path well-trodden. On the basis of our analysis of site mapping data accumulated from the literature and also through targeted site mapping of an entirely intrinsically disordered protein by mass spectrometry, I counter argue that OGT preferentially targets substrates which can be intrinsically disordered.

Second, I describe a study aimed to gain insight into cellular proteomic response due to lowering of O-GlcNAc levels. There is mounting evidence O-GlcNAcylation is both linked with protein folding and intracellular proteome stability. While stability is measured by turnover it is also tied to misfolding. We investigated a possible relationship between lowered O-GlcNAc levels and instability of a segment of the proteome using stable isotope labelling by amino acids in cell culture mass (SILAC). This data reveals a change in protein stability between the entire sample populations that differ in O-GlcNAc levels, which is also observed for many individual proteins.

Keywords: mass spectrometry; *O*-GlcNAc; *N*-acetylglucosamine transferase (OGT); site mapping; SILAC; protein stability

Dedication

Rosslyn, Ross and Julie.

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List of Abbreviations and Acronyms

5S-GlcNAc	2-acetamido-2-deoxy-5-thio-D-glucopyranose
CID	Collision Induced Dissociation
DTT	Dithiothreitol
ECD	Electron Capture Dissociation
ESI	Electro Spray Ionization
ETD	Electron Transfer Dissociation
HCD	Higher energy Collisional Dissociation
HEK	Human Embryonic Kidney
HPLC	High Performance Liquid Chromatography
IAA	Iodoacetamide
MEF	Mouse Embryonic Fibroblast
MORF	MOlecular Recognition Feature
MS	Mass Spectrometer
OGA	β-N-acetylglucosaminidase
OGT	Uridine diphosphate *N*-Acetylglucosamine: polypeptidyl transferase
SILAC	Stable Isotope Labelling by Amino acids in Cell culture

Chapter 1.

Introduction

Historical introduction

Just over 500 million years ago during the Pre-Cambrian explosion, life forms evolved rapidly with the emergence of metazoans which eventually included humans (Wray, Levinton et al. 1996). It is remarkable to note in 1897 J.J. Thomson, a scientist known for so many disruptive contributions also built the first example of a mass spectrometer (Thomson 1897). By 1953, Watson and Crick published their famous article, "Molecular Structure of Nucleic Acids: A Structure for Deoxyribose Nucleic Acid", detailing their model of deoxyribonucleic acid (DNA) which holds the code necessary for the biosynthesis of thousands of different proteins (Watson and Crick 1953). The biosynthesis of the vast majority of proteins is carried out in two steps: transcription and translation. First, ribonucleic acid (RNA) is transcribed from DNA in the nucleus. Next, RNA is translated to protein in the cytoplasm by ribosomes. Fischer and Krebs were later awarded the Nobel prize in physiology or medicine for uncovering an entirely new dimension of complexity as to how cells are regulated by the addition and removal of the post translational modification phosphorylation (Fischer and Krebs 1966). An enzyme is a type of protein that catalyzes a chemical reaction, by lowering the energy barrier for a chemical process that governs the rate of the reaction. The activities of many enzymes are regulated by post translational modifications (Fersht 1984). Understanding the

temporal and spatial changes in cells that are created by post translational modifications which extend far beyond what is simply coded within genes has meant that the regulation of specific biological pathways involves a far larger number of proteins species than were initially anticipated through early genomics research. Among the many types of protein modifications, glycosylation is highly abundant (Khoury, Baliban et al. 2011). Several types of protein glycosylation are known including N-linked glycosylation, O-linked glycosylation with N-acetylgalactosamine, C-mannosylation and O-linked glycosylation with N-acetylglucosamine (O-GlcNAc) (Brooks 2002). Early techniques used to study protein glycosylation included radio-isotopic labelling to trace the transfer of monosaccharide groups added onto proteins; followed by Edman degradation of the proteins, separation by liquid chromatography and finally radiolabel detection such as scintillation or gamma counting (Kelly, Dahmus et al. 1993). However, these methods are cumbersome and have limitations in terms of determining the sequence around the sites of modification unless used in conjunction with other techniques such as site-directed mutagenesis. In 1984, Fenn et al. invented electrospray ionization for the purpose of detecting biomolecules (Yamashita and Fenn 1984) on the basis of theoretical speculation in 1968 by Malcom Dole (Wilm 2011). By the turn of the 21st century, mass spectrometry was established as the primary analytical chemistry tool for the enormous task of investigating the nature of the many thousands of proteins present within organisms. Now with the advent of more advanced mass spectrometers and isotopic labelling techniques such as stable isotope labelling of amino acids in cell culture (SILAC) the great sensitivity and accuracy in protein analysis afforded by these technologies is helping us to better understand of the complexity of the proteome. This thesis investigates some aspects of the post-translational glycosylation of proteins with *O*-GlcNAc through the use of mass spectrometry. Although many groups have studied the use of mass spectrometry for

analyzing PTMS such as phosphorylation, little method development has been pursued in the study of protein glycosylation with *O*-GlcNAc due to some of the intrinsic properties of this modification. In this thesis I will describe studies directed toward explaining some of the current ambiguity regarding the role of O-GlcNAcylation in protein structure and function as well as describe some trends in the protein sequences that define modification sites that are *O*-GlcNAcylated.

O-GlcNAcylation

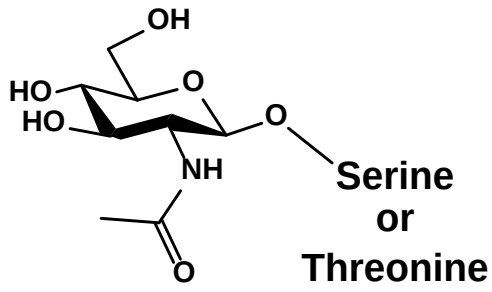

Figure 1.1. O-GlcNAc is covalently attached to serine and threonine hydroxyl groups

O-GlcNAcylation (Figure 1.1) is the enzymatic transfer of the monosaccharide *N*-acetylglucosamine (GlcNAc) from uridine diphosphate *N*-acetylglucosamine (UDP)-GlcNAc onto specific serine and threonine residues of target proteins within metazoans (Torres and Hart 1984, Groves, Lee et al. 2013). There is only a single known enzyme responsible for this intracellular form of *O*-linked glycosylation, Uridine diphosphate *N*-acetylglucosamine:polypeptidyl transferase or OGT (Vocadlo 2012). OGT is essential for life at the cellular level (Shafi, Iyer et al. 2000); however, we have yet to discover whether *O*-GlcNAc itself is what defines this absolute requirement for OGT or whether the protein scaffold plays the essential role at the single cell level. Recently, OGT was shown to have the remarkable ability to cleave proteins (Lazarus, Jiang et al. 2013). Another metazoan

GlcNAc transferase known as eOGT has no homology to OGT and *O*-GlcNAcylates proteins within the secretory pathway (Sakaidani, Nomura et al. 2011). β-N-acetylglucosaminidase (OGA) acts to hydrolyse *O*-GlcNAc from substrate proteins (Gao, Wells et al. 2001). Accordingly OGT catalyzed O-GlcNAcylation is reversible and occurs within the nucleus and cytoplasm where it can compete with serine and threonine phosphorylation on some proteins (Hart, Kreppel et al. 1996). There has been significant research interest in *O*-GlcNAcylation over the past decade resulting in recent X-ray crystal structures of human OGT (Lazarus, Nam et al. 2011) and OGA homologs (Dennis, Taylor et al. 2006, Schimpl, Schuttelkopf et al. 2010), increased mapping of O-GlcNAc sites by mass spectrometry as tabulated in the appendix, and inhibitors of these two enzymes (Gloster, Zandberg et al. 2011, Yuzwa, Shan et al. 2014) created specifically for understanding this carbohydrate modification. This PTM appears to play a role in multiple physiological and pathophysiological processes including, transcription (Fujiki, Hashiba et al. 2011) and translation (Ranuncolo, Ghosh et al. 2012), diabetes (Vaidyanathan and Wells 2014), neural development (Rexach, Clark et al. 2012), Alzheimer disease (Yuzwa, Shan et al. 2012, Zhu, Shan et al. 2014), cell cycle (Tan, Caro et al. 2013), cancer (Ma and Vosseller 2014), and cellular stress response (Slawson, Zachara et al. 2005, Reeves, Lee et al. 2014). Interestingly, loss of OGT in mice is deleterious at the single cell level for reasons for which are not fully understood (Shafi, Iyer et al. 2000). This observation indicates that OGT is critical for development and has a unique function that cannot be compensated for by other related proteins. More recently, *O*-GlcNAcylation have been described as an epigenetic marker (Fujiki, Chikanishi et al. 2009, Sinclair, Syrzycka et al. 2009, Dehennaut, Leprince et al. 2014, Lewis and Hanover 2014), and playing a role in the unfolded protein response (Ngoh, Hamid et al. 2009, Zachara, Molina et al. 2011,

Groves, Lee et al. 2013, Wang, Deng et al. 2014). This thesis will focus primarily on intracellular *O*-GlcNAcylation of proteins in mammalian cells.

Mass spectrometry

A mass spectrometer is an analytical instrument used to identify or quantify molecules that can be ionized. Sample is introduced into a mass spectrometer and the output is a measure of signal intensity versus mass to charge (m/z) ratio. Through the manipulation of an ion by the controlled electromagnetic fields of the mass spectrometer, molecules can be separated in both time and space. In cases where better than atomic mass unit resolution can be obtained, the charge of an ion is determined and observed as integer multiples of an electron charge. Once the charge state is known one can easily derive the mass of the ion from the measured m/z, which is a critical step in the analysis of peptides as performed later within this thesis.

Mass spectrometers are purpose built in order to maximize their performance characteristics towards either quantitative or qualitative applications. However, one needs to understand the limitations of the various parts of a mass spectrometer and how these different components match the needs for the intended application whether it be quantitative or qualitative. For proteomics applications most mass spectrometers have at least one of each of the following; an ion source, an interface to an evacuated chamber, an ion guide, an ion filter, a fragmentation cell, a detector and a set of data processing and analysis tools, which are also accompanied by a chromatography system.

An ion source ionizes molecules and transfers them into the gas phase. For all of our experiments in this thesis we used electrospray ionization (ESI) (Kebarle and Verkerk

2009, Wilm 2011). The efficiency of electrospray ionization mass spectrometry is concentration dependent at the point of exit from the ion source to the mass spectrometer. This type of ionization is achieved by transferring charge to the ion solution as opposed to charge transfer the ion in the gas phase, in which case it would be called an atmospheric pressure ionization source (Horning, Carroll et al. 1974) which is not as strongly concentration dependent. Nano-electrospray ionization is generally performed using flow rates of nanoliters per min by employing narrow bore tubing as small at 5 µm internal diameter. This low flow rate and narrow bore enables one to increase the concentration of analyte being transferred into the gas phase and thereby improve the lower limit of detections in combination with ESI. Electrospray ionization is one of the soft ionization techniques, meaning it is less likely to fragment large biomolecules within the ion source. Electrospray ionization actually results from the competition of two different processes by which charge is transferred to a molecule: the ion evaporation process (Iribarne and Thomson 1976) and the charge residue process (Fenn, Mann et al. 1989). Even though we have not utilized matrix assisted laser desorption ionization (MALDI) (Zenobi and Knochenmuss 1998) in this thesis, it is worth mentioning at this point because a handful of *O*-GlcNAc site mapping spectra were rejected when compiling our list of mapped *O*-GlcNAc sites from the literature. These experiments often cited MALDI as a soft ionization technique but unfortunately failed to generate MSMS data that would support identification of the site of *O*-GlcNAc modification (de Jesus Perez, Juarez et al. 2006, Kang, Han et al. 2008, Hoffmann, Liu et al. 2012). MALDI-TOFTOF (Time Of Flight - Time Of Flight) mass spectrometry is a cornerstone method used in proteomics studies (Aebersold and Mann 2003, Kuzyk, Ohlund et al. 2009) and the MALDI in combination with a TOF will produce a quality precursor spectrum for a peptide with an *O*-GlcNAc PTM. However, it is the opinion of the author that fragmentation of such a peptide within a TOFTOF instrument

requires the precursor to be rapidly decelerated into the fragmentation cell, fragmented then rapidly accelerated into the second time of flight path, all of which imparts too much internal energy on the peptide to retain the labile *O*-GlcNAc modification even in the absence of additional neutral collision gas above the residual base pressure.

Mass filters come in many different designs. The quadrupole mass filters (Miller and Denton 1986, Douglas 2009) are the standard for use in applications requiring absolute quantitation but offer relatively less in terms of ion transmission efficiency and resolution as compared to other mass filters. Time of flight filters offer reasonable resolution and good signal to noise ratios but as noted above for O-GlcNAc, tends to impart too much energy to labile molecules when configured in a tandem TOF-TOF design. The Linear ion trap (Douglas and Konenkov 2014) offers one of the best places to recover or produce labile peptide fragments prior to delivery to a detector but has a low mass cut-off that limits detection of low molecular weight species, cannot compete with the quadrupole for absolute quantitative repeatability and when overloaded with ions will thermalize the ions causing a mass shift. The Fourier transform ion cyclotron resonance (FT-ICR) mass spectrometer produces the highest resolution and sensitivity but has a low mass cut-off. These systems are also overly expensive and are too slow to accommodate high throughput proteomics. The orbitrap mass filter is a type of ion trap that has a low cycle time, very high resolution and good sensitivity but is limited by an upper limit in the amount of sample that can be loaded into the trap. Hybrid mass spectrometers combine multiple different mass filters to excellent effect in qualitative mass spectrometry such the quadrupole with time of flight (Ens and Standing 2005) or orbitrap with linear ion trap and quadrupole (Ledvina, Rose et al. 2013, Hebert, Richards et al. 2014).

The choice of fragmentation strategy used is a critical element in both the design of an *O*-GlcNAc site mapping experiment due to the lability of this modification, and the design of a SILAC experiment where the length of the cycle time affects the number of peptides identified. Cycle time is the measure of the time it takes for the mass spectrometer to go through one period of carrying out a number of requested functions, returning to the point of detection of data of the same type and point in the mass range. There are four common types of hardware and corresponding chemical fragmentation mechanisms available: CID, HCD, ETD and ECD. Collision induced dissociation (CID) and higher energy collisional dissociation (HCD) both fragment peptides along the peptide backbone at the same locations between amino acids, mostly generating b-ions and y-ions (Figure 1.2). Electron transfer dissociation (ETD) and electron capture dissociation (ECD) both fragment peptides along the peptide backbone at the same locations between amino acids, mostly generating c-ions and z-ions (Figure 1.2).

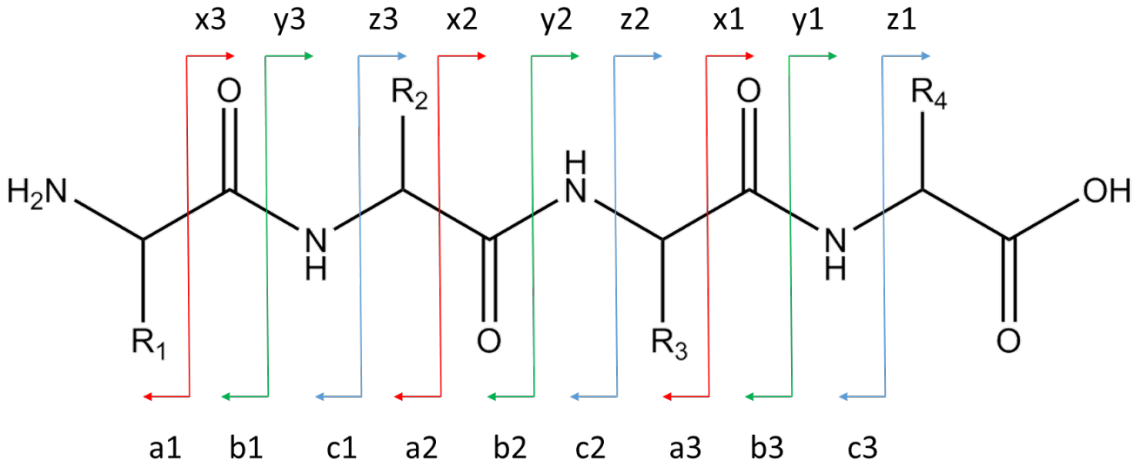

Figure 1.2. Peptide backbone showing fragmentation ladder. CID and HCD fragment the peptide to produce b- and y-ions. ETD and ECD fragment the peptide to produce c- and z-ions.

CID fragments ions by introducing neutral gas molecules into a collision cell. The ionized analytes are imparted sufficient kinetic energy by way of an electric potential to induce

fragmentation. The density of the neutral collision gas is such that the collisional cross section does not favor direct collisions but rather favors the absorption of energy internally within the peptide through multiple near collisions. The molecule then dissociates after reaching an excess of internal energy to yield several fragment ions that are subsequently analyzed (Mitchell Wells and McLuckey 2005). HCD is actually a form of CID but fragmentation occurs within a "c-trap" that is, analogous to a linear ion trap where the quadrupoles have been shaped into a 'C'. The higher energy terms in HCD does not refer to the radio frequency (RF) applied to induce resonant motion and resulting CID fragmentation but rather the higher RF applied field to contain the ions within the 'C-trap' (Olsen, Macek et al. 2007). ETD fragments ions by aligning the beam path of energized ions to be fragmented into a DC potential well within close proximity to an electron donor reagent under vacuum conditions (Syka, Coon et al. 2004). ECD is used only in FTICR instruments where the magnetic field strength is sufficient to trap a bath of energized electrons produced by electronic means, in close proximity with the ion being fragmented. ECD is a very efficient, effective and reliable way of consistently producing c- and z- ion fragmentation but is rare due the great cost of ECD which must be added to the already high cost of a high field FT-ICR (Zubarev, Kelleher et al. 1998).

Quantifying the concentration of molecules in a sample is also a common application of mass spectrometry. The area of peaks found at various masses correlates with the concentration of that particular analyte in the sample if recordings are made within the linear dynamic range of the instrument. The use of quadrapole, fragmentation cell, and quadrapole design, often referred to as a 'QQQ' or 'triple quad' produces the most repeatable and reproducible absolute quantitation results but lacks the resolution required for analysis of unknowns in complex biological samples. Further, absolute quantitation

requires knowledge of the sample contents to meet the required use of an external or internal standard appropriate for use with the analyte of interest.

Stable isotope labelling by amino acids in cell culture (SILAC) is a relative quantitation strategy (Mann 2006) that is employed within this thesis (Figure 1.3). SILAC is one of several labelling strategies where high performance, hybrid mass spectrometers are generally more suited to qualitative analytical chemistry work and can be used to good effect for relative quantitation of proteins. In the simplest design and therefore more reliable, control group cells are fed media where some essential amino acids have been replaced by amino acids labelled with stable isotopes while experimental cells that have had some treatment and are fed media where the same essential amino acids have been substituted with amino acids with a different isotopic label. The amino acids that are used in these studies typically correspond with the amino acids found at the cleavage sites of endoproteineases used to generate the peptides that will be analyzed. For example lysine and arginine are the common amino acids chosen for labelling, as trypsin is used to digest proteins into smaller peptides that are more amenable to mass spectrometric analysis, preferentially cleave C-terminal to lysine and arginine residues. In this way, a perfect digestion of a protein mixture would leave a single labelled amino acid per peptide. Cells are cultured in media that contain the isotopic labelled amino acids, and through repeated cell divisions the labelled amino acids are gradually incorporated into the proteins of the cell. The incorporation of labelled amino acids into proteins to a level enabling one to conclude that the proteins in the cells in one labelled group are homogeneously labelled typically takes five passages or cell doublings. It has been shown the incorporation of isotopic labelled amino acids does not alter cell growth “as evidenced by cell morphology, doubling time, and ability to differentiate” (Ong, Blagoev et al. 2002).

Mass spectrometry is then used to detect the labelled peptides after separation by liquid chromatography. The mass to charge ratio of each full length peptide is measured along with the fragmentation spectrum of each peptide. Precursor ions are then found in clusters of the same peptide but with different mass shifts due to having different isotopic labels. There are two ways to identify peptides that belong to the same isotopic cluster of the same peptides. One method is to identify the amino acid sequence and map additional post translational modifications of each precursor ion based on the fragmentation spectra obtained. The other method is to measure m/z with high mass precision and high mass accuracy to distinguish precursor ions according to the mass of the isotopic labels incorporated. In this last method, only one of the precursor ions needs to have an accompanying MSMS fragmentation spectrum that confidently identifies the peptide sequence. It should be noted the isotopic labelled peptides tend to elute from reverse phase C18 chromatography a very short time earlier than their unlabelled counterparts. To account for this time separation and also benefit from increased data sample sizes, software applications used for SILAC reconstruct the spectra in three dimensional space with the addition of a time axis showing the chromatogram orthogonal to the typical peak intensity vs m/z (Figure 1.4). In the simplest design used in SILAC experiments the experimental and control groups are then mixed and the relative intensities of resulting precursor ions are indicative of the relative amounts of peptides and in turn the corresponding relative protein abundance between the control and treated groups. More complex experiments can be designed with correspondingly increased experimental errors. One can, as we have done in chapter 3, completely separate a control group from the experimental treated group using identical labelling strategies where the isotopic ratios track protein synthesis, degradation and turnover as will be discussed.

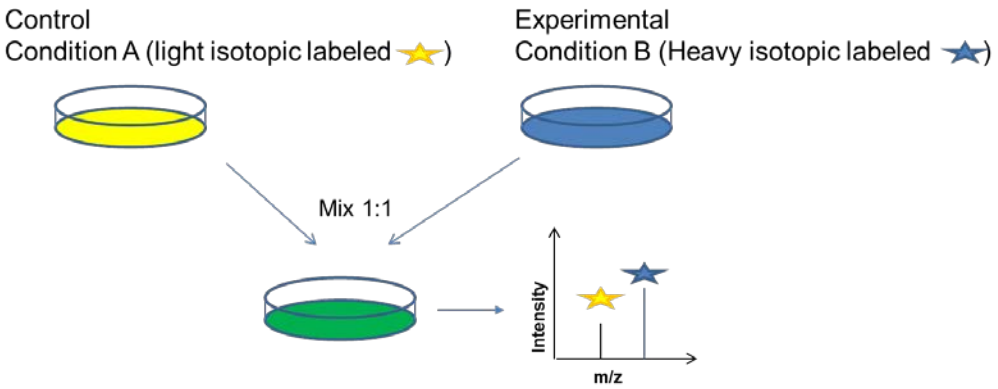

Figure 1.3. **The simplest SILAC experiment. The intensity of the signals between the Heavy (Blue) and Light (Yellow) labelled peptides gives relative protein abundance between conditions A and B, as measured by precursor ion ratio from mass spectrometry results.**

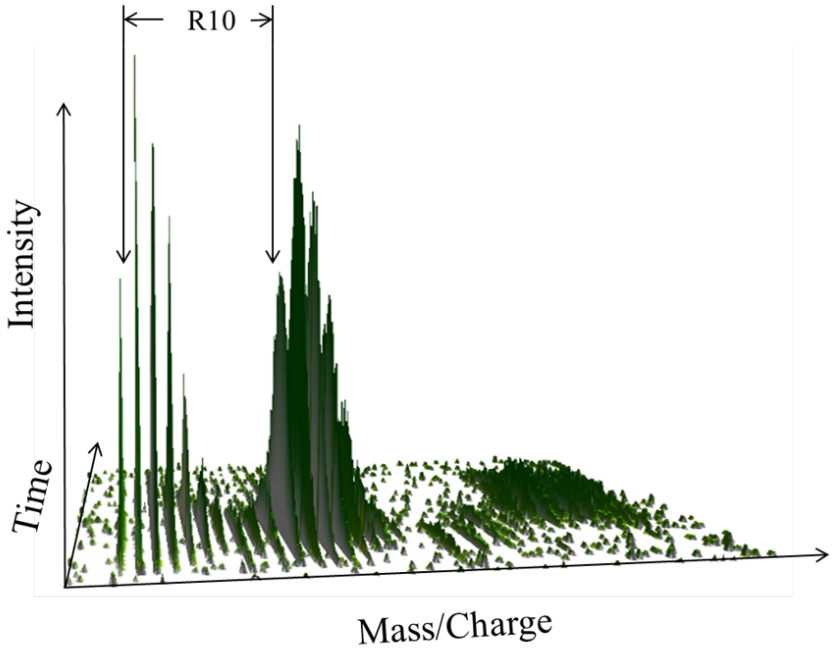

Figure 1.4. **Mass spectra reconstructed in time and mass/charge ratio three dimensional space from the MEF cells showing two peptide precursor ions with natural isotopic distribution separated by a mass/charge ratio equivalent to the addition of an Arginine10 label**

Chapter 2.

Analysis of *O*-GlcNAc mapped sites reveals OGT targets regions of intrinsic disorder and unstable structures

Introduction

It is in this chapter we provide evidence to support the hypothesis that OGT targets sections of substrate proteins for *O*-GlcNAcylation that are assigned on the basis of bioinformatics as being intrinsically disordered. We also map ten O-GlcNAc sites (eight novel sites) and reference from the literature a few other mapped sites on a protein known to be entirely intrinsically disordered (Figure 2.4). Intrinsic disorder with regard to proteins or regions of proteins are defined as polypeptide regions that, “exist as dynamic ensembles, within which atom positions and Ramachandran angles exhibit extreme temporal fluctuation without equilibrium values” (Habchi, Tompa et al. 2014). Intrinsic disorder (ID), however, is difficult to measure directly (Receveur-Brechot, Bourhis et al. 2006). In fact, the intrinsically disordered regions of proteins are not homogeneous in terms of their three dimensional structure and thus, such regions are not observed within protein crystals by X-ray diffraction spectroscopy. Similarly, intrinsic disordered regions are also too flexible to have their structures readily determined by NMR (Ota, Koike et al. 2013). Data in this section of the thesis was obtained by a combination of mass spectrometry, bioinformatics approaches, and annotated databases.

Intrinsic disorder and the absence of structural data

We obtained site mapping data through critical review of proposed mapped *O*-GlcNAc sites in the literature. This data set containing *O*-GlcNAcylation sites of proteins was formatted into a set of peptides 101 amino acids long, centered on the *O*-GlcNAcylated residue extracted from protein sequence information stored in the NCBI protein database and secondary and tertiary structural elements observed with these peptide sequences were then obtained using PHYRE2 software (Kelley and Sternberg 2009) which uses algorithms to correlate sequence similarity against archived peptides and sequences for which structural information is already reported by either X-ray crystallography or nuclear magnetic resonance (NMR). What we found is that *O*-GlcNAc sites are most often found in, or near, regions where data collection by either X-ray crystallography or NMR is absent. This observation suggests that these regions are likely difficult to elucidate from a structural perspective and therefore be intrinsically disordered. We validate these findings by submitting our peptide data set to a bioinformatics predictor of intrinsic disorder, PONDR-FIT (Xue, Dunbrack et al. 2010).

We reviewed over 4000 proposed claims of O-GlcNAc sites reported in the literature as having been mapped. We take into account redundancies within these reports and have compiled the data into the appendix based on assessment of the experimental data. Using this approach we compiled 1670 uniquely mapped *O*-GlcNAc sites published from the time O-GlcNAc was discovered by the Gerald Hart laboratory in 1984 (Torres and Hart 1984, Holt and Hart 1986) extending to through June 2012 (Hahne, Moghaddas Gholami et al. 2012). We further applied an empirical algorithm to score the quality of each mapped site based on general experimental parameters including the biological source of the proteins, the chemical methods used to identify sites, the analytical

instrumentation employed and the quality of the data. Based on the empirical scores obtained in this algorithm we identified 559 high confidence sites for further analysis.

Uversky and Dunker have categorized the common amino acids into three groups according to whether they have a statistical propensity to be associated with order, intrinsic disorder or neutral structure (Campen, Williams et al. 2008). We calculate the frequency of each category for individual positions around the O-GlcNAc mapped residue relative to natural abundance (Figure 2.1). The individual amino acids are characterized in the legend below.

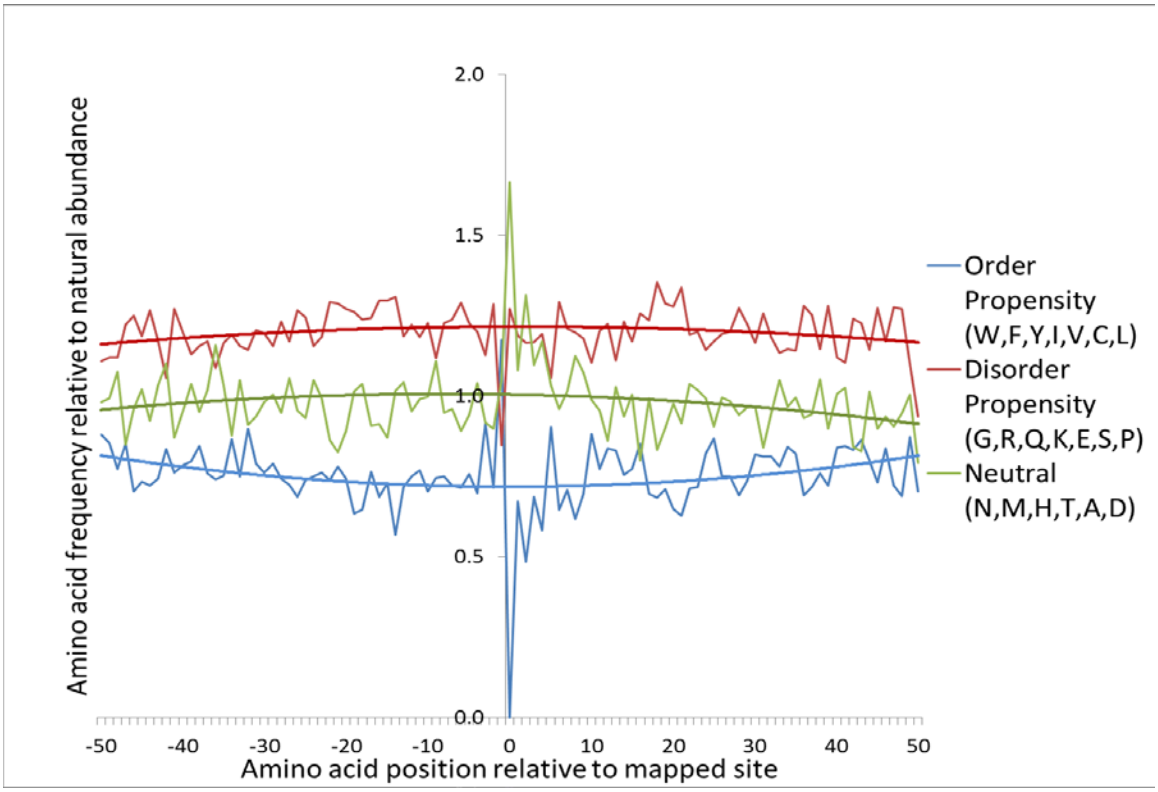

Figure 2.1. Frequency of amino acids categorized according to their propensity for association with intrinsic disorder relative to the natural abundance of each amino acid and plotted relative to the mapped site located in the center of the 101 amino acid polypeptide.

Intrinsic disorder is difficult to identify using conventional analytical techniques. We used our database containing the 559 mapped sites and computationally constructed a database of peptides each 101 amino acids in length centered on the *O*-GlcNAcylation sites using the known protein sequences from the NCBI protein database that contain the modification site. These peptides were generated using a program written in Pearl to automatically access and retrieve data from the NCBI website and then access the DISPROT website to use the PONDR-FIT utility to return intrinsically disordered probability scores along the length of each peptide (Figure 2.2).

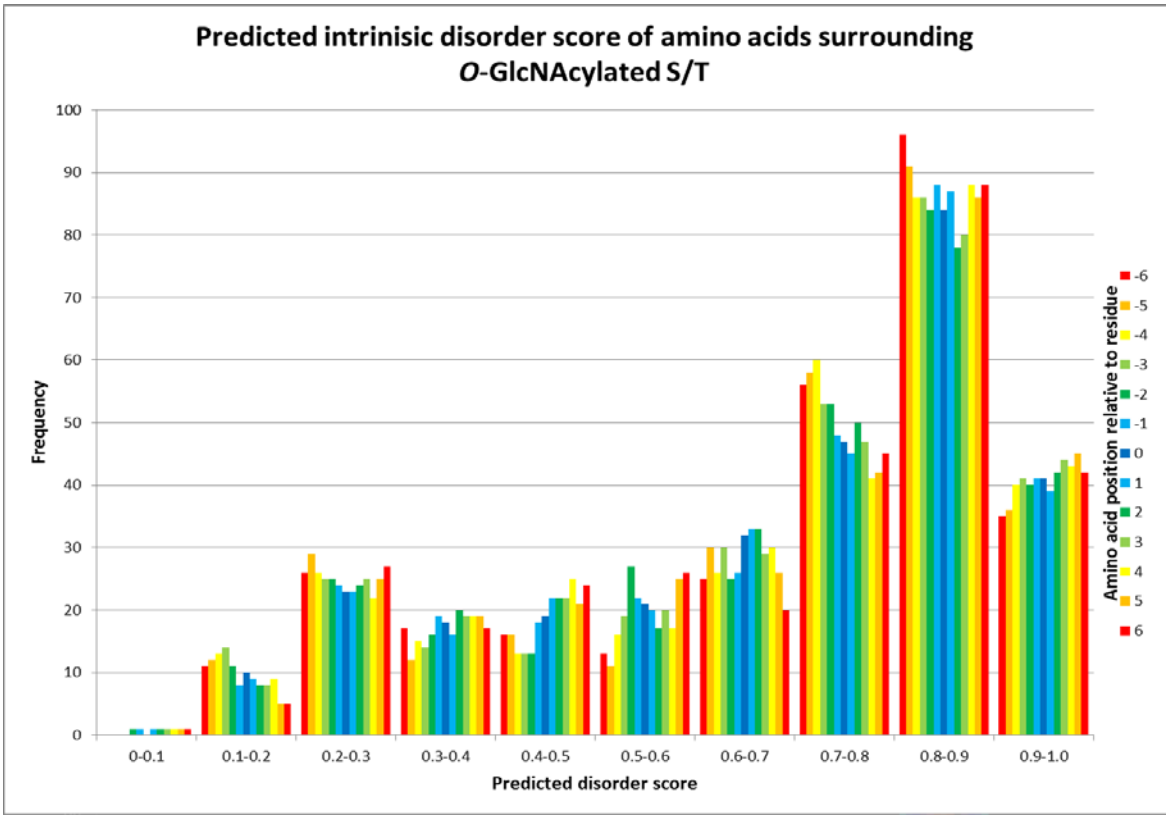

Figure 2.2. Intrinsic disorder scores for 559 O-GlcNAc 11 amino acids centered on the mapped sites using PONDR-FIT software. Dark blue represents the mapped site while other colors represent disorder scores at residues offset from the mapped site according to the legend.

Programs such as PONDR-FIT are excellent bioinformatics tools for exploring structural properties of proteins but we needed independent experimental data to validate these computationally predicted intrinsically disorder sequences observed amongst the database of *O*-GlcNAc modified peptides. Protein structure databases are populated with data generated from X-ray crystallographic and nuclear magnetic resonance experiments but are underrepresented by protein domains and regions that are either hydrophobic in nature or highly repetitive or intrinsically disordered. We therefore, accessed a second online program, PHYRE2 in order to assess the likelihood that each peptide is structured. PHYRE2 searches a redundant database of protein sequences to find proteins having high sequence similarity to each query sequence. The redundant protein sequences in the database are linked to known protein structures. PHYRE2 then returns a list of predicted protein structures for the query along with an associated confidence score for the model as compared to the known structures.

We used the data returned from PHYRE2 to examine whether protein regions that were predicted to not be folded would correlate with the intrinsic disorder prediction obtained from PONDR-FIT. Clearly the distribution of results for the prediction of intrinsic disorder results as shown in figure 2.2 reveal a higher probability of intrinsic disorder and in the region flanking the site of O-GlcNAcylation suggesting O-GlcNAc is found predominantly in regions of intrinsic disorder. From inspection of figure 2.3, a visually dense group of proteins that are predicted to be intrinsically disordered are seen and these also have a corresponding low confidence of assignment in that structure based on homology modelling. Correlation between PONDR-FIT intrinsic disorder scores and PHYRE2 structure assignment confidence is quite weakly anti-correlated with a Pearson correlation coefficient of -0.41. Many of the proteins that lie outside of the densely

populated area of intrinsic disorder and low confidence of assignment to measured structures can be explained as either being associated with the secretory pathway, have unstable second order structure such as part of an amphipathic α-helix, or located in the neighbourhood of a mostly well-defined structure or fold which contains a small region of intrinsic disorder.

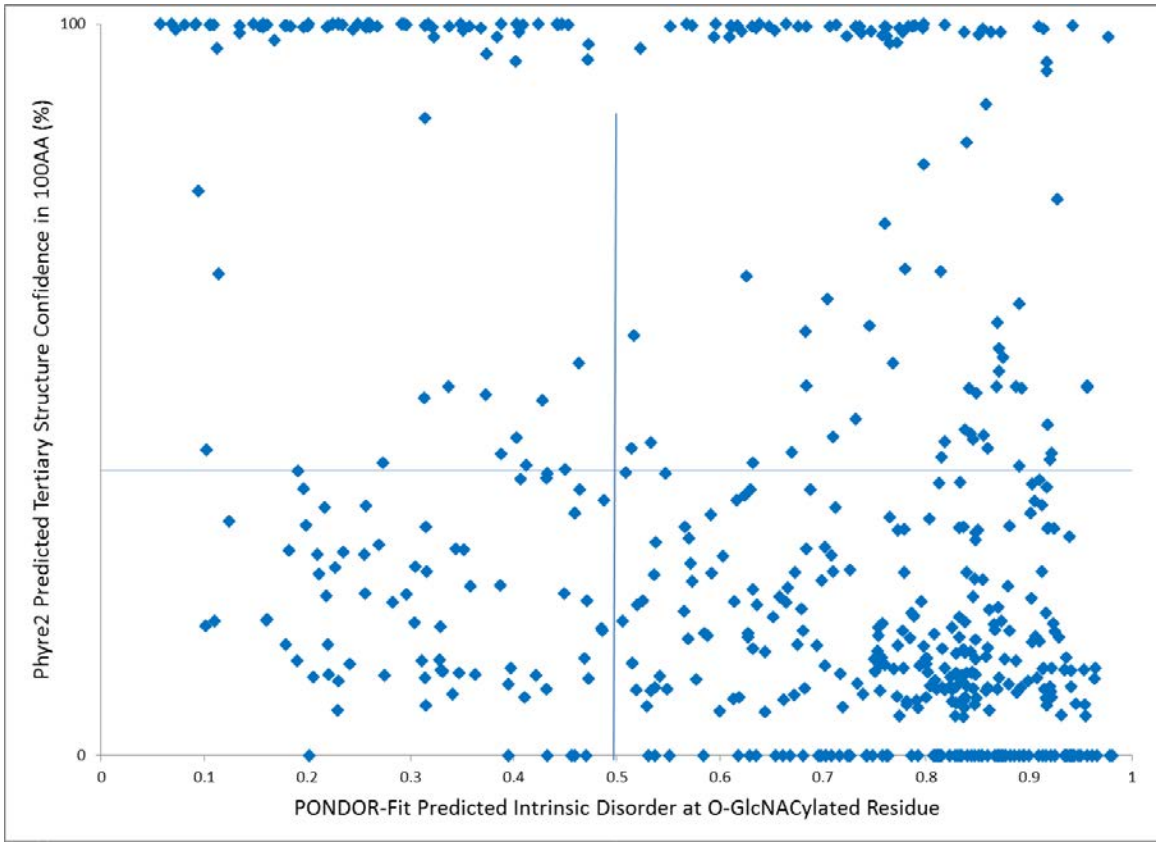

Figure 2.3. Intrinsic disorder probability assigned to O-GlcNAcylated residues by PONDR-FIT versus PHYRE2 confidence in assigning a tertiary structure to the sequence of 101 amino acids containing the O-GlcNAc modification site. There is a weak correlation between intrinsic disorder prediction based on primary structure and an absence of predicted tertiary structure proposed to be due to intrinsic disorder. The majority of data points are located in the lower right hand quadrant which supports our hypothesis that O-GlcNAc is found in intrinsically disordered regions.

Sites mapped on an entirely intrinsic disorder protein

The microtubule associated protein Tau is unique for being intrinsically disordered along the entire primary sequence.

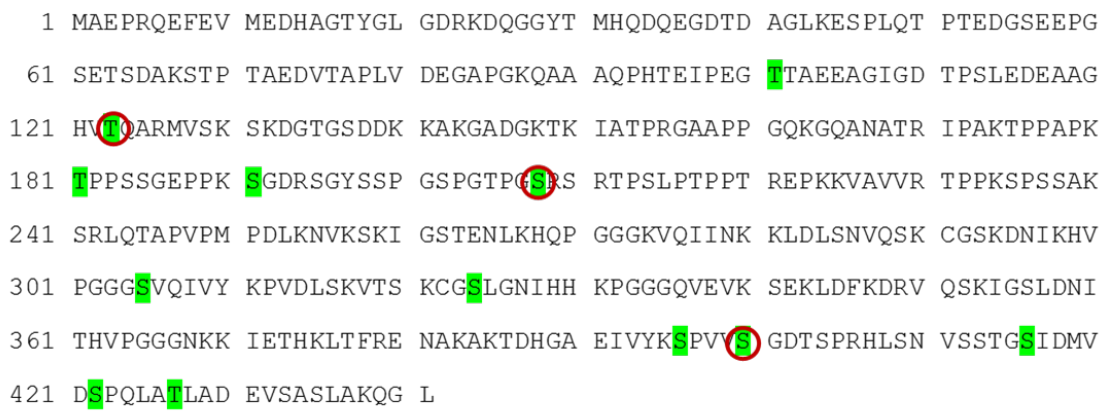

Figure 2.4. The *O*-GlcNAc mapped sites of microtubule associated protein Tau are highlighted in green based on data acquired in this thesis. Residues circled in red are already published mapped sites. : Yuzwa et al *Nat. Chem. Biol. (2012)* 8,393–399; Yuzwa et al *Amino Acids (2011)* 40,857–868; Wang et al *Mol. Cell. Proteomics (2010)* 9, 153–160.

Here we site map *O*-GlcNAc to Threonine 181, Serine 396, Serine 422, Serine 305, Serine 400, Threonine 427, Serine 416 and Serine 208 using HCD. We also site map *O*-GlcNAc to Serine 191 and Serine 324 using ETD on the full length isoform of Tau. Tau was recombinantly co-expressed in *Escherichia coli* with human OGT as per (Yuzwa, Yadav et al. 2011). Two of the above sites, Serine 400 and Serine 208 we already mapped and published using CID (Yuzwa, Yadav et al. 2011). One site Threonine 123 we have not mapped above is also previously published (Yuzwa, Shan et al. 2012).

The mapped sites above when combined include 10 O-GlcNAc mapped sites clearly mapped on Tau while there exist several more that are difficult to associate with a single residue amongst neighbouring serine and threonine residues due to insufficient

information contained within the MSMS spectra. Before showing the unambiguous assignment of each site using MSMS data, we'd like to point out the following table which clearly shows how the intrinsically disordered protein Tau has such a greater than usual density of *O*-GlcNAc mapped sites derived using the table of mapped sites from the literature contained in the appendix.

Table 2.1. Frequency of *O*-GlcNAc mapped sites among various proteins in decreasing order of density of *O*-GlcNAc mapped sites. The entirely intrinsically disordered protein Tau is 9th most densely *O*-GlcNAc mapped site out of 1674 proteins with some published *O*-GlcNAcylated residues.

# Mapped Sites Full List (1997 Mapped Sites)	Protein	Species	GI	Length (amino acids)	# Mapped Sites / 101 amino acids
124	Protein bassoon	Mouse	341940634	3942	3.1
74	Protein piccolo	Mouse	94730407	5038	1.5
46	host cell factor 1 **	Human	160332311	2035	2.3
34	Host cell factor 1	Mouse	341940790	2045	1.7
24	Myosin-6	Rat	127741	1938	1.2
23	nuclear pore complex protein Nup153 ***	Human	24430146	1475	1.6
18	Protein EMSY	Mouse	47605694	1264	1.4
14	host cell factor 1 **	Human	98986457	2035	0.7
12	Tau	Human	6754638	441	2.3
12	Catenin delta-2	Mouse	20177853	1247	1.0
12	Nuclear pore complex protein Nup214	Human	205831380	2090	0.6
12	Synapsin-1	Mouse	73920802	706	1.7
11	SH3 and multiple ankyrin repeat domains protein 2	Mouse	341942027	1476	0.7
9	Alpha-adducin	Mouse	10719868		
9	Neurofilament medium polypeptide	Mouse	146345468		

# Mapped Sites Full List (1997 Mapped Sites)	Protein	Species	GI	Length (amino acids)	# Mapped Sites / 101 amino acids
9	Signal-induced proliferation-associated 1-like protein 1	Mouse	50401562		
8	Actin-binding LIM protein 3	Mouse	56404493		
8	Band 4.1-like protein 1	Mouse	134047752		
8	Keratin, type II cytoskeletal 2 epidermal	Mouse	123796763		
8	Serine/threonine-protein kinase WNK1	Mouse	313104051		
7	12 proteins				
6	14 proteins				
5	15 proteins				
4	31 proteins				
3	66 proteins				
2	110 proteins				
1	422 proteins				

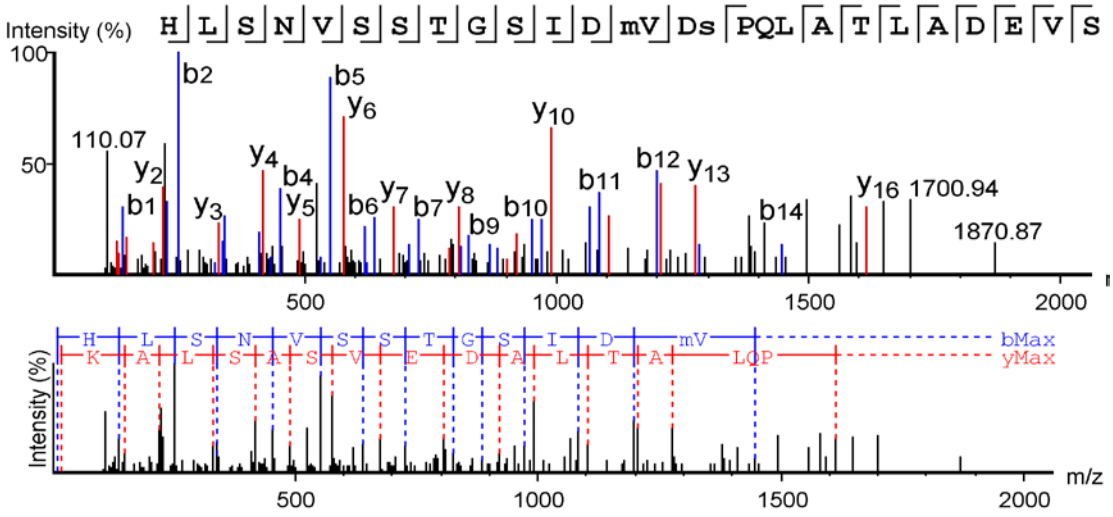

Figure 2.5. MSMS spectrum obtained by HCD reveals an O-GlcNAc site at S422.

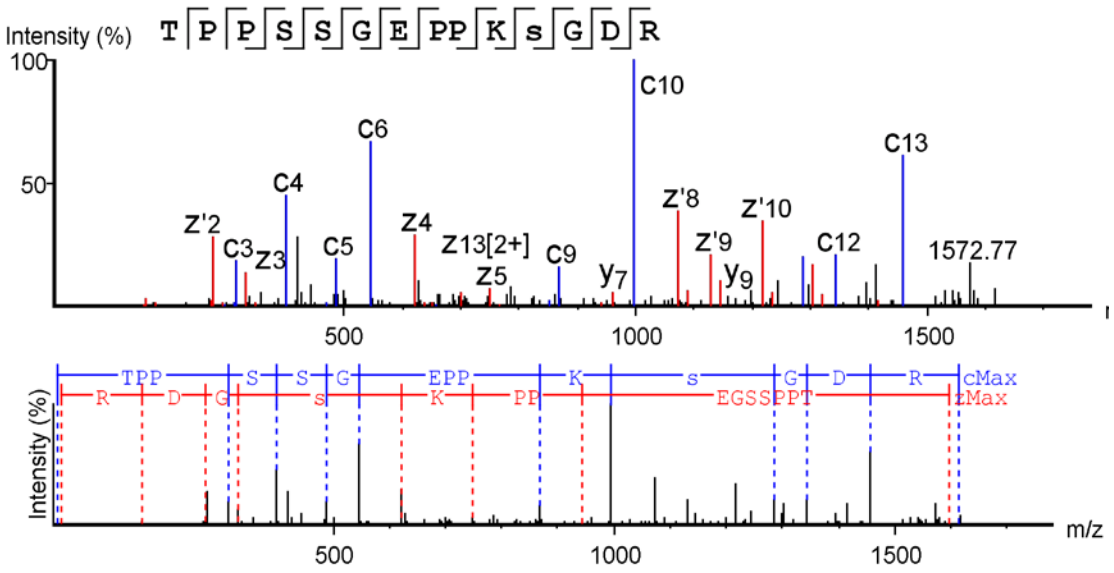

Figure 2.6. MSMS spectrum obtained by ETD reveals an O-GlcNAc site at S191.

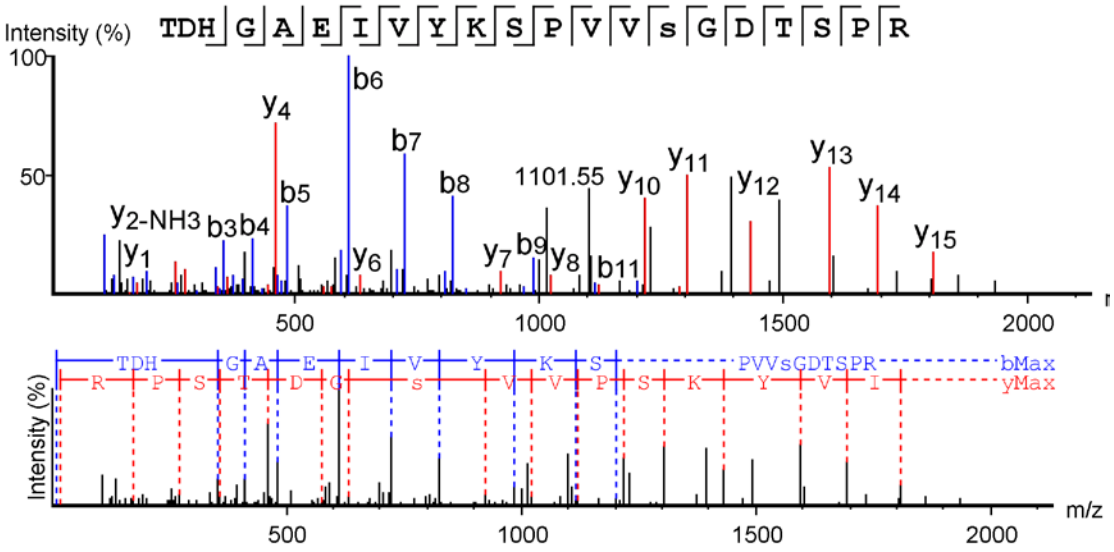

Figure 2.7. MSMS spectrum obtained by HCD reveals an O-GlcNAc site at S400.

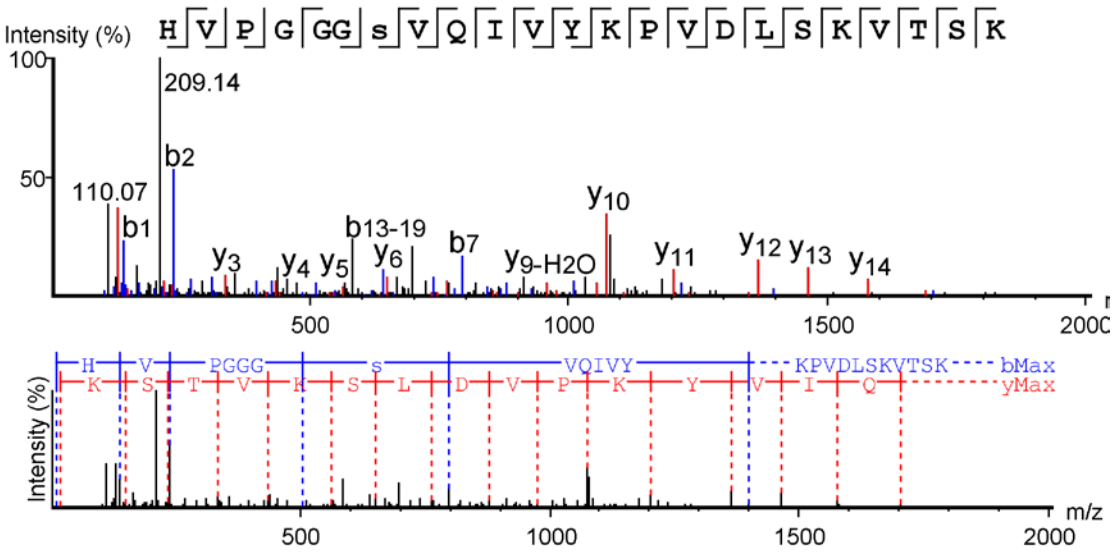

Figure 2.8. MSMS spectrum obtained by HCD reveals an O-GlcNAc site at S305.

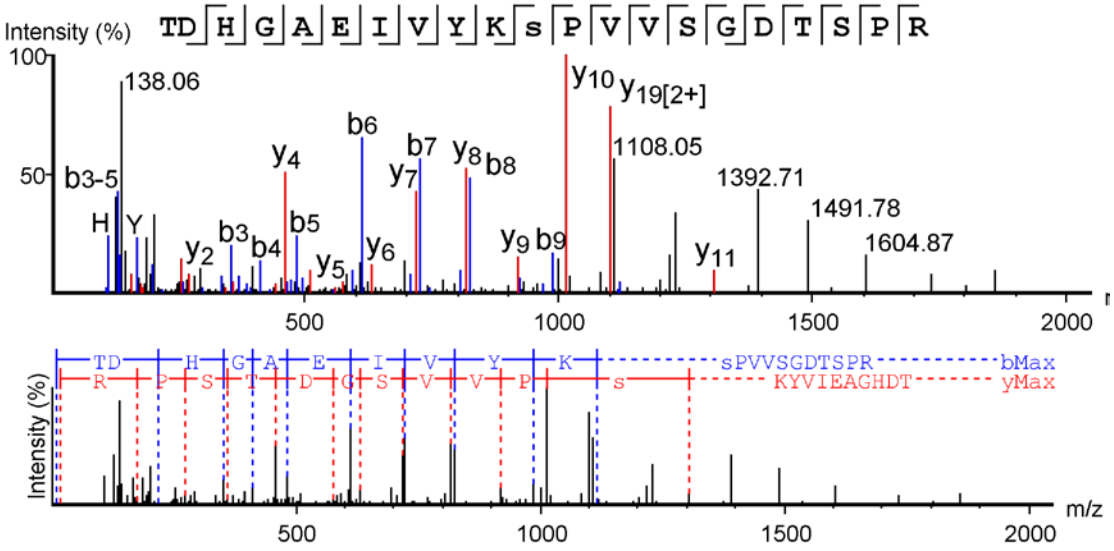

Figure 2.9. MSMS spectrum obtained by HCD reveals an O-GlcNAc site at S396.

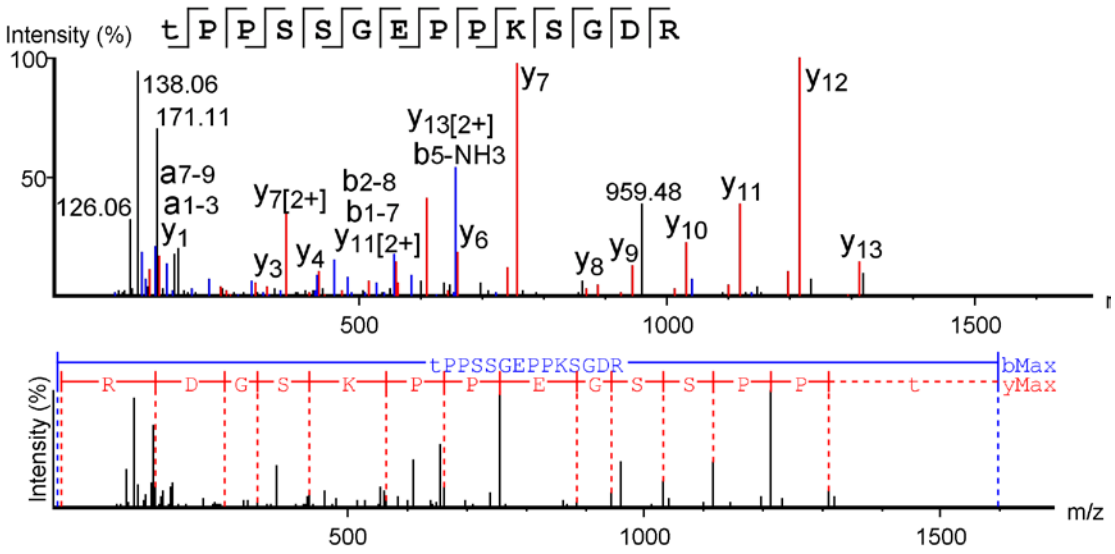

Figure 2.10. MSMS spectrum obtained by HCD reveals an O-GlcNAc site at T181.

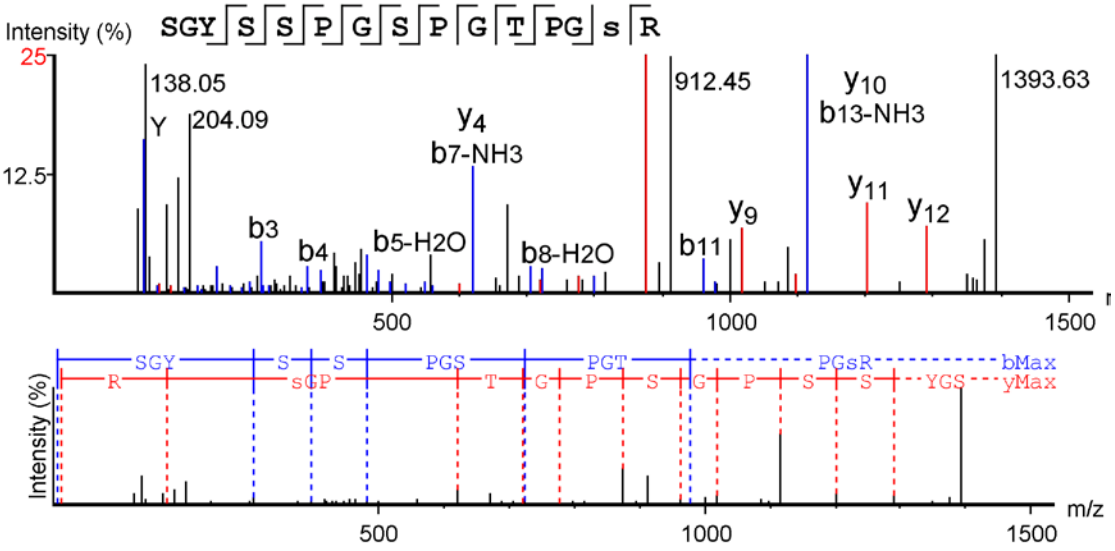

Figure 2.11. MSMS spectrum obtained by HCD reveals an O-GlcNAc site at S208.

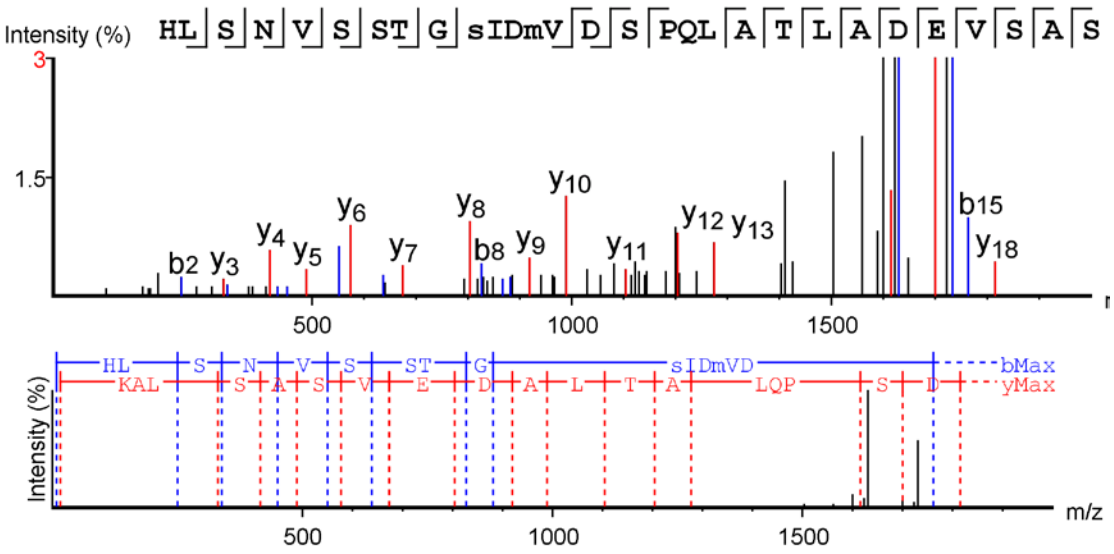

Figure 2.12. MSMS spectrum obtained by HCD reveals an O-GlcNAc site at S416.

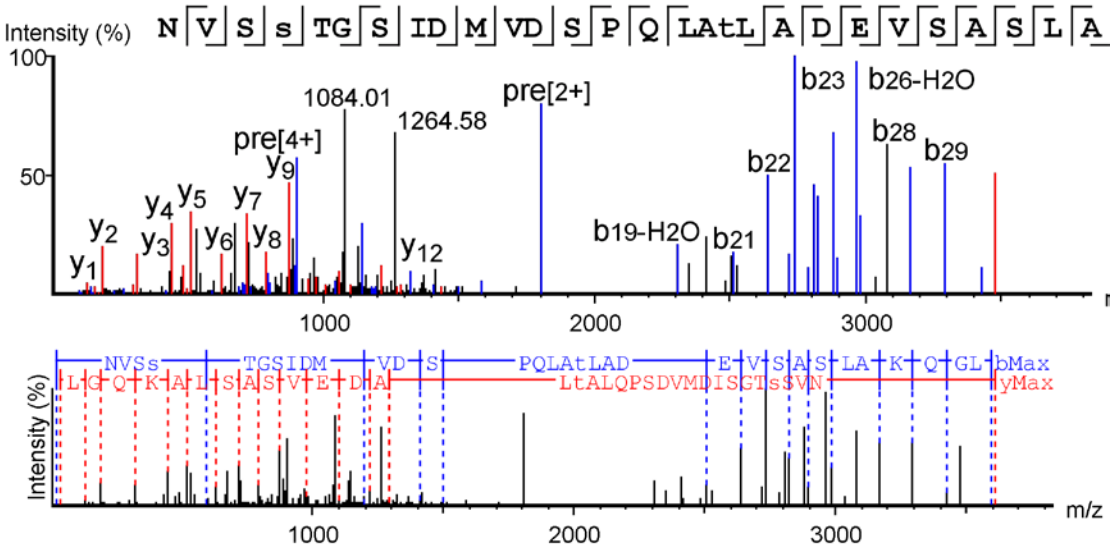

Figure 2.13. MSMS spectrum obtained by HCD reveals an O-GlcNAc site at S427.

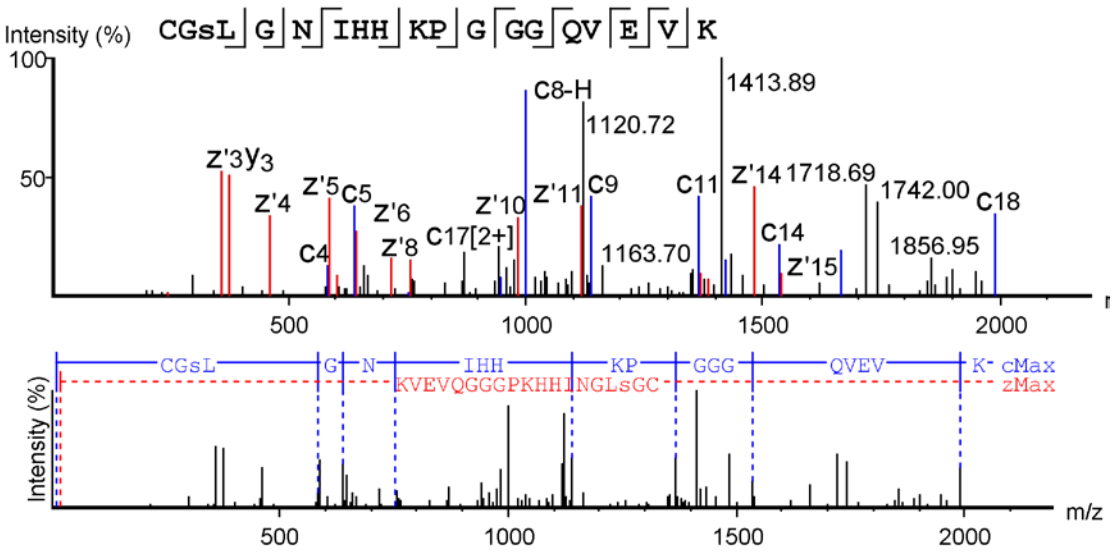

Figure 2.14. MSMS spectrum obtained by ETD reveals an O-GlcNAc site at S324.

#	Immonium	b	b-H2O	b-NH3	b (2+)	Seq	y	y-H2O	y-NH3	y (2+)	#
1	110.07	138.05	120.06	121.04	69.53	H					32
2	86.10	251.15	233.14	234.12	126.08	L	3325.62	3307.61	3308.59	1663.31	31
3	60.04	338.18	320.17	321.16	169.59	S	3212.54	3194.53	3195.51	1606.77	30
4	87.06	452.23	434.22	435.20	226.61	N	3125.50	3107.49	3108.48	1563.25	29
5	72.08	551.29	533.29	534.27	276.15	V	3011.46	2993.45	2994.43	1506.23	28
6	60.04	638.32	620.31	621.30	319.66	S	2912.39	2894.38	2895.37	1456.70	27
7	60.04	725.36	707.35	708.33	363.18	S	2825.36	2807.35	2808.33	1413.18	26
8	74.06	826.41	808.41	809.38	413.70	T	2738.33	2720.32	2721.30	1369.66	25
9	30.03	883.43	865.42	866.40	442.21	G	2637.28	2619.27	2620.25	1319.14	24
10	60.04	970.46	952.45	953.43	485.73	S	2580.26	2562.25	2563.23	1290.63	23
11	86.10	1083.55	1065.53	1066.52	542.27	I	2493.23	2475.22	2476.20	1247.11	22
12	88.04	1198.57	1180.56	1181.54	599.79	D	2380.14	2362.13	2363.12	1190.57	21
13	120.05	1345.61	1327.60	1328.58	673.30	M(+15.99)	2265.12	2247.11	2248.09	1133.06	20
14	72.08	1444.69	1426.66	1427.65	722.84	V	2118.08	2100.07	2101.05	1059.54	19
15	88.04	1559.70	1541.69	1542.67	780.35	D	2019.01	2001.00	2001.99	1010.01	18
16	263.12	1849.81	1831.80	1832.79	925.41	S(+203.08)	1903.99	1885.98	1886.96	952.49	17
17	70.07	1946.87	1928.85	1929.84	973.93	P	1613.91	1595.86	1596.85	807.44	16
18	101.07	2074.92	2056.91	2057.90	1037.96	Q	1516.82	1498.81	1499.79	758.91	15
19	86.10	2188.01	2170.00	2170.98	1094.50	L	1388.76	1370.75	1371.74	694.88	14
20	44.05	2259.05	2241.03	2242.02	1130.02	A	1275.69	1257.67	1258.65	638.34	13
21	74.06	2360.09	2342.08	2343.07	1180.55	T	1204.66	1186.63	1187.61	602.82	12
22	86.10	2473.18	2455.17	2456.15	1237.09	L	1103.61	1085.58	1086.57	552.30	11
23	44.05	2544.21	2526.20	2527.19	1272.61	A	990.51	972.50	973.48	495.76	10
24	88.04	2659.24	2641.23	2642.21	1330.12	D	919.48	901.46	902.45	460.24	9
25	102.06	2788.28	2770.27	2771.26	1394.64	E	804.45	786.44	787.42	402.72	8
26	72.08	2887.35	2869.34	2870.32	1444.18	V	675.40	657.39	658.38	338.20	7
27	60.04	2974.38	2956.37	2957.36	1487.69	S	576.34	558.32	559.31	288.67	6
28	44.05	3045.42	3027.41	3028.39	1523.21	A	489.30	471.29	472.28	245.15	5
29	60.04	3132.45	3114.44	3115.43	1566.73	S	418.27	400.26	401.24	209.63	4
30	86.10	3245.54	3227.53	3228.51	1623.27	L	331.23	313.22	314.21	166.12	3
31	44.05	3316.57	3298.56	3299.55	1658.79	A	218.15	200.14	201.12	109.57	2
32	101.11					K	147.11	129.10	130.09	74.06	1

Figure 2.15. Interpretation of HCD MSMS data enables *O*-GlcNAc site mapping to S422 of a peptide obtained by trypsin digestion of recombinant tau protein.

#	b	c	c-H	c (2+)	Seq	y	z	z'	z (2+)	z' (2+)	#
1	102.06	119.08	118.07	60.04	T						14
2	199.11	216.14	215.13	108.57	P	1513.71	1496.69	1497.69	748.54	749.46	13
3	296.34	313.19	312.30	157.09	P	1416.69	1399.63	1400.64	700.32	701.10	12
4	383.19	400.34	399.43	200.61	S	1319.47	1302.58	1303.76	651.75	652.29	11
5	470.29	487.32	486.38	244.13	S	1232.89	1215.55	1216.64	608.27	608.78	10
6	527.25	544.34	543.27	272.64	G	1145.48	1128.52	1129.71	564.76	565.26	9
7	656.65	673.32	672.31	337.16	E	1088.56	1071.49	1072.55	536.25	536.75	8
8	753.34	770.37	769.36	385.68	P	959.70	942.62	943.46	471.73	472.23	7
9	850.48	867.51	866.41	434.21	P	862.43	845.40	846.41	423.20	423.70	6
10	978.49	995.62	994.51	498.26	K	765.45	748.54	749.46	374.67	375.18	5
11	1268.60	1285.81	1284.62	643.31	S(+203.08)	637.28	620.49	621.27	310.63	311.13	4
12	1325.62	1342.78	1341.64	671.82	G	347.30	330.34	331.21	165.57	166.07	3
13	1440.65	1457.71	1456.67	729.34	D	290.23	273.54	274.18	137.06	137.56	2
14					R	175.10	158.21	159.13	79.55	80.05	1

Figure 2.16. Interpretation of ETD MSMS data enables O-GlcNAc site mapping to S191 of a peptide obtained by trypsin digestion of recombinant tau protein.

Discussion

The data presented here (Figure 2.2) using the intrinsic disorder prediction algorithm is supportive of the hypothesis, that regions containing *O*-GlcNAcylation sites tend to be intrinsically disordered. This data is consistent with previous data reported by (Trinidad, Barkan et al. 2012). Mapping sites of *O*-GlcNAc on the intrinsically disordered Tau protein *in vitro* also supports *O*-GlcNAcylated peptides are preferentially intrinsically disordered. There are, however, outliers in some regions of the chart in figure 2.3 that need to be explained.

It may seem contradictory for PHYREII to successfully return a tertiary structure with near 100% confidence, while PONDR-FIT identifies the *O*-GlcNAcylated residue as having greater than 50% probability of being intrinsically disordered. Many of these cases can be explained by the mapped site being located in or near a small intrinsically disordered region within a larger well known protein fold. An example is shown below of

the intrinsically disordered region in the Thioredoxin fold of endoplasmic reticulum (ER) resident protein 44, the structure of which was obtained using X-ray crystallography (Wang, Wang et al. 2008). Serine 381, Serine 385 and Serine 386 are shown in red and are all known O-GlcNAcylation sites (Hahne, Moghaddas Gholami et al. 2012). Intrinsic disorder probability scores obtained from PONDR-FIT for these three mapped sites are 0.72, 0.61 and 0.60 respectively. The corresponding confidences in tertiary structure association returned by PHYRE2 are 98.4%, 98.2% and 98.2%. These high confidences of tertiary structure are associated with the well-defined Thioredoxin fold, which routinely shows a small region of intrinsic disorder in many X-ray and NMR obtained structures within the RCSB protein data bank (Berman, Westbrook et al. 2000).

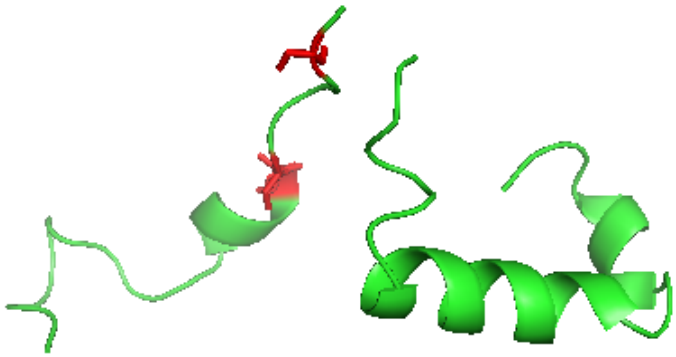

Figure 2.17. The structure of an O-GlcNAc modified 101 amino acid peptide known to adopt a thioredoxin fold. The absent data is proposed to be due to intrinsic disorder. Instrinsically disordered regions cannot be crystalized and therefore cannot be reported to have secondary or tertiary structure by X-ray crystallography or nuclear magnetic resonance. The O-GlcNAc mapped residues are highlighted in red. This explains why some of the outlier data points in Figure 2.3 can be assigned an ordered structure with high confidence.

In addition to this complication, there is a possibility that some of the outlier O-GlcNAc sites can be attributed to the action of this glycosylation by eOGT. Some proteins are biosynthesized within the endoplasmic reticulum (ER) while others span the ER

membrane such that the ER-localized section may be *O*-GlcNAcylated by eOGT while the cytoplasmic part maybe modified by OGT.

Nevertheless, correlation between PONDR-FIT intrinsic disorder scores and confidence values for PHYRE2 structure assignment are weakly anti-correlated with a Pearson correlation coefficient of -0.41. This information considered in combination with the data presented in figure 2.2 and figure 2.3, support the view that there are unaccounted for variables in the data sets such as *O*-GlcNAcylation by eOGT. For the hypothesis proposed here to be generally true the anti-correlation between confidence of structure assignment and probability of intrinsic disorder should be stronger. A more rigorous application of statistics for categorical data can be made through a 'goodness of fit' test using Chi-squared testing. To accomplish this analysis we categorized the four areas of figure 2.3 divided by the lines defining a PHYRE2 homology confidence threshold of 0.4 and probability of intrinsic disorder of 0.5.

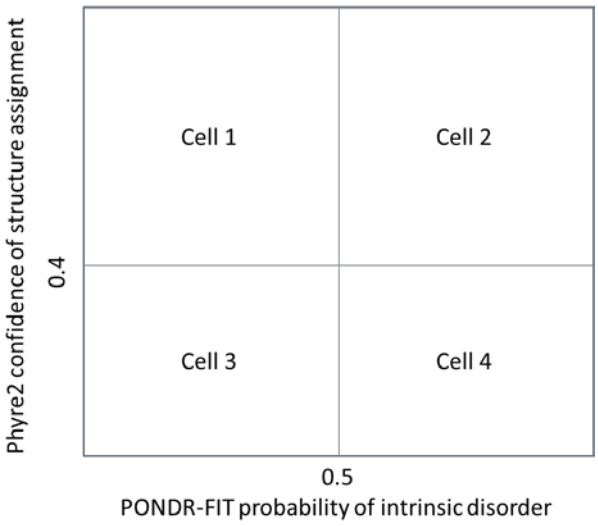

Table 2.2. Chi-squared test results for anti-correlation of PONDR-FIT intrinsic probability scores and PHYRE2 confidence of structural assignment. This is a schematic representation of Figure 2.13.

	Cell #			
	1	2	3	4
Observed n	81	94	76	308
Expected n	19	19	19	502

$$\chi 2 = \sum_{i=1}^{4} \frac{[\mathrm{ni} - \mathrm{E(ni)}]^2}{\mathrm{E(ni)}} = 969$$

10% combined error assignment in algorithm prediction was assumed and this was divided equally amongst cells 1, 2 and 3. Despite a clear tendency towards cell 4, we still cannot eliminate the fact there may be some other factor(s) affecting the structure-disorder preference amongst O-GlcNAc mapped sites, based on chi-squared value of 969. Manual analysis of those presumably structured O-GlcNAc sites will be necessary to refine this data set to obtain more clear conclusions.

Despite some factors including those discussed above, contributing to some protein sequences containing *O*-GlcNAc being characterized as ordered, we can see from figure 2.2 and figure 2.3 that regions of proteins containing *O*-GlcNAcylated sites are preferentially intrinsically disordered. This assertion is supported by the mapping of many *O*-GlcNAc sites reported in this thesis on the intrinsically disordered protein Tau in addition to other mapped sites (Yuzwa, Yadav et al. 2011, Yuzwa, Shan et al. 2012) on this protein. Notably, the data makes Tau one of the most extensively O-GlcNAc mapped proteins in terms of density of *O*-GlcNAc modifications per protein length.

Methods

Data mining from literature

Mapped O-GlcNAcylated sites were manually accumulated from reading peer reviewed articles. For proteins having unambiguous *O*-GlcNAc site assignment, species and GI number (sequence identification number system used by NCBI) were obtained. In many cases, the GI number had to be cross referenced from another database if the protein was referenced according to another database such as UNIPROT or EMBL. A Perl program was written to access the NCBI website, seek out the current FASTA file and verify that the peptide reported in the literature and the residue number of the O-GlcNAc mapped site matched. If successful, the program would obtain information from the database site including accession number, protein length and a sequence of 101 amino acids long from the deposited protein sequence centered on the mapped residue. The range of different experimental parameters used to map *O*-GlcNAc sites combined with the diverse data reporting methods in the literature made a true comparison of confidence in different mapped sites wholly impractical. Notes were taken from each entry to support an empirical scoring algorithm as follows, where lower scoring suggest higher confidence in the assignment of a modification site. A score was assigned for the biological experiment aimed at defining the source of the protein sample. Samples extracted from *in vivo*, tissue culture and bacterial cells were assigned scores of 0, 1 and 2 respectively. Next scoring was assigned for chemical preparation with a penalty of 1 for chemo-enzymatic labelling (Rexach, Rogers et al. 2010) and 2 for chemical substitution of O-GlcNAc (Wells, Vosseller et al. 2002). Scoring for the analytical method used was in hindsight possibly unfairly biased as 0 was assigned to mass spectrometry data MS_n (n>1) with conclusive raw data shown, 2 for mass spectrometry data MS_n (n>1) with raw data

not shown or accessible, and 3 for Edman degradation sequencing. During review of the reported data analysis for each site, much data was rejected for MSMS data for which isolating the mapped site between neighbouring residues was not unambiguously assigned. The data analysis step was assigned a score of 1 if the original journal article and the mapped residue along with the peptide was shifted +/- 1 amino acid, 2 if the false discovery rate was greater than 1% and for high throughput site mapping a score of 3 was assigned if sampling of the data revealed errors or there was insufficient automated scoring reported. Additionally, independent reporting of the same mapped site in different publications was incorporated into improving the mapped site assignment score. The top 559 mapped sites with empirical scores equal to or below 4.0 were used for the analysis described in this chapter. All of the mapped sites from the literature independent of any empirical scoring applied can be found in the appendices.

Phyre2 Protein Homology/analogY Recognition Engine

Mapped sites and their associated data were tagged with a file name that is the concatenation of the GI number and mapped site amino acid residue code and residue number to distinguish between mapped sites on the same protein and track their usage. Entries of the top 559 mapped sites were made into PHYRE2 v2.0 (Kelley and Sternberg 2009) according to their file name with the 101 amino acid peptide centered on the mapped site submitted to the search engine. The search engine returned in each case a list of tertiary structures ordered and their associated confidence reported as a percent value.

PONDR-FIT: A meta-predictor of intrinsically disordered amino acids

PONDR-FIT is a meta-predictor of intrinsic disorder that only accepts a single submission at a time. 101 amino acid sequences centered on the mapped sites for all of

the top 559 mapped sites were submitted one at a time using a PERL program we wrote which also collected the returned predictions of intrinsic disorder for each amino acid in every sequence as a probability score between 0 and 1.

Site mapping Tau

Human tau protein was co-expressed in *Escherichia coli* with human OGT to enable its glycosylation within the bacterium and then purified as per an earlier published protocol (Yuzwa, Yadav et al. 2011). The sample was digested using immobilized trypsin (V9012, Promega) exactly according to the manufacturer's protocol. Site mapping was accomplished using an LTQ Orbitrap Elite (Thermo Fisher Scientific) coupled with nano-flow 2D LC (Eksigent) operated in a 1D using a C18 trap column (360 µm ID × 4mm) which was reverse phase eluted over a C18 analytical column (150 µm ID x 10 cm, packed with 3 µm, 300 Angstrom beads). Flow rate was set to 600 nL/min and gradient elution was performed using water and acetonitrile (0-55%) over 50 min. Data was analyzed first using the Mascot (Matrix science) (Perkins, Pappin et al. 1999) and then using the PEAKS search engines (Zhang, Xin et al. 2012). Both Mascot and PEAKS search engines confirm these same two mapped site with false discovery rates much lower than 1%.

Chapter conclusions and future speculation

O-GlcNAcylation occurs primarily on residues in intrinsically disordered (ID) regions. This view is supported by the prevalence of amino acids with ID propensity, primary structure bioinformatics intrinsic disorder prediction, and the general absence of tertiary structures found in polypeptide sequences surrounding O-GlcNAc mapped sites.

Further, we have also shown the entirely intrinsically disordered protein Tau is densely O-GlcNAcylated relative to other proteins for which residues have been site mapped.

Looking forward and speculating on the significance of O-GlcNAcylated polypeptides primarily being intrinsically disordered, we suggest that it might be useful for intrinsic disorder to be considered a protein domain. Proteins can be very structurally dynamic and adopt many conformations depending on their location and interacting partners. Multiple conformations found for the same region of a protein are being studied as part of a relatively new concept called molecular recognition features or MORFs (Mohan, Oldfield et al. 2006). Alternating between these domain conformations, including intrinsically disordered conformations, consumes energy. It may be that *O*-GlcNAc helps preserve either ordered or disordered folds for some proteins to help prevent inadvertent conformational changes.

Chapter 3.

Proteome response to the removal and inhibition of OGT

Introduction

In 1959, Eagle, Piez and Fleischman wrote an article, “Protein Turnover in Mammalian Cell Cultures” (Eagle, Piez et al. 1959). This is an important paper in cellular proteomics because they reasoned that proteins are not stable in growing or resting human cells. Instead, they observed that proteins are constantly turned over through a cycle of protein degradation and synthesis. They realized this by monitoring synthesis using isotopically labelled amino acids fed to the cells that become incorporated into the newly synthesized proteins. This seminal work helped define the concepts of protein stability and protein turnover that are now commonly used. In this chapter we use a stable isotope amino acid labelling strategy but combined this labeling method with modern mass spectrometry to investigate whether a change in O-GlcNAc levels alters protein stability. We do this by measuring cumulative protein turnover at various time points. Although the experiment can be improved through continual investment of resources until it matches the latest experimental excellence of the Mann and Coon laboratories, it is still currently not possible nor practical to quantify changes in turnover for every protein in the human proteome across all time points in an experiment. This issue arises not only because, by our estimations, no lab has detected more than 80% of the human proteome in any single experiment, but also because “normal” protein turnover rates are varied across all the proteins. This has two effects, the first being that over the course of the experiment there are proteins with such small changes in turnover and insufficient statistical supporting data

to detect such changes that we cannot draw any conclusions regarding their turnover. The second effect is that some rapidly changing turnover rates result in changes that exceed the dynamic range of protein abundances detectable by our experimental apparatus. Nonetheless, here we look for occurrences of change in protein stability due to the reduction of O-GlcNAc levels and whether the number of proteins undergoing changes in turnover increases over time. We also consider protein folding as a factor contributing to possible changes and therefore investigate the stability of chaperones. We already know that proteins which are incorrectly folded are targeted for increased degradation through the process of ubiquitination (Guo, Giasson et al. 2014). As such we hypothesize that changes in O-GlcNAc levels may change the turnover rates of the global proteome and also of chaperones and other proteins involved in protein folding. We observe an increasing trend in the number of proteins showing variations in their synthesis and degradation as a function of time following a stimulus that results in lowered O-GlcNAc levels as data to support the concept that lowered O-GlcNAc levels elicit changes in protein stability.

In this chapter we perform stable isotope labelling of amino acids in cell culture (SILAC) experiments on MEF and HEK293 cells with the aim of uncovering changes in protein synthesis, degradation and turnover between cells with reduced O-GlcNAc levels and untreated cells. In these experiments we compare parallel control experiments with cells that have either the OGT gene knocked out or OGT inhibited using 2-acetamido-2-deoxy-5-thio-D-glucopyranose (5S-GlcNAc). A SILAC experiment involves feeding cells in different samples with different isotopic labelled amino acids that are then incorporated into proteins being synthesized as a function of time. Mass spectrometry is then employed to measure the relative abundance of one isotope to another within peptides obtained from

tryptic digestion of the same proteins from the different samples. This approach enables a relative quantitative comparison of the abundance of proteins at specified time points, permitting us to measure changes in protein stability

Experimental design

SILAC experimental designs can vary significantly and a detailed explanation follows. An authoritative introduction to SILAC experiments was written by Matthias Mann (Mann 2006). This particular experiment was designed by Dr. Yanping Zhou based on papers from the Lamond laboratory (Boisvert, Ahmad et al. 2012) and Krijgsveld laboratory (Hughes and Krijgsveld 2012). The object of this version of SILAC is to measure the synthesis, degradation and turnover of proteins independently in a treated group of cells where OGT is either knocked out or inhibited and for comparison another independent experiment which employs the same set of SILAC isotopes to also measure synthesis, degradation and turnover in cells that have not been treated.

Let us first describe the cells treated with 5S-GlcNAc in MEF cells and clarify that at no time during the experiment were samples from the control group mixed with samples from the treated group. Two days in advance of “time zero” two batches of cells were separated. At this time, both batches began the process of incorporating different isotopic labelled amino acids through five cell divisions. One batch was labelled ‘light’ and incorporated the natural isotopologues of arginine and lysine. The other batch was labelled ‘medium’ and the proteins were metabolically labelled with arginine 13C6 (R6) and lysine D4 (K4). Immediately prior to time zero, before any further changes, samples of equal quantities were taken from the ‘light’ and the ‘medium’ batches, mixed and prepared for mass spectrometry. At time zero, the media used in the medium batch was exchanged

from one that contained the previously mentioned medium isotopes K4 and R6 to one that contained heavy isotopic labelled amino acids, lysine 13C6, 15N2 (K8) and arginine 13C6, 15N4 (R10). The light batch remained in light or natural abundance amino acids for the duration of the experiment. In this way, for the 5S-GlcNAc treated group, medium labelled proteins would be replaced by heavy labelled proteins and treated light labelled proteins would be replaced by light labelled proteins, thus remaining constant. The ratio of medium to light amino acids would be expected to decline over time, representing protein degradation and the ratio of heavy to light would be expected to increase over time, representing protein synthesis. At 2, 6 and 11 hour time points, equal amounts of treated light cells and treated medium/heavy cells were removed, mixed and prepared for analysis by mass spectrometry.

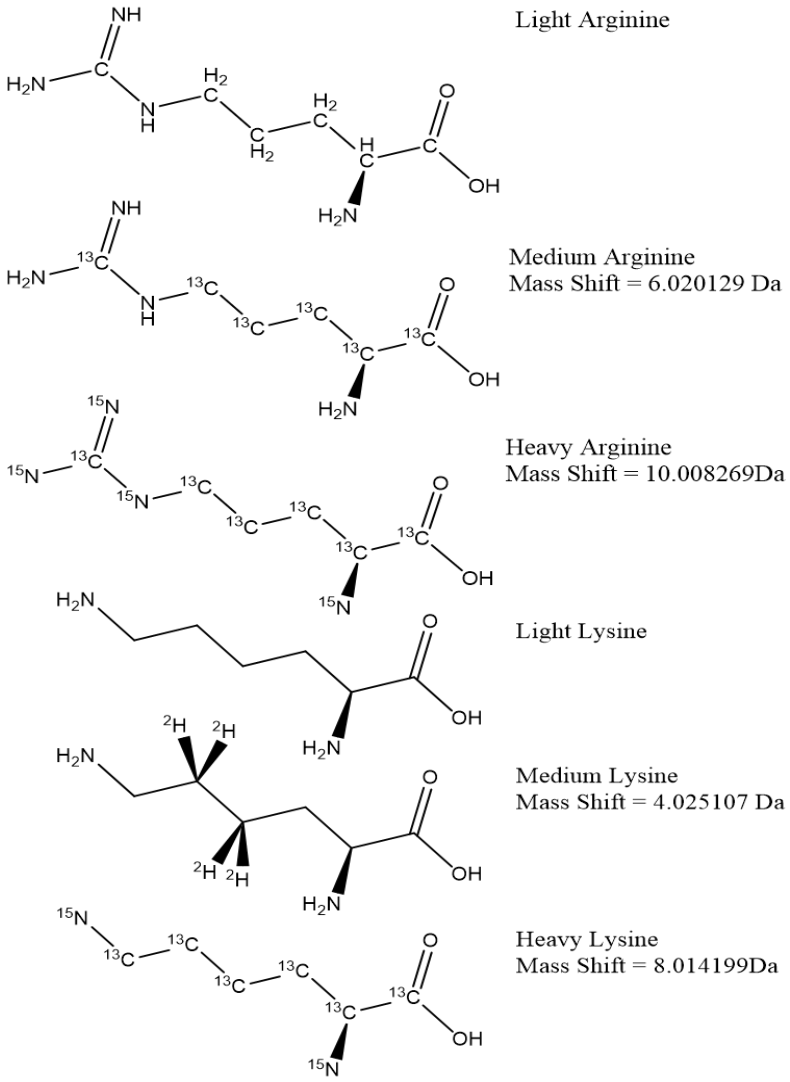

Figure 3.1. **The isotopic labelled amino acids used in the metabolic labelling of MEF cells indicating the amount by which their masses differ from 'light' arginine.**

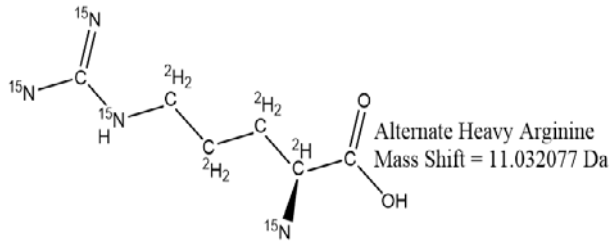

Figure 3.2. Arginine 11 was used in place of Arginine 10 for experiments involving the HEK293 cell line as explained in the analysis and methods sections of this thesis.

In the exact same way, independent experiments were carried out for control samples (no treatment in medium and light batches) for MEF cells. This was also done for cells treated by knocking out the gene for OGT. For HEK 293 cells we also have completed 5S-GlcNAc treated and control (no treatment) as independent experiments where the collection and mixing times were done at 0, 2, 5, 8, 12 and 24 hours. Only after independent mass spec data acquisition of each of the five experiments, were treated groups compared with control groups.

The following experiment is carried independently for control and treated groups.

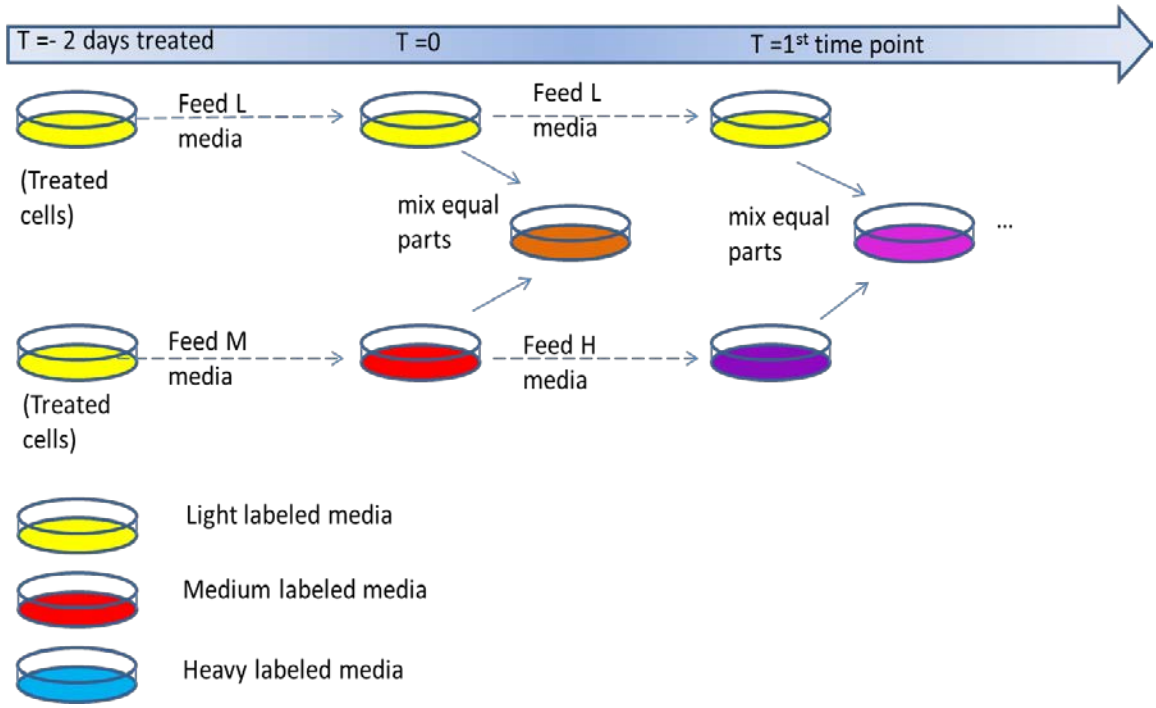

Figure 3.3. **Experimental design for the SILAC experiment performed in this thesis showing one arm of the study. Treated cells refer to cells treated with inhibitor. The orange media indicates a mixure of the 'light' and 'medium' labeled samples and the light purple indicates a mixture of the 'light', 'medium' and 'heavy' labeled samples. An identical parallel arm of the study was performed for the untreated cells except that those cells were not treated with inhibitor. At various time points, equal amounts from both batches were mixed, the proteins recovered and prepared for mass spectrometer detection and analysis.**

Results

Global comparison of population means for protein turnover between 5S-GlcNAc treated and untreated HEK293 cells.

Here we compare the means of two populations of protein turnover data between 5S-GlcNAc treated and untreated cells. In this way we test for a global shift in protein stability resulting from reduced O-GlcNAc levels. For this comparison we used raw data that has not been normalized and has only undergone a Log2 transformation. We filtered our dataset of 3210 proteins with turnover data for at some time points down to 831

proteins with complete data at all time points for both populations, treated and untreated. The distributions for these data sets are not clearly associated with any particular commonly seen distribution. In Figure 3.16 we show two example distributions of H/M rations for 2 hours and 24 hours for raw data from proteins relatively quantitated at all time points in both treated and control samples. We used Minitab statistical software V.17 (Minitab Inc.) to numerically calculate the bootstrapped mean of each distribution using 831 iterations with a 95% confidence interval. Plotted in Figure 3.17 are all the means of each distribution comparing the global turn over between untreated and 5S-GlcNAc inhibited cells. The error bars indicate the 95% confidence intervals for the numerical calculation of the means of each distribution. The means of global protein turnover from untreated cells and from cells with reduced O-GlcNAc levels clearly diverge at time zero, then return to the same rate global rate of change at around 10 hours.

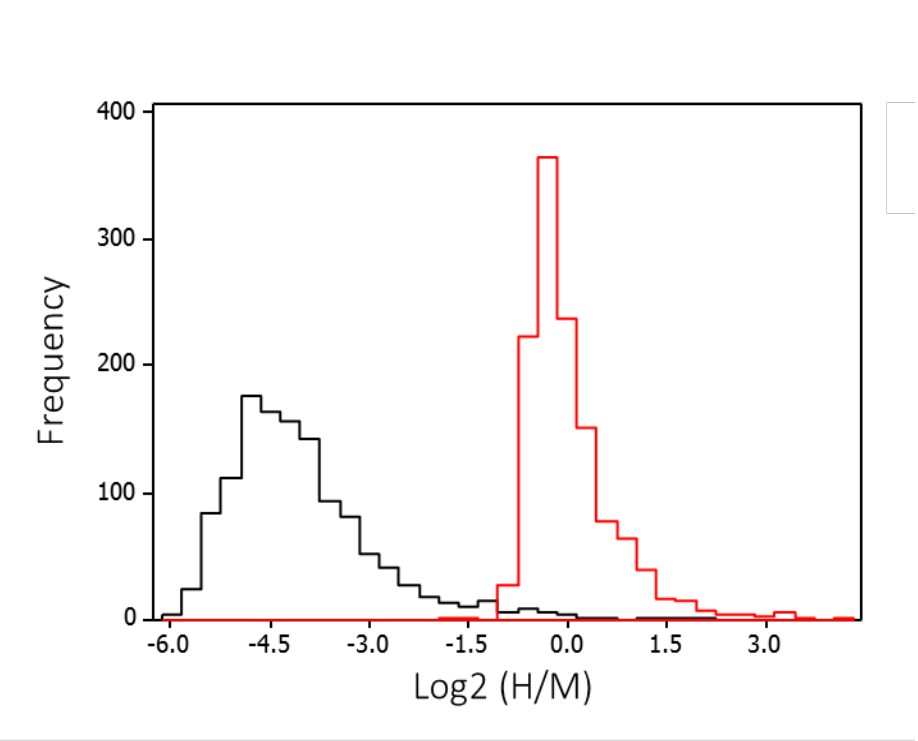

Figure 3.4. **Example raw data distributions used in Figure 3.16. In both cases distributions are from untreated HEK293 cells. Red is collected at 24 hours and black is collected at the 2 hours. The numerically collected means of these distributions are plotted in Figure 3.16.**

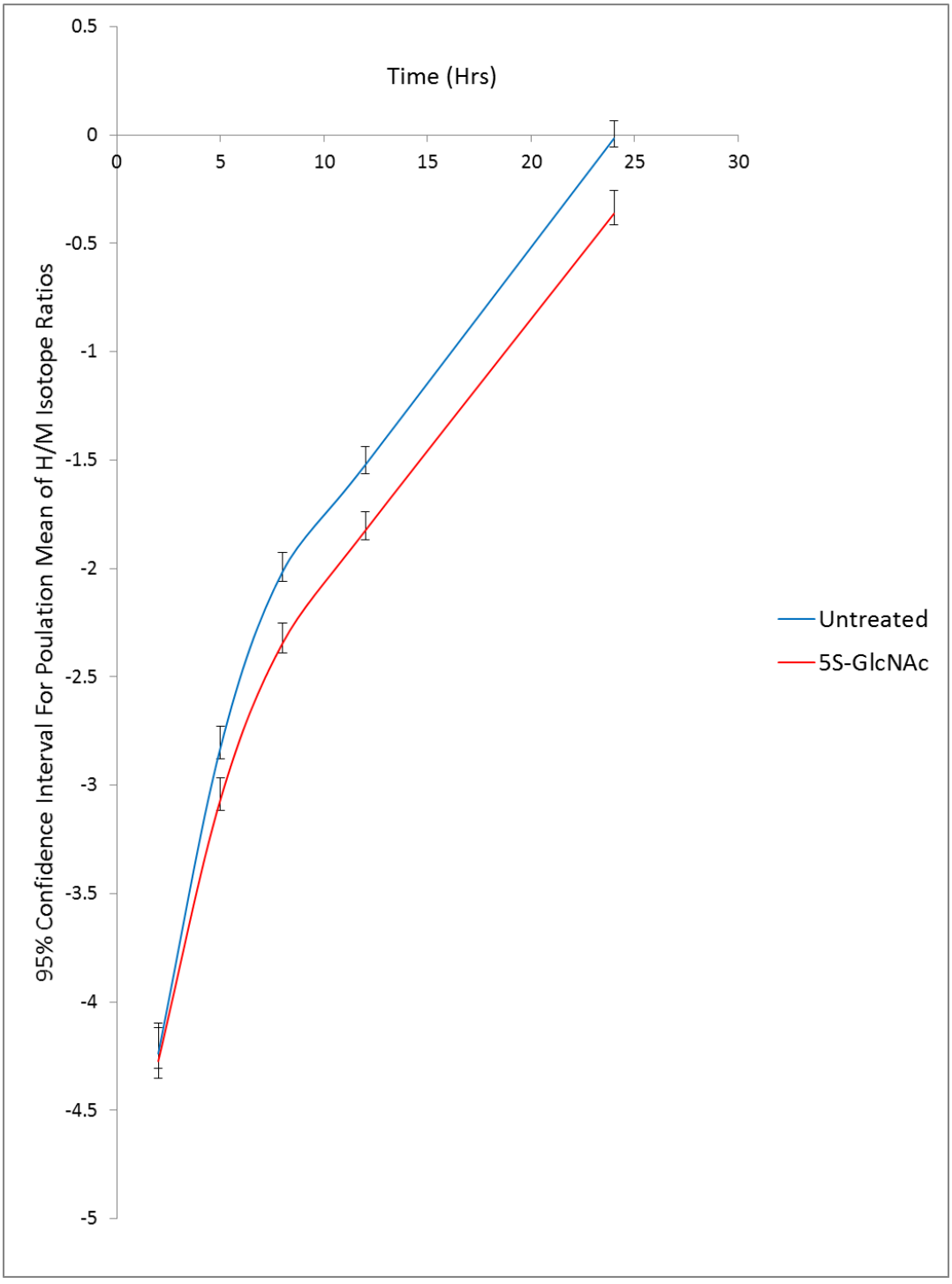

Figure 3.5. **Comparison of sample means for distributions of protein H/M ratios (turnover) at five time points between 5S-GlcNAc and untreated in HEK293 cells. Means were numerically calculated and error bars correspond to the 95% confidence intervals from the calculation of each mean turnover value.**

Summary of relative quantitation data collected for individual proteins using volcano plots

Table 3.1. Summary of proteins that are statistically differentiated between treated and control as measured using volcano plots. In brackets are the total numbers of protein that are both identified with greater than 99% confidence and have valid isotopic ratios for relative quantitation based on at least two peptides.

Treatment	Experimental Observation	Quantity of MEF cell derived proteins showing statistically significant difference between treated and control			Quantity of HEK293 cell derived proteins showing statistically significant difference between treated and control				
Experimental time point		2 hrs	6 hrs	11 hrs	2 hrs	5 hrs	8 hrs	12 hrs	24 hrs
5S-GlcNAc	Increased synthesis	5 (284)	6 (288)	2 (330)	7 (970)	11 (1274)	3 (1918)	15 (1269)	8 (1971)
5S-GlcNAc	Decreased synthesis	0 (284)	8 (288)	8 (330)	1 (970)	17 (1274)	4 (1918)	72 (1269)	36 (1971)
OGT Knockout	Increased synthesis	7 (318)	13 (371)	27 (367)	N/A				
OGT Knockout	Decreased synthesis	3 (318)	9 (317)	7 (367)	N/A				
5S-GlcNAc	Increased degradation	Rejected data			2 (1230)	8 (1368)	0 (2087)	13 (1278)	3 (1984)
5S-GlcNAc	Decreased degradation	Rejected data			5 (1230)	180 (1368)	16 (2087)	100 (1278)	35 (1984)
5S-GlcNAc	Increased turnover	Rejected data			5 (990)	0 (1284)	2 (1955)	1 (1274)	10 (1976)
5S-GlcNAc	Decreased turnover	Rejected data			3 (990)	0 (1284)	26 (1955)	30 (1274)	119 (1976)

Differentiated protein synthesis measured by heavy to light isotope ratios due to reduced O-GlcNAcylation

By employing a strategy involving volcano plots we have identified many proteins with differentiated rates of protein synthesis between HEK293 cells not treated and HEK293 cells that have been treated using 5S-GlcNAc, an inhibitor of OGT. The volcano plots are employed as a useful comparison of two groups, in this case the log10 ratio of H/L isotopes observed for proteins from treated cells to the H/L ratio for proteins from untreated cells is plotted along the x-axis. The y-axis represents a statistical test, defined in the methods section, which is used to delineate whether there is a statistically significant change in synthesis between the two groups. The curved lines separate the null hypothesis from the hypothesis; the null hypothesis being that there is not a difference between the groups treated with the inhibitor as compared to the untreated group. The upper left hand side of the chart above and to the left of the curved line are proteins which undergo decreased synthesis due to the reduction in O-GlcNAcylation induced by the inhibitor. The upper right hand side represents significantly increased synthesis of individual proteins in response to reduced O-GlcNAc levels. The proteins identified with differentiated cumulative protein synthesis are tabulated in the appendix.

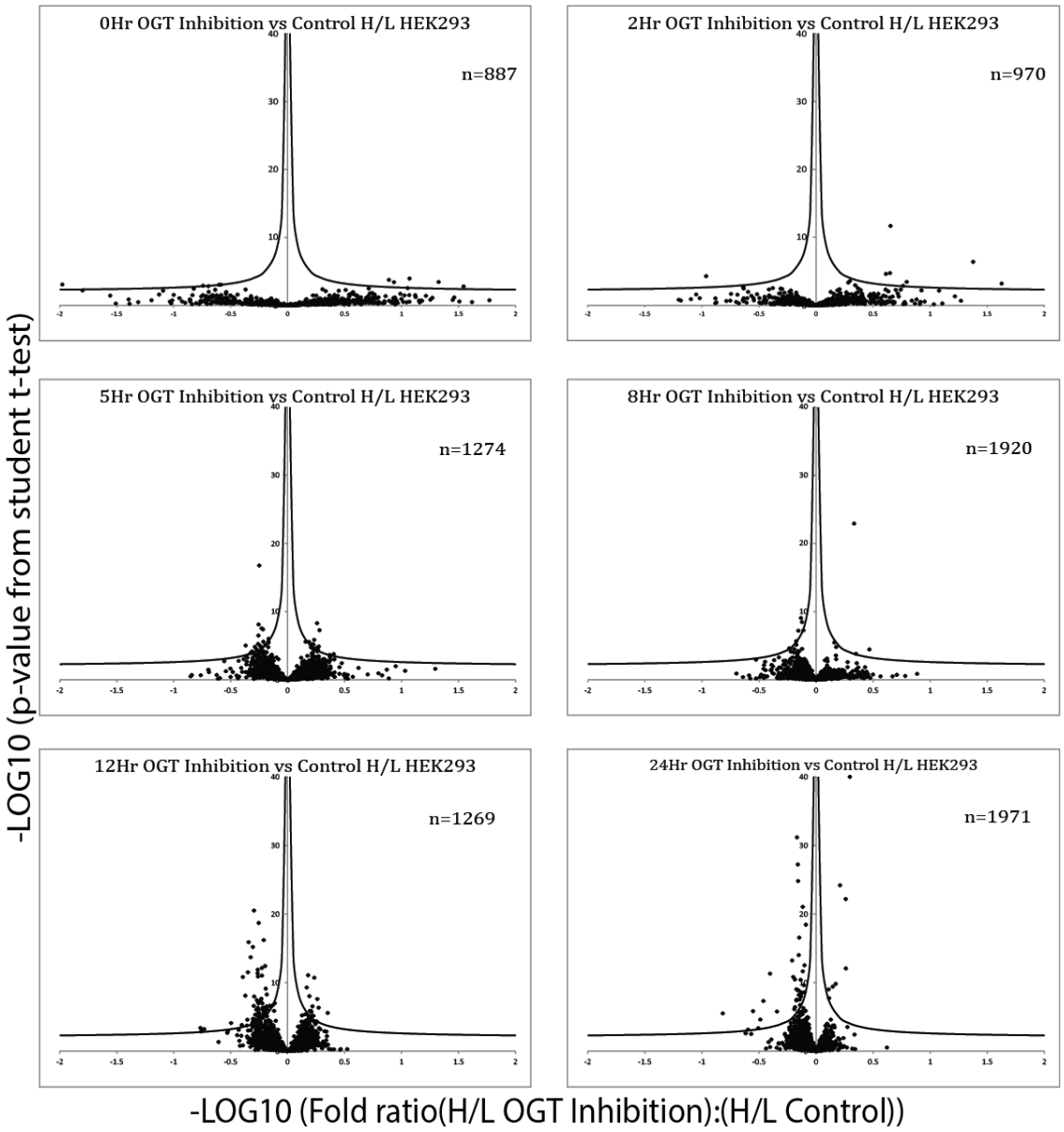

Figure 3.6. Time progression of proteins differentiated in rates of synthesis between Control and 5Thio-GlcNAc inhibited in HEK293 cells. Note the altered protein stability represented over time.

Similarly, we have the comparison of H/L protein synthesis ratios between 5S-GlcNAc treated and untreated from MEF cells. Again, the differentiated proteins between treated and control can be found tabulated in the appendix.

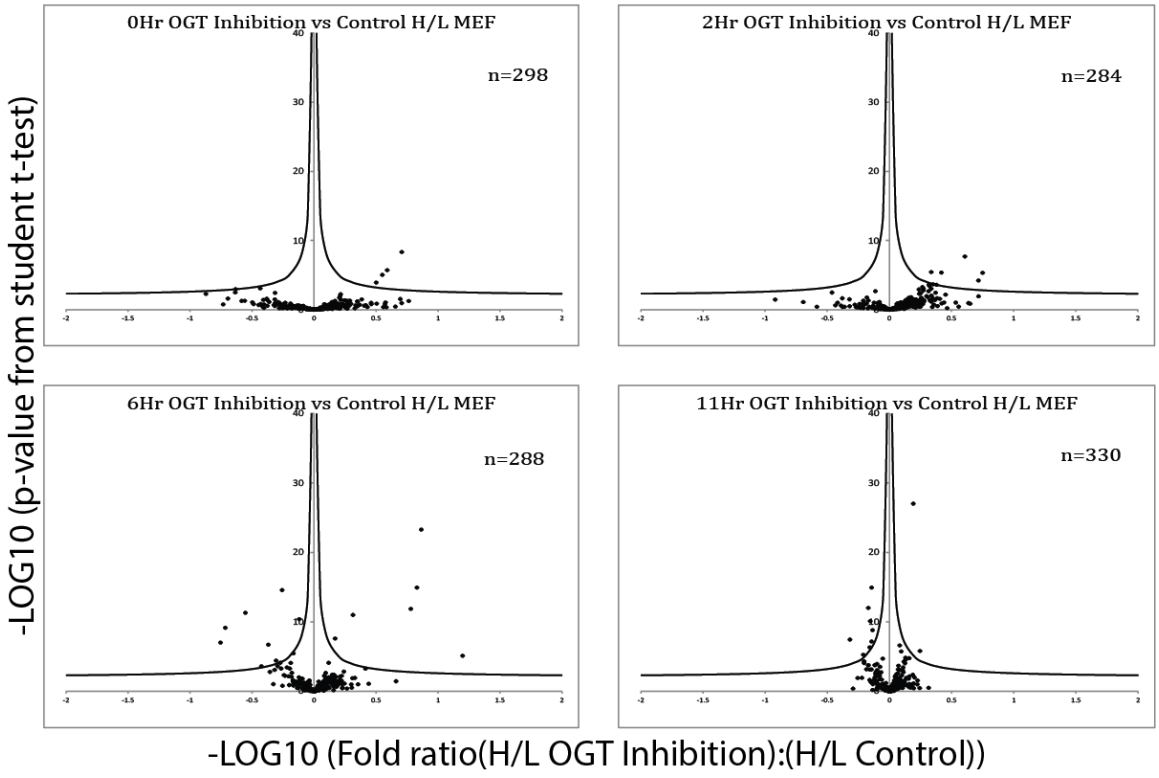

Figure 3.7. Differentiated in rates of synthesis control and 5Thio-GlcNAc inhibited in MEF cells. Note the altered protein stability represented over time.

Below, we show the volcano plots for H/L ratios comparing OGT knockout vs untreated, also in MEF cells. Again the proteins measured with significant difference in H/L ratios are tabulated in appendix 1.

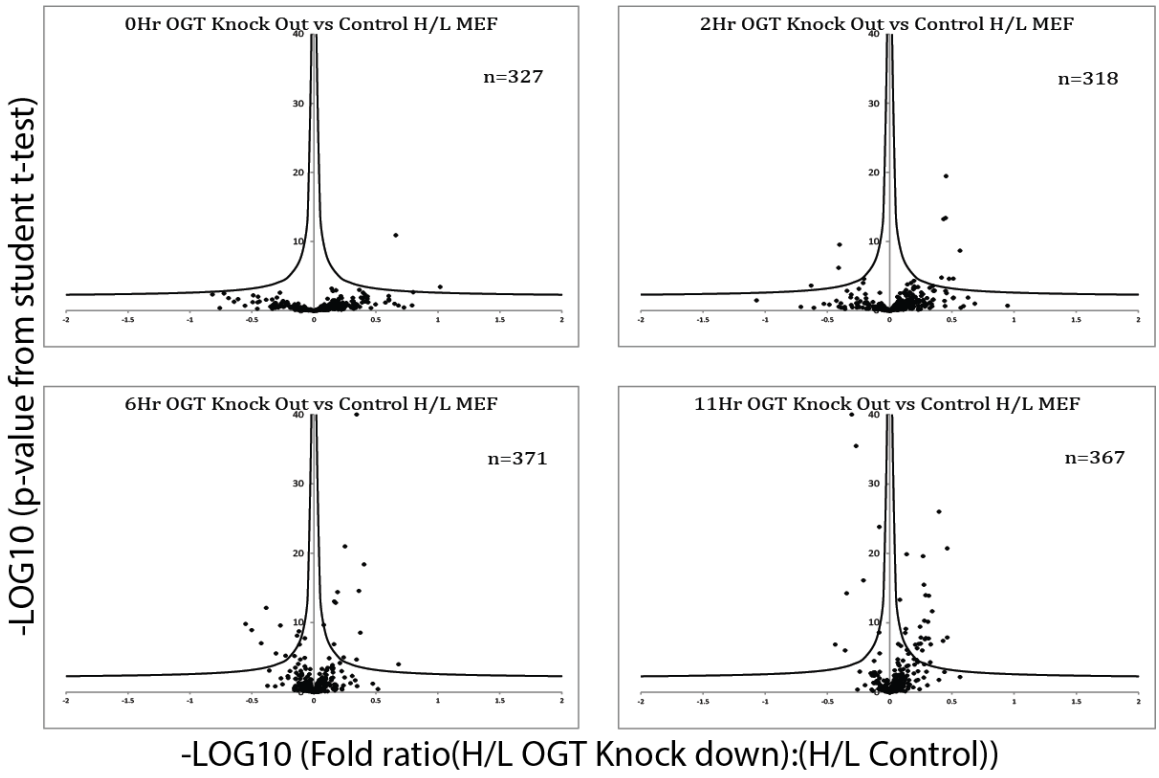

Figure 3.8. Differentiated in rates of synthesis between control and OGT knock out in MEF cells. Note the altered protein stability represented over time.

Differentiated protein degradation measured by medium to light isotope ratios due to reduced O-GlcNAcylation

We have rejected the data sets for protein degradation as measured by M/L isotopes for MEF cells. The reasoning for this decision will be discussed in the discussion section of this thesis.

For HEK293 cells we show the volcano plots below for medium to light ratios which are indicative of protein degradation. The proteins that are statistically differentiated in terms of the observed values for medium to light ratios at any time point are tabulated in appendix 1.

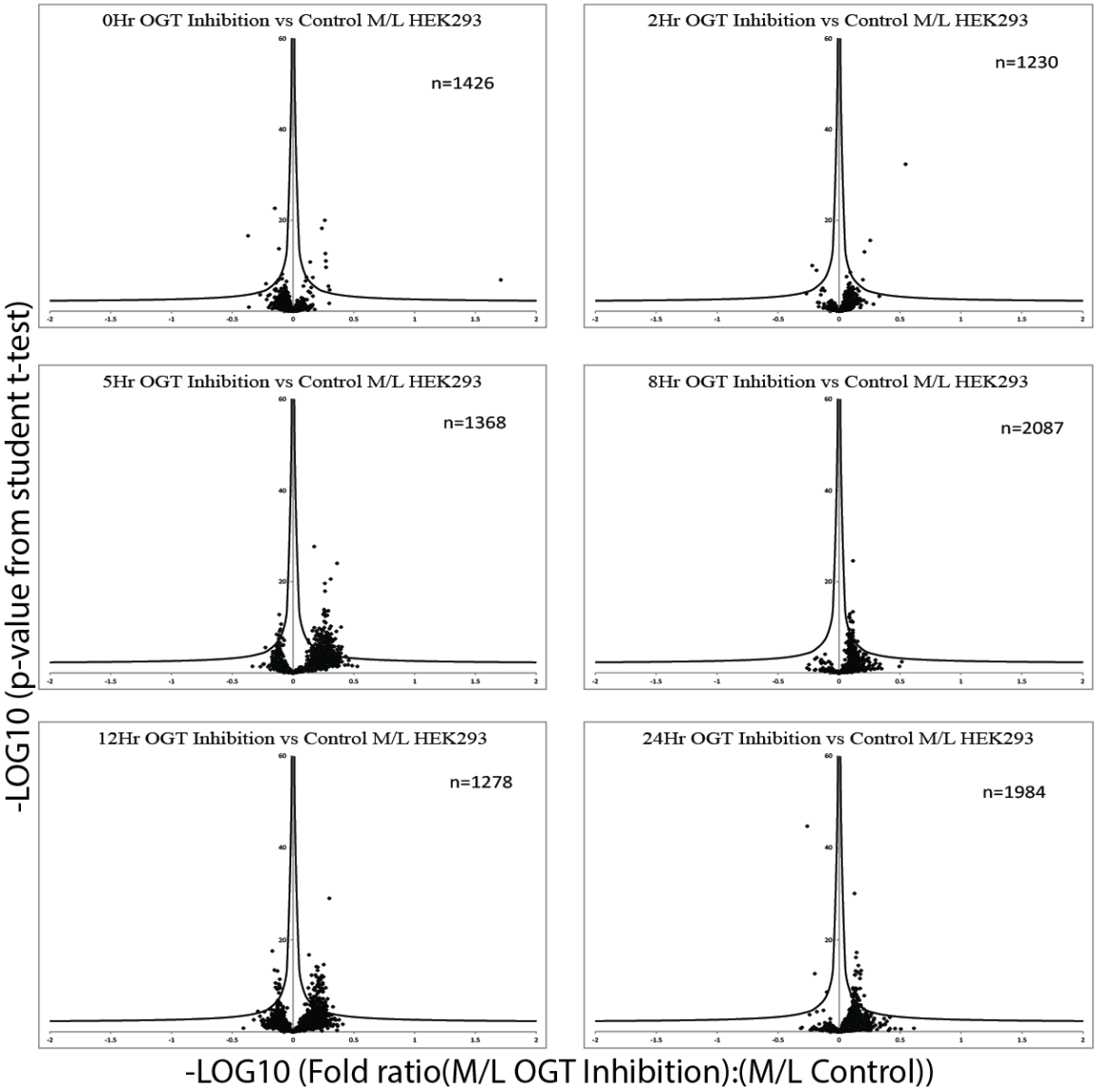

Figure 3.9. For volcano plots showing M/L isotopic rations, increased degradation is observed in the left hand side of each plot and vice versa. Note the altered protein stability represented over time.

Differentiated protein degradation measured by medium to light isotope ratios due to reduced O-GlcNAcylation

Again, by employing volcano plots, for turnover as measured by H/M isotopes we differentiate proteins that show a statistical difference in turnover due to reduced O-

GlcNAc levels in HEK293 cells. Proteins that are differentiated in this measure due to reduced O-GlcNAc levels are tabulated in the appendix.

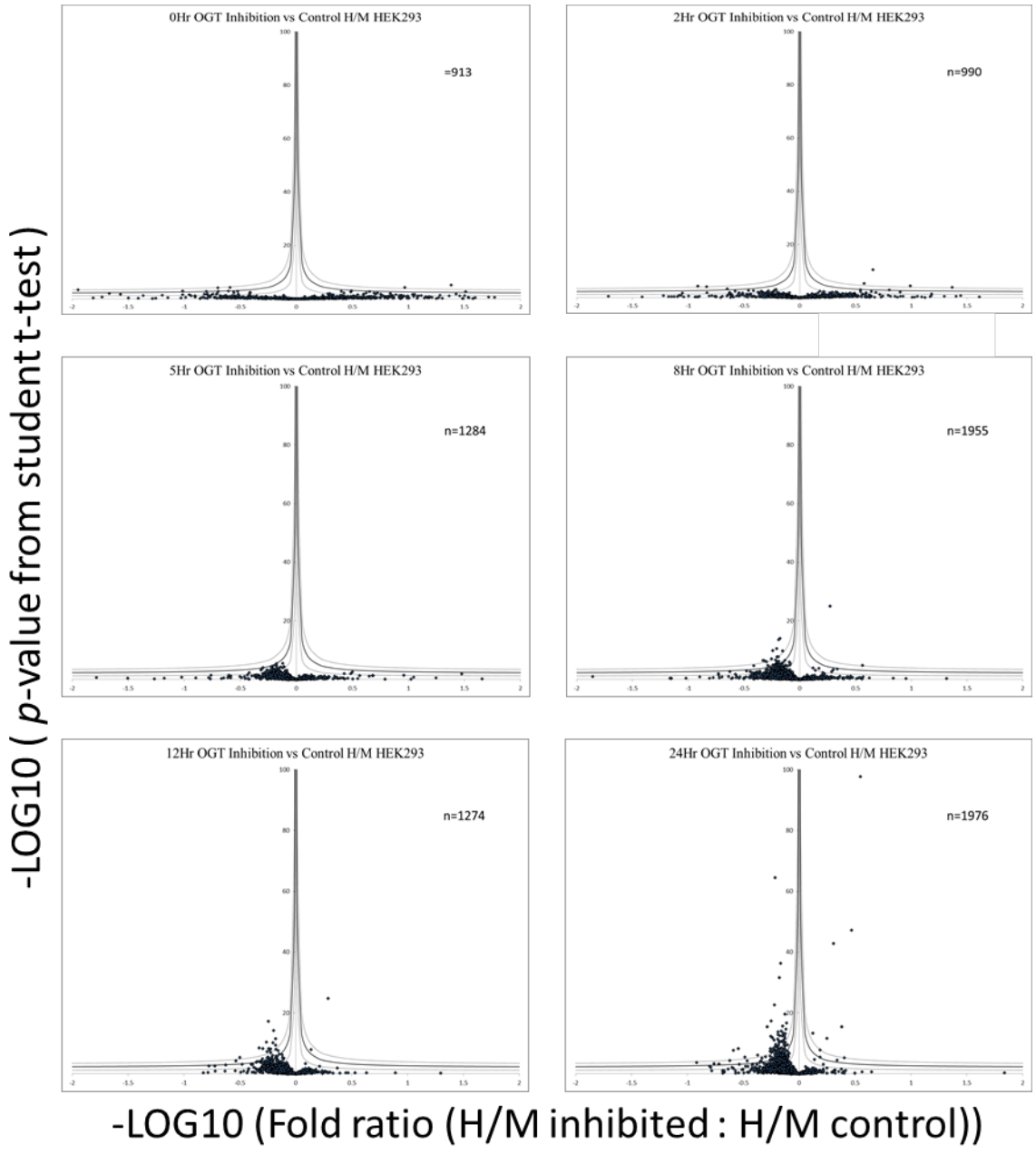

Figure 3.10. Sequential time series of volcano plots showing protein turnover in HEK293 cells as measured by H/M ratios due to 5S-GlcNAc inhibition of OGT.

Proteins with differentiated synthesis conserved across experiments due to reduced levels of O-GlcNAcylation

We have three experiments that track the H/L isotopic ratios that reflect changes in the rate of protein synthesis: MEF cells where OGT is inhibited by 5S-GlcNAc, MEF cells with OGT knocked out, and HEK293 in which OGT is inhibited by 5S-GlcNAc. Perhaps a powerful approach to identifying proteins that are likely of high significance in a set of experiments like these is to note those proteins that are identified in both species and also when both strategies are used to lower O-GlcNAc levels.

Table 3.2. Conserved proteins with increased synthesis due to the lowering of O-GlcNAc levels.

HEK293-5S-GlcNAc	MEF-5S-GlcNAc	MEF-OGTKO
78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	78 kDa glucose-regulated protein (GRP-78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	
	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (HDP-1) (Helix-destabilizing protein) (Single-strand-binding protein) (Topoisomerase-inhibitor suppressed) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (HDP-1) (Helix-destabilizing protein) (Single-strand-binding protein) (Topoisomerase-inhibitor suppressed) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]
	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)
	Myosin regulatory light chain 12B (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2)	Myosin regulatory light chain 12B (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2)

HEK293-5S-GlcNAc	MEF-5S-GlcNAc	MEF-OGTKO
Nascent polypeptide-associated complex subunit alpha (NAC-alpha) (Alpha-NAC) (allergen Hom s 2)		Nascent polypeptide-associated complex subunit alpha (Alpha-NAC) (Alpha-NAC/1.9.2)
	NEDD8 (Neddylin) (Neural precursor cell expressed developmentally down-regulated protein 8) (NEDD-8) (Ubiquitin-like protein Nedd8)	NEDD8 (Neddylin) (Neural precursor cell expressed developmentally down-regulated protein 8) (NEDD-8) (Ubiquitin-like protein Nedd8)
	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)
	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)

Table 3.3. Conserved proteins with decreased synthesis due to the lowering of O-GlcNAc levels.

HEK293-5S-GlcNAc	MEF-5S-GlcNAc	MEF-OGTKO
Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (HDP-1) (Helix-destabilizing protein) (Single-strand-binding protein) (Topoisomerase-inhibitor suppressed) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	
Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	
Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	
Histone H2A.V (H2A.F/Z)	Histone H2A.V (H2A.F/Z)	Histone H2A.V (H2A.F/Z)
	Histone H2B type 3-A	Histone H2B type 3-A
Histone H3.2 (Histone H3/m) (Histone H3/o)	Histone H3.2	Histone H3.2
Histone H4	Histone H4	Histone H4

HEK293-5S-GlcNAc	MEF-5S-GlcNAc	MEF-OGTKO
Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)		Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)
Nucleolin (Protein C23)	Nucleolin (Protein C23)	
Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)
Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	Prelamin-A/C [Cleaved into: Lamin-A/C]	Prelamin-A/C [Cleaved into: Lamin-A/C]
	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta)	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta)

Using the volcano plots served both to determine which data sets had sufficiently low errors and also permitted identification of all measured proteins with differentiated protein synthesis and degradation rates. We can now use the valid data sets to measure protein turnover on proteins of interest and attempt to answer some fundamental questions about the response of the proteome to the lowering of *O*-GlcNAc levels.

Results surrounding a question of whether reduced O-GlcNAcylation levels alters the turnover of chaperone proteins

The identification of chaperones with an altered turnover rate due to a reduction in *O*-GlcNAc levels supports our hypothesis. Altering O-GlcNAc levels elicits changes in protein stability. Within the lists of proteins with altered synthesis and degradation as previously discussed we observe many chaperones. Turnover is defined as the balance of synthesis and degradation and can be expressed in terms of isotopic ratios:

$$\text{Protein turnover} = \frac{\text{protein synthesis}}{\text{protein degradation}} = \frac{\frac{\Delta \text{ heavy isotope}}{\Delta \text{ light isotope}}}{\frac{\Delta \text{ medium isotope}}{\Delta \text{ light isotope}}} = \frac{\Delta \text{ heavy isotope}}{\Delta \text{ medium isotope}} = \frac{\text{H}}{\text{M}}$$

We next represent changes in protein turnover for proteins measured at each experimental time point in HEK293 cells. Observed turnover for cells treated with 5S-GlcNAc are plotted against observed turnover for proteins for proteins without treatment. A perfect experiment where no proteins display an alteration in turnover due to reduced levels of O-GlcNAcylation would yield a series of data points along the line of equality (y=x). We have plotted two lines parallel to y = x that represent a fold change threshold of 2 or 0.5. Distributions of measured cumulative turnover are not normal distributions and are not represented by any of the common probability distributions. We show the HEK293 differences in accumulated protein turnover over five time points between OGT inhibited and control groups. The entire population of proteins detected with valid H/M ratios in both the control and experimental are plotted in grey while the measured chaperone proteins are plotted in blue. Chaperones identified as having two standard deviations difference in H/M isotope ratios between 5S-GlcNAc treated and untreated are highlighted in each plot. The data are from 3210 proteins with H/M ratios measured in both treated and untreated cells for at least one of the five time points where sample was collected, following removal of proteins defined as contaminant proteins and proteins only identified by modification peptides. The reviewed list of human chaperone proteins was downloaded from UNIPROT.org.

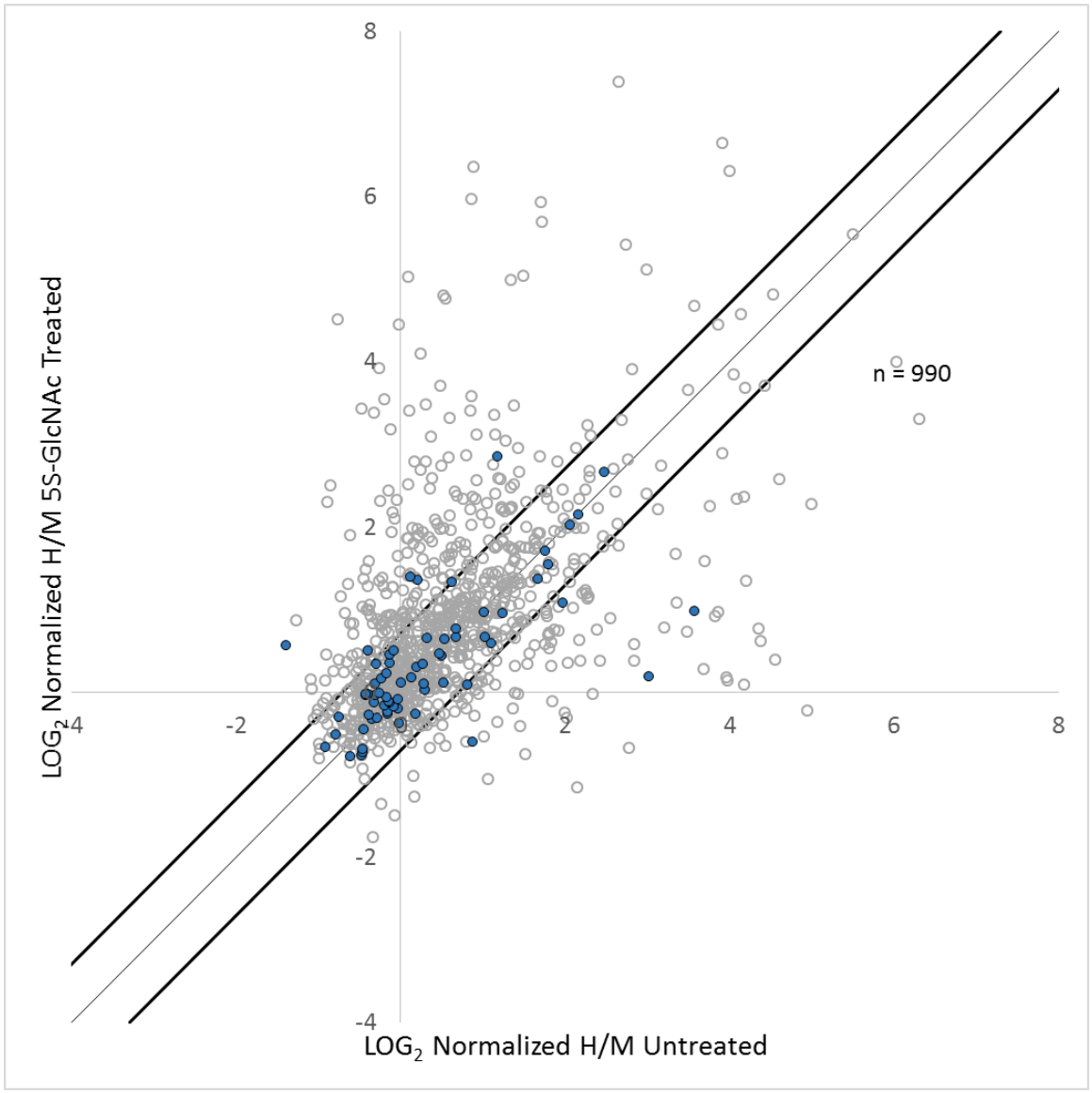

Figure 3.11. **2 hour comparison of H/M (protein turnover) between 5S-GlcNAc and untreated cells. Two thick diagonal lines represent doubling (or half) on Log2 scale. Chaperones are colored blue and tabulated below.**

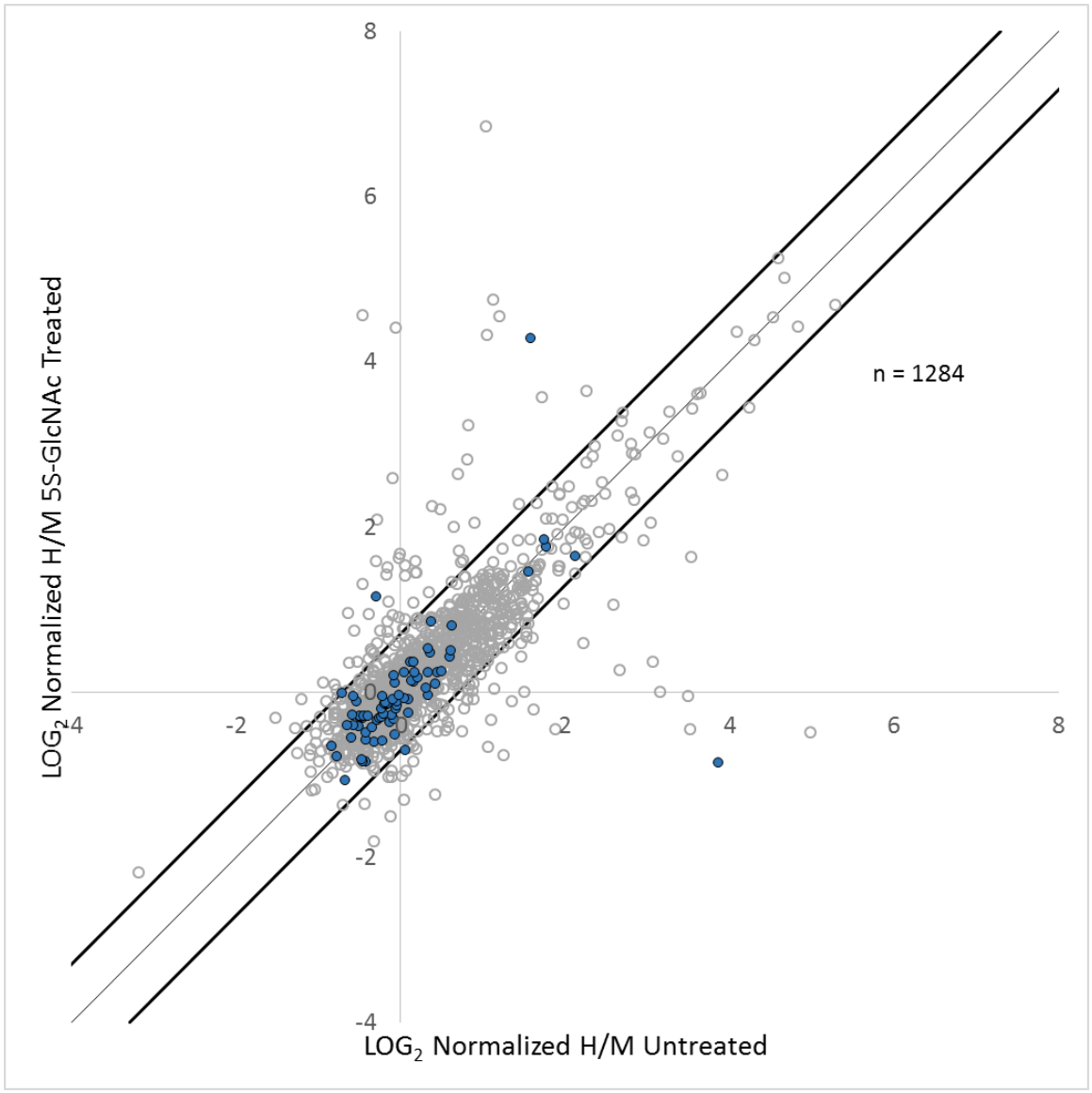

Figure 3.12. **5 hour comparison of H/M (protein turnover) between 5S-GlcNAc and untreated cells. Two thick diagonal lines represent doubling (or half) on Log_2 scale. Chaperones are colored blue and tabulated below.**

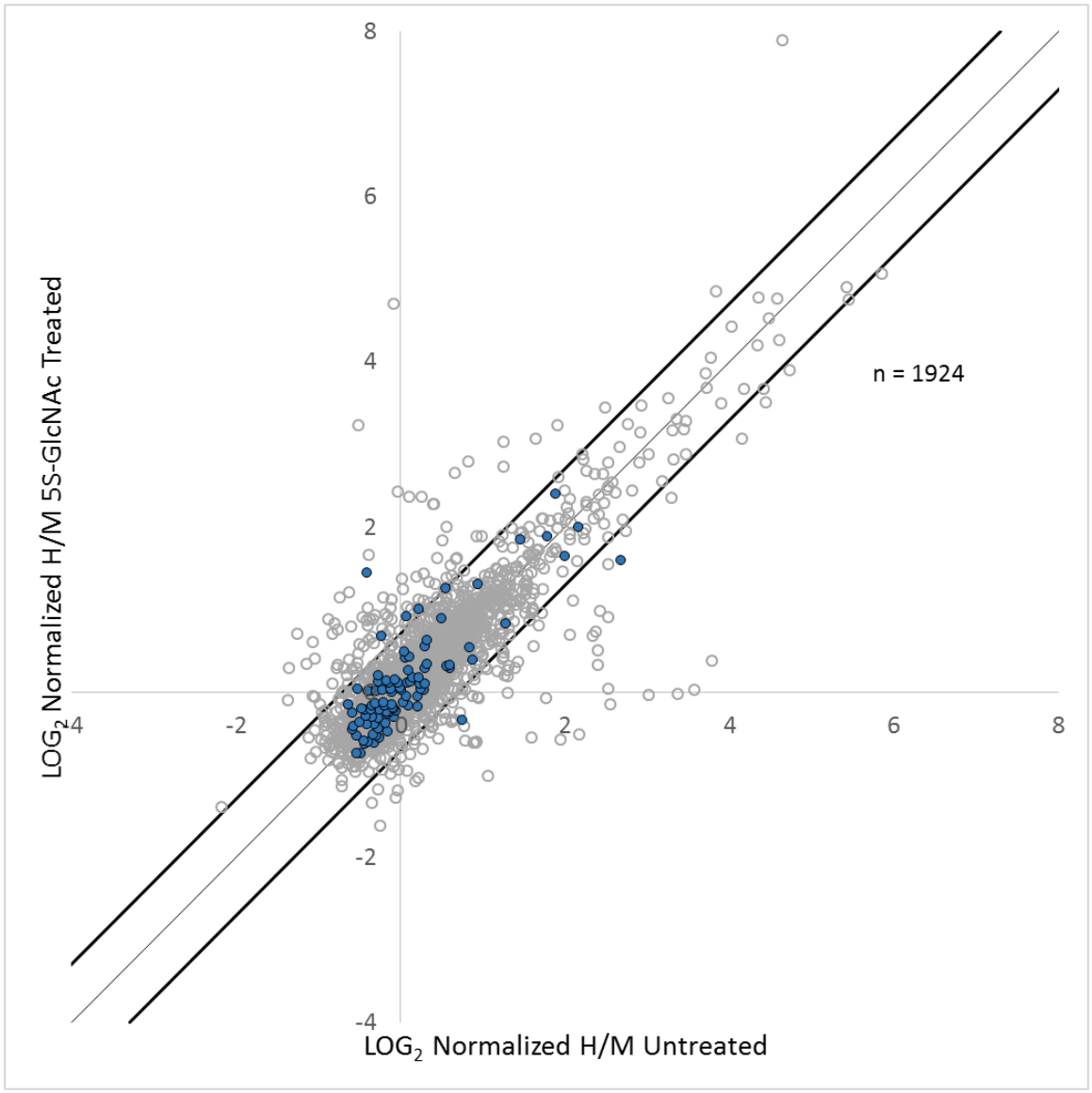

Figure 3.13. **8 hour comparison of H/M (protein turnover) between 5S-GlcNAc and untreated cells. Two thick diagonal lines represent doubling (or half) on Log2 scale. Chaperones are colored blue and tabulated below.**

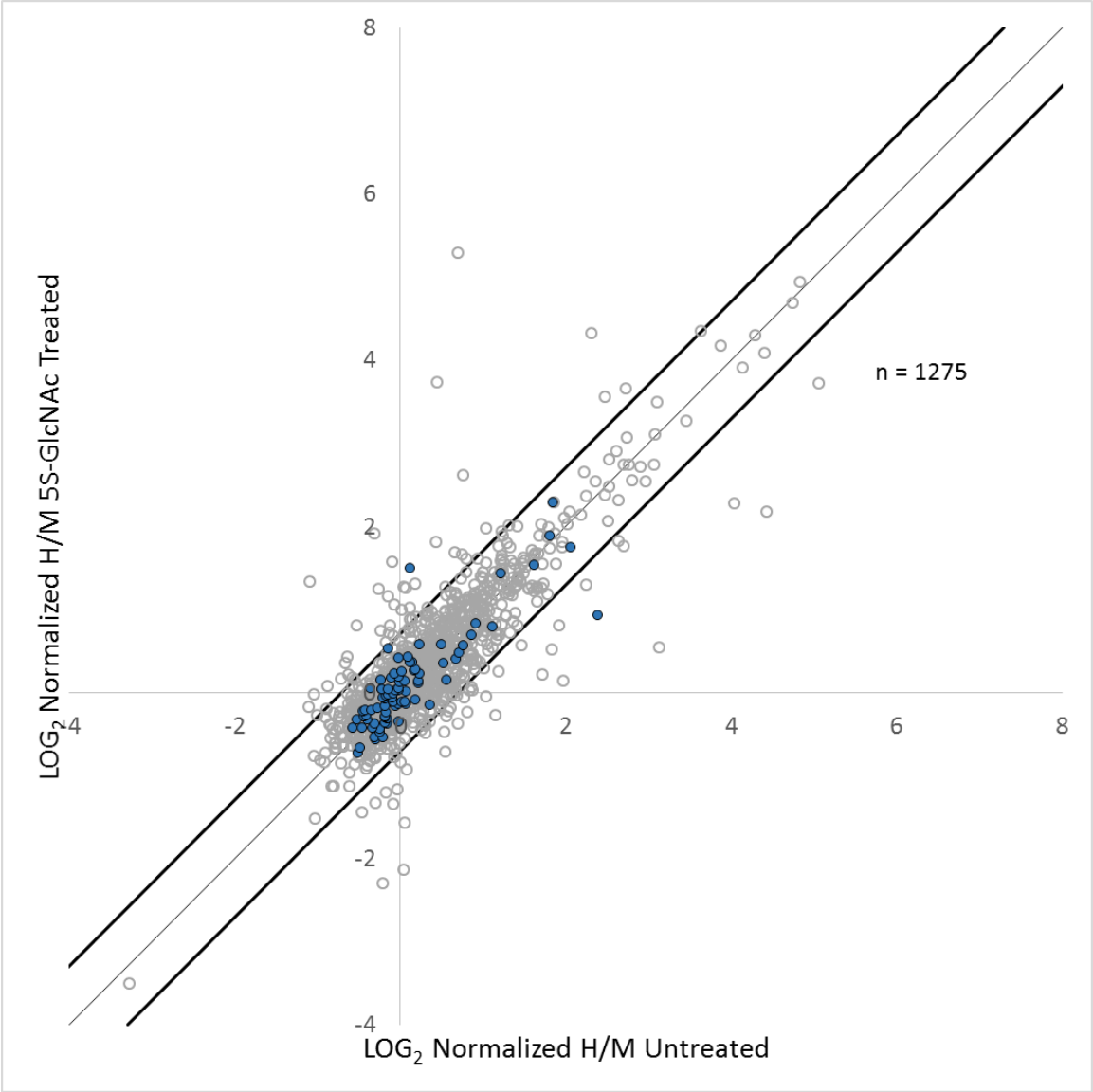

Figure 3.14. **12 hour comparison of H/M (protein turnover) between 5S-GlcNAc and untreated cells. Two thick diagonal lines represent doubling (or half) on Log2 scale. Chaperones are colored blue and tabulated below.**

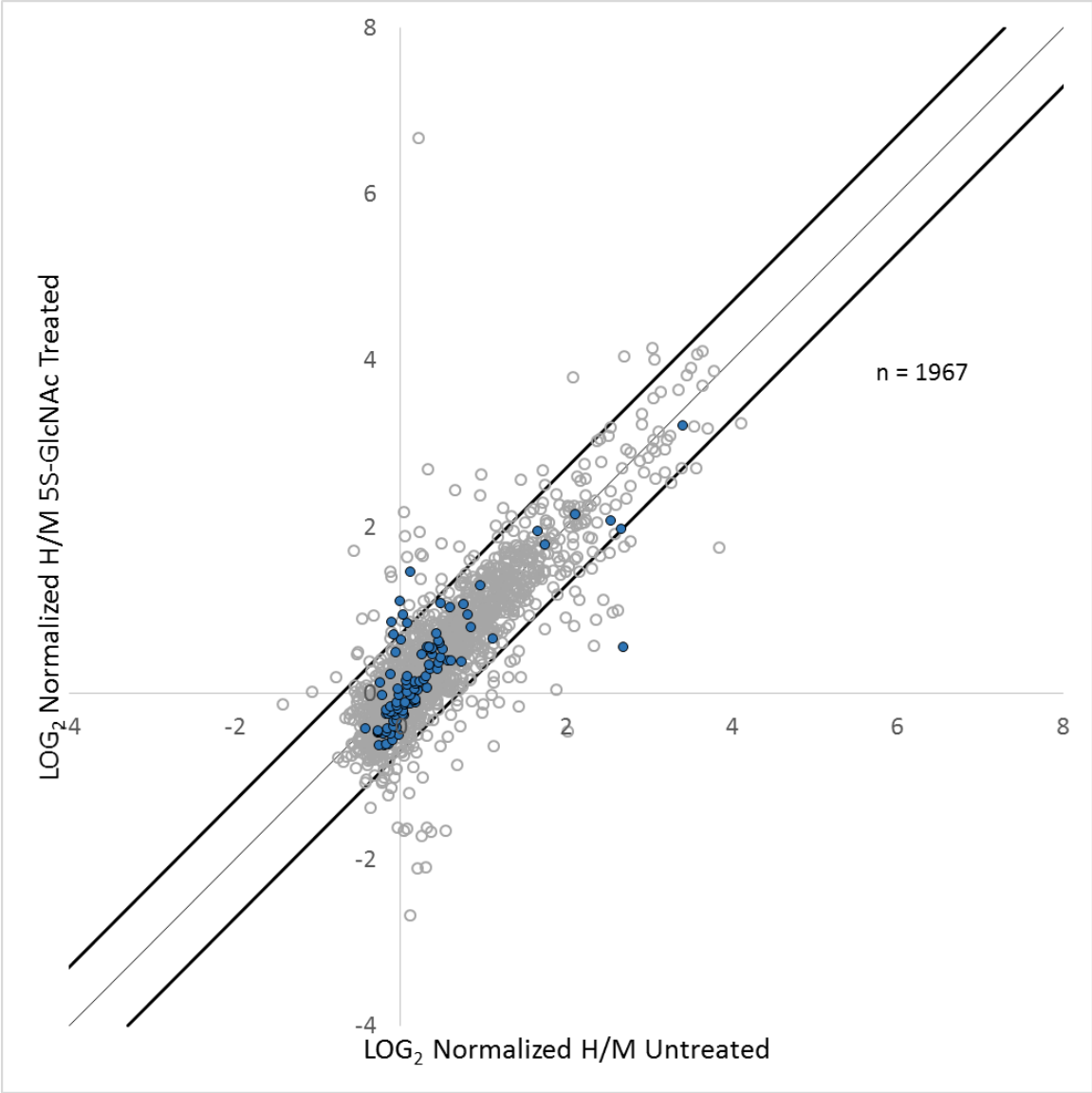

Figure 3.15. **24 hour comparison of H/M (protein turnover) between 5S-GlcNAc and untreated cells. Two thick diagonal lines represent doubling (or half) on Log2 scale. Chaperones are colored blue and tabulated below.**

Table 3.4. Chaperones with more than doubled the measured turnover due to treatment with 5S-GlcNAc compared to untreated HEK293 cells

HR	Entry	Entry name	Protein names	Gene names
2	Q99615	DNJC7_HUMAN	DnaJ homolog subfamily C member 7 (Tetratricopeptide repeat protein 2) (TPR repeat protein 2)	DNAJC7 TPR2 TTC2
2	O15212	PFD6_HUMAN	Prefoldin subunit 6 (Protein Ke2)	PFDN6 HKE2 PFD6
2	O75832	PSD10_HUMAN	26S proteasome non-ATPase regulatory subunit 10 (26S proteasome regulatory subunit p28) (Gankyrin) (p28(GANK))	PSMD10
2	O43765	SGTA_HUMAN	Small glutamine-rich tetratricopeptide repeat-containing protein alpha (Alpha-SGT) (Vpu-binding protein) (UBP)	SGTA SGT SGT1
2	Q86V81	THOC4_HUMAN	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF ALY BEF THOC4
2	Q9BS26	ERP44_HUMAN	Endoplasmic reticulum resident protein 44 (ER protein 44) (ERp44) (Thioredoxin domain-containing protein 4)	ERP44 KIAA0573 TXNDC4 UNQ532/PRO1075
5	Q16576	RBBP7_HUMAN	Histone-binding protein RBBP7 (Histone acetyltransferase type B subunit 2) (Nucleosome-remodeling factor subunit RBAP46) (Retinoblastoma-binding protein 7) (RBBP-7) (Retinoblastoma-binding protein p46)	RBBP7 RBAP46
5	O43819	SCO2_HUMAN	Protein SCO2 homolog, mitochondrial	SCO2
8	Q15813	TBCE_HUMAN	Tubulin-specific chaperone E (Tubulin-folding cofactor E)	TBCE
8	P61221	ABCE1_HUMAN	ATP-binding cassette sub-family E member 1 (2'-5'-oligoadenylate-binding protein) (HuHP68) (RNase L inhibitor) (Ribonuclease 4 inhibitor) (RNS4I)	ABCE1 RLI RNASEL1 RNASELI RNS4I OK/SW-cl.40
8	O14618	CCS_HUMAN	Copper chaperone for superoxide dismutase (Superoxide dismutase copper chaperone)	CCS
8	O75607	NPM3_HUMAN	Nucleoplasmin-3	NPM3

HR	Entry	Entry name	Protein names	Gene names
8	Q7KZ85	SPT6H_HUMAN	Transcription elongation factor SPT6 (hSPT6) (Histone chaperone suppressor of Ty6) (Tat-cotransactivator 2 protein) (Tat-CT2 protein)	SUPT6H KIAA0162 SPT6H
12	O43819	SCO2_HUMAN	Protein SCO2 homolog, mitochondrial	SCO2
24	P27824	CALX_HUMAN	Calnexin (IP90) (Major histocompatibility complex class I antigen-binding protein p88) (p90)	CANX
24	Q9UBS4	DJB11_HUMAN	DnaJ homolog subfamily B member 11 (APOBEC1-binding protein 2) (ABBP-2) (DnaJ protein homolog 9) (ER-associated DNAJ) (ER-associated Hsp40 co-chaperone) (Endoplasmic reticulum DNA J domain-containing protein 3) (ER-resident protein ERdj3) (ERdj3) (ERj3p) (HEDJ) (Human DnaJ protein 9) (hDj-9) (PWP1-interacting protein 4)	DNAJB11 EDJ ERJ3 HDJ9 PSEC0121 UNQ537/PRO1080
24	P27797	CALR_HUMAN	Calreticulin (CRP55) (Calregulin) (Endoplasmic reticulum resident protein 60) (ERp60) (HACBP) (grp60)	CALR CRTC
24	Q9Y4L1	HYOU1_HUMAN	Hypoxia up-regulated protein 1 (150 kDa oxygen-regulated protein) (ORP-150) (170 kDa glucose-regulated protein) (GRP-170)	HYOU1 GRP170 ORP150
24	Q15084	PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6 ERP5 P5 TXNDC7
24	P14625	ENPL_HUMAN	Endoplasmin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1 GRP94 TRA1

Table 3.5. Chaperones with measured turnover reduced to less than one half due to treatment with 5S-GlcNAc compared to untreated HEK293 cellls.

HR	Entry	Entry name	Protein names	Gene names
2	O95817	BAG3_HUMAN	BAG family molecular chaperone regulator 3 (BAG-3) (Bcl-2-associated athanogene 3) (Bcl-2-binding protein Bis) (Docking protein CAIR-1)	BAG3 BIS
2	Q16543	CDC37_HUMAN	Hsp90 co-chaperone Cdc37 (Hsp90 chaperone protein kinase-targeting subunit) (p50Cdc37) [Cleaved into: Hsp90 co-chaperone Cdc37, N-terminally processed]	CDC37 CDC37A
2	Q9UHD1	CHRD1_HUMAN	Cysteine and histidine-rich domain-containing protein 1 (CHORD domain-containing protein 1) (CHORD-containing protein 1) (CHP-1) (Protein morgana)	CHORDC1 CHP1
2	Q9Y4L1	HYOU1_HUMAN	Hypoxia up-regulated protein 1 (150 kDa oxygen-regulated protein) (ORP-150) (170 kDa glucose-regulated protein) (GRP-170)	HYOU1 GRP170 ORP150
2	O75937	DNJC8_HUMAN	DnaJ homolog subfamily C member 8 (Splicing protein spf31)	DNAJC8 SPF31 HSPC315 HSPC331
5	O75880	SCO1_HUMAN	Protein SCO1 homolog, mitochondrial	SCO1 SCOD1
5	Q13451	FKBP5_HUMAN	Peptidyl-prolyl cis-trans isomerase FKBP5 (PPIase FKBP5) (EC 5.2.1.8) (51 kDa FK506-binding protein) (51 kDa FKBP) (FKBP-51) (54 kDa progesterone receptor-associated immunophilin) (Androgen-regulated protein 6) (FF1 antigen) (FK506-binding protein 5) (FKBP-5) (FKBP54) (p54) (HSP90-binding immunophilin) (Rotamase)	FKBP5 AIG6 FKBP51
8	Q8TAA5	GRPE2_HUMAN	GrpE protein homolog 2, mitochondrial (Mt-GrpE#2)	GRPEL2
8	Q5F1R6	DJC21_HUMAN	DnaJ homolog subfamily C member 21 (DnaJ homolog subfamily A member 5) (Protein GS3)	DNAJC21 DNAJA5

HR	Entry	Entry name	Protein names	Gene names
12	P46379	BAG6_HUMAN	Large proline-rich protein BAG6 (BAG family molecular chaperone regulator 6) (BCL2-associated athanogene 6) (BAG-6) (BAG6) (HLA-B-associated transcript 3) (Protein G3) (Protein Scythe)	BAG6 BAT3 G3
24	Q7KZ85	SPT6H_HUMAN	Transcription elongation factor SPT6 (hSPT6) (Histone chaperone suppressor of Ty6) (Tat-cotransactivator 2 protein) (Tat-CT2 protein)	SUPT6H KIAA0162 SPT6H

Glucose regulated proteins synthesis regulation in HEK293 cells treated with 5Thio-GlcNAc and untreated.

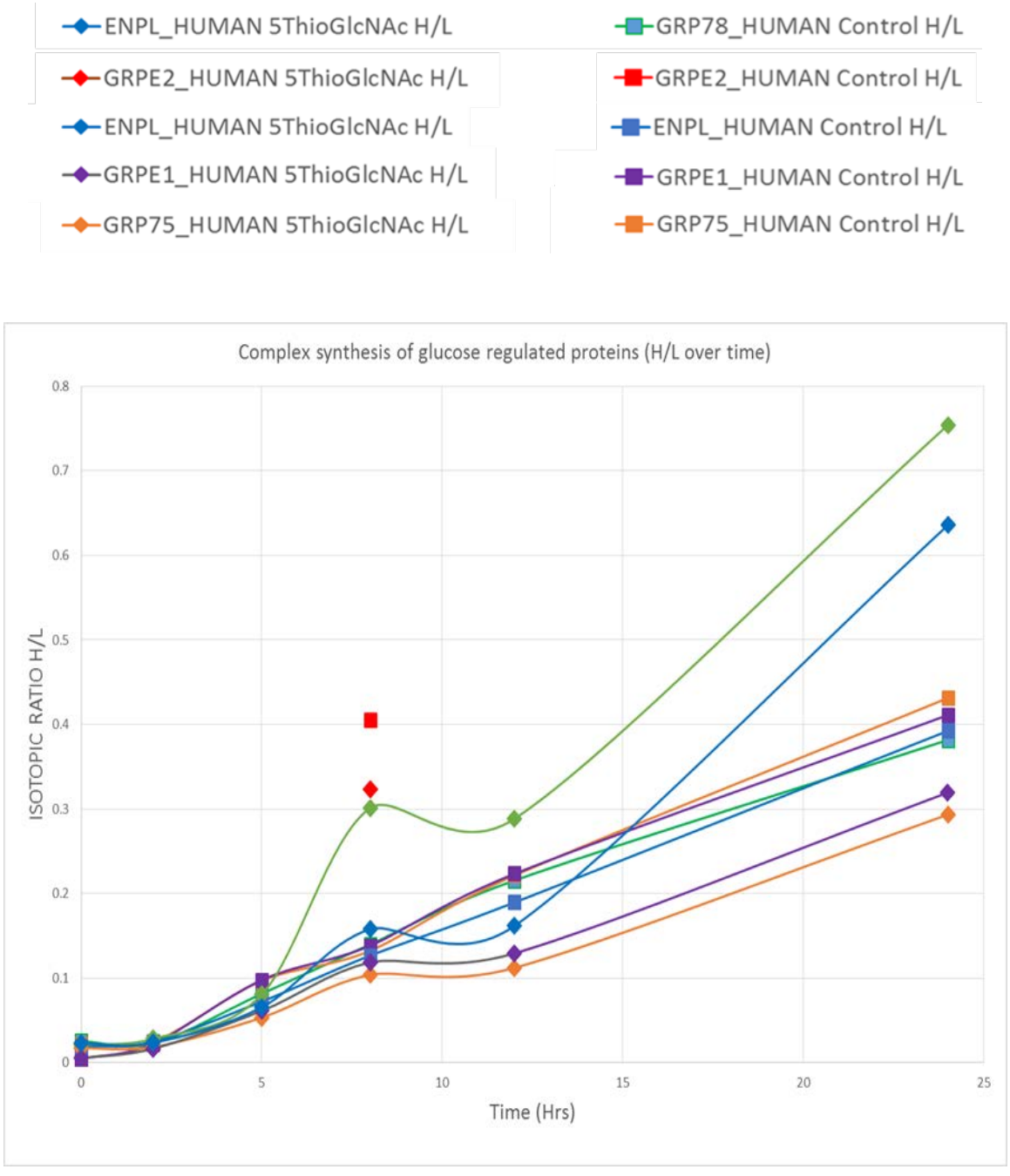

Figure 3.16. With a decrease in O-GlcNAcylation in HEK293 cells, GRP78 and ENPL also known as GRP170 both undergo increased synthesis while GRPE2, GRPE1 and GRP75 undergo decreased rates of synthesis. Proteins from 5S-GlcNAc treated cells are labelled with diamonds. Untreated are labelled with squares of the same color.

Time dependent kurtosis of H/M turnover data

Kurtosis is a generalized term that has attracted a variety of mathematical models, meaning the movement of distributed data from the tails to the centralized peak of a distribution (Balanda and Macgillivray 1988). Using the same data from the 2D plots of H/M 5S-GlcNAc treated versus untreated, we measured each minimum distance between each point mapped by (Log2 H/M untreated, Log2 H/M treated) and the line of equality. We then compiled these distances into a histogram and repeated this process for each time point. The curves overlying the histograms, to the naked eye look like normal distributions; however, formal tests for normality including Anderson-Darling, Ryan-Joiner (similar to Shapiro-Wilk) and Kolmogorov-Smirnov, all conclude these distributions are far for from normal. These distributions deviate from the normal distribution in way that is more dependent on kurtosis than skewness, although both parameters contribute to failure of normality. Rather astoundingly, the following charts show a remarkable increase in kurtosis over time. We would expect treatment or in the absence of the effects of treatment, experimental error and entropy to all contribute to the broadening of these distributions of over time.

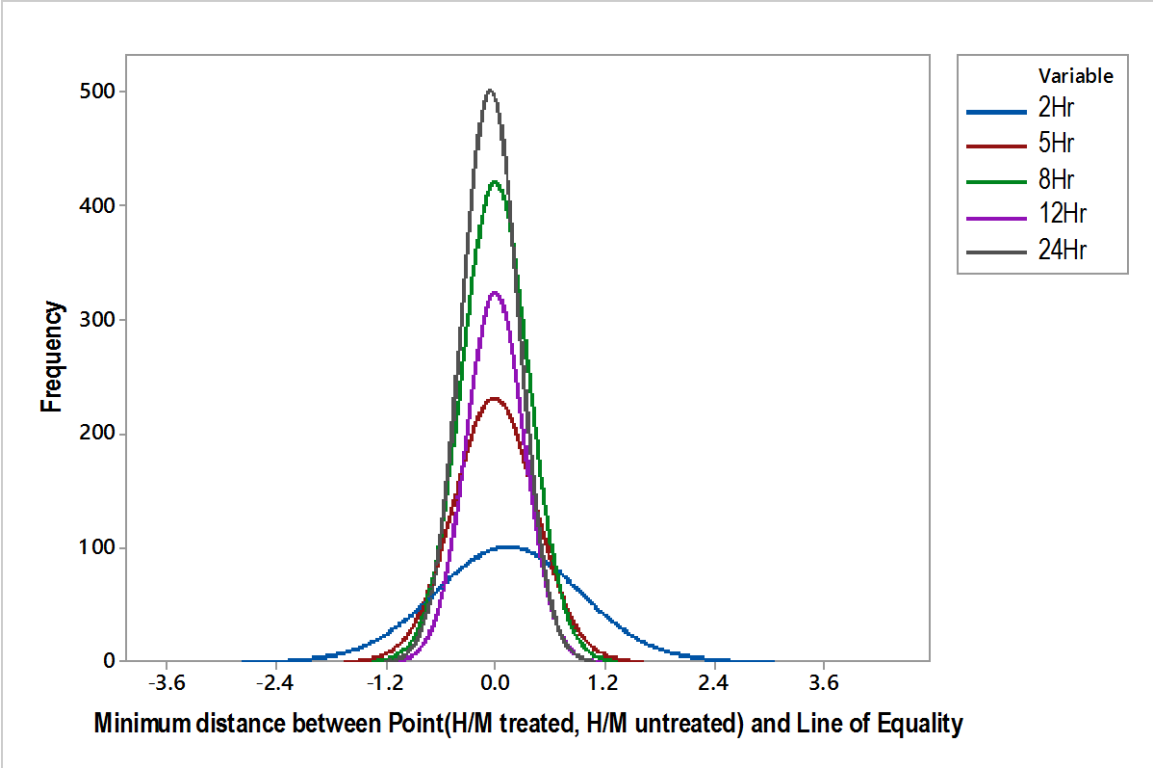

Figure 3.17. **Increasing kurtosis of Log2 data for H/M 5S-GlcNAc versus H/M untreated about the line of equality over time, from HEK293 cells. Based on natural entropy in the absence of an active cellular response, one would expect the kurtosis to increase and the peaks broaden over time, contrary to what is observed. An alterantive explanation could be the significant depletion of available inhibitor over time.**

Discussion

Discussion or results

We have hypothesized that changes in O-GlcNAc levels affects protein stability. The altered turnover rates of chaperones and other proteins involved in protein folding combined with upward trends in the numbers of proteins with differentiated synthesis and degradation rates as a function of time due to lowered O-GlcNAc levels is evidence that lowered O-GlcNAc levels elicit changes in protein stability. This proposal is supported by the data obtained using HEK293 cell and MEF cells in which O-GlcNAc levels were lowered by way of inhibition of OGT using 5S-GlcNAc or by OGT knock down. Additionally, one should note the expansion of the volcano plots over time into greater statistical significance of there being differential protein synthesis and degradation for intracellular proteins obtained from treated and untreated – which is consistent with our hypothesis. Even more supportive of the idea that lowered O-GlcNAc results in changes in protein stability among chaperones is the data which has targeted protein chaperones showing changes in cumulative turnover that are either more than doubled or cut to less than one half at the various time points. We have also made a global comparison of 831 proteins with complete turnover data at all time points which clearly shows a consistent departure between the mean values for turnover (95% confidence intervals) between 5S-GlcNAc treated and untreated HEK293 cells (Figure 3.14).

The unfolded protein response (UPR), also known as the ER stress response, has been proposed as being linked with O-GlcNAcylation (Ngoh, Hamid et al. 2009, Zachara, Molina et al. 2011, Groves, Lee et al. 2013, Wang, Deng et al. 2014). There is data to suggest that there may exist an alternative unfolded protein response outside of the

endoplasmic reticulum. We have found as outliers glucose regulated proteins (GRP) throughout our data in terms of synthesis, degradation and turnover. The GRP proteins play a key role in the UPR, with GPR78 being critical to endoplasmic reticulum protein quality control which involves N-glycosylation (Ron and Walter 2007). It appears from our data (fig. 3.12), that the glucose regulated proteins respond in a complex manner to reduction in *O*-GlcNAcylation levels. We also observe synthesis regulation of proteins belonging to the DnaJ family which are known to regulate Hsp70 (GRP78). Additionally, we observe many chaperones with increased turnover and the expression of endoribonucleic activity, changes in protein synthesis and degradation all of which suggest the existence of an alternative unfolded protein response.

What is truly puzzling is the increase over time in kurtosis of the distributions measuring the distance from the line (x=y) to points mapped by the normalized Log_2 H/M treated vs the normalized Log_2 H/M untreated ratios. If anything, in the absence of any other factors, one would expect these distributions to broaden over time due to experimental error and entropy. Perhaps this narrowing of the distribution of H/M differentials over time is a result of the cell actively re-equilibrating following treatment to reduce *O*-GlcNAc levels. Turnover data using gene knockout of OGT for comparison would be useful in understanding this phenomenon. It may be that the increase of kurtosis supports the re-equilibration of changes mean global protein turnover previously described. Alterantively, the increase in kurtosis over time suggests therefore that decreased levels of O-GlcNAc or aspects of the experimental design are driving this process.

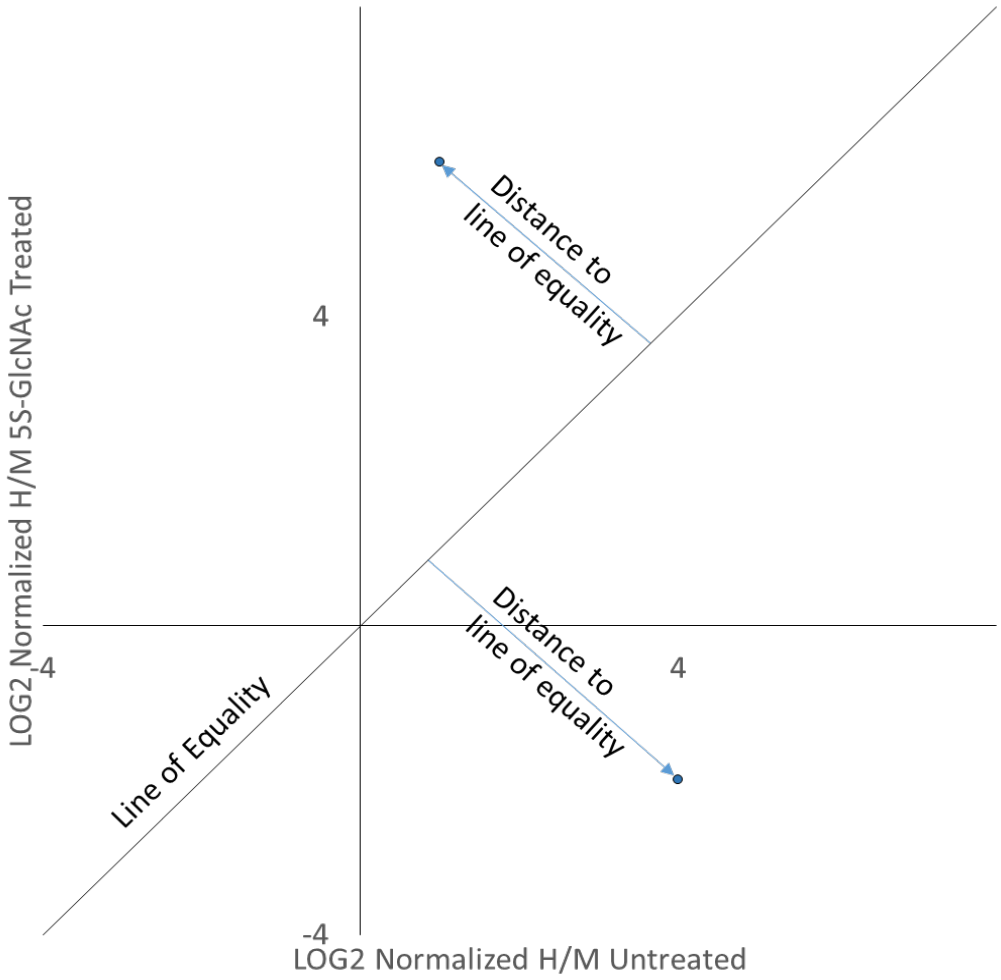

Figure 3.18. Diagram explaining parameters used in construction of distributions in Figures 3.12 through 3.15.

Discussion of the rejection of MEF medium to light data sets.

The experimental design for the MEF cells is that one batch of cells is split into two separate pools and both undergo the similar treatments, with the only difference being that one pool incorporates medium isotopic labelled amino acids while the other group remains light isotopically labelled. It stands to reason that the ratio of medium to light isotopes after mixing equal parts from each pool should be equal to one or at least be a tight distribution

about a ratio of one. If one then does the same analysis with a second control group where both medium and light isotopic pools have no treatment then this group should also have an M/L ratio of one, following mixing equal parts from each pool. If we then compare the M/L ratio between treated and untreated, we should also find no difference between the groups, assuming our experimental protocol contains no systematic errors, except for random error. We performed this comparison using volcano plots where we expected to be able to fine tune the volcano plot regularization coefficient (Li, 2012) such that the data reflected an acceptable 1% false discovery rate due to random error. We retain this regularization coefficient for all later time points in the same experiment. We found for the two data sets of M/L in MEF cells, we could not adjust the regularization coefficient to reduce the false discovery rate below 1%, indicating the presence of non-random error. After investigating this problem further, we found the ratios of M/L for both OGT knockdown and 5S-GlcNAc inhibition deviated from 1 with wide non-normal distributions. The lack of normality in these distributions made it unreasonable to employ correction factors and thus we rejected the MEF M/L and MEF H/M data sets from analysis.

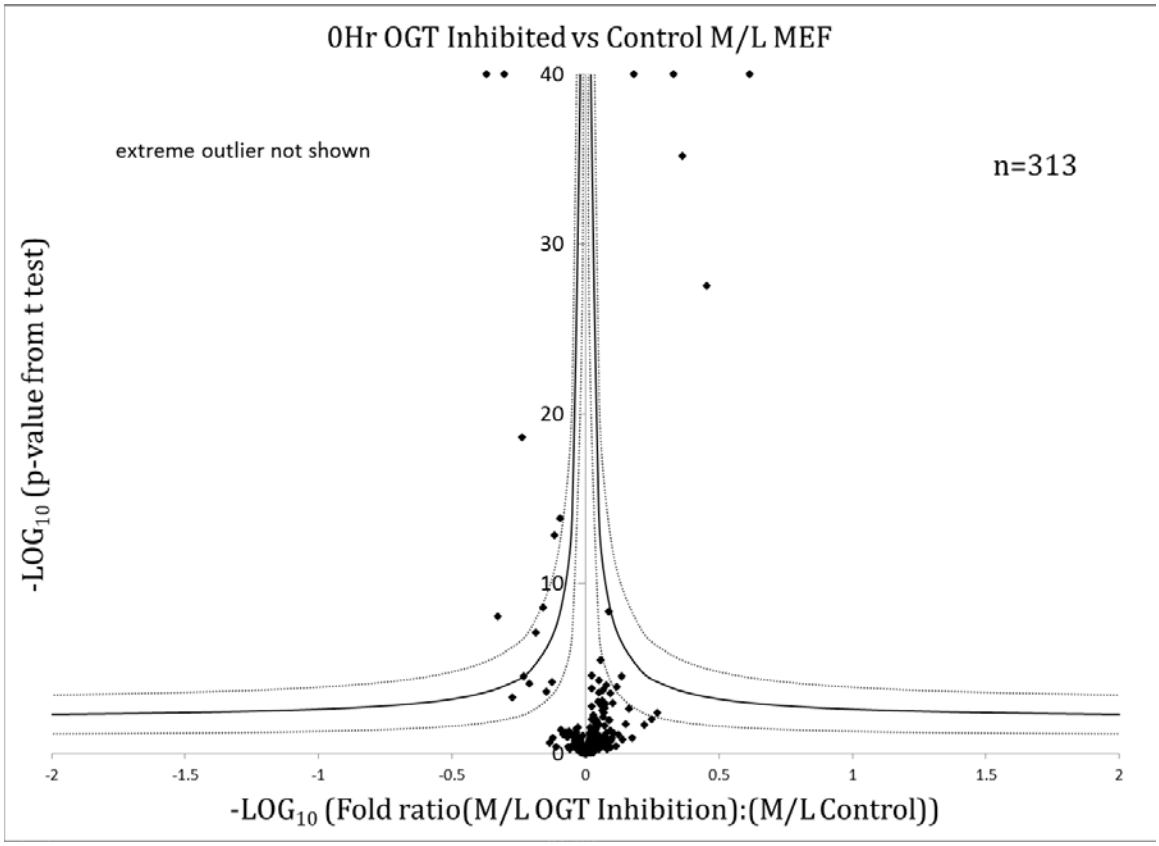

Figure 3.19. Example volcano plot where renormalization of data was not possible at T=0.

Table 3.6. Summary Statistics of 5S-GlcNAc Treated MEF cells M/L at T = 0

Mean	0.884798691
Standard Error	0.011488867
Median	0.8755
Mode	0.88917
Standard Deviation	0.203258799
Sample Variance	0.041314139
Kurtosis	99.34754791
Skewness	7.616431492
Range	3.5587098
Minimum	0.0034902
Maximum	3.5622
Sum	276.9419902
Count	313
Largest(1)	3.5622
Smallest(1)	0.0034902
Confidence Level (95.0%)	0.022605454

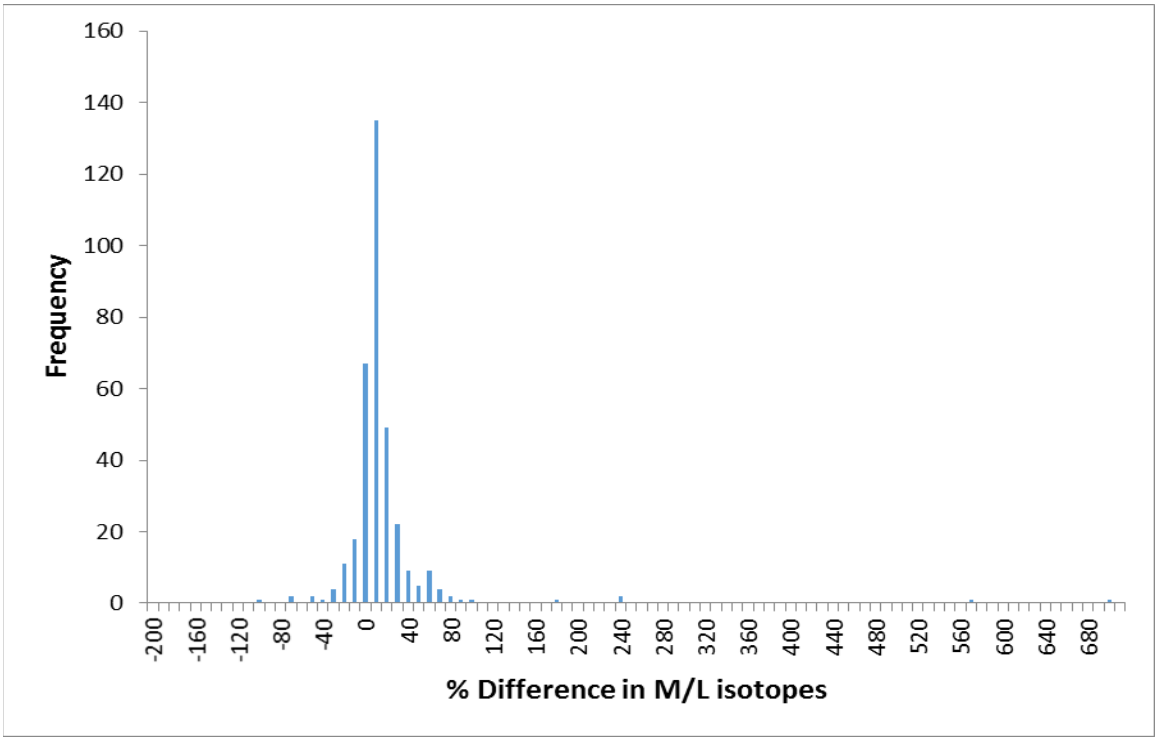

Figure 3.20. Percent difference in M/L isotopes at time zero between 5S-GlcNAc treated and control

False positives in preliminary MEF cell experiment traced to missed cleavages and high background

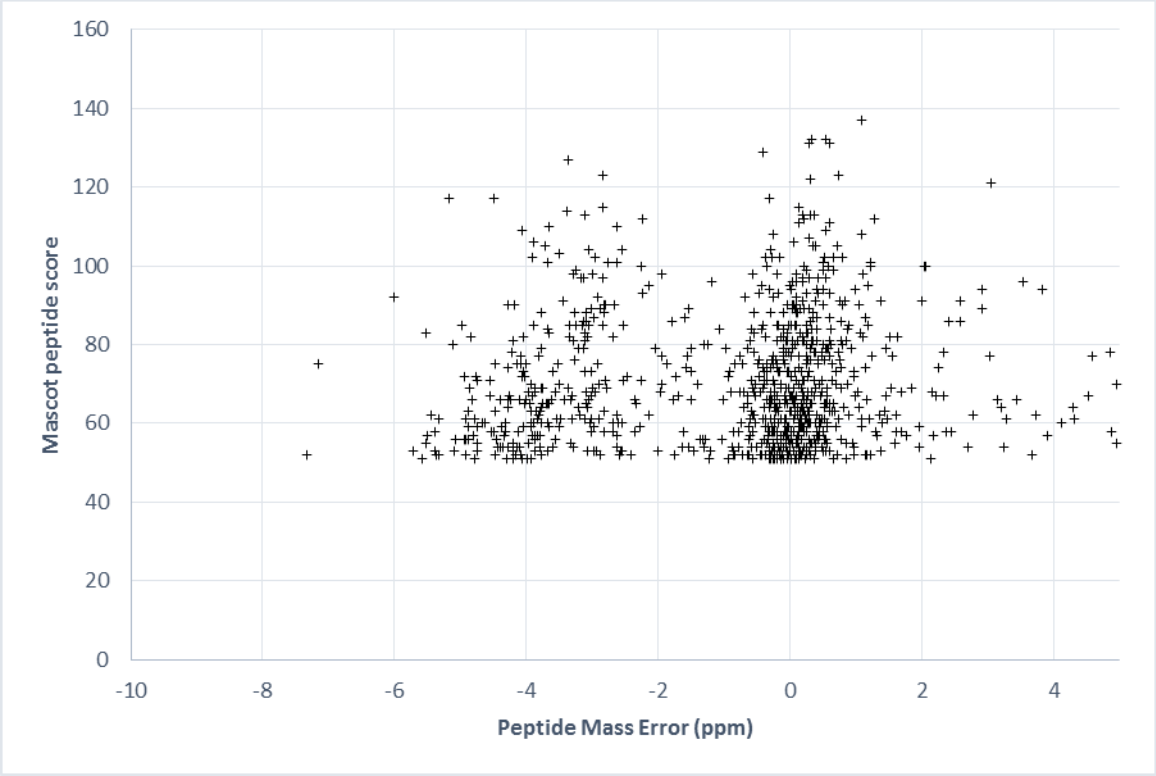

Figure 3.21. Bimodal plot of the mass error in initial MEF data for 1000 peptides. The mass shift largely corresponds to the difference between a peptide having a single R10 label versus having one K4 and one R6 label.

There was a gross excess of false positives that were identified in the initial MEF cell line data. Data analysis that showed an obvious excess of false positives included the volcano plots based on MaxQuant data tables for heavy to light which showed a great number of hits at time zero for a sample that does not yet contain any heavy isotopes and also the distribution of peptide mass errors based on

Mascot searches were bi-modal (figure 3.18). Investigation of these proteins that showed significant change in ratios containing heavy isotopes, most had one missed cleavage, typically due to a proline C-terminal to the missed cleavage site. They also typically had a single arginine and a single lysine. We found that the quantitation software was unable to distinguish between a peptide double labelled with K4 and R6 and a peptide single labelled with R10. The mass shift for R10 is +10.008269Da while the combined mass shift of K4 + R6 is +10.045236Da, the difference being 0.036967Da. Inspection of the MSMS spectra reveals sufficient peptide sequence coverage to confidently associate the correct peptide identification but lacked the information to determine the amino acid location of labels. This last point regarding MSMS spectra is not taken into consideration by all quantitation software in assigning the label used; rather, the MS data is used to find the presence and volume/area of the labelled peptide using the high mass accuracy of the Orbitrap. The Orbitrap Velos has very good mass accuracy and 10 ppm is standard for a well maintained instrument, while the default settings in MaxQuant software for first pass searches are 20 ppm as a guide. For peptides at high mass and high charge state, the difference between K4 + R6 and R10 is less than 10ppm, while peptides with low charge state and low mass are supposed to be excluded due to a difference of K4 + R6 and R10 being significantly greater than 10 ppm. Visual inspection of these latter cases reveals co-eluting peaks including polymer peaks also interfering with the distribution of the ions of interest and further interfering with the assignment of labels. The MEF sample data was indeed immersed in an unusually high chemical back ground of polymer ions due

to acetonitrile precipitation in a plastic vial for the purposes of removing biological detergents. Nonetheless, we can learn from this rather extreme case that by swapping R10 with R11 we can reduce the error in other, cleaner SILAC experiments such as done with our HEK293 samples.

We took corrective action to alleviate this problem. For the MEF cells, we changed the search parameters to allow for no missed cleavages and also by setting the tryptic enzyme cleavage specificity to cleave exclusively after all lysine and arginine residues. This resulted in removal of the unworkable false discovery rate of proteins with a difference in H/L ratios at time zero but a cost of a reduced number of proteins identified. For the HEK293 cell line experiment, this problem was completely removed. A changed cell lysis strategy more in line with FASP sample preparation (Wisniewski, 2009) to include fewer contaminants, combined with switching R10 isotope (arginine with +10Da label) with R11 (arginine with +11Da label) and also employing an Orbitrap fusion where the precursor mass accuracy is on the order of 2 ppm were all implemented.

Conversion of Arginine to Proline in SILAC Experiments

As part of the improvements we incorporated into the HEK293 cell line experiments we follow the protocol outlined by Lajoie et al. in order to prevent the conversion of arginine to proline (Bendall, Hughes et al. 2008). Specifically increased amounts of proline (minimum of 200 mg/L) were used in their experiment where arginine (R) to proline (P) conversion did not occur. Similarly some have also used the complementary strategy and have reduced the amount of arginine added to the media but there is no evidence to

support that method. These approaches aim to offset the balance of arginine to proline, so as to have the same effect but the data does not support a decrease in arginine as reducing conversion. Only an adequate amount of proline does.

Inhibition of over alkylation by Iodoacetaminic acid

We changed our protocol for the breaking and capping of cysteine disulfide bonds between the MEF cell line and HEK293 cell line experiments. Indeed leading labs and some commercial protocols have recently started to avoid alkylation of cysteine thiol groups altogether. Over-alkylation of samples results in *N*-alkylation of lysines, arginines, histidines and N-termini along with *O*-alkylation of glutamic and aspartic acid residues. The solution we followed is to carefully proportion the amount of DTT and IAA used, followed by the additional step of quenching the IAA reactions with more DTT (Boja and Fales 2001). We also routinely replace the conventional fixed modification of carbamidomethylation with a variable one during data processing.

Improving proteome coverage through comparison of fragmentation mechanisms

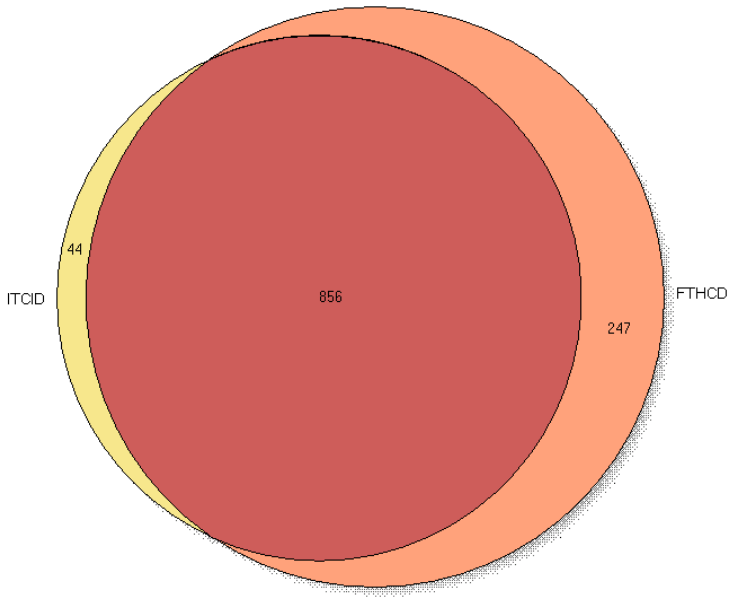

Figure 3.22. Comparison of MSMS data collection strategies used for the MEF cell line and HEK293 cell line experiments. Data shows a small observable increase in the number of proteins identified when collecting fragmentation data using the orbitrap and HCD fragmentation as compared to collecting fragments in the linear ion trap and employing CID fragments.

We compared several different arrangements before and after these SILAC experiments by changing the fragmentation type and filter/detector combinations for the detection of MSMS spectra. In all cases, MS data was collected in the orbitrap as described in the methods section. Above is the comparison of the two parameters that were changed between MEF and HEK293 cells. Data in the Venn diagram (Figure 3.19) shows the number of proteins acquired during a short LC run after injecting 1 µg of commercial *E.coli* digest onto the column and detect using the orbitrap fusion. We found the number of

peptides detected by using the ion trap with CID (ITCID) for MSMS data collection to be higher but the number of proteins detected to be greater by using the Orbitrap with HCD (FTHCD) for MSMS data collection. For the MEF cell line experiments, we used CID fragmentation of peptides which were then detected after filtration through the linear ion trap. The HEK293 cell line was fragmented by HCD then the fragments were filtered in the orbitrap. Later we found HCD in combination the linear ion trap to detect the greatest number of proteins and peptides, which should be used going forward. The increased speed of the both HCD over CID fragmentation and ion trap filtration over orbitrap filtration highlights reduced cycle time as the predominant parameter for improved proteome coverage.

We also determined that the minimum precursor height for triggering MSMS data collection plays a critical role in the quality of SILAC data. Most experiments published with the aim of acquiring the greatest number of proteins utilize a precursor trigger height of 5000 cps on the orbitrap Velos and Fusion. We also used 5000 cps, as the precursor trigger height on the Orbitrap Velos for the MEF SILAC experiment. However, we observed peak shape quality is frequently poor at 5000 cps such that the ratio of the natural isotopic ratio abundances had obvious errors. For our experiment on HEK293 cells using the Orbitrap Fusion, we raised the minimum precursor trigger height to 50000 cps.

Methods

We performed successive experiments including a preliminary investigation using MEF cells followed by improved methodologies using HEK293. Cell culture, SILAC labelling, and treatment were carried out by Dr. Yanping Zhou and briefly summarized here.

Cell Culture

Mouse embryonic fibroblast (MEF) cell line containing lentivirus encoding mutated estrogen receptor (mER)-Cre-2A-GFP construct was a gift from Zachara's group (Kazemi, Chang et al. 2010). Cells were cultured in Dulbecco's modified Eagle's medium (DMEM; 1 g/l glucose) with 10% (v/v) fetal bovine serum (FBS) and 1% (v/v) penicillin/streptomycin at 37 °C in a water-jacketed, humidified CO_2 (5%) incubator. Typically, cells were plated at 10-25% confluency. Unless otherwise noted, Cre-recombinase was activated to knock out OGT through incubation with 0.7 μM 4-hydroxytamoxifen (4HT, Bioshop) 1 day post-plating. 4HT was removed 24 hours later. To inhibit the OGT activity, Ac5SGlcNAc (5sInh) was added into cell culture to final concentration of 50 μM.

HEK cells were maintained in high glucose DMEM (Gibco) supplemented with 10% fetal bovine serum (Gibco), 100 IU/ml penicillin, and 100 μg/ml streptomycin (Gibco). For inhibition of OGT, Ac5SGlcNAc was added into cell cultures to yield 200 μM final concentrations of compounds.

SILAC Labelling

Cells were grown in media containing arginine and lysine, either with the normal light isotopes of carbon, hydrogen and nitrogen (i.e. 12C14N) (light – “L”), or else with L-lysine-$^{2}H_{4}$ (K4) and L-arginine-$^{13}C_{6}$ (R6) (medium – “M”) for at least five cell divisions, resulting in 99% incorporation of the M amino acids. The culture media with the M amino acids is then replaced with media containing L-lysine-13C6-15N2 (K8) and L-arginine- 13C6-15N4 (R10) or 2H7-15N4 (R11) (heavy – “H”). H amino acids are pulsed into cells with M-labelled proteins for varying times. L-proline was added into the medium to final 500 mg/L for preventing interconversion between arginine and proline. All stable amino acid isotopologues were order from Cambridge Isotope Lab (CIL), Andover, MA, USA.

HEK293 Cells were harvested at 0, 2, 5, 8, 12, and 24 h time points following the H amino acid-pulse. Cells were lysed in 100 mM ABC buffer containing 0.2% SDS, and boiled for 5 min. After sonicated for 10 s at 4 °C, cell lysates were mixed with equal volume of 6 M guanidine HCl and centrifuged at 17,000 g for 10 min. Clear solution containing the protein samples in the middle layer was transferred to a new tube. At each time point, protein samples from the pulsed cells (M-H) was mixed with an equal amount of samples prepared from cells grown in normal (i.e. light – “L”) culture media.

SILAC experiment with MEF cells

Twelve MEF samples (4 time points each of Control, OGT knockout and OGT inhibitor) were prepared in parallel. Further sample purification was required from biological detergents not compatible with mass spectrometry and samples underwent an acetone precipitation.

For this procedure we estimate the recoverable MEF protein amounts to be 105 µg. Proteins were denatured in 200 µL of 6M guanidinium hydrochloride (prepared by dissolving 8.6 g GnHCl (98% Sigma) in water (lcms chromasolv, Fluka) and topping volume up to 15 mL in glass containers. Denaturing ran for 50 min at 90 ºC while shaking at 300 rpm (Thermo Mixer, Eppendorf). We regularly use GnHCl for denaturing proteins without any observed unwanted reactions, having abandoned use of Urea due to previous observations of extensive carbamylation, while we are aware of the alternative agent, sodium deoxycholate (Proc, Kuzyk et al. 2010). Cysteine disulfide bonds were reduced by adding dithiothreitol to a final concentration of 5 mM taken from a freshly prepared stock solution of 80 mM DTT (prepared by dissolving 12.34 mg DTT (99.5%, Sigma) in a final volume of 1 mL water) and heated to 56 ºC for 30 min. We employ the traditional DTT in place of the more potent TCEP due to our interest in glycoproteomics as TCEP is known to alter the stereochemistry of carbohydrates. The choice to use 5 mM of reducing agent was motivated by the commercial trypsin digestion protocol (Promega). The free thiol groups of Cysteines were then covalently alkylated to prevent the reformation of disulfide bonds by adding iodoacetamide to a final concentration of 8 mM using a freshly prepared 200mM stock solution (37 mg IAA (bioultra, Sigma) dissolved in water to a final volume of 1 mL), wrapped in tin foil to prevent light induced degradation of IAA and left at room temperature for an additional 20 min. Samples were transferred to 10 kDa 0.5 mL spin

filters (Amicon ultra, Millipore) using an excess of digestion buffer (10% acetonitrile, 40 mM ammonium bicarbonate). Samples were centrifuged (5415D centrifuge, Eppendorf) at 9000 rpm down to 40 µL and 400 µL of digestion buffer which was first used to rinse original vials was added. This transfer, sample washing and buffer exchange step was repeated three times with the final volume of 20 µL. Spin filters were inverted in new plastic vials and centrifuged at 13000 rpm for 5 min. Trypsin enzyme (V511A, Promega) was removed from -20ºC and resuspended in freshly thawed trypsin resuspension buffer (V511A, 50mM acetic acid, Promega) as per manufacturer's protocol where we skipped the suggested heating step of 30 ºC for 15 min. Trypsin solution was immediately added to each sample vial containing an estimated 105 µg protein in 20 µL of digestion buffer in a 1:40 sample to enzyme : sample ratio. Samples were digested at 37 ºC while shaking at 300 rpm under a vacuum hood. Digestion was stopped after 15 hrs by freezing samples in -80 ºC freezer. Holes were pierced into the top of each vial and then samples were lyophilized to complete dryness. Samples were reconstituted in 65 µL 2% acetonitrile, 0.1% formic acid and mixed thoroughly on vortex mixer.

Samples were reconstituted in 50 µL of 2% acetonitrile, 0.1% trifluoroacetic acid and vails were vortex mixed, centrifuged and vortex mixed again. Samples were then desalted with desalting tips (Supel-tips, TPSC18, Sigma-Aldrich).

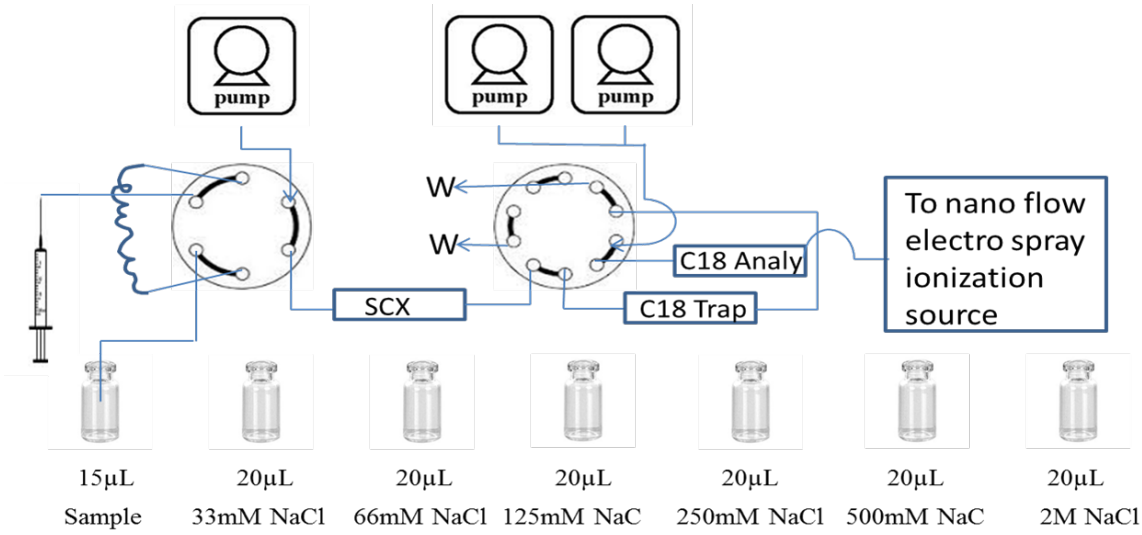

Figure 3.23. 2D on line chromatography apparatus employing SCX and C18 solid phase materials used in separation of peptides for MEF cells.

Two dimensional online chromatography was employed using an Eksigent nano-LC 1D, with a 20 µL sample loop, 5.4 µL sample needle and a 100 µL loading syringe and batch sample controlled by programming Eksigent run manager v2.8,. 2D chromatography was accomplished by introducing an SCX column (POROS 10S, 300 µm x 10 cm) placed between sample loop loading valve and an external 10-port switch valve (Vici Valco) that housed the trap column (C18 pepmap, 5 µm, 100 Å, 300 µm x 15 mm, Dionex). An analytical column was packed in house (2.7µm HALO core C18, 140mm x 75µm) and plumbed immediately before a nano spray tip (New objective, 20 µm ID, terminating in 10 µm ID). All plumbing used in loading through the SCX column was 75 µm ID fused silica, and all tubing used in conjunction with C18 columns were 20 µm ID fused silica. SCX columns were cleaned and regenerated with 20 µL 1 M NaCl salt plug injection across the column followed by 30 min wash at 5 µL/min with regeneration solution (1.38 g monosodium phosphate, monohydrate, 0.3 mg disodium phosphate, heptahydrate in 1 L of MS grade water) and this was repeated between injections of sample from different groups (Control, OGT inhibitor, OGT knockout). C18 columns were pre-conditioned with

repeated 100 fmol BSA digest (Michrom) injections on full gradient elution as used for samples until retention times and intensities of BSA digest peaks stabilized. Flow rates for all three mobile phase pumps were calibrated in the range of their intended use. The injection needle was pre washed in 100 µL loading mobile phase before samples were picked up at 20 µL/min from trays cooled to 7 ºC. Aqueous mobile phase A was composed of 0.1% FA, 3% ACN, organic mobile phase B was composed of 85% ACN, 0.08% FA and the loading solvent was made of 2% ACN, 0.025% TFA. Before the first injection of sample two blank injections were performed using an aliquot of mobile phase B to clear any residue from the previous sample. Additionally, between each run of sample and salt plug injections, the interface capillary was cleaned with water, then methanol and dried with high pressure nitrogen. Within each run, the first injection was 20 µL from the sample vial which was loaded onto the SCX column. The initial eluent not retained on the SCX column was directed onto the C18 trap column as the first run and washed for 15 min at 7 µL/min, after which time the C18 trap gradient eluted onto the C18 analytical commenced and a start signal was sent to the mass spectrometer to start data acquisition. Gradient elution jumped from 0-5% B between 15 and 17 min then linearly ramped to 55% by minute 74, then ramped to 85% B in 3 min which was held for 5min, then dropped to 0% B over 3min and the C18 column was equilibrated in mobile phase A from minutes 85 through 95. This first sample injection is labelled 0 mM (NaCl) in all data file names. Then sequential 20 µL injections followed with the same gradient using increasing concentrations of salt (31, 63, 125, 250, 500 and 2000 mM NaCl) to dislodge aliquots of peptides from the SCX column onto the C18 trap column for desalting.

Samples were exposed in solution using a tee holding platinum wire with a relative 2300 V applied potential positioned directly before the analytical column. The nano-spray

tip was positioned 15 mm back and 3 mm to the side on the horizontal plane of the capillary inlet (nano-spray Flex ion source, Thermo). A thermo orbitrap velos (with velos pro upgrade) was used for data acquisition employing Thermo Tune Plus v 2.7.0.1103sp1 and Thermo Xcalibur v2.8sp1.48. The Eksigent LC system was not in the Thermo foundations library so both sets of software operated on separate computers with communication cables made in house to accommodate a ready state request to be sent to the LC from Xcalibur system, a ready state signal to be received by the Xcalibur software and a start signal to be sent from the Eksient AS1 autosampler to the Orbitrap Velos to commence data acquisition. Prior to experiment, ion optics were cleaned, tuned and calibrated. As per the automatic gain control integrated into this mass spectrometer, analytes were sampled in the linear ion trap with two orthogonal detectors to estimate the amount of ions eluting at that particular point in the gradient elution and the calibrated automatic gain control adjusted the time permitted for an optimized amount of sample ions to be injected into the orbitrap where an FTMS scan captured mass spectra targeted at 60000 resolution with a mass range of 350 to 2000 m/z and a collision voltage of 0.0 V. MS AGC target of 100000 cps in FT with a maximum time of 500 ms and MSn AGC target of 10000 for the linear ion trap with a maximum time of 100 ms. From each MS acquisition, a maximum of nine MSMS scans were accumulated by CID fragmentation in the linear ion trap in the interests of striking a balance between minimizing cycle time and producing conventional spectra easily evaluated by commercial software without further clean-up of harmonic signals. Ions selected for MSMS acquisition had to be greater than 5000 cps with charge state discernable by the software and greater than singly charged. MSMS fragmentation occurred in the linear ion trap with a precursor isolation width of 2 Da, with a normalized collision energy of 35eV and an activation time set to 10ms. Ions were measured in positive ion mode while employing an active lock mass of 445.120024 Da which

corresponds to $[C_2H_6SiO]_6$ from polysiloxane found to be pervasive in laboratory air and solvents (Keller, Sui et al. 2008). The mass spectrometer cycled through this MS and maximum set of nine MSMS spectra in a cycle time that varied depending on the AGC response to signal intensity and the availability of ions to fragment. Ions were permitted to be fragmented twice within 15 s, then placed on an exclusion list for 30 min, with a rolling exclusion list having a maximum size of 500. For peaks interpreted to co-elute with data already collected within the mass exclusion time with a mass difference equal to or less than 10ppm, no fragmentation data was collected.

Protein prospector (Chalkley, Baker et al. 2008) employing the Mascot search algorithm was used to roughly and comparatively quantify the total number of proteins found in each sample. And with priority given to samples with the least number of proteins identified, those samples were re-injected into the Orbitrap Velos along with an exclusion list to avoid reacquisition of previously acquired data. The exclusion list was created from protein prospector data and included masses for peptides with a Mascot peptide score greater than 50 and imported into individual Thermo tune methods along with the previously acquired retention time, using a retention time window of 2 min and a mass tolerance for exclusion of 10 ppm. Reacquired data from the same sample were assigned to data files of the same name with an ‘X’ after the file name. If a sample was injected a third time, the file name was followed by ‘XX’. Multiple data files from the same sample would later be combined using Maxquant software, discussed later.

MEF raw data files were modified solely and consistently by removing the first 15 min of each 90 min data acquisition by the Slicer algorithm (Thermo) and these files were renamed with the suffix ‘Refined’. The first 15 min of spectra were dominated by polymer

ions assumed to originate from the acetone precipitation done in plastic vials. Removal of the first 15min of spectra sped data analysis and reduced file size.

SILAC experiment with HEK293 cells

For our second and improved experimental method, twelve HEK293 samples (6 time points each of control and OGT inhibitor) were prepared in parallel starting with roughly 67 µg each. Samples were dissolved in 800 µL 6 M GnHCl (98% Sigma) and were briefly spun on a vortex mixer (Thermo, vortex mixer). Samples were then placed on a thermo mixer (Eppendorf) at 37ºC and 300 rpm for 2 hours. 4 µL of 1 µmol/µL solution of dithiothreitol (10.7 mg DTT in 69.5 µL water) was added to each vial and temperature was increased to 60ºC for 1 hour. 8 µL of fresh iodoacetamide solution (16.4mg IAA in 88.6µL water) was added to each vial which were immediately transferred to dark and room temperature for 30 min. 10 µL of 1 µmol/µL of DTT was then added to each vial which was then briefly centrifuged an then mixed on vortex mixer. Samples were sequentially loaded onto centrifuge filters (0.5 mL 10 kDa Amicon) and spun at 11000 rpm and reloaded until all samples were loaded onto filters. Samples were buffer exchanged by reducing volume to 100 µL and topping off with 400 µL of 50 mM ammonium bicarbonate (98.8 mg ABC in 25 mL of water). This buffer exchange step was repeated with a final volume of 40 µL. Filters were inverted into new tubes and centrifuged at 13000 rpm. Samples were digested with trypsin gold in a 1:25 sample to enzyme ratio at 37ºC and 300 rpm for 15 hrs. Digestion was stopped by freezing to -80ºC and lyophilization to dryness.

Off line high pH fractionation was accomplished as our first dimension of peptide separation as set forth here (Percy, Simon et al. 2014). Samples were reconstituted in 1 mL of 10% 100 mM NaOH and 3% ACN. Samples were separated across a high pH C18

column (XBridge BEH300, 4.6 x 150 mm, 5 µm particles, Waters) in a column heater at 40ºC (Agilent). UV Vis at 240 nm. Fraction collector distributed the samples from left to right across 48 fractions. Fractions were pooled down from 48 to 11 fractions as outlined in the figure below so as to compensate for the lack of total orthogonally between high pH and subsequent low pH separations on C18 media.

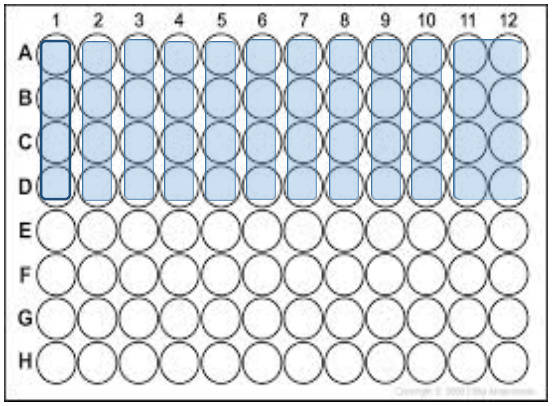

Figure 3.24. Pooling strategy of peptides following off-line high pH reverse phase C18 fractionation. Blue rectangles encapsulate each pool of 11 samples which were in turn separated online using low pH C18 chromatography.

Each of the 11 sample fractions for each experiment (Control, 5THio-GlcNAc) were divided in half and one of each was stored for insurance purposes. Remaining samples were in some cases less than 1 µg and so were each desalted twice using C18 desalting tips (PIERCE, CAPI87782, C18 TIPS 10 µL). Samples were lyophilized then re-suspended in 22 µL of mobile phase A.

Online liquid chromatography. Proxeon easynLC1000 µHPLC. 1D chromatography was set up using an enrichment trap column (100 µm ID x 280 mm) packed in house (2.7 µm HALO core C18) and an analytical column (75 µm ID x 380 mm) packed with the same material. Samples were picked up in 18 µl at a flow rate of 20 µl/min. Samples were loaded onto trap column by volume measurement of 30 µl using a maximum

pressure of 450 bar. Trap column was equilibrated using 8 µl of mobile phase A. Analytical column was equilibrated using 2 µl of mobile phase A. Reverse phase gradient elution was as per the table below using 2% acetonitrile, 0.1% formic acid for mobile phase A and 90% acetonitrile, 0.1% formic acid for mobile phase B.

Time [min]	Duration [min]	Flow [nl/min]	Mixture [%B]
0	0	200	0
1	1	200	3
47	46	200	45
49	2	200	47
50	1	200	50
51	1	200	100
66	15	200	100

Figure 3.25. Liquid chromatography gradient parameters for online separation of HEK293 peptides.

Mass spectrometry was performed with an Orbitrap Fusion with a nano-flow electrospray ionization source set to a potential difference of 2300 V. A custom nano-spray head supplied a nebulizer nitrogen gas warmed by passing through a column heater set to 50ºC at a flow rate of 0.6 cm^3/min. Ion transfer tube temperature was 275ºC. Positive internal calibration was 445.12002 Da which corresponds to ubiquitous polysiloxane. Cycle time was set to a maximum of 3 s. MS data acquisition settings included 120 k resolution, over an m/z range of 380-2000 amu using a maximum injection time of 200 ms in the orbitrap employing an AGC target of 400000 counts. Only mono-isotopic precursor ions with a known charge state of 2-7. Dynamic exclusion of precursors for fragmentation was set such that if precursor has already been fragmented within the last 15 s, it is excluded for another 12 s. The decision tree for fragmentation for fragmentation was based on most intense ions first and all ions having greater than 50000 counts. MSMS fragmentation was done on precursor ions directed through a quadrapole mass filter with an isolation window of 1.6 amu, followed by fragmentation by HCD and detection in the

Orbitrap at 30 k resolution with maximum injection time 64 ms, first mass set to 110 Da and an AGC Target of 50000.

Data processing and analysis

Identification and relative quantitation of proteins was carried out by using the computer program MaxQuant v1.5.0.30 (Cox and Mann 2008) in combination with the Andromeda search engine v1.4.0.0. (Cox, Neuhauser et al. 2011). FASTA files were downloaded from uniprot.org and included the canonical databases filtered for reviewed entries only and included isoforms. Separate FASTA files were downloaded for Mus musculus (Oct 12, 2014) and Homo sapiens (Aug 22, 2014).

MaxQuant settings for HEK293 cells were multiplicity 3, maximum number of labelled peptides 3, light isotopes were unlabelled, medium isotopes included K4 and R6, heavy isotopes K8 and R11, digestion according to normal cleavage after Lysine and Arginine residues unless followed by Proline, and allowed up to 2 missed cleavages. MaxQuant setting particular to MEF cells were multiplicity 3, maximum number of labelled peptides 3, light isotopes were unlabelled, medium isotopes included K4 and R6, heavy isotopes K8 and R10, digestion according to exclusive cleavage after Lysine and Arginine residues and no tolerance for missed cleavages. Variable modifications of amino acids were acetylation of protein N-terminus, carbamidomethylation of Cysteines, deamidation of Asparagines and Glutamines and oxidation of methionines, histidines and tryptophans. First search peptide mass tolerance was 20 ppm for the Velos and 10 ppm for the Fusion and both had a main search tolerance of 4 ppm. Decoy data set was by random sequence generation. For protein identification false discovery rate was set at 1% both at the peptide and protein levels, minimum peptide length was set at 5 and minimum score for modified

peptide was set at 40. For protein quantitation, a minimum of 2 unique plus razor peptides were required and used including unmodified peptides and peptides with the four previously mentioned modifications. For the Velos, MSMS tolerance was set to 0.8 Da using the linear ion trap. For the Fusion, MSMS tolerance was set to 20 ppm using the Orbitrap.

Volcano plots have been frequently used in genomics studies over the past decade and are highly appropriate for the analysis of growing populations of relative quantitative proteomics data (Cui and Churchill 2003). Volcano plots offer a way to display all of the data including marginal data to satisfaction of some researchers using the x-axis as some appropriate function of the fold change observed between the control and experimental groups while y-axis represents the statistical validity of the differences observed between the two groups in the data. We employ volcano plots as a difference of means hypothesis test, using the p-value from student t-test statistic to test difference between isotopic ratios for proteins which are taken as a mean of a number peptides isotopic ratio and variance reported by the max quant software. We plot the y-axis as the Log_{10} of the p-value. Our x-axis if the difference of Log_{10} of the measured isotopic ratios of the treated and control groups. Our volcano plots are made from scratch in excel and the curves separating data points between groups that pass or fail the null hypothesis are made as suggested by Li (Li 2012).

Taking the protein GRP-78 which shows significant altered synthesis as example data point in the Volcano plots, we start with the ratio H/L plot at the 24 hour time point in HEK293 samples. We have collected 129 peptides (n1) in the control sample with a mean H/L ratio of 0.38167 and a % variability of 18.16 which we use to calculate our variance^2 of 0.00518 ($Var^2 1$). For the 5S-GlcNAc treated group we have 132 peptides (n2), a mean

H/L ratio of 0.75417, a % variability of 11.968 and a variance^2 of 0.00815 (Var^{2}2). From the data above we can calculate the x-axis Log_{10} (0.75417) – Log_{10} (0.38167) = 0.296. For the y-axis, we first need to define and calculate our test statistic (TS):

$$TS = \frac{\left(\frac{H}{L}\right) treated - \left(\frac{H}{L}\right) control}{\sqrt{\frac{Var^2 2}{n2} - \frac{Var^2 1}{n1}} + RegCoef}$$

TS = 32.38, where the regularization coefficient is found from the time zero entire population of collected H/L data and equal to 0.0015. We use the test statistic to calculate the *p*-value based on the student t-test, where the degrees of freedom (DOF = n1+n2-2) is 263. *p*-value (|TS|,DOF) = 9.43 x 10^{-94}. We then plot the –Log10 (*p*-value) = 93.03 as our y-axis coordinate.

Perseus v.1.5.0.31 (Cox and Mann 2012) software was used for the cross-referencing of columns of categorized data, and data manipulation for the purposes of producing 2-dimensional plots of H/M ratios for HEK293. The entire reviewed list of known human chaperone proteins was downloaded from UNIPROT.org

Global comparison of population means for protein turnover between 5S-GlcNAc treated and untreated HEK293 cells.

Data for H/M ratios from Orbitrap Fusion acquired as previously mentioned was analyzed. Data sets were from HEK293 from untreated and 5S-GlcNAc. Three dimensional peak reconstruction was performed using MaxQuant software as previously mentioned and non-normalized data was used. Data has only undergone a Log2 transformation using Perseus software. We filtered our dataset of 3210 proteins with turnover data for at some time points down to 831 proteins with complete data at all time

points for both populations, treated and untreated using Excel (Microsoft inc.). The distributions for these data sets are smooth and continuous but not normal and not clearly associated with any particular distribution. We then used Minitab statistical software V.17 (Minitab Inc.), to numerically calculate the bootstrapped mean using 831 iterations and a 95% confidence interval for each distribution from each time point and sample group. The lower and upper bounds of the 95% confidence intervals of the means were plotted using Excel in figure 3.14. Below, we show the Minitab graphical results at each time point.

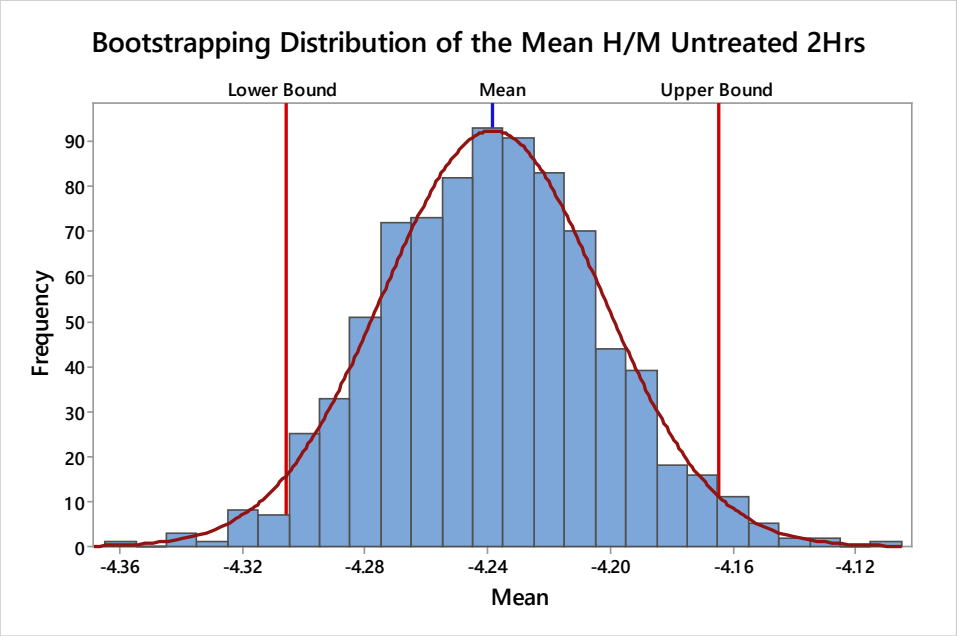

Figure 3.26. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 untreated 2 hrs.

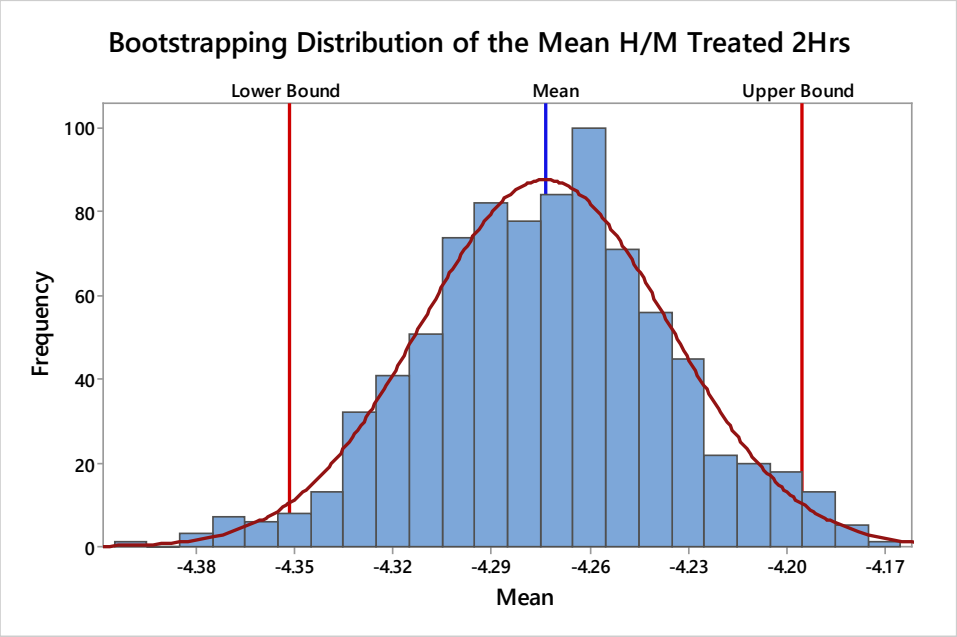

Figure 3.27. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 treated 2 hrs.

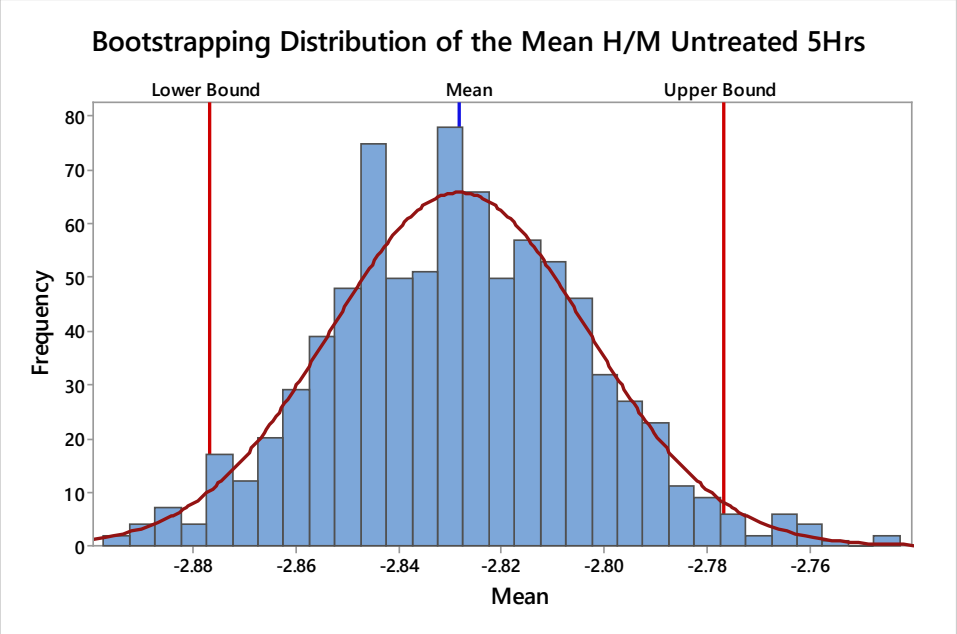

Figure 3.28. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 untreated 5 hrs.

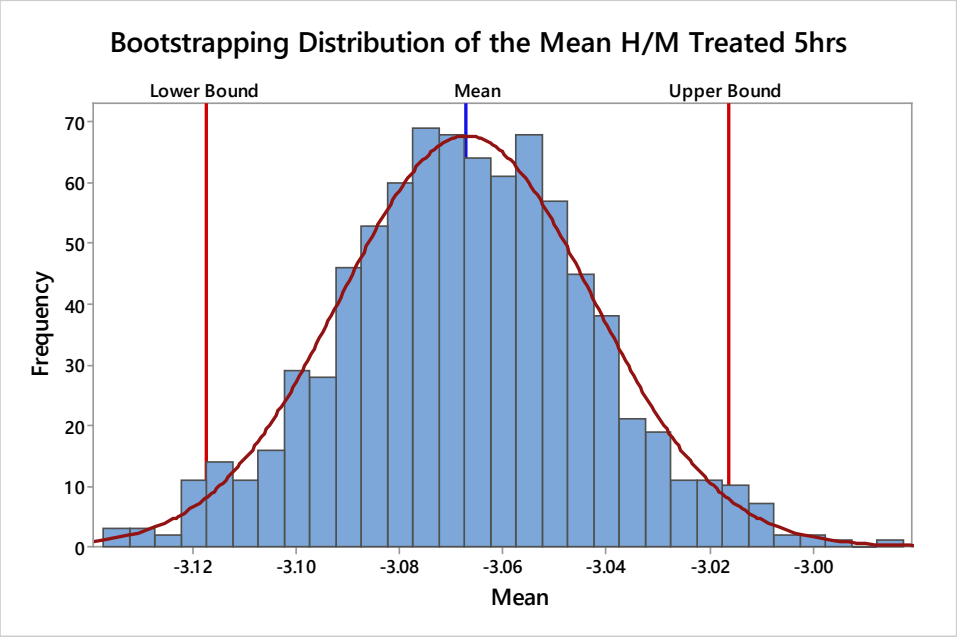

Figure 3.29. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 treated 5 hrs.

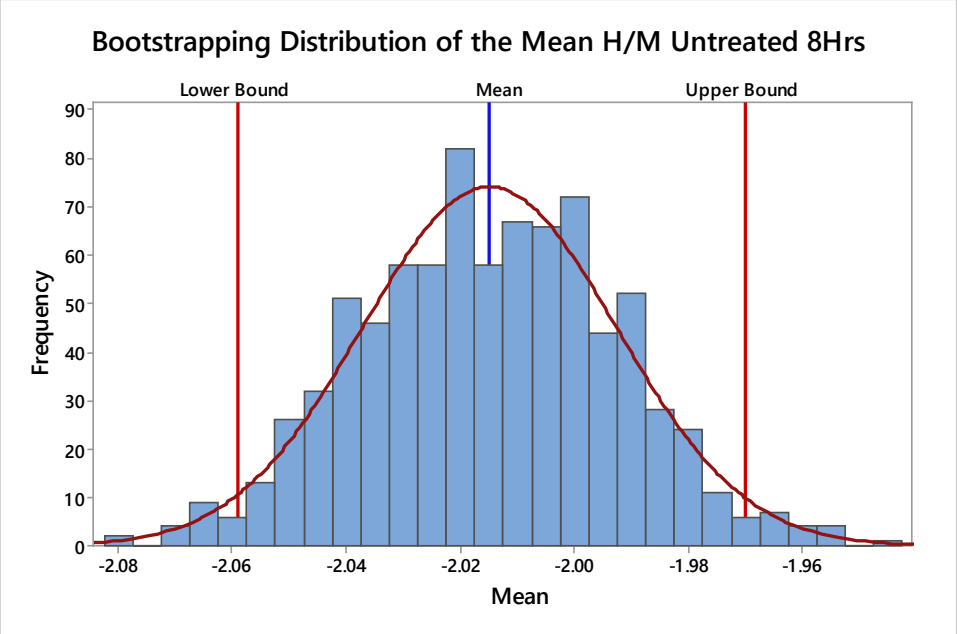

Figure 3.30. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 untreated 8 hrs.

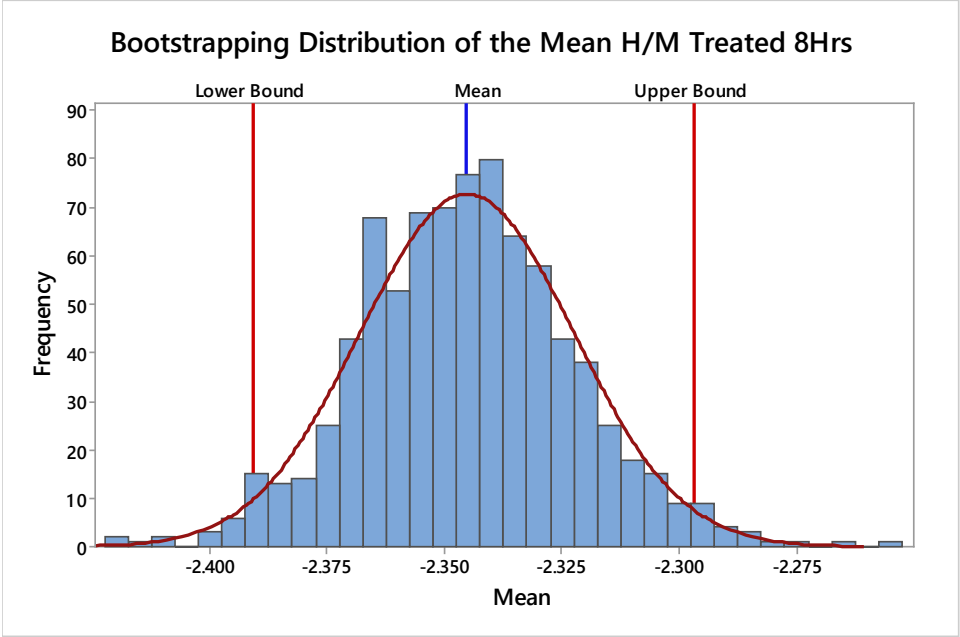

Figure 3.31. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 treated 8 hrs.

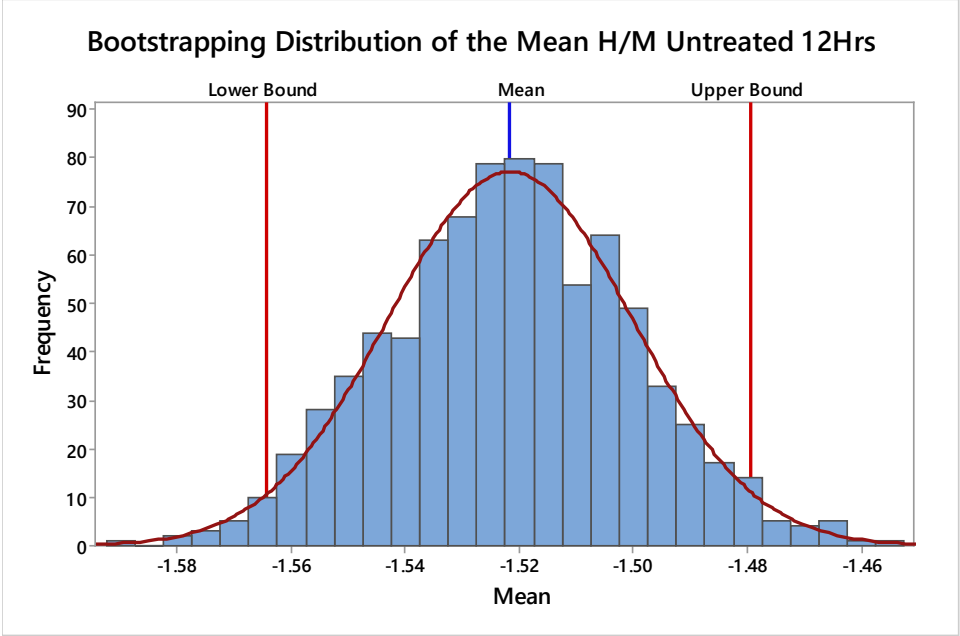

Figure 3.32. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 untreated 12 hrs.

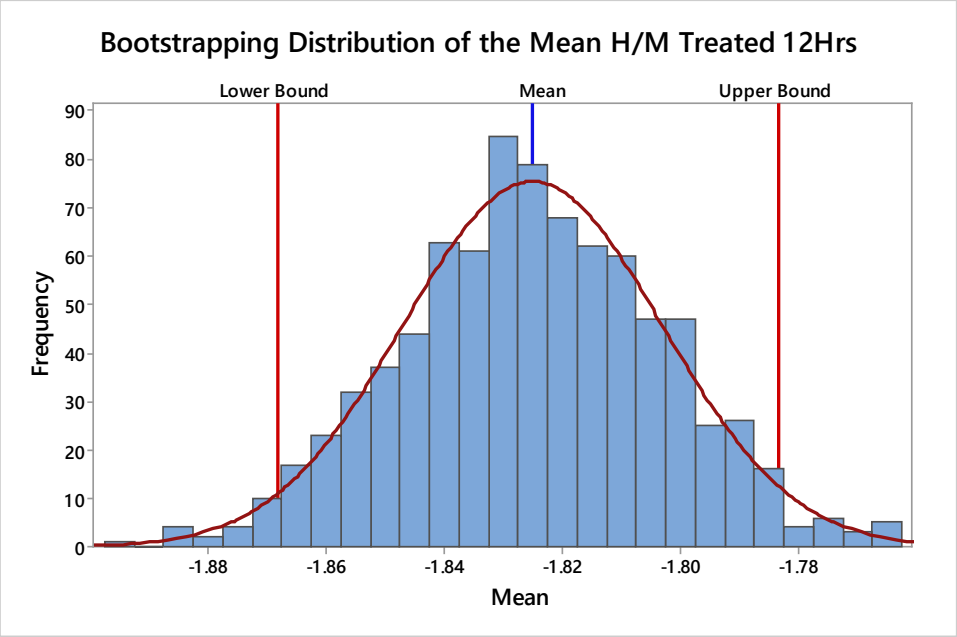

Figure 3.33. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 treated 12 hrs.

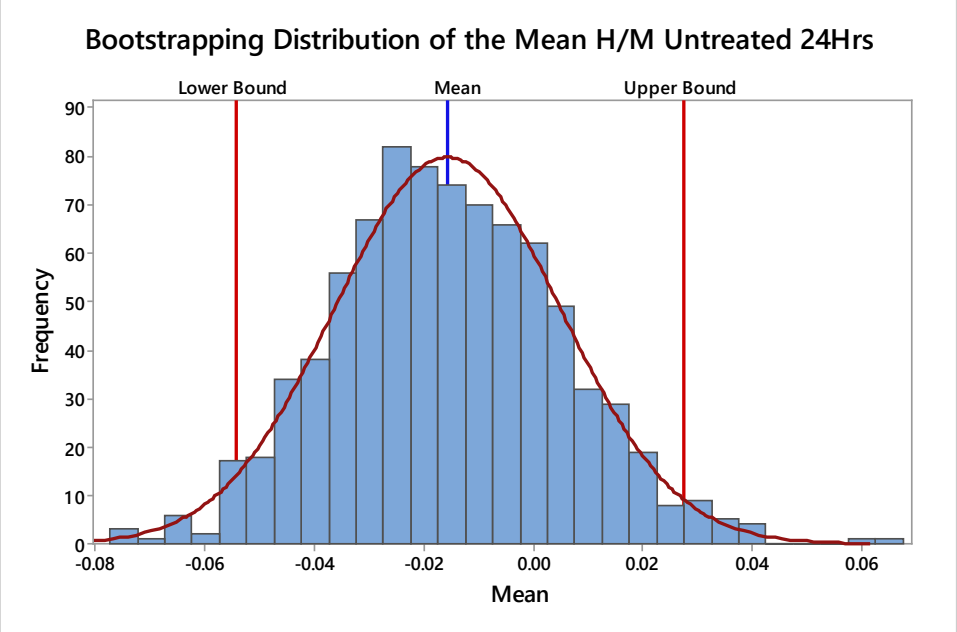

Figure 3.34. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 untreated 24 hrs.

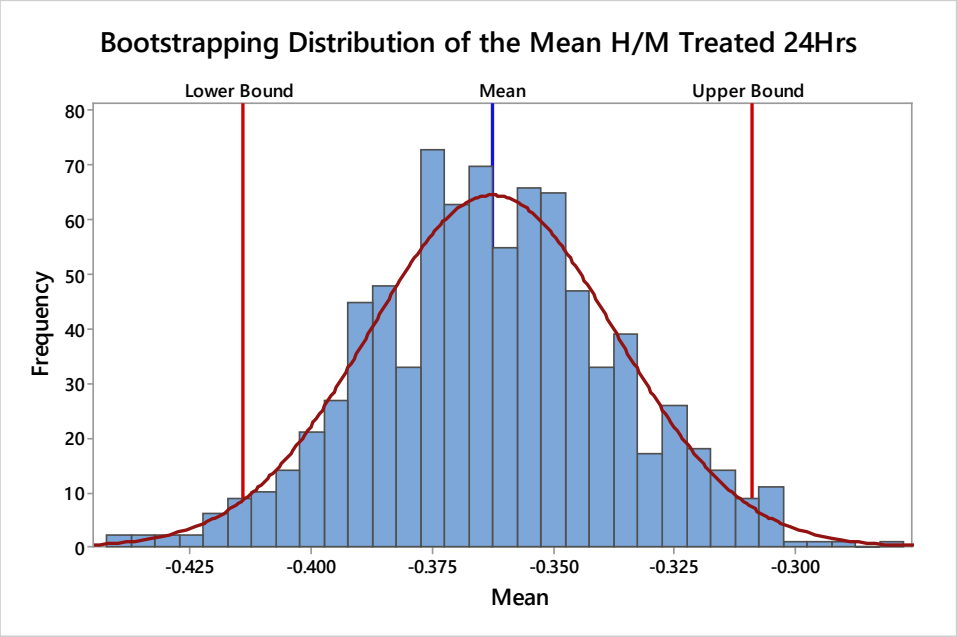

Figure 3.35. Minitab bootstrapping calculation of 95% confidence interval for mean of non-parametric data. H/M HEK293 treated 24 hrs.

Chapter conclusions and future directions

Reduced O-GlcNAcylation alters proteome stability. This conclusion is supported by our observations showing that there are changes in mean global proteome turnover upon inhibition of OGT. Levels of many individual proteins show altered degradation, synthesis and turnover as seen in both HEK293 and MEF cells where treatments included either inhibition or knockout of OGT.

Looking forward, there is an abundance of data compiled here that suggests O-GlcNAcylation may be involved in a novel type of unfolded protein response in the nucleus and cytoplasm. This is a preliminary conclusion based on altered synthesis of GRP's, altered synthesis of DnaJ proteins known to regulate GRP 78, and the regulation of phosphatidylethanolamine binding protein. The ATF proteins, ATF3, ATF4, ATF5 and ATF6 are all known to be play a part in the canonical unfolded protein response and are

activated by phosphorylation. Interestingly ATF1 and ATF2 have had some O-GlcNAc sites mapped. The three arms of canonical UPR are altered (synthesis, degradation and chaperones) and all show evidence of changes to reduced O-GlcNAc levels. Protein degradation pathways that are altered not only include the chaperone mediated autophagy pathway, as eveidenced by increased HSP70 turnover as described above, but also the macroautophagy pathway, as evidenced by the significantly upregulated core ATG proteins GABARAPL2 and GATE-16. Transription may be influenced by changes in the turnover of transcriptional activators shuch as Pinin. A survey of the proteins tabulated in the appendices yields a common theme amongst their UNIPROT functions and descriptions which, albeit sometimes loosely, associates many of these proteins with either a response to protein folding or the canonical unfolded protein response. An example includes the protein NACA which has been proposed to prevent inadvertent targeting of non-secretory polypeptides to the ER (Moller 1998). We know O-GlcNAcylation is localized to the nucleus and cytoplasm but not the endoplasmic reticulum and so it is interesting to find examples such as Mesencephalic astrocyte-derived neurotrophic factor which is also localized to the nucleus and cytoplasm, has a response to unfolded protein (by UNIPROT electronic annotation) and responded to reduced O-GlcNAc levels with a 2.4 fold increase in protein turnover. However, biological work needs to be done to define and or validate any novel UPR pathway. Nonetheless, seven proteins showing increased synthesis and eight proteins showing decreased synthesis due to reduced *O*-GlcNAc levels are laid out in Table 3.3 and Table 3.4 respectively which are validated by both OGT knockout and OGT inhibition. In these same tables, there are ten proteins with reduced synthesis rates due to reduced O-GlcNAc levels and two proteins, 78kDa glucose regulated protein and Nascent polypeptide-associated complex subunit alpha which show increased synthesis rates validated in both human and mouse cells.

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Appendices.

Results Tables

Appendix A: Table of volcano plot derived proteins with increased synthesis in MEF cells due to 5Thio-GlcNAc inhibition:

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q8VDD5	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	Myh9	15.8	MEF	5S-GlcNAc	6
Q60605	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	Myl6 Myln	7.33	MEF	5S-GlcNAc	6
P09602	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)	Hmgn2 Hmg-17 Hmg17	6.76	MEF	5S-GlcNAc	6
Q3THE2	Myosin regulatory light chain 12B (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2)	Myl12b Mrlc2 Mylc2b	6.04	MEF	5S-GlcNAc	6

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P29595	NEDD8 (Neddylin) (Neural precursor cell expressed developmentally down-regulated protein 8) (NEDD-8) (Ubiquitin-like protein Nedd8)	Nedd8 Nedd-8	5.63	MEF	5S-GlcNAc	2
Q8VDD5	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	Myh9	5.21	MEF	5S-GlcNAc	2
P05213	Tubulin alpha-1B chain (Alpha-tubulin 2) (Alpha-tubulin isotype M-alpha-2) (Tubulin alpha-2 chain)	Tuba1b Tuba2	4.05	MEF	5S-GlcNAc	2
P09602	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)	Hmgn2 Hmg-17 Hmg17	2.62	MEF	5S-GlcNAc	2
Q60605	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	Myl6 Myln	2.17	MEF	5S-GlcNAc	2

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q61937	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	Npm1	2.06	MEF	5S-GlcNAc	6
P14069	Protein S100-A6 (5B10) (Calcyclin) (Prolactin receptor-associated protein) (S100 calcium-binding protein A6)	S100a6 Cacy	1.76	MEF	5S-GlcNAc	11
P20029	78 kDa glucose-regulated protein (GRP-78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	Hspa5 Grp78	1.55	MEF	5S-GlcNAc	11
P49312	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (HDP-1) (Helix-destabilizing protein) (Single-strand-binding protein) (Topoisomerase-inhibitor suppressed) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	Hnrnpa1 Fli-2 Hnrpa1 Tis	1.48	MEF	5S-GlcNAc	6

Appendix B: Table of volcano plot derived proteins with increased synthesis in MEF cells due to OGT knockout:

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P45591	Cofilin-2 (Cofilin, muscle isoform)	Cfl2	4.822	MEF	OGTKO	6
Q3THE2	Myosin regulatory light chain 12B (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2)	Myl12b Mrlc2 Mylc2b	3.683	MEF	OGTKO	2
P29595	NEDD8 (Neddylin) (Neural precursor cell expressed developmentally down-regulated protein 8) (NEDD-8) (Ubiquitin-like protein Nedd8)	Nedd8 Nedd-8	3.255	MEF	OGTKO	2
P25206	DNA replication licensing factor MCM3 (EC 3.6.4.12) (DNA polymerase alpha holoenzyme-associated protein P1) (P1-MCM3)	Mcm3 Mcmd Mcmd3	3.008	MEF	OGTKO	2
P84228	Histone H3.2	Hist1h3b H3-53 H3.2 H3b; Hist1h3c H3-143; Hist1h3d H3-B; Hist1h3e H3-F; Hist1h3f H3.2-221 H3f; Hist2h3b H3.2-616; Hist2h3c1 H3.2-615 Hist2h3ca1; Hist2h3c2 H3.2-614 Hist2h3ca2	2.899	MEF	OGTKO	11
P62806	Histone H4	Hist1h4a; Hist1h4b H4-53; Hist1h4c H4-12; Hist1h4d; Hist1h4f; Hist1h4h; Hist1h4i; Hist1h4j; Hist1h4k; Hist1h4m; Hist2h4a Hist2h4; Hist4h4	2.896	MEF	OGTKO	11
Q61937	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	Npm1	2.844	MEF	OGTKO	2

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P09602	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)	Hmgn2 Hmg-17 Hmg17	2.818	MEF	OGTKO	2
Q60605	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	Myl6 Myln	2.719	MEF	OGTKO	2
P84099	60S ribosomal protein L19	Rpl19	2.686	MEF	OGTKO	11
P70349	Histidine triad nucleotide-binding protein 1 (EC 3.-.-.-) (Adenosine 5'-monophosphoramidase) (Protein kinase C inhibitor 1) (Protein kinase C-interacting protein 1) (PKCI-1)	Hint1 Hint Pkci Pkci1 Prkcnh1	2.614	MEF	OGTKO	2
Q60605	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	Myl6 Myln	2.538	MEF	OGTKO	6
Q9D2U9	Histone H2B type 3-A	Hist3h2ba	2.491	MEF	OGTKO	11
Q3THE2	Myosin regulatory light chain 12B (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2)	Myl12b Mrlc2 Mylc2b	2.366	MEF	OGTKO	6
P09602	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)	Hmgn2 Hmg-17 Hmg17	2.307	MEF	OGTKO	6

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q61937	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	Npm1	2.212	MEF	OGTKO	6
O08784	Treacle protein (Treacher Collins syndrome protein homolog)	Tcof1	2.206	MEF	OGTKO	6
P47915	60S ribosomal protein L29	Rpl29 Rpl43	2.195	MEF	OGTKO	11
P35980	60S ribosomal protein L18	Rpl18	2.136	MEF	OGTKO	11
P62267	40S ribosomal protein S23	Rps23	2.115	MEF	OGTKO	11
O09167	60S ribosomal protein L21	Rpl21	2.06	MEF	OGTKO	11
P47963	60S ribosomal protein L13 (A52)	Rpl13	2.056	MEF	OGTKO	11
P62900	60S ribosomal protein L31	Rpl31	2.029	MEF	OGTKO	11
P62843	40S ribosomal protein S15 (RIG protein)	Rps15 Rig	1.954	MEF	OGTKO	11
P62702	40S ribosomal protein S4, X isoform	Rps4x Rps4	1.942	MEF	OGTKO	11
P62960	Nuclease-sensitive element-binding protein 1 (CCAAT-binding transcription factor I subunit A) (CBF-A) (DNA-binding protein B) (DBPB) (Enhancer factor I subunit A) (EFI-A) (Y-box transcription factor) (Y-box-binding protein 1) (YB-1)	Ybx1 Msy-1 Msy1 Nsep1 Yb1	1.916	MEF	OGTKO	11
P97351	40S ribosomal protein S3a (Protein TU-11)	Rps3a Rps3a1	1.898	MEF	OGTKO	11
P48678	Prelamin-A/C [Cleaved into: Lamin-A/C]	Lmna Lmn1	1.883	MEF	OGTKO	11
Q9CPR4	60S ribosomal protein L17	Rpl17	1.853	MEF	OGTKO	11
P25444	40S ribosomal protein S2 (40S ribosomal protein S4) (Protein LLRep3)	Rps2 Llrep3 Rps4	1.829	MEF	OGTKO	11
P35979	60S ribosomal protein L12	Rpl12	1.782	MEF	OGTKO	11

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P49312	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (HDP-1) (Helix-destabilizing protein) (Single-strand-binding protein) (Topoisomerase-inhibitor suppressed) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	Hnrnpa1 Fli-2 Hnrpa1 Tis	1.78	MEF	OGTKO	6
P62889	60S ribosomal protein L30	Rpl30	1.771	MEF	OGTKO	11
Q3THW5	Histone H2A.V (H2A.F/Z)	H2afv H2av	1.752	MEF	OGTKO	11
P14206	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37 kDa oncofetal antigen) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (OFA/iLRP)	Rpsa Lamr1 P40-8	1.738	MEF	OGTKO	6
P61255	60S ribosomal protein L26 (Silica-induced gene 20 protein) (SIG-20)	Rpl26	1.704	MEF	OGTKO	11
P62918	60S ribosomal protein L8	Rpl8	1.66	MEF	OGTKO	11
P14069	Protein S100-A6 (5B10) (Calcyclin) (Prolactin receptor-associated protein) (S100 calcium-binding protein A6)	S100a6 Cacy	1.608	MEF	OGTKO	11
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	Hnrnpa2b1 Hnrpa2b1	1.551	MEF	OGTKO	6
P29341	Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding protein 1)	Pabpc1 Pabp1	1.499	MEF	OGTKO	6
P60843	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	Eif4a1 Ddx2a Eif4a	1.46	MEF	OGTKO	6

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q99020	Heterogeneous nuclear ribonucleoprotein A/B (hnRNP A/B) (CArG-binding factor-A) (CBF-A)	Hnrnpab Cbf-a Cgbfa Hnrpab	1.452	MEF	OGTKO	6
P09405	Nucleolin (Protein C23)	Ncl Nuc	1.367	MEF	OGTKO	11
O89086	Putative RNA-binding protein 3 (RNA-binding motif protein 3)	Rbm3	1.347	MEF	OGTKO	11
Q60817	Nascent polypeptide-associated complex subunit alpha (Alpha-NAC) (Alpha-NAC/1.9.2)	Naca	1.333	MEF	OGTKO	11
P62984	Ubiquitin-60S ribosomal protein L40 (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (CEP52)]	Uba52 Ubcep2	1.207	MEF	OGTKO	11
P16110	Galectin-3 (Gal-3) (35 kDa lectin) (Carbohydrate-binding protein 35) (CBP 35) (Galactose-specific lectin 3) (IgE-binding protein) (L-34 galactoside-binding lectin) (Laminin-binding protein) (Lectin L-29) (Mac-2 antigen)	Lgals3	1.2	MEF	OGTKO	6

Appendix C: Table of volcano plot derived proteins with increased synthesis in HEK293 cells due to treatment with 5Thio-GlcNAc:

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P28838	Cytosol aminopeptidase (EC 3.4.11.1) (Leucine aminopeptidase 3) (LAP-3) (Leucyl aminopeptidase) (Peptidase S) (Proline aminopeptidase) (EC 3.4.11.5) (Prolyl aminopeptidase)	LAP3 LAPEP PEPS	42.32	HEK293	5S-GlcNAc	2
Q8N9T8	Protein KRI1 homolog	KRI1	23.82	HEK293	5S-GlcNAc	2
P07305	Histone H1.0 (Histone H1') (Histone H1(0)) [Cleaved into: Histone H1.0, N-terminally processed]	H1F0 H1FV	6.23	HEK293	5S-GlcNAc	2
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 (PPIase) (EC 5.2.1.8) (Rotamase PPIL1)	PPIL1 CYPL1 CGI-124 UNQ2425/PRO4984	5.78	HEK293	5S-GlcNAc	2
Q9H307	Pinin (140 kDa nuclear and cell adhesion-related phosphoprotein) (Desmosome-associated protein) (Domain-rich serine protein) (DRS protein) (DRSP) (Melanoma metastasis clone A protein) (Nuclear protein SDK3) (SR-like protein)	PNN DRS MEMA	4.49	HEK293	5S-GlcNAc	2
P26639	Threonine--tRNA ligase, cytoplasmic (EC 6.1.1.3) (Threonyl-tRNA synthetase) (ThrRS)	TARS	4.45	HEK293	5S-GlcNAc	2

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P49327	Fatty acid synthase (EC 2.3.1.85) [Includes: [Acyl-carrier-protein] S-acetyltransferase (EC 2.3.1.38); [Acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39); 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41); 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100); 3-hydroxyacyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.59); Enoyl-[acyl-carrier-protein] reductase (EC 1.3.1.39); Oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14)]	FASN FAS	4.10	HEK293	5S-GlcNAc	2
P35613	Basigin (5F7) (Collagenase stimulatory factor) (Extracellular matrix metalloproteinase inducer) (EMMPRIN) (Leukocyte activation antigen M6) (OK blood group antigen) (Tumor cell-derived collagenase stimulatory factor) (TCSF) (CD antigen CD147)	BSG UNQ6505/PRO21383	2.94	HEK293	5S-GlcNAc	8
Q9UK76	Hematological and neurological expressed 1 protein (Androgen-regulated protein 2) [Cleaved into: Hematological and neurological expressed 1 protein, N-terminally processed]	HN1 ARM2	2.54	HEK293	5S-GlcNAc	5
O60664	Perilipin-3 (47 kDa mannose 6-phosphate receptor-binding protein) (47 kDa MPR-binding protein) (Cargo selection protein TIP47) (Mannose-6-phosphate receptor-binding protein 1) (Placental protein 17) (PP17)	PLIN3 M6PRBP1 TIP47	2.34	HEK293	5S-GlcNAc	5
Q9H6Z4	Ran-binding protein 3 (RanBP3)	RANBP3	2.25	HEK293	5S-GlcNAc	12
Q8N1F7	Nuclear pore complex protein Nup93 (93 kDa nucleoporin) (Nucleoporin Nup93)	NUP93 KIAA0095	2.24	HEK293	5S-GlcNAc	8

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P11021	78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	HSPA5 GRP78	2.15	HEK293	5S-GlcNAc	8
P11021	78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	HSPA5 GRP78	1.98	HEK293	5S-GlcNAc	24
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 (PPIase FKBP4) (EC 5.2.1.8) (51 kDa FK506-binding protein) (FKBP51) (52 kDa FK506-binding protein) (52 kDa FKBP) (FKBP-52) (59 kDa immunophilin) (p59) (FK506-binding protein 4) (FKBP-4) (FKBP59) (HSP-binding immunophilin) (HBI) (Immunophilin FKBP52) (Rotamase) [Cleaved into: Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed]	FKBP4 FKBP52	1.90	HEK293	5S-GlcNAc	5
Q9UHV9	Prefoldin subunit 2	PFDN2 PFD2 HSPC231	1.88	HEK293	5S-GlcNAc	5
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1 (UCH-L1) (EC 3.4.19.12) (EC 6.-.-.-) (Neuron cytoplasmic protein 9.5) (PGP 9.5) (PGP9.5) (Ubiquitin thioesterase L1)	UCHL1	1.87	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P07900	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1 HSP90A HSPC1 HSPCA	1.84	HEK293	5S-GlcNAc	5
P30086	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPpp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1 PBP PEBP	1.82	HEK293	5S-GlcNAc	12
P55145	Mesencephalic astrocyte-derived neurotrophic factor (Arginine-rich protein) (Protein ARMET)	MANF ARMET ARP	1.82	HEK293	5S-GlcNAc	24
P13667	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4 ERP70 ERP72	1.82	HEK293	5S-GlcNAc	24
O75347	Tubulin-specific chaperone A (TCP1-chaperonin cofactor A) (Tubulin-folding cofactor A) (CFA)	TBCA	1.81	HEK293	5S-GlcNAc	5
P49321	Nuclear autoantigenic sperm protein (NASP)	NASP	1.79	HEK293	5S-GlcNAc	5
P60174	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	TPI1 TPI	1.71	HEK293	5S-GlcNAc	12
P22392	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2 NM23B	1.71	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q14247	Src substrate cortactin (Amplaxin) (Oncogene EMS1)	CTTN EMS1	1.69	HEK293	5S-GlcNAc	5
P00558	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1 PGKA MIG10 OK/SW-cl.110	1.68	HEK293	5S-GlcNAc	12
O60925	Prefoldin subunit 1	PFDN1 PFD1	1.65	HEK293	5S-GlcNAc	12
Q13765	Nascent polypeptide-associated complex subunit alpha (NAC-alpha) (Alpha-NAC) (allergen Hom s 2)	NACA HSD48	1.65	HEK293	5S-GlcNAc	5
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2 (GABA(A) receptor-associated protein-like 2) (Ganglioside expression factor 2) (GEF-2) (General protein transport factor p16) (Golgi-associated ATPase enhancer of 16 kDa) (GATE-16) (MAP1 light chain 3-related protein)	GABARAPL2 FLC3A GEF2	1.64	HEK293	5S-GlcNAc	12
P14625	Endoplasmin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1 GRP94 TRA1	1.62	HEK293	5S-GlcNAc	24
P37837	Transaldolase (EC 2.2.1.2)	TALDO1 TAL TALDO TALDOR	1.61	HEK293	5S-GlcNAc	12
Q8WW12	PEST proteolytic signal-containing nuclear protein (PCNP) (PEST-containing nuclear protein)	PCNP	1.60	HEK293	5S-GlcNAc	12
P61758	Prefoldin subunit 3 (HIBBJ46) (Von Hippel-Lindau-binding protein 1) (VBP-1) (VHL-binding protein 1)	VBP1 PFDN3	1.58	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
O75347	Tubulin-specific chaperone A (TCP1-chaperonin cofactor A) (Tubulin-folding cofactor A) (CFA)	TBCA	1.57	HEK293	5S-GlcNAc	12
Q04760	Lactoylglutathione lyase (EC 4.4.1.5) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (Methylglyoxalase) (S-D-lactoylglutathione methylglyoxal lyase)	GLO1	1.55	HEK293	5S-GlcNAc	12
P08238	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1 HSP90B HSPC2 HSPCB	1.54	HEK293	5S-GlcNAc	5
P06733	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1 ENO1L1 MBPB1 MPB1	1.51	HEK293	5S-GlcNAc	12
Q15084	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6 ERP5 P5 TXNDC7	1.48	HEK293	5S-GlcNAc	24
P63241	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A	1.47	HEK293	5S-GlcNAc	12
P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1 (UCH-L1) (EC 3.4.19.12) (EC 6.-.-.-) (Neuron cytoplasmic protein 9.5) (PGP 9.5) (PGP9.5) (Ubiquitin thioesterase L1)	UCHL1	1.40	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P30101	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3 ERP57 ERP60 GRP58	1.30	HEK293	5S-GlcNAc	24
P23284	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB CYPB	1.29	HEK293	5S-GlcNAc	24

Appendix D: Table of volcano plot derived proteins with decreased synthesis in MEF cells due to 5Thio-GlcNAc inhibition

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62806	Histone H4	Hist1h4a; Hist1h4b H4-53; Hist1h4c H4-12; Hist1h4d; Hist1h4f; Hist1h4h; Hist1h4i; Hist1h4j; Hist1h4k; Hist1h4m; Hist2h4a Hist2h4; Hist4h4	0.18	MEF	5S-GlcNAc	6
P84228	Histone H3.2	Hist1h3b H3-53 H3.2 H3b; Hist1h3c H3-143; Hist1h3d H3-B; Hist1h3e H3-F; Hist1h3f H3.2-221 H3f; Hist2h3b H3.2-616; Hist2h3c1 H3.2-615 Hist2h3ca1; Hist2h3c2 H3.2-614 Hist2h3ca2	0.19	MEF	5S-GlcNAc	6
Q9D2U9	Histone H2B type 3-A	Hist3h2ba	0.28	MEF	5S-GlcNAc	6
P42932	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta)	Cct8 Cctq	0.38	MEF	5S-GlcNAc	6
Q3THW5	Histone H2A.V (H2A.F/Z)	H2afv H2av	0.43	MEF	5S-GlcNAc	6
Q9Z204	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	Hnrnpc Hnrpc	0.48	MEF	5S-GlcNAc	11
P35979	60S ribosomal protein L12	Rpl12	0.49	MEF	5S-GlcNAc	6
P48678	Prelamin-A/C [Cleaved into: Lamin-A/C]	Lmna Lmn1	0.55	MEF	5S-GlcNAc	6
P62918	60S ribosomal protein L8	Rpl8	0.62	MEF	5S-GlcNAc	11
O88569	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	Hnrnpa2b1 Hnrpa2b1	0.68	MEF	5S-GlcNAc	11
Q9D2U9	Histone H2B type 3-A	Hist3h2ba	0.69	MEF	5S-GlcNAc	11
Q61937	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	Npm1	0.70	MEF	5S-GlcNAc	11

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P49312	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (HDP-1) (Helix-destabilizing protein) (Single-strand-binding protein) (Topoisomerase-inhibitor suppressed) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	Hnrnpa1 Fli-2 Hnrpa1 Tis	0.72	MEF	5S-GlcNAc	11
P09405	Nucleolin (Protein C23)	Ncl Nuc	0.72	MEF	5S-GlcNAc	11
Q9CPR4	60S ribosomal protein L17	Rpl17	0.73	MEF	5S-GlcNAc	11
P62984	Ubiquitin-60S ribosomal protein L40 (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into: Ubiquitin; 60S ribosomal protein L40 (CEP52)]	Uba52 Ubcep2	0.76	MEF	5S-GlcNAc	6

Appendix E: Table of volcano plot derived proteins with decreased synthesis in MEF cells due to OGT knockout:

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P84228	Histone H3.2	Hist1h3b H3-53 H3.2 H3b; Hist1h3c H3-143; Hist1h3d H3-B; Hist1h3e H3-F; Hist1h3f H3.2-221 H3f; Hist2h3b H3.2-616; Hist2h3c1 H3.2-615 Hist2h3ca1; Hist2h3c2 H3.2-614 Hist2h3ca2	0.234	MEF	OGTKO	2
P84228	Histone H3.2	Hist1h3b H3-53 H3.2 H3b; Hist1h3c H3-143; Hist1h3d H3-B; Hist1h3e H3-F; Hist1h3f H3.2-221 H3f; Hist2h3b H3.2-616; Hist2h3c1 H3.2-615 Hist2h3ca1; Hist2h3c2 H3.2-614 Hist2h3ca2	0.281	MEF	OGTKO	6
P62806	Histone H4	Hist1h4a; Hist1h4b H4-53; Hist1h4c H4-12; Hist1h4d; Hist1h4f; Hist1h4h; Hist1h4i; Hist1h4j; Hist1h4k; Hist1h4m; Hist2h4a Hist2h4; Hist4h4	0.315	MEF	OGTKO	6
Q8VDD5	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	Myh9	0.364	MEF	OGTKO	11
P42932	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta)	Cct8 Cctq	0.376	MEF	OGTKO	6
P15532	Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (EC 2.7.4.6) (Metastasis inhibition factor NM23) (NDPK-A) (Tumor metastatic process-associated protein) (nm23-M1)	Nme1 Nm23	0.389	MEF	OGTKO	2
Q9D2U9	Histone H2B type 3-A	Hist3h2ba	0.396	MEF	OGTKO	2
Q9D2U9	Histone H2B type 3-A	Hist3h2ba	0.412	MEF	OGTKO	6

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q9CYR0	Single-stranded DNA-binding protein, mitochondrial (Mt-SSB) (MtSSB)	Ssbp1	0.438	MEF	OGTKO	11
P09602	Non-histone chromosomal protein HMG-17 (High mobility group nucleosome-binding domain-containing protein 2)	Hmgn2 Hmg-17 Hmg17	0.451	MEF	OGTKO	11
Q61553	Fascin (Singed-like protein)	Fscn1 Fan1 Snl	0.494	MEF	OGTKO	6
Q61937	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	Npm1	0.495	MEF	OGTKO	11
Q3THW5	Histone H2A.V (H2A.F/Z)	H2afv H2av	0.536	MEF	OGTKO	6
Q60605	Myosin light polypeptide 6 (17 kDa myosin light chain) (LC17) (Myosin light chain 3) (MLC-3) (Myosin light chain alkali 3) (Myosin light chain A3) (Smooth muscle and nonmuscle myosin light chain alkali 6)	Myl6 Myln	0.537	MEF	OGTKO	11
P02340	Cellular tumor antigen p53 (Tumor suppressor p53)	Tp53 P53 Trp53	0.591	MEF	OGTKO	6
Q3THE2	Myosin regulatory light chain 12B (Myosin regulatory light chain 2-B, smooth muscle isoform) (Myosin regulatory light chain 20 kDa) (MLC20) (Myosin regulatory light chain MRLC2)	Myl12b Mrlc2 Mylc2b	0.615	MEF	OGTKO	11
P48678	Prelamin-A/C [Cleaved into: Lamin-A/C]	Lmna Lmn1	0.73	MEF	OGTKO	6
Q64339	Ubiquitin-like protein ISG15 (Interferon-induced 15 kDa protein) (Interferon-induced 17 kDa protein) (IP17) (Ubiquitin cross-reactive protein)	Isg15 G1p2 Ucrp	0.757	MEF	OGTKO	6

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P63260	Actin, cytoplasmic 2 (Gamma-actin) [Cleaved into: Actin, cytoplasmic 2, N-terminally processed]	Actg1 Actg	0.824	MEF	OGTKO	11

Appendix F: Table of volcano plot derived proteins with decreased synthesis in HEK293 cells due to treatment with 5Thio-GlcNAc

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
O75947	ATP synthase subunit d, mitochondrial (ATPase subunit d)	ATP5H My032	0.109	HEK293	5S-GlcNAc	2
O00115	Deoxyribonuclease-2-alpha (EC 3.1.22.1) (Acid DNase) (Deoxyribonuclease II alpha) (DNase II alpha) (Lysosomal DNase II) (R31240_2)	DNASE2 DNASE2A DNL2	0.152	HEK293	5S-GlcNAc	24
P11279	Lysosome-associated membrane glycoprotein 1 (LAMP-1) (Lysosome-associated membrane protein 1) (CD107 antigen-like family member A) (CD antigen CD107a)	LAMP1	0.172	HEK293	5S-GlcNAc	12
Q92542	Nicastrin	NCSTN KIAA0253 UNQ1874/PRO4317	0.174	HEK293	5S-GlcNAc	12
Q5JRX3	Presequence protease, mitochondrial (hPreP) (EC 3.4.24.-) (Pitrilysin metalloproteinase 1) (Metalloprotease 1) (hMP1)	PITRM1 KIAA1104 MP1	0.185	HEK293	5S-GlcNAc	12
Q92542	Nicastrin	NCSTN KIAA0253 UNQ1874/PRO4317	0.253	HEK293	5S-GlcNAc	24
P15586	N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) (Glucosamine-6-sulfatase) (G6S)	GNS	0.281	HEK293	5S-GlcNAc	24
Q92820	Gamma-glutamyl hydrolase (EC 3.4.19.9) (Conjugase) (GH) (Gamma-Glu-X carboxypeptidase)	GGH	0.312	HEK293	5S-GlcNAc	24
Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10 (PPIase FKBP10) (EC 5.2.1.8) (65 kDa FK506-binding protein) (65 kDa FKBP) (FKBP-65) (FK506-binding protein 10) (FKBP-10) (Immunophilin FKBP65) (Rotamase)	FKBP10 FKBP65 PSEC0056	0.319	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial (P5C reductase 1) (P5CR 1) (EC 1.5.1.2)	PYCR1	0.324	HEK293	5S-GlcNAc	24
P13473	Lysosome-associated membrane glycoprotein 2 (LAMP-2) (Lysosome-associated membrane protein 2) (CD107 antigen-like family member B) (CD antigen CD107b)	LAMP2	0.345	HEK293	5S-GlcNAc	24
Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10 (PPIase FKBP10) (EC 5.2.1.8) (65 kDa FK506-binding protein) (65 kDa FKBP) (FKBP-65) (FK506-binding protein 10) (FKBP-10) (Immunophilin FKBP65) (Rotamase)	FKBP10 FKBP65 PSEC0056	0.395	HEK293	5S-GlcNAc	24
Q86U42	Polyadenylate-binding protein 2 (PABP-2) (Poly(A)-binding protein 2) (Nuclear poly(A)-binding protein 1) (Poly(A)-binding protein II) (PABII) (Polyadenylate-binding nuclear protein 1)	PABPN1 PAB2 PABP2	0.396	HEK293	5S-GlcNAc	12
P05141	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5 ANT2	0.404	HEK293	5S-GlcNAc	12
P42704	Leucine-rich PPR motif-containing protein, mitochondrial (130 kDa leucine-rich protein) (LRP 130) (GP130)	LRPPRC LRP130	0.425	HEK293	5S-GlcNAc	12
Q9NZM5	Glioma tumor suppressor candidate region gene 2 protein (p60)	GLTSCR2	0.428	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q13151	Heterogeneous nuclear ribonucleoprotein A0 (hnRNP A0)	HNRNPA0 HNRPA0	0.439	HEK293	5S-GlcNAc	12
Q6UB35	Monofunctional C1-tetrahydrofolate synthase, mitochondrial (EC 6.3.4.3) (Formyltetrahydrofolate synthetase)	MTHFD1L FTHFSDC1	0.443	HEK293	5S-GlcNAc	12
P20700	Lamin-B1	LMNB1 LMN2 LMNB	0.448	HEK293	5S-GlcNAc	12
P61916	Epididymal secretory protein E1 (Human epididymis-specific protein 1) (He1) (Niemann-Pick disease type C2 protein)	NPC2 HE1	0.454	HEK293	5S-GlcNAc	24
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	0.455	HEK293	5S-GlcNAc	12
Q8IV08	Phospholipase D3 (PLD 3) (EC 3.1.4.4) (Choline phosphatase 3) (HindIII K4L homolog) (Hu-K4) (Phosphatidylcholine-hydrolyzing phospholipase D3)	PLD3	0.469	HEK293	5S-GlcNAc	5
Q99879	Histone H2B type 1-M (Histone H2B.e) (H2B/e)	HIST1H2BM H2BFE	0.473	HEK293	5S-GlcNAc	12
P11388	DNA topoisomerase 2-alpha (EC 5.99.1.3) (DNA topoisomerase II, alpha isozyme)	TOP2A TOP2	0.486	HEK293	5S-GlcNAc	5
P84103	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3 SFRS3 SRP20	0.488	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q71DI3	Histone H3.2 (Histone H3/m) (Histone H3/o)	HIST2H3A; HIST2H3C H3F2 H3FM; HIST2H3D	0.494	HEK293	5S-GlcNAc	12
Q99878	Histone H2A type 1-J (Histone H2A/e)	HIST1H2AJ H2AFE	0.495	HEK293	5S-GlcNAc	12
P34897	Serine hydroxymethyltransferase, mitochondrial (SHMT) (EC 2.1.2.1) (Glycine hydroxymethyltransferase) (Serine methylase)	SHMT2	0.496	HEK293	5S-GlcNAc	12
Q9Y277	Voltage-dependent anion-selective channel protein 3 (VDAC-3) (hVDAC3) (Outer mitochondrial membrane protein porin 3)	VDAC3	0.498	HEK293	5S-GlcNAc	12
P46013	Antigen KI-67	MKI67	0.503	HEK293	5S-GlcNAc	12
O76021	Ribosomal L1 domain-containing protein 1 (CATX-11) (Cellular senescence-inhibited gene protein) (Protein PBK1)	RSL1D1 CATX11 CSIG PBK1 L12	0.504	HEK293	5S-GlcNAc	12
P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9 GRP75 HSPA9B mt-HSP70	0.507	HEK293	5S-GlcNAc	12
Q96PK6	RNA-binding protein 14 (Paraspeckle protein 2) (PSP2) (RNA-binding motif protein 14) (RRM-containing coactivator activator/modulator) (Synaptotagmin-interacting protein) (SYT-interacting protein)	RBM14 SIP	0.508	HEK293	5S-GlcNAc	12
Q13247	Serine/arginine-rich splicing factor 6 (Pre-mRNA-splicing factor SRP55) (Splicing factor, arginine/serine-rich 6)	SRSF6 SFRS6 SRP55	0.515	HEK293	5S-GlcNAc	5
P07339	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	CTSD CPSD	0.517	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q13838	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B BAT1 UAP56	0.52	HEK293	5S-GlcNAc	12
P23246	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ PSF	0.524	HEK293	5S-GlcNAc	12
Q8N5N7	39S ribosomal protein L50, mitochondrial (L50mt) (MRP-L50)	MRPL50	0.53	HEK293	5S-GlcNAc	5
P22695	Cytochrome b-c1 complex subunit 2, mitochondrial (Complex III subunit 2) (Core protein II) (Ubiquinol-cytochrome-c reductase complex core protein 2)	UQCRC2	0.531	HEK293	5S-GlcNAc	12
O60814	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK H2BFT HIRIP1	0.536	HEK293	5S-GlcNAc	12
Q07065	Cytoskeleton-associated protein 4 (63-kDa cytoskeleton-linking membrane protein) (Climp-63) (p63)	CKAP4	0.539	HEK293	5S-GlcNAc	12
P49792	E3 SUMO-protein ligase RanBP2 (EC 6.3.2.-) (358 kDa nucleoporin) (Nuclear pore complex protein Nup358) (Nucleoporin Nup358) (Ran-binding protein 2) (RanBP2) (p270)	RANBP2 NUP358	0.541	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q00839	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU HNRPU SAFA U21.1	0.545	HEK293	5S-GlcNAc	12
P24752	Acetyl-CoA acetyltransferase, mitochondrial (EC 2.3.1.9) (Acetoacetyl-CoA thiolase) (T2)	ACAT1 ACAT MAT	0.546	HEK293	5S-GlcNAc	12
O75367	Core histone macro-H2A.1 (Histone macroH2A1) (mH2A1) (Histone H2A.y) (H2A/y) (Medulloblastoma antigen MU-MB-50.205)	H2AFY MACROH2A1	0.546	HEK293	5S-GlcNAc	12
P54886	Delta-1-pyrroline-5-carboxylate synthase (P5CS) (Aldehyde dehydrogenase family 18 member A1) [Includes: Glutamate 5-kinase (GK) (EC 2.7.2.11) (Gamma-glutamyl kinase); Gamma-glutamyl phosphate reductase (GPR) (EC 1.2.1.41) (Glutamate-5-semialdehyde dehydrogenase) (Glutamyl-gamma-semialdehyde dehydrogenase)]	ALDH18A1 GSAS P5CS PYCS	0.548	HEK293	5S-GlcNAc	12
P45880	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	VDAC2	0.55	HEK293	5S-GlcNAc	12
Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13	TIMM13 TIM13B TIMM13A TIMM13B	0.55	HEK293	5S-GlcNAc	12
P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9 GRP75 HSPA9B mt-HSP70	0.551	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P05141	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5 ANT2	0.553	HEK293	5S-GlcNAc	5
Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13	TIMM13 TIM13B TIMM13A TIMM13B	0.555	HEK293	5S-GlcNAc	5
P35232	Prohibitin	PHB	0.556	HEK293	5S-GlcNAc	12
P14866	Heterogeneous nuclear ribonucleoprotein L (hnRNP L)	HNRNPL HNRPL P/OKcl.14	0.557	HEK293	5S-GlcNAc	12
P25705	ATP synthase subunit alpha, mitochondrial	ATP5A1 ATP5A ATP5AL2 ATPM	0.557	HEK293	5S-GlcNAc	12
P10412	Histone H1.4 (Histone H1b) (Histone H1s-4)	HIST1H1E H1F4	0.558	HEK293	5S-GlcNAc	12
P30042	ES1 protein homolog, mitochondrial (Protein GT335) (Protein KNP-I)	C21orf33 HES1 KNPI	0.558	HEK293	5S-GlcNAc	12
P05114	Non-histone chromosomal protein HMG-14 (High mobility group nucleosome-binding domain-containing protein 1)	HMGN1 HMG14	0.559	HEK293	5S-GlcNAc	12
P09651	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1 HNRPA1	0.56	HEK293	5S-GlcNAc	12
Q9NVI7	ATPase family AAA domain-containing protein 3A	ATAD3A	0.56	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P54819	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleaved into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2 ADK2	0.561	HEK293	5S-GlcNAc	12
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2	0.563	HEK293	5S-GlcNAc	12
P46013	Antigen KI-67	MKI67	0.563	HEK293	5S-GlcNAc	5
P38159	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX HNRPG RBMXP1	0.568	HEK293	5S-GlcNAc	12
Q9BVP2	Guanine nucleotide-binding protein-like 3 (E2-induced gene 3 protein) (Novel nucleolar protein 47) (NNP47) (Nucleolar GTP-binding protein 3) (Nucleostemin)	GNL3 E2IG3 NS	0.576	HEK293	5S-GlcNAc	5
Q9HAV7	GrpE protein homolog 1, mitochondrial (HMGE) (Mt-GrpE#1)	GRPEL1 GREPEL1	0.579	HEK293	5S-GlcNAc	12
P35579	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9	0.581	HEK293	5S-GlcNAc	8

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	0.585	HEK293	5S-GlcNAc	5
P43243	Matrin-3	MATR3 KIAA0723	0.587	HEK293	5S-GlcNAc	12
O60814	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK H2BFT HIRIP1	0.591	HEK293	5S-GlcNAc	5
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC HNRPC	0.594	HEK293	5S-GlcNAc	12
P06576	ATP synthase subunit beta, mitochondrial (EC 3.6.3.14)	ATP5B ATPMB ATPSB	0.595	HEK293	5S-GlcNAc	12
Q14684	Ribosomal RNA processing protein 1 homolog B (RRP1-like protein B)	RRP1B KIAA0179	0.6	HEK293	5S-GlcNAc	12
Q12931	Heat shock protein 75 kDa, mitochondrial (HSP 75) (TNFR-associated protein 1) (Tumor necrosis factor type 1 receptor-associated protein) (TRAP-1)	TRAP1 HSP75	0.6	HEK293	5S-GlcNAc	12
Q15233	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO NRB54	0.605	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P21796	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1 VDAC	0.605	HEK293	5S-GlcNAc	12
Q99879	Histone H2B type 1-M (Histone H2B.e) (H2B/e)	HIST1H2BM H2BFE	0.607	HEK293	5S-GlcNAc	5
P07197	Neurofilament medium polypeptide (NF-M) (160 kDa neurofilament protein) (Neurofilament 3) (Neurofilament triplet M protein)	NEFM NEF3 NFM	0.611	HEK293	5S-GlcNAc	5
Q9UQ35	Serine/arginine repetitive matrix protein 2 (300 kDa nuclear matrix antigen) (Serine/arginine-rich splicing factor-related nuclear matrix protein of 300 kDa) (SR-related nuclear matrix protein of 300 kDa) (Ser/Arg-related nuclear matrix protein of 300 kDa) (Splicing coactivator subunit SRm300) (Tax-responsive enhancer element-binding protein 803) (TaxREB803)	SRRM2 KIAA0324 SRL300 SRM300 HSPC075	0.612	HEK293	5S-GlcNAc	12
P51991	Heterogeneous nuclear ribonucleoprotein A3 (hnRNP A3)	HNRNPA3 HNRPA3	0.612	HEK293	5S-GlcNAc	12
P20700	Lamin-B1	LMNB1 LMN2 LMNB	0.616	HEK293	5S-GlcNAc	24
P10809	60 kDa heat shock protein, mitochondrial (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1 HSP60	0.617	HEK293	5S-GlcNAc	12
O75947	ATP synthase subunit d, mitochondrial (ATPase subunit d)	ATP5H My032	0.619	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P19338	Nucleolin (Protein C23)	NCL	0.621	HEK293	5S-GlcNAc	12
P30084	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1	0.624	HEK293	5S-GlcNAc	12
Q9UKM9	RNA-binding protein Raly (Autoantigen p542) (Heterogeneous nuclear ribonucleoprotein C-like 2) (hnRNP core protein C-like 2) (hnRNP associated with lethal yellow protein homolog)	RALY HNRPCL2 P542	0.627	HEK293	5S-GlcNAc	12
P48047	ATP synthase subunit O, mitochondrial (Oligomycin sensitivity conferral protein) (OSCP)	ATP5O ATPO	0.63	HEK293	5S-GlcNAc	12
Q71UI9	Histone H2A.V (H2A.F/Z)	H2AFV H2AV	0.63	HEK293	5S-GlcNAc	12
Q08211	ATP-dependent RNA helicase A (RHA) (EC 3.6.4.13) (DEAH box protein 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II)	DHX9 DDX9 LKP NDH2	0.632	HEK293	5S-GlcNAc	24
P61604	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPE1	0.635	HEK293	5S-GlcNAc	12
P10412	Histone H1.4 (Histone H1b) (Histone H1s-4)	HIST1H1E H1F4	0.637	HEK293	5S-GlcNAc	5
P50454	Serpin H1 (47 kDa heat shock protein) (Arsenic-transactivated protein 3) (AsTP3) (Cell proliferation-inducing gene 14 protein) (Collagen-binding protein) (Colligin) (Rheumatoid arthritis-related antigen RA-A47)	SERPINH1 CBP1 CBP2 HSP47 SERPINH2 PIG14	0.642	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q07021	Complement component 1 Q subcomponent-binding protein, mitochondrial (ASF/SF2-associated protein p32) (Glycoprotein gC1qBP) (C1qBP) (Hyaluronan-binding protein 1) (Mitochondrial matrix protein p32) (gC1q-R protein) (p33)	C1QBP GC1QBP HABP1 SF2P32	0.646	HEK293	5S-GlcNAc	24
P35637	RNA-binding protein FUS (75 kDa DNA-pairing protein) (Oncogene FUS) (Oncogene TLS) (POMp75) (Translocated in liposarcoma protein)	FUS TLS	0.651	HEK293	5S-GlcNAc	12
Q00059	Transcription factor A, mitochondrial (mtTFA) (Mitochondrial transcription factor 1) (MtTF1) (Transcription factor 6) (TCF-6) (Transcription factor 6-like 2)	TFAM TCF6 TCF6L2	0.652	HEK293	5S-GlcNAc	12
P06748	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1 NPM	0.652	HEK293	5S-GlcNAc	24
P02545	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA LMN1	0.653	HEK293	5S-GlcNAc	12
P38159	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX HNRPG RBMXP1	0.655	HEK293	5S-GlcNAc	24
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1 HNRPA2B1	0.656	HEK293	5S-GlcNAc	12
Q13813	Spectrin alpha chain, non-erythrocytic 1 (Alpha-II spectrin) (Fodrin alpha chain) (Spectrin, non-erythroid alpha subunit)	SPTAN1 NEAS SPTA2	0.662	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P05387	60S acidic ribosomal protein P2 (Renal carcinoma antigen NY-REN-44)	RPLP2 D11S2243E RPP2	0.669	HEK293	5S-GlcNAc	8
Q86V81	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF ALY BEF THOC4	0.673	HEK293	5S-GlcNAc	24
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2	0.673	HEK293	5S-GlcNAc	24
P35232	Prohibitin	PHB	0.676	HEK293	5S-GlcNAc	24
Q00839	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU HNRPU SAFA U21.1	0.677	HEK293	5S-GlcNAc	5
P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9 GRP75 HSPA9B mt-HSP70	0.68	HEK293	5S-GlcNAc	24
Q9NR30	Nucleolar RNA helicase 2 (EC 3.6.4.13) (DEAD box protein 21) (Gu-alpha) (Nucleolar RNA helicase Gu) (Nucleolar RNA helicase II) (RH II/Gu)	DDX21	0.681	HEK293	5S-GlcNAc	5
O14979	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D-like) (hnRNP DL) (AU-rich element RNA-binding factor) (JKT41-binding protein) (Protein laAUF1)	HNRNPDL HNRPDL JKTBP	0.689	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	0.692	HEK293	5S-GlcNAc	24
P40926	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	MDH2	0.695	HEK293	5S-GlcNAc	12
Q99879	Histone H2B type 1-M (Histone H2B.e) (H2B/e)	HIST1H2BM H2BFE	0.696	HEK293	5S-GlcNAc	24
P21796	Voltage-dependent anion-selective channel protein 1 (VDAC-1) (hVDAC1) (Outer mitochondrial membrane protein porin 1) (Plasmalemmal porin) (Porin 31HL) (Porin 31HM)	VDAC1 VDAC	0.699	HEK293	5S-GlcNAc	24
P13639	Elongation factor 2 (EF-2)	EEF2 EF2	0.699	HEK293	5S-GlcNAc	8
P07237	Protein disulfide-isomerase (PDI) (EC 5.3.4.1) (Cellular thyroid hormone-binding protein) (Prolyl 4-hydroxylase subunit beta) (p55)	P4HB ERBA2L PDI PDIA1 PO4DB	0.705	HEK293	5S-GlcNAc	12
P09651	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1 HNRPA1	0.705	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P54819	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleaved into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2 ADK2	0.707	HEK293	5S-GlcNAc	24
P61604	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPE1	0.712	HEK293	5S-GlcNAc	24
P23246	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ PSF	0.719	HEK293	5S-GlcNAc	24
P46778	60S ribosomal protein L21	RPL21	0.724	HEK293	5S-GlcNAc	24
P50454	Serpin H1 (47 kDa heat shock protein) (Arsenic-transactivated protein 3) (AsTP3) (Cell proliferation-inducing gene 14 protein) (Collagen-binding protein) (Colligin) (Rheumatoid arthritis-related antigen RA-A47)	SERPINH1 CBP1 CBP2 HSP47 SERPINH2 PIG14	0.732	HEK293	5S-GlcNAc	24
P08670	Vimentin	VIM	0.737	HEK293	5S-GlcNAc	12
O75475	PC4 and SFRS1-interacting protein (CLL-associated antigen KW-7) (Dense fine speckles 70 kDa protein) (DFS 70) (Lens epithelium-derived growth factor) (Transcriptional coactivator p75/p52)	PSIP1 DFS70 LEDGF PSIP2	0.737	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8 HSC70 HSP73 HSPA10	0.738	HEK293	5S-GlcNAc	8
Q99878	Histone H2A type 1-J (Histone H2A/e)	HIST1H2AJ H2AFE	0.739	HEK293	5S-GlcNAc	24
P43243	Matrin-3	MATR3 KIAA0723	0.741	HEK293	5S-GlcNAc	24
P46013	Antigen KI-67	MKI67	0.752	HEK293	5S-GlcNAc	8
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1 HNRPA2B1	0.765	HEK293	5S-GlcNAc	24
P10809	60 kDa heat shock protein, mitochondrial (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1 HSP60	0.765	HEK293	5S-GlcNAc	24
Q00839	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU HNRPU SAFA U21.1	0.782	HEK293	5S-GlcNAc	24
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC HNRPC	0.791	HEK293	5S-GlcNAc	24
P08670	Vimentin	VIM	0.792	HEK293	5S-GlcNAc	24
P08107	Heat shock 70 kDa protein 1A/1B (Heat shock 70 kDa protein 1/2) (HSP70-1/HSP70-2) (HSP70.1/HSP70.2)	HSPA1A HSPA1 HSX70; HSPA1B	0.814	HEK293	5S-GlcNAc	24

Appendix G: Table of volcano plot derived proteins showing increased degradation in HEK293 cells due to 5Thio-GlcNAc inhibition.

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q92922	SWI/SNF complex subunit SMARCC1 (BRG1-associated factor 155) (BAF155) (SWI/SNF complex 155 kDa subunit) (SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 1)	SMARCC1 BAF155	0.51	HEK293	5S-GlcNAc	12
P11021	78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	HSPA5 GRP78	0.55	HEK293	5S-GlcNAc	24
Q5UIP0	Telomere-associated protein RIF1 (Rap1-interacting factor 1 homolog)	RIF1	0.59	HEK293	5S-GlcNAc	5
P08559	Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial (EC 1.2.4.1) (PDHE1-A type I)	PDHA1 PHE1A	0.60	HEK293	5S-GlcNAc	2
P13667	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4 ERP70 ERP72	0.63	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q9Y230	RuvB-like 2 (EC 3.6.4.12) (48 kDa TATA box-binding protein-interacting protein) (48 kDa TBP-interacting protein) (51 kDa erythrocyte cytosolic protein) (ECP-51) (INO80 complex subunit J) (Repressing pontin 52) (Reptin 52) (TIP49b) (TIP60-associated protein 54-beta) (TAP54-beta)	RUVBL2 INO80J TIP48 TIP49B CGI-46	0.65	HEK293	5S-GlcNAc	2
P11021	78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	HSPA5 GRP78	0.68	HEK293	5S-GlcNAc	12
P20700	Lamin-B1	LMNB1 LMN2 LMNB	0.70	HEK293	5S-GlcNAc	12
Q99879	Histone H2B type 1-M (Histone H2B.e) (H2B/e)	HIST1H2BM H2BFE	0.72	HEK293	5S-GlcNAc	12
P02545	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA LMN1	0.72	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	0.73	HEK293	5S-GlcNAc	5
P49411	Elongation factor Tu, mitochondrial (EF-Tu) (P43)	TUFM	0.74	HEK293	5S-GlcNAc	12
P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9 GRP75 HSPA9B mt-HSP70	0.74	HEK293	5S-GlcNAc	12
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	0.75	HEK293	5S-GlcNAc	12
O60814	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK H2BFT HIRIP1	0.76	HEK293	5S-GlcNAc	5
Q99878	Histone H2A type 1-J (Histone H2A/e)	HIST1H2AJ H2AFE	0.76	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q13813	Spectrin alpha chain, non-erythrocytic 1 (Alpha-II spectrin) (Fodrin alpha chain) (Spectrin, non-erythroid alpha subunit)	SPTAN1 NEAS SPTA2	0.76	HEK293	5S-GlcNAc	12
Q99878	Histone H2A type 1-J (Histone H2A/e)	HIST1H2AJ H2AFE	0.77	HEK293	5S-GlcNAc	12
P46013	Antigen KI-67	MKI67	0.77	HEK293	5S-GlcNAc	5
P43243	Matrin-3	MATR3 KIAA0723	0.77	HEK293	5S-GlcNAc	12
P02545	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	LMNA LMN1	0.78	HEK293	5S-GlcNAc	5
P10809	60 kDa heat shock protein, mitochondrial (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1 HSP60	0.78	HEK293	5S-GlcNAc	12
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1 HNRPA2B1	0.78	HEK293	5S-GlcNAc	12
Q13813	Spectrin alpha chain, non-erythrocytic 1 (Alpha-II spectrin) (Fodrin alpha chain) (Spectrin, non-erythroid alpha subunit)	SPTAN1 NEAS SPTA2	0.79	HEK293	5S-GlcNAc	5
P14625	Endoplasmin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1 GRP94 TRA1	0.79	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P10809	60 kDa heat shock protein, mitochondrial (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1 HSP60	0.80	HEK293	5S-GlcNAc	5

Appendix H: Table of volcano plot derived proteins showing decreased degradation in HEK293 cells due to 5Thio-GlcNAc inhibition.

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
O14776	Transcription elongation regulator 1 (TATA box-binding protein-associated factor 2S) (Transcription factor CA150)	TCERG1 CA150 TAF2S	3.52	HEK293	5S-GlcNAc	2
Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 (P1)	NUCKS1 NUCKS JC7	2.71	HEK293	5S-GlcNAc	5
Q9NTK5	Obg-like ATPase 1 (DNA damage-regulated overexpressed in cancer 45) (DOC45) (GTP-binding protein 9)	OLA1 GTPBP9 PRO2455 PTD004	2.52	HEK293	5S-GlcNAc	5
P49321	Nuclear autoantigenic sperm protein (NASP)	NASP	2.49	HEK293	5S-GlcNAc	5
P25786	Proteasome subunit alpha type-1 (EC 3.4.25.1) (30 kDa prosomal protein) (PROS-30) (Macropain subunit C2) (Multicatalytic endopeptidase complex subunit C2) (Proteasome component C2) (Proteasome nu chain)	PSMA1 HC2 NU PROS30 PSC2	2.47	HEK293	5S-GlcNAc	5
Q9UHD1	Cysteine and histidine-rich domain-containing protein 1 (CHORD domain-containing protein 1) (CHORD-containing protein 1) (CHP-1) (Protein morgana)	CHORDC1 CHP1	2.47	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
O43242	26S proteasome non-ATPase regulatory subunit 3 (26S proteasome regulatory subunit RPN3) (26S proteasome regulatory subunit S3) (Proteasome subunit p58)	PSMD3	2.43	HEK293	5S-GlcNAc	5
P50395	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2 RABGDIB	2.41	HEK293	5S-GlcNAc	5
P00568	Adenylate kinase isoenzyme 1 (AK 1) (EC 2.7.4.3) (EC 2.7.4.6) (ATP-AMP transphosphorylase 1) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) (Myokinase)	AK1	2.37	HEK293	5S-GlcNAc	5
P23193	Transcription elongation factor A protein 1 (Transcription elongation factor S-II protein 1) (Transcription elongation factor TFIIS.o)	TCEA1 GTF2S TFIIS	2.33	HEK293	5S-GlcNAc	5
Q96EI5	Transcription elongation factor A protein-like 4 (TCEA-like protein 4) (Transcription elongation factor S-II protein-like 4)	TCEAL4 NPD017	2.33	HEK293	5S-GlcNAc	5
P27695	DNA-(apurinic or apyrimidinic site) lyase (EC 3.1.-.-) (EC 4.2.99.18) (APEX nuclease) (APEN) (Apurinic-apyrimidinic endonuclease 1) (AP endonuclease 1) (APE-1) (REF-1) (Redox factor-1) [Cleaved into: DNA-(apurinic or apyrimidinic site) lyase, mitochondrial]	APEX1 APE APE1 APEX APX HAP1 REF1	2.31	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P06454	Prothymosin alpha [Cleaved into: Prothymosin alpha, N-terminally processed; Thymosin alpha-1]	PTMA TMSA	2.30	HEK293	5S-GlcNAc	5
P29401	Transketolase (TK) (EC 2.2.1.1)	TKT	2.27	HEK293	5S-GlcNAc	5
O00273	DNA fragmentation factor subunit alpha (DNA fragmentation factor 45 kDa subunit) (DFF-45) (Inhibitor of CAD) (ICAD)	DFFA DFF1 DFF45 H13	2.23	HEK293	5S-GlcNAc	5
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A (PPIase FKBP1A) (EC 5.2.1.8) (12 kDa FK506-binding protein) (12 kDa FKBP) (FKBP-12) (Calstabin-1) (FK506-binding protein 1A) (FKBP-1A) (Immunophilin FKBP12) (Rotamase)	FKBP1A FKBP1 FKBP12	2.23	HEK293	5S-GlcNAc	5
P41567	Eukaryotic translation initiation factor 1 (eIF1) (A121) (Protein translation factor SUI1 homolog) (Sui1iso1)	EIF1 SUI1	2.23	HEK293	5S-GlcNAc	5
P00558	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1 PGKA MIG10 OK/SW-cl.110	2.19	HEK293	5S-GlcNAc	5
P37837	Transaldolase (EC 2.2.1.2)	TALDO1 TAL TALDO TALDOR	2.17	HEK293	5S-GlcNAc	5
Q9HC38	Glyoxalase domain-containing protein 4	GLOD4 C17orf25 CGI-150 My027	2.17	HEK293	5S-GlcNAc	5
Q9HD15	Steroid receptor RNA activator 1 (Steroid receptor RNA activator protein) (SRAP)	SRA1 PP7684	2.16	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q9UBT2	SUMO-activating enzyme subunit 2 (EC 6.3.2.-) (Anthracycline-associated resistance ARX) (Ubiquitin-like 1-activating enzyme E1B) (Ubiquitin-like modifier-activating enzyme 2)	UBA2 SAE2 UBLE1B HRIHFB2115	2.16	HEK293	5S-GlcNAc	5
Q9UHV9	Prefoldin subunit 2	PFDN2 PFD2 HSPC231	2.14	HEK293	5S-GlcNAc	5
Q15181	Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-hydrolase) (PPase)	PPA1 IOPPP PP	2.14	HEK293	5S-GlcNAc	5
Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog (Protein 40-6-3) (Sgt1)	SUGT1	2.13	HEK293	5S-GlcNAc	12
Q9Y2Z0	Suppressor of G2 allele of SKP1 homolog (Protein 40-6-3) (Sgt1)	SUGT1	2.12	HEK293	5S-GlcNAc	5
Q04760	Lactoylglutathione lyase (EC 4.4.1.5) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (Methylglyoxalase) (S-D-lactoylglutathione methylglyoxal lyase)	GLO1	2.11	HEK293	5S-GlcNAc	5
P30043	Flavin reductase (NADPH) (FR) (EC 1.5.1.30) (Biliverdin reductase B) (BVR-B) (EC 1.3.1.24) (Biliverdin-IX beta-reductase) (Green heme-binding protein) (GHBP) (NADPH-dependent diaphorase) (NADPH-flavin reductase) (FLR)	BLVRB FLR	2.11	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P31939	Bifunctional purine biosynthesis protein PURH [Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (ATIC) (IMP synthase) (Inosinicase)]	ATIC PURH OK/SW-cl.86	2.09	HEK293	5S-GlcNAc	5
P30086	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPpp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1 PBP PEBP	2.09	HEK293	5S-GlcNAc	5
Q01469	Fatty acid-binding protein, epidermal (Epidermal-type fatty acid-binding protein) (E-FABP) (Fatty acid-binding protein 5) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	FABP5	2.09	HEK293	5S-GlcNAc	5
Q96CP2	FLYWCH family member 2	FLYWCH2	2.09	HEK293	5S-GlcNAc	5
P60174	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	TPI1 TPI	2.08	HEK293	5S-GlcNAc	5
P33552	Cyclin-dependent kinases regulatory subunit 2 (CKS-2)	CKS2	2.08	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P13693	Translationally-controlled tumor protein (TCTP) (Fortilin) (Histamine-releasing factor) (HRF) (p23)	TPT1	2.08	HEK293	5S-GlcNAc	5
Q9H910	Hematological and neurological expressed 1-like protein (HN1-like protein)	HN1L C16orf34 L11	2.08	HEK293	5S-GlcNAc	5
P09429	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1 HMG1	2.06	HEK293	5S-GlcNAc	5
P63241	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A	2.05	HEK293	5S-GlcNAc	5
P42771	Cyclin-dependent kinase inhibitor 2A, isoforms 1/2/3 (Cyclin-dependent kinase 4 inhibitor A) (CDK4I) (Multiple tumor suppressor 1) (MTS-1) (p16-INK4a) (p16-INK4) (p16INK4A)	CDKN2A CDKN2 MTS1	2.05	HEK293	5S-GlcNAc	5
O75347	Tubulin-specific chaperone A (TCP1-chaperonin cofactor A) (Tubulin-folding cofactor A) (CFA)	TBCA	2.04	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Acidic nuclear phosphoprotein pp32) (pp32) (Leucine-rich acidic nuclear protein) (LANP) (Mapmodulin) (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Putative HLA-DR-associated protein I) (PHAPI)	ANP32A C15orf1 LANP MAPM PHAP1	2.04	HEK293	5S-GlcNAc	5
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase Pin1) (PPIase Pin1) (Rotamase Pin1)	PIN1	2.03	HEK293	5S-GlcNAc	5
P60981	Destrin (Actin-depolymerizing factor) (ADF)	DSTN ACTDP DSN	2.03	HEK293	5S-GlcNAc	5
P12081	Histidine--tRNA ligase, cytoplasmic (EC 6.1.1.21) (Histidyl-tRNA synthetase) (HisRS)	HARS HRS	2.02	HEK293	5S-GlcNAc	5
Q9H3K6	BolA-like protein 2	BOLA2 BOLA2A My016; BOLA2B	2.02	HEK293	5S-GlcNAc	5
O15212	Prefoldin subunit 6 (Protein Ke2)	PFDN6 HKE2 PFD6	2.01	HEK293	5S-GlcNAc	5
P55036	26S proteasome non-ATPase regulatory subunit 4 (26S proteasome regulatory subunit RPN10) (26S proteasome regulatory subunit S5A) (Antisecretory factor 1) (AF) (ASF) (Multiubiquitin chain-binding protein)	PSMD4 MCB1	2.01	HEK293	5S-GlcNAc	5
P37802	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2 KIAA0120 CDABP0035	2.00	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
O00299	Chloride intracellular channel protein 1 (Chloride channel ABP) (Nuclear chloride ion channel 27) (NCC27) (Regulatory nuclear chloride ion channel protein) (hRNCC)	CLIC1 G6 NCC27	1.99	HEK293	5S-GlcNAc	5
P60900	Proteasome subunit alpha type-6 (EC 3.4.25.1) (27 kDa prosomal protein) (PROS-27) (p27K) (Macropain iota chain) (Multicatalytic endopeptidase complex iota chain) (Proteasome iota chain)	PSMA6 PROS27	1.99	HEK293	5S-GlcNAc	5
P26583	High mobility group protein B2 (High mobility group protein 2) (HMG-2)	HMGB2 HMG2	1.99	HEK293	5S-GlcNAc	5
P06454	Prothymosin alpha [Cleaved into: Prothymosin alpha, N-terminally processed; Thymosin alpha-1]	PTMA TMSA	1.99	HEK293	5S-GlcNAc	12
P22314	Ubiquitin-like modifier-activating enzyme 1 (Protein A1S9) (Ubiquitin-activating enzyme E1)	UBA1 A1S9T UBE1	1.99	HEK293	5S-GlcNAc	5
P78417	Glutathione S-transferase omega-1 (GSTO-1) (EC 2.5.1.18) (Glutathione S-transferase omega 1-1) (GSTO 1-1) (Glutathione-dependent dehydroascorbate reductase) (EC 1.8.5.1) (Monomethylarsonic acid reductase) (MMA(V) reductase) (EC 1.20.4.2) (S-(Phenacyl)glutathione reductase) (SPG-R)	GSTO1 GSTTLP28	1.98	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P22102	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (Glycinamide ribonucleotide synthetase) (GARS) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (5'-phosphoribosylglycinamide transformylase) (GAR transformylase) (GART)]	GART PGFT PRGS	1.97	HEK293	5S-GlcNAc	5
P14174	Macrophage migration inhibitory factor (MIF) (EC 5.3.2.1) (Glycosylation-inhibiting factor) (GIF) (L-dopachrome isomerase) (L-dopachrome tautomerase) (EC 5.3.3.12) (Phenylpyruvate tautomerase)	MIF GLIF MMIF	1.97	HEK293	5S-GlcNAc	5
P49368	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRiC5)	CCT3 CCTG TRIC5	1.96	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P30041	Peroxiredoxin-6 (EC 1.11.1.15) (1-Cys peroxiredoxin) (1-Cys PRX) (24 kDa protein) (Acidic calcium-independent phospholipase A2) (aiPLA2) (EC 3.1.1.-) (Antioxidant protein 2) (Liver 2D page spot 40) (Non-selenium glutathione peroxidase) (NSGPx) (EC 1.11.1.9) (Red blood cells page spot 12)	PRDX6 AOP2 KIAA0106	1.96	HEK293	5S-GlcNAc	5
Q9UK76	Hematological and neurological expressed 1 protein (Androgen-regulated protein 2) [Cleaved into: Hematological and neurological expressed 1 protein, N-terminally processed]	HN1 ARM2	1.96	HEK293	5S-GlcNAc	5
P13984	General transcription factor IIF subunit 2 (EC 3.6.4.12) (ATP-dependent helicase GTF2F2) (General transcription factor IIF 30 kDa subunit) (Transcription initiation factor IIF subunit beta) (TFIIF-beta) (Transcription initiation factor RAP30)	GTF2F2 RAP30	1.95	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 (PPIase FKBP4) (EC 5.2.1.8) (51 kDa FK506-binding protein) (FKBP51) (52 kDa FK506-binding protein) (52 kDa FKBP) (FKBP-52) (59 kDa immunophilin) (p59) (FK506-binding protein 4) (FKBP-4) (FKBP59) (HSP-binding immunophilin) (HBI) (Immunophilin FKBP52) (Rotamase) [Cleaved into: Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed]	FKBP4 FKBP52	1.95	HEK293	5S-GlcNAc	5
P40222	Alpha-taxilin	TXLNA TXLN	1.95	HEK293	5S-GlcNAc	5
Q9Y5Z4	Heme-binding protein 2 (Placental protein 23) (PP23) (Protein SOUL)	HEBP2 C6orf34 SOUL	1.93	HEK293	5S-GlcNAc	5
P04075	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA ALDA	1.93	HEK293	5S-GlcNAc	5
P09211	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	GSTP1 FAEES3 GST3	1.93	HEK293	5S-GlcNAc	5
Q99497	Protein DJ-1 (EC 3.4.-.-) (Oncogene DJ1) (Parkinson disease protein 7)	PARK7	1.93	HEK293	5S-GlcNAc	5
P27348	14-3-3 protein theta (14-3-3 protein T-cell) (14-3-3 protein tau) (Protein HS1)	YWHAQ	1.93	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62937	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA CYPA	1.93	HEK293	5S-GlcNAc	5
Q15056	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	EIF4H KIAA0038 WBSCR1 WSCR1	1.92	HEK293	5S-GlcNAc	5
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Acidic nuclear phosphoprotein pp32) (pp32) (Leucine-rich acidic nuclear protein) (LANP) (Mapmodulin) (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Putative HLA-DR-associated protein I) (PHAPI)	ANP32A C15orf1 LANP MAPM PHAP1	1.92	HEK293	5S-GlcNAc	12
Q14847	LIM and SH3 domain protein 1 (LASP-1) (Metastatic lymph node gene 50 protein) (MLN 50)	LASP1 MLN50	1.92	HEK293	5S-GlcNAc	5
Q92734	Protein TFG (TRK-fused gene protein)	TFG	1.92	HEK293	5S-GlcNAc	5
P07741	Adenine phosphoribosyltransferase (APRT) (EC 2.4.2.7)	APRT	1.92	HEK293	5S-GlcNAc	5
O14818	Proteasome subunit alpha type-7 (EC 3.4.25.1) (Proteasome subunit RC6-1) (Proteasome subunit XAPC7)	PSMA7 HSPC	1.92	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q06830	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PRDX1 PAGA PAGB TDPX2	1.91	HEK293	5S-GlcNAc	5
Q9UKY7	Protein CDV3 homolog	CDV3 H41	1.91	HEK293	5S-GlcNAc	5
Q9UNZ2	NSFL1 cofactor p47 (UBX domain-containing protein 2C) (p97 cofactor p47)	NSFL1C UBXN2C	1.90	HEK293	5S-GlcNAc	5
P46779	60S ribosomal protein L28	RPL28	1.90	HEK293	5S-GlcNAc	5
P31949	Protein S100-A11 (Calgizzarin) (Metastatic lymph node gene 70 protein) (MLN 70) (Protein S100-C) (S100 calcium-binding protein A11) [Cleaved into: Protein S100-A11, N-terminally processed]	S100A11 MLN70 S100C	1.90	HEK293	5S-GlcNAc	5
P61758	Prefoldin subunit 3 (HIBBJ46) (Von Hippel-Lindau-binding protein 1) (VBP-1) (VHL-binding protein 1)	VBP1 PFDN3	1.90	HEK293	5S-GlcNAc	5
P14618	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM OIP3 PK2 PK3 PKM2	1.90	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q14320	Protein FAM50A (Protein HXC-26) (Protein XAP-5)	FAM50A DXS9928E HXC26 XAP5	1.90	HEK293	5S-GlcNAc	5
Q9Y617	Phosphoserine aminotransferase (EC 2.6.1.52) (Phosphohydroxythreonine aminotransferase) (PSAT)	PSAT1 PSA	1.90	HEK293	5S-GlcNAc	12
P41227	N-alpha-acetyltransferase 10 (EC 2.3.1.-) (EC 2.3.1.88) (N-terminal acetyltransferase complex ARD1 subunit homolog A) (NatA catalytic subunit Naa10)	NAA10 ARD1 ARD1A TE2	1.90	HEK293	5S-GlcNAc	5
P61088	Ubiquitin-conjugating enzyme E2 N (EC 6.3.2.19) (Bendless-like ubiquitin-conjugating enzyme) (Ubc13) (UbcH13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	UBE2N BLU	1.89	HEK293	5S-GlcNAc	5
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2 (GABA(A) receptor-associated protein-like 2) (Ganglioside expression factor 2) (GEF-2) (General protein transport factor p16) (Golgi-associated ATPase enhancer of 16 kDa) (GATE-16) (MAP1 light chain 3-related protein)	GABARAPL2 FLC3A GEF2	1.89	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q99426	Tubulin-folding cofactor B (Cytoskeleton-associated protein 1) (Cytoskeleton-associated protein CKAPI) (Tubulin-specific chaperone B)	TBCB CG22 CKAP1	1.89	HEK293	5S-GlcNAc	5
Q15819	Ubiquitin-conjugating enzyme E2 variant 2 (DDVit 1) (Enterocyte differentiation-associated factor 1) (EDAF-1) (Enterocyte differentiation-promoting factor 1) (EDPF-1) (MMS2 homolog) (Vitamin D3-inducible protein)	UBE2V2 MMS2 UEV2	1.88	HEK293	5S-GlcNAc	5
P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (Renal carcinoma antigen NY-REN-11) (Transformation-sensitive protein IEF SSP 3521)	STIP1	1.88	HEK293	5S-GlcNAc	5
P00441	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Superoxide dismutase 1) (hSod1)	SOD1	1.88	HEK293	5S-GlcNAc	5
P29401	Transketolase (TK) (EC 2.2.1.1)	TKT	1.88	HEK293	5S-GlcNAc	12
P43487	Ran-specific GTPase-activating protein (Ran-binding protein 1) (RanBP1)	RANBP1	1.88	HEK293	5S-GlcNAc	5
O00233	26S proteasome non-ATPase regulatory subunit 9 (26S proteasome regulatory subunit p27)	PSMD9	1.88	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P08758	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5 ANX5 ENX2 PP4	1.88	HEK293	5S-GlcNAc	5
P05455	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjoegren syndrome type B antigen) (SS-B)	SSB	1.87	HEK293	5S-GlcNAc	5
O60749	Sorting nexin-2 (Transformation-related gene 9 protein) (TRG-9)	SNX2 TRG9	1.86	HEK293	5S-GlcNAc	5
Q99436	Proteasome subunit beta type-7 (EC 3.4.25.1) (Macropain chain Z) (Multicatalytic endopeptidase complex chain Z) (Proteasome subunit Z)	PSMB7 Z	1.86	HEK293	5S-GlcNAc	5
Q8WZA0	Protein LZIC (Leucine zipper and CTNNBIP1 domain-containing protein) (Leucine zipper and ICAT homologous domain-containing protein)	LZIC	1.86	HEK293	5S-GlcNAc	5
Q99614	Tetratricopeptide repeat protein 1 (TPR repeat protein 1)	TTC1 TPR1	1.86	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q01469	Fatty acid-binding protein, epidermal (Epidermal-type fatty acid-binding protein) (E-FABP) (Fatty acid-binding protein 5) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	FABP5	1.86	HEK293	5S-GlcNAc	12
Q15417	Calponin-3 (Calponin, acidic isoform)	CNN3	1.86	HEK293	5S-GlcNAc	5
O76003	Glutaredoxin-3 (PKC-interacting cousin of thioredoxin) (PICOT) (PKC-theta-interacting protein) (PKCq-interacting protein) (Thioredoxin-like protein 2)	GLRX3 PICOT TXNL2 HUSSY-22	1.86	HEK293	5S-GlcNAc	5
Q15691	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	MAPRE1	1.85	HEK293	5S-GlcNAc	5
P07900	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1 HSP90A HSPC1 HSPCA	1.85	HEK293	5S-GlcNAc	5
Q15185	Prostaglandin E synthase 3 (EC 5.3.99.3) (Cytosolic prostaglandin E2 synthase) (cPGES) (Hsp90 co-chaperone) (Progesterone receptor complex p23) (Telomerase-binding protein p23)	PTGES3 P23 TEBP	1.85	HEK293	5S-GlcNAc	5
P17987	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	TCP1 CCT1 CCTA	1.85	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q9Y266	Nuclear migration protein nudC (Nuclear distribution protein C homolog)	NUDC	1.85	HEK293	5S-GlcNAc	5
Q13765	Nascent polypeptide-associated complex subunit alpha (NAC-alpha) (Alpha-NAC) (allergen Hom s 2)	NACA HSD48	1.84	HEK293	5S-GlcNAc	5
P41250	Glycine--tRNA ligase (EC 6.1.1.14) (Diadenosine tetraphosphate synthetase) (AP-4-A synthetase) (Glycyl-tRNA synthetase) (GlyRS)	GARS	1.84	HEK293	5S-GlcNAc	5
P49321	Nuclear autoantigenic sperm protein (NASP)	NASP	1.84	HEK293	5S-GlcNAc	12
P60842	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1 DDX2A EIF4A	1.84	HEK293	5S-GlcNAc	5
Q8WW12	PEST proteolytic signal-containing nuclear protein (PCNP) (PEST-containing nuclear protein)	PCNP	1.84	HEK293	5S-GlcNAc	12
P60520	Gamma-aminobutyric acid receptor-associated protein-like 2 (GABA(A) receptor-associated protein-like 2) (Ganglioside expression factor 2) (GEF-2) (General protein transport factor p16) (Golgi-associated ATPase enhancer of 16 kDa) (GATE-16) (MAP1 light chain 3-related protein)	GABARAPL2 FLC3A GEF2	1.84	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P23588	Eukaryotic translation initiation factor 4B (eIF-4B)	EIF4B	1.84	HEK293	5S-GlcNAc	5
P49915	GMP synthase [glutamine-hydrolyzing] (EC 6.3.5.2) (GMP synthetase) (Glutamine amidotransferase)	GMPS	1.83	HEK293	5S-GlcNAc	5
O75534	Cold shock domain-containing protein E1 (N-ras upstream gene protein) (Protein UNR)	CSDE1 D1S155E KIAA0885 NRU UNR	1.83	HEK293	5S-GlcNAc	5
P06733	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1 ENO1L1 MBPB1 MPB1	1.83	HEK293	5S-GlcNAc	5
P50990	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Renal carcinoma antigen NY-REN-15)	CCT8 C21orf112 CCTQ KIAA0002	1.83	HEK293	5S-GlcNAc	5
O00273	DNA fragmentation factor subunit alpha (DNA fragmentation factor 45 kDa subunit) (DFF-45) (Inhibitor of CAD) (ICAD)	DFFA DFF1 DFF45 H13	1.83	HEK293	5S-GlcNAc	12
O95433	Activator of 90 kDa heat shock protein ATPase homolog 1 (AHA1) (p38)	AHSA1 C14orf3 HSPC322	1.83	HEK293	5S-GlcNAc	5
P13639	Elongation factor 2 (EF-2)	EEF2 EF2	1.83	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q9UBT2	SUMO-activating enzyme subunit 2 (EC 6.3.2.-) (Anthracycline-associated resistance ARX) (Ubiquitin-like 1-activating enzyme E1B) (Ubiquitin-like modifier-activating enzyme 2)	UBA2 SAE2 UBLE1B HRIHFB2115	1.83	HEK293	5S-GlcNAc	12
P23528	Cofilin-1 (18 kDa phosphoprotein) (p18) (Cofilin, non-muscle isoform)	CFL1 CFL	1.82	HEK293	5S-GlcNAc	5
O95793	Double-stranded RNA-binding protein Staufen homolog 1	STAU1 STAU	1.82	HEK293	5S-GlcNAc	12
Q9Y5Z4	Heme-binding protein 2 (Placental protein 23) (PP23) (Protein SOUL)	HEBP2 C6orf34 SOUL	1.82	HEK293	5S-GlcNAc	12
P07108	Acyl-CoA-binding protein (ACBP) (Diazepam-binding inhibitor) (DBI) (Endozepine) (EP)	DBI	1.82	HEK293	5S-GlcNAc	5
P04406	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH GAPD CDABP0047 OK/SW-cl.12	1.82	HEK293	5S-GlcNAc	5
Q13442	28 kDa heat- and acid-stable phosphoprotein (PDGF-associated protein) (PAP) (PDGFA-associated protein 1) (PAP1)	PDAP1 HASPP28	1.82	HEK293	5S-GlcNAc	5
Q99497	Protein DJ-1 (EC 3.4.-.-) (Oncogene DJ1) (Parkinson disease protein 7)	PARK7	1.81	HEK293	5S-GlcNAc	12
P63104	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ	1.81	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	CCT6A CCT6 CCTZ	1.81	HEK293	5S-GlcNAc	5
P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	EEF1D EF1D	1.81	HEK293	5S-GlcNAc	5
P51858	Hepatoma-derived growth factor (HDGF) (High mobility group protein 1-like 2) (HMG-1L2)	HDGF HMG1L2	1.81	HEK293	5S-GlcNAc	5
P13797	Plastin-3 (T-plastin)	PLS3	1.81	HEK293	5S-GlcNAc	5
P48643	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	CCT5 CCTE KIAA0098	1.81	HEK293	5S-GlcNAc	5
P07195	L-lactate dehydrogenase B chain (LDH-B) (EC 1.1.1.27) (LDH heart subunit) (LDH-H) (Renal carcinoma antigen NY-REN-46)	LDHB	1.81	HEK293	5S-GlcNAc	5
O43390	Heterogeneous nuclear ribonucleoprotein R (hnRNP R)	HNRNPR HNRPR	1.80	HEK293	5S-GlcNAc	2
P08238	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1 HSP90B HSPC2 HSPCB	1.80	HEK293	5S-GlcNAc	5
P22392	Nucleoside diphosphate kinase B (NDK B) (NDP kinase B) (EC 2.7.4.6) (C-myc purine-binding transcription factor PUF) (Histidine protein kinase NDKB) (EC 2.7.13.3) (nm23-H2)	NME2 NM23B	1.80	HEK293	5S-GlcNAc	5
O43768	Alpha-endosulfine (ARPP-19e)	ENSA	1.79	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q06323	Proteasome activator complex subunit 1 (11S regulator complex subunit alpha) (REG-alpha) (Activator of multicatalytic protease subunit 1) (Interferon gamma up-regulated I-5111 protein) (IGUP I-5111) (Proteasome activator 28 subunit alpha) (PA28a) (PA28alpha)	PSME1 IFI5111	1.79	HEK293	5S-GlcNAc	12
Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3 (PPIase FKBP3) (EC 5.2.1.8) (25 kDa FK506-binding protein) (25 kDa FKBP) (FKBP-25) (FK506-binding protein 3) (FKBP-3) (Immunophilin FKBP25) (Rapamycin-selective 25 kDa immunophilin) (Rotamase)	FKBP3 FKBP25	1.79	HEK293	5S-GlcNAc	5
P61923	Coatomer subunit zeta-1 (Zeta-1-coat protein) (Zeta-1 COP)	COPZ1 COPZ CGI-120 HSPC181	1.79	HEK293	5S-GlcNAc	5
P05455	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjoegren syndrome type B antigen) (SS-B)	SSB	1.79	HEK293	5S-GlcNAc	12
Q99584	Protein S100-A13 (S100 calcium-binding protein A13)	S100A13	1.78	HEK293	5S-GlcNAc	5
P50395	Rab GDP dissociation inhibitor beta (Rab GDI beta) (Guanosine diphosphate dissociation inhibitor 2) (GDI-2)	GDI2 RABGDIB	1.78	HEK293	5S-GlcNAc	12
P60174	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	TPI1 TPI	1.78	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P26641	Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma)	EEF1G EF1G PRO1608	1.78	HEK293	5S-GlcNAc	5
O60841	Eukaryotic translation initiation factor 5B (eIF-5B) (Translation initiation factor IF-2)	EIF5B IF2 KIAA0741	1.77	HEK293	5S-GlcNAc	5
P62258	14-3-3 protein epsilon (14-3-3E)	YWHAE	1.77	HEK293	5S-GlcNAc	5
Q7L1Q6	Basic leucine zipper and W2 domain-containing protein 1 (Protein Orf)	BZW1 BZAP45 KIAA0005	1.77	HEK293	5S-GlcNAc	5
P54577	Tyrosine--tRNA ligase, cytoplasmic (EC 6.1.1.1) (Tyrosyl-tRNA synthetase) (TyrRS) [Cleaved into: Tyrosine--tRNA ligase, cytoplasmic, N-terminally processed]	YARS	1.77	HEK293	5S-GlcNAc	5
Q15056	Eukaryotic translation initiation factor 4H (eIF-4H) (Williams-Beuren syndrome chromosomal region 1 protein)	EIF4H KIAA0038 WBSCR1 WSCR1	1.77	HEK293	5S-GlcNAc	12
P23193	Transcription elongation factor A protein 1 (Transcription elongation factor S-II protein 1) (Transcription elongation factor TFIIS.o)	TCEA1 GTF2S TFIIS	1.77	HEK293	5S-GlcNAc	12
Q15819	Ubiquitin-conjugating enzyme E2 variant 2 (DDVit 1) (Enterocyte differentiation-associated factor 1) (EDAF-1) (Enterocyte differentiation-promoting factor 1) (EDPF-1) (MMS2 homolog) (Vitamin D3-inducible protein)	UBE2V2 MMS2 UEV2	1.77	HEK293	5S-GlcNAc	12
P09429	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1 HMG1	1.76	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62633	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9)	CNBP RNF163 ZNF9	1.76	HEK293	5S-GlcNAc	12
Q9UHV9	Prefoldin subunit 2	PFDN2 PFD2 HSPC231	1.75	HEK293	5S-GlcNAc	12
O75347	Tubulin-specific chaperone A (TCP1-chaperonin cofactor A) (Tubulin-folding cofactor A) (CFA)	TBCA	1.75	HEK293	5S-GlcNAc	12
O60869	Endothelial differentiation-related factor 1 (EDF-1) (Multiprotein-bridging factor 1) (MBF1)	EDF1	1.75	HEK293	5S-GlcNAc	5
P61758	Prefoldin subunit 3 (HIBBJ46) (Von Hippel-Lindau-binding protein 1) (VBP-1) (VHL-binding protein 1)	VBP1 PFDN3	1.75	HEK293	5S-GlcNAc	12
P37837	Transaldolase (EC 2.2.1.2)	TALDO1 TAL TALDO TALDOR	1.75	HEK293	5S-GlcNAc	12
Q15417	Calponin-3 (Calponin, acidic isoform)	CNN3	1.74	HEK293	5S-GlcNAc	12
Q9H910	Hematological and neurological expressed 1-like protein (HN1-like protein)	HN1L C16orf34 L11	1.74	HEK293	5S-GlcNAc	12
P07311	Acylphosphatase-1 (EC 3.6.1.7) (Acylphosphatase, erythrocyte isozyme) (Acylphosphatase, organ-common type isozyme) (Acylphosphate phosphohydrolase 1)	ACYP1 ACYPE	1.74	HEK293	5S-GlcNAc	12
Q14320	Protein FAM50A (Protein HXC-26) (Protein XAP-5)	FAM50A DXS9928E HXC26 XAP5	1.74	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P53365	Arfaptin-2 (ADP-ribosylation factor-interacting protein 2) (Partner of RAC1) (Protein POR1)	ARFIP2 POR1	1.74	HEK293	5S-GlcNAc	5
P31946	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAB	1.74	HEK293	5S-GlcNAc	5
Q9BUL8	Programmed cell death protein 10 (Cerebral cavernous malformations 3 protein) (TF-1 cell apoptosis-related protein 15)	PDCD10 CCM3 TFAR15	1.73	HEK293	5S-GlcNAc	5
P26583	High mobility group protein B2 (High mobility group protein 2) (HMG-2)	HMGB2 HMG2	1.73	HEK293	5S-GlcNAc	12
P37802	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	TAGLN2 KIAA0120 CDABP0035	1.73	HEK293	5S-GlcNAc	12
P16949	Stathmin (Leukemia-associated phosphoprotein p18) (Metablastin) (Oncoprotein 18) (Op18) (Phosphoprotein p19) (pp19) (Prosolin) (Protein Pr22) (pp17)	STMN1 C1orf215 LAP18 OP18	1.72	HEK293	5S-GlcNAc	5
O60925	Prefoldin subunit 1	PFDN1 PFD1	1.72	HEK293	5S-GlcNAc	12
P54727	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B	1.72	HEK293	5S-GlcNAc	5
P62633	Cellular nucleic acid-binding protein (CNBP) (Zinc finger protein 9)	CNBP RNF163 ZNF9	1.72	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P12277	Creatine kinase B-type (EC 2.7.3.2) (B-CK) (Creatine kinase B chain)	CKB CKBB	1.71	HEK293	5S-GlcNAc	5
C9JLW8	Protein FAM195B	FAM195B	1.71	HEK293	5S-GlcNAc	5
P62701	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein)	RPS4X CCG2 RPS4 SCAR	1.71	HEK293	5S-GlcNAc	5
P68363	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain)	TUBA1B	1.71	HEK293	5S-GlcNAc	5
Q13642	Four and a half LIM domains protein 1 (FHL-1) (Skeletal muscle LIM-protein 1) (SLIM) (SLIM-1)	FHL1 SLIM1	1.71	HEK293	5S-GlcNAc	12
O75822	Eukaryotic translation initiation factor 3 subunit J (eIF3j) (Eukaryotic translation initiation factor 3 subunit 1) (eIF-3-alpha) (eIF3 p35)	EIF3J EIF3S1 PRO0391	1.70	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P63244	Guanine nucleotide-binding protein subunit beta-2-like 1 (Cell proliferation-inducing gene 21 protein) (Guanine nucleotide-binding protein subunit beta-like protein 12.3) (Human lung cancer oncogene 7 protein) (HLC-7) (Receptor for activated C kinase) (Receptor of activated protein kinase C 1) (RACK1) [Cleaved into: Guanine nucleotide-binding protein subunit beta-2-like 1, N-terminally processed]	GNB2L1 HLC7 PIG21	1.70	HEK293	5S-GlcNAc	5
Q9UQ80	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErbB3-binding protein 1)	PA2G4 EBP1	1.70	HEK293	5S-GlcNAc	5
P20042	Eukaryotic translation initiation factor 2 subunit 2 (Eukaryotic translation initiation factor 2 subunit beta) (eIF-2-beta)	EIF2S2 EIF2B	1.70	HEK293	5S-GlcNAc	12
P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2 99D8.1 CCTB	1.70	HEK293	5S-GlcNAc	5
Q9UKY7	Protein CDV3 homolog	CDV3 H41	1.70	HEK293	5S-GlcNAc	12
P41227	N-alpha-acetyltransferase 10 (EC 2.3.1.-) (EC 2.3.1.88) (N-terminal acetyltransferase complex ARD1 subunit homolog A) (NatA catalytic subunit Naa10)	NAA10 ARD1 ARD1A TE2	1.69	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q13561	Dynactin subunit 2 (50 kDa dynein-associated polypeptide) (Dynactin complex 50 kDa subunit) (DCTN-50) (p50 dynamitin)	DCTN2 DCTN50	1.69	HEK293	5S-GlcNAc	5
P20810	Calpastatin (Calpain inhibitor) (Sperm BS-17 component)	CAST	1.69	HEK293	5S-GlcNAc	5
Q04760	Lactoylglutathione lyase (EC 4.4.1.5) (Aldoketomutase) (Glyoxalase I) (Glx I) (Ketone-aldehyde mutase) (Methylglyoxalase) (S-D-lactoylglutathione methylglyoxal lyase)	GLO1	1.69	HEK293	5S-GlcNAc	12
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha (Alpha-SGT) (Vpu-binding protein) (UBP)	SGTA SGT SGT1	1.69	HEK293	5S-GlcNAc	5
P18206	Vinculin (Metavinculin) (MV)	VCL	1.68	HEK293	5S-GlcNAc	5
P48444	Coatomer subunit delta (Archain) (Delta-coat protein) (Delta-COP)	ARCN1 COPD	1.68	HEK293	5S-GlcNAc	5
P12004	Proliferating cell nuclear antigen (PCNA) (Cyclin)	PCNA	1.68	HEK293	5S-GlcNAc	12
P0CW22	40S ribosomal protein S17-like	RPS17L	1.68	HEK293	5S-GlcNAc	12
P40222	Alpha-taxilin	TXLNA TXLN	1.67	HEK293	5S-GlcNAc	12
P40925	Malate dehydrogenase, cytoplasmic (EC 1.1.1.37) (Cytosolic malate dehydrogenase) (Diiodophenylpyruvate reductase) (EC 1.1.1.96)	MDH1 MDHA	1.67	HEK293	5S-GlcNAc	12
P13639	Elongation factor 2 (EF-2)	EEF2 EF2	1.66	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P04075	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA ALDA	1.66	HEK293	5S-GlcNAc	12
O43633	Charged multivesicular body protein 2a (Chromatin-modifying protein 2a) (CHMP2a) (Putative breast adenocarcinoma marker BC-2) (Vacuolar protein sorting-associated protein 2-1) (Vps2-1) (hVps2-1)	CHMP2A BC2 CHMP2	1.66	HEK293	5S-GlcNAc	5
P61088	Ubiquitin-conjugating enzyme E2 N (EC 6.3.2.19) (Bendless-like ubiquitin-conjugating enzyme) (Ubc13) (UbcH13) (Ubiquitin carrier protein N) (Ubiquitin-protein ligase N)	UBE2N BLU	1.66	HEK293	5S-GlcNAc	12
P05387	60S acidic ribosomal protein P2 (Renal carcinoma antigen NY-REN-44)	RPLP2 D11S2243E RPP2	1.66	HEK293	5S-GlcNAc	5
P63104	14-3-3 protein zeta/delta (Protein kinase C inhibitor protein 1) (KCIP-1)	YWHAZ	1.65	HEK293	5S-GlcNAc	12
P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2 99D8.1 CCTB	1.65	HEK293	5S-GlcNAc	12
O75821	Eukaryotic translation initiation factor 3 subunit G (eIF3g) (Eukaryotic translation initiation factor 3 RNA-binding subunit) (eIF-3 RNA-binding subunit) (Eukaryotic translation initiation factor 3 subunit 4) (eIF-3-delta) (eIF3 p42) (eIF3 p44)	EIF3G EIF3S4	1.65	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P55036	26S proteasome non-ATPase regulatory subunit 4 (26S proteasome regulatory subunit RPN10) (26S proteasome regulatory subunit S5A) (Antisecretory factor 1) (AF) (ASF) (Multiubiquitin chain-binding protein)	PSMD4 MCB1	1.65	HEK293	5S-GlcNAc	12
P51858	Hepatoma-derived growth factor (HDGF) (High mobility group protein 1-like 2) (HMG-1L2)	HDGF HMG1L2	1.65	HEK293	5S-GlcNAc	12
P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	EEF1D EF1D	1.65	HEK293	5S-GlcNAc	12
O15212	Prefoldin subunit 6 (Protein Ke2)	PFDN6 HKE2 PFD6	1.65	HEK293	5S-GlcNAc	12
P63241	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A	1.64	HEK293	5S-GlcNAc	12
P27816	Microtubule-associated protein 4 (MAP-4)	MAP4	1.64	HEK293	5S-GlcNAc	5
P46108	Adapter molecule crk (Proto-oncogene c-Crk) (p38)	CRK	1.64	HEK293	5S-GlcNAc	12
P23396	40S ribosomal protein S3	RPS3 OK/SW-cl.26	1.64	HEK293	5S-GlcNAc	12
P63220	40S ribosomal protein S21	RPS21	1.64	HEK293	5S-GlcNAc	5
O95347	Structural maintenance of chromosomes protein 2 (SMC protein 2) (SMC-2) (Chromosome-associated protein E) (hCAP-E) (XCAP-E homolog)	SMC2 CAPE SMC2L1 PRO0324	1.64	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P60866	40S ribosomal protein S20	RPS20	1.64	HEK293	5S-GlcNAc	5
Q13263	Transcription intermediary factor 1-beta (TIF1-beta) (E3 SUMO-protein ligase TRIM28) (EC 6.3.2.-) (KRAB-associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-1) (Nuclear corepressor KAP-1) (RING finger protein 96) (Tripartite motif-containing protein 28)	TRIM28 KAP1 RNF96 TIF1B	1.63	HEK293	5S-GlcNAc	5
P62249	40S ribosomal protein S16	RPS16	1.63	HEK293	5S-GlcNAc	5
P39019	40S ribosomal protein S19	RPS19	1.63	HEK293	5S-GlcNAc	12
P62937	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA CYPA	1.63	HEK293	5S-GlcNAc	12
P53999	Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (SUB1 homolog) (p14)	SUB1 PC4 RPO2TC1	1.63	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 (PPIase FKBP4) (EC 5.2.1.8) (51 kDa FK506-binding protein) (FKBP51) (52 kDa FK506-binding protein) (52 kDa FKBP) (FKBP-52) (59 kDa immunophilin) (p59) (FK506-binding protein 4) (FKBP-4) (FKBP59) (HSP-binding immunophilin) (HBI) (Immunophilin FKBP52) (Rotamase) [Cleaved into: Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed]	FKBP4 FKBP52	1.62	HEK293	5S-GlcNAc	12
Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein)	CCT7 CCTH NIP7-1	1.62	HEK293	5S-GlcNAc	2
P63220	40S ribosomal protein S21	RPS21	1.62	HEK293	5S-GlcNAc	12
P08758	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	ANXA5 ANX5 ENX2 PP4	1.61	HEK293	5S-GlcNAc	12
Q9Y490	Talin-1	TLN1 KIAA1027 TLN	1.61	HEK293	5S-GlcNAc	5
P16949	Stathmin (Leukemia-associated phosphoprotein p18) (Metablastin) (Oncoprotein 18) (Op18) (Phosphoprotein p19) (pp19) (Prosolin) (Protein Pr22) (pp17)	STMN1 C1orf215 LAP18 OP18	1.61	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P61758	Prefoldin subunit 3 (HIBBJ46) (Von Hippel-Lindau-binding protein 1) (VBP-1) (VHL-binding protein 1)	VBP1 PFDN3	1.61	HEK293	5S-GlcNAc	24
Q9NTK5	Obg-like ATPase 1 (DNA damage-regulated overexpressed in cancer 45) (DOC45) (GTP-binding protein 9)	OLA1 GTPBP9 PRO2455 PTD004	1.60	HEK293	5S-GlcNAc	12
Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein)	CCT7 CCTH NIP7-1	1.60	HEK293	5S-GlcNAc	12
P62857	40S ribosomal protein S28	RPS28	1.60	HEK293	5S-GlcNAc	5
P04406	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH GAPD CDABP0047 OK/SW-cl.12	1.60	HEK293	5S-GlcNAc	12
P15311	Ezrin (Cytovillin) (Villin-2) (p81)	EZR VIL2	1.59	HEK293	5S-GlcNAc	5
P67809	Nuclease-sensitive element-binding protein 1 (CCAAT-binding transcription factor I subunit A) (CBF-A) (DNA-binding protein B) (DBPB) (Enhancer factor I subunit A) (EFI-A) (Y-box transcription factor) (Y-box-binding protein 1) (YB-1)	YBX1 NSEP1 YB1	1.59	HEK293	5S-GlcNAc	12
P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (Renal carcinoma antigen NY-REN-11) (Transformation-sensitive protein IEF SSP 3521)	STIP1	1.59	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q14157	Ubiquitin-associated protein 2-like (Protein NICE-4)	UBAP2L KIAA0144 NICE4	1.59	HEK293	5S-GlcNAc	5
Q02878	60S ribosomal protein L6 (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6 TXREB1	1.59	HEK293	5S-GlcNAc	5
P06733	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1 ENO1L1 MBPB1 MPB1	1.58	HEK293	5S-GlcNAc	12
P60866	40S ribosomal protein S20	RPS20	1.58	HEK293	5S-GlcNAc	12
P14618	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM OIP3 PK2 PK3 PKM2	1.58	HEK293	5S-GlcNAc	12
P61247	40S ribosomal protein S3a (v-fos transformation effector protein) (Fte-1)	RPS3A FTE1 MFTL	1.57	HEK293	5S-GlcNAc	5
Q9Y266	Nuclear migration protein nudC (Nuclear distribution protein C homolog)	NUDC	1.57	HEK293	5S-GlcNAc	12
Q92598	Heat shock protein 105 kDa (Antigen NY-CO-25) (Heat shock 110 kDa protein)	HSPH1 HSP105 HSP110 KIAA0201	1.57	HEK293	5S-GlcNAc	2

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P11940	Polyadenylate-binding protein 1 (PABP-1) (Poly(A)-binding protein 1)	PABPC1 PAB1 PABP1 PABPC2	1.57	HEK293	5S-GlcNAc	5
P55072	Transitional endoplasmic reticulum ATPase (TER ATPase) (EC 3.6.4.6) (15S Mg(2+)-ATPase p97 subunit) (Valosin-containing protein) (VCP)	VCP	1.57	HEK293	5S-GlcNAc	5
P62857	40S ribosomal protein S28	RPS28	1.57	HEK293	5S-GlcNAc	12
Q13561	Dynactin subunit 2 (50 kDa dynein-associated polypeptide) (Dynactin complex 50 kDa subunit) (DCTN-50) (p50 dynamitin)	DCTN2 DCTN50	1.56	HEK293	5S-GlcNAc	12
P23396	40S ribosomal protein S3	RPS3 OK/SW-cl.26	1.56	HEK293	5S-GlcNAc	5
P62258	14-3-3 protein epsilon (14-3-3E)	YWHAE	1.56	HEK293	5S-GlcNAc	12
P67809	Nuclease-sensitive element-binding protein 1 (CCAAT-binding transcription factor I subunit A) (CBF-A) (DNA-binding protein B) (DBPB) (Enhancer factor I subunit A) (EFI-A) (Y-box transcription factor) (Y-box-binding protein 1) (YB-1)	YBX1 NSEP1 YB1	1.54	HEK293	5S-GlcNAc	5
P23588	Eukaryotic translation initiation factor 4B (eIF-4B)	EIF4B	1.54	HEK293	5S-GlcNAc	12
P16989	Y-box-binding protein 3 (Cold shock domain-containing protein A) (DNA-binding protein A) (Single-strand DNA-binding protein NF-GMB)	YBX3 CSDA DBPA	1.54	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P22102	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (Glycinamide ribonucleotide synthetase) (GARS) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (5'-phosphoribosylglycinamide transformylase) (GAR transformylase) (GART)]	GART PGFT PRGS	1.53	HEK293	5S-GlcNAc	12
P62249	40S ribosomal protein S16	RPS16	1.53	HEK293	5S-GlcNAc	12
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8 HSC70 HSP73 HSPA10	1.53	HEK293	5S-GlcNAc	12
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8 HSC70 HSP73 HSPA10	1.53	HEK293	5S-GlcNAc	5

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P60842	Eukaryotic initiation factor 4A-I (eIF-4A-I) (eIF4A-I) (EC 3.6.4.13) (ATP-dependent RNA helicase eIF4A-1)	EIF4A1 DDX2A EIF4A	1.52	HEK293	5S-GlcNAc	12
P68104	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1 EEF1A EF1A LENG7	1.51	HEK293	5S-GlcNAc	24
P62701	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein)	RPS4X CCG2 RPS4 SCAR	1.51	HEK293	5S-GlcNAc	12
P61247	40S ribosomal protein S3a (v-fos transformation effector protein) (Fte-1)	RPS3A FTE1 MFTL	1.51	HEK293	5S-GlcNAc	12
O00273	DNA fragmentation factor subunit alpha (DNA fragmentation factor 45 kDa subunit) (DFF-45) (Inhibitor of CAD) (ICAD)	DFFA DFF1 DFF45 H13	1.50	HEK293	5S-GlcNAc	24
Q14677	Clathrin interactor 1 (Clathrin-interacting protein localized in the trans-Golgi region) (Clint) (Enthoprotin) (Epsin-4) (Epsin-related protein) (EpsinR)	CLINT1 ENTH EPN4 EPNR KIAA0171	1.50	HEK293	5S-GlcNAc	5
P31946	14-3-3 protein beta/alpha (Protein 1054) (Protein kinase C inhibitor protein 1) (KCIP-1) [Cleaved into: 14-3-3 protein beta/alpha, N-terminally processed]	YWHAB	1.50	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P30086	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPpp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	PEBP1 PBP PEBP	1.50	HEK293	5S-GlcNAc	24
P06753	Tropomyosin alpha-3 chain (Gamma-tropomyosin) (Tropomyosin-3) (Tropomyosin-5) (hTM5)	TPM3	1.50	HEK293	5S-GlcNAc	5
P09429	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1 HMG1	1.49	HEK293	5S-GlcNAc	24
P08107	Heat shock 70 kDa protein 1A/1B (Heat shock 70 kDa protein 1/2) (HSP70-1/HSP70-2) (HSP70.1/HSP70.2)	HSPA1A HSPA1 HSX70; HSPA1B	1.49	HEK293	5S-GlcNAc	5
P16949	Stathmin (Leukemia-associated phosphoprotein p18) (Metablastin) (Oncoprotein 18) (Op18) (Phosphoprotein p19) (pp19) (Prosolin) (Protein Pr22) (pp17)	STMN1 C1orf215 LAP18 OP18	1.49	HEK293	5S-GlcNAc	24
O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha (Alpha-SGT) (Vpu-binding protein) (UBP)	SGTA SGT SGT1	1.48	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P07900	Heat shock protein HSP 90-alpha (Heat shock 86 kDa) (HSP 86) (HSP86) (Lipopolysaccharide-associated protein 2) (LAP-2) (LPS-associated protein 2) (Renal carcinoma antigen NY-REN-38)	HSP90AA1 HSP90A HSPC1 HSPCA	1.48	HEK293	5S-GlcNAc	12
P16989	Y-box-binding protein 3 (Cold shock domain-containing protein A) (DNA-binding protein A) (Single-strand DNA-binding protein NF-GMB)	YBX3 CSDA DBPA	1.48	HEK293	5S-GlcNAc	12
P18206	Vinculin (Metavinculin) (MV)	VCL	1.48	HEK293	5S-GlcNAc	24
P27694	Replication protein A 70 kDa DNA-binding subunit (RP-A p70) (Replication factor A protein 1) (RF-A protein 1) (Single-stranded DNA-binding protein) [Cleaved into: Replication protein A 70 kDa DNA-binding subunit, N-terminally processed]	RPA1 REPA1 RPA70	1.48	HEK293	5S-GlcNAc	12
O75821	Eukaryotic translation initiation factor 3 subunit G (eIF3g) (Eukaryotic translation initiation factor 3 RNA-binding subunit) (eIF-3 RNA-binding subunit) (Eukaryotic translation initiation factor 3 subunit 4) (eIF-3-delta) (eIF3 p42) (eIF3 p44)	EIF3G EIF3S4	1.48	HEK293	5S-GlcNAc	12
P48643	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	CCT5 CCTE KIAA0098	1.48	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62993	Growth factor receptor-bound protein 2 (Adapter protein GRB2) (Protein Ash) (SH2/SH3 adapter GRB2)	GRB2 ASH	1.47	HEK293	5S-GlcNAc	12
P15880	40S ribosomal protein S2 (40S ribosomal protein S4) (Protein LLRep3)	RPS2 RPS4	1.47	HEK293	5S-GlcNAc	12
P50990	T-complex protein 1 subunit theta (TCP-1-theta) (CCT-theta) (Renal carcinoma antigen NY-REN-15)	CCT8 C21orf112 CCTQ KIAA0002	1.46	HEK293	5S-GlcNAc	12
P26583	High mobility group protein B2 (High mobility group protein 2) (HMG-2)	HMGB2 HMG2	1.46	HEK293	5S-GlcNAc	24
O60869	Endothelial differentiation-related factor 1 (EDF-1) (Multiprotein-bridging factor 1) (MBF1)	EDF1	1.46	HEK293	5S-GlcNAc	12
P17066	Heat shock 70 kDa protein 6 (Heat shock 70 kDa protein B')	HSPA6 HSP70B'	1.46	HEK293	5S-GlcNAc	5
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	CCT6A CCT6 CCTZ	1.45	HEK293	5S-GlcNAc	24
Q14247	Src substrate cortactin (Amplaxin) (Oncogene EMS1)	CTTN EMS1	1.44	HEK293	5S-GlcNAc	5
P62750	60S ribosomal protein L23a	RPL23A	1.44	HEK293	5S-GlcNAc	12
P63241	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A	1.44	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q9UQ80	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErbB3-binding protein 1)	PA2G4 EBP1	1.44	HEK293	5S-GlcNAc	12
P33176	Kinesin-1 heavy chain (Conventional kinesin heavy chain) (Ubiquitous kinesin heavy chain) (UKHC)	KIF5B KNS KNS1	1.43	HEK293	5S-GlcNAc	24
P00558	Phosphoglycerate kinase 1 (EC 2.7.2.3) (Cell migration-inducing gene 10 protein) (Primer recognition protein 2) (PRP 2)	PGK1 PGKA MIG10 OK/SW-cl.110	1.42	HEK293	5S-GlcNAc	24
Q13838	Spliceosome RNA helicase DDX39B (EC 3.6.4.13) (56 kDa U2AF65-associated protein) (ATP-dependent RNA helicase p47) (DEAD box protein UAP56) (HLA-B-associated transcript 1 protein)	DDX39B BAT1 UAP56	1.42	HEK293	5S-GlcNAc	8
Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1 RPL26P1	1.42	HEK293	5S-GlcNAc	12
P08238	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1 HSP90B HSPC2 HSPCB	1.42	HEK293	5S-GlcNAc	12
P22061	Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PIMT) (EC 2.1.1.77) (L-isoaspartyl protein carboxyl methyltransferase) (Protein L-isoaspartyl/D-aspartyl methyltransferase) (Protein-beta-aspartate methyltransferase)	PCMT1	1.41	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B (Acidic protein rich in leucines) (Putative HLA-DR-associated protein I-2) (PHAPI2) (Silver-stainable protein SSP29)	ANP32B APRIL PHAPI2	1.41	HEK293	5S-GlcNAc	24
P60174	Triosephosphate isomerase (TIM) (EC 5.3.1.1) (Triose-phosphate isomerase)	TPI1 TPI	1.40	HEK293	5S-GlcNAc	24
O00151	PDZ and LIM domain protein 1 (C-terminal LIM domain protein 1) (Elfin) (LIM domain protein CLP-36)	PDLIM1 CLIM1 CLP36	1.40	HEK293	5S-GlcNAc	12
Q9Y266	Nuclear migration protein nudC (Nuclear distribution protein C homolog)	NUDC	1.39	HEK293	5S-GlcNAc	24
P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (Renal carcinoma antigen NY-REN-11) (Transformation-sensitive protein IEF SSP 3521)	STIP1	1.39	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P22102	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (Glycinamide ribonucleotide synthetase) (GARS) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (5'-phosphoribosylglycinamide transformylase) (GAR transformylase) (GART)]	GART PGFT PRGS	1.38	HEK293	5S-GlcNAc	24
Q14677	Clathrin interactor 1 (Clathrin-interacting protein localized in the trans-Golgi region) (Clint) (Enthoprotin) (Epsin-4) (Epsin-related protein) (EpsinR)	CLINT1 ENTH EPN4 EPNR KIAA0171	1.37	HEK293	5S-GlcNAc	12
P62258	14-3-3 protein epsilon (14-3-3E)	YWHAE	1.37	HEK293	5S-GlcNAc	24
P62937	Peptidyl-prolyl cis-trans isomerase A (PPIase A) (EC 5.2.1.8) (Cyclophilin A) (Cyclosporin A-binding protein) (Rotamase A) [Cleaved into: Peptidyl-prolyl cis-trans isomerase A, N-terminally processed]	PPIA CYPA	1.37	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2 99D8.1 CCTB	1.37	HEK293	5S-GlcNAc	24
P14618	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM OIP3 PK2 PK3 PKM2	1.37	HEK293	5S-GlcNAc	24
Q99497	Protein DJ-1 (EC 3.4.-.-) (Oncogene DJ1) (Parkinson disease protein 7)	PARK7	1.36	HEK293	5S-GlcNAc	24
P13639	Elongation factor 2 (EF-2)	EEF2 EF2	1.36	HEK293	5S-GlcNAc	24
P09496	Clathrin light chain A (Lca)	CLTA	1.35	HEK293	5S-GlcNAc	5
P08107	Heat shock 70 kDa protein 1A/1B (Heat shock 70 kDa protein 1/2) (HSP70-1/HSP70-2) (HSP70.1/HSP70.2)	HSPA1A HSPA1 HSX70; HSPA1B	1.35	HEK293	5S-GlcNAc	12
P04406	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH GAPD CDABP0047 OK/SW-cl.12	1.35	HEK293	5S-GlcNAc	24
P08238	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1 HSP90B HSPC2 HSPCB	1.34	HEK293	5S-GlcNAc	24
P04075	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA ALDA	1.34	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P08107	Heat shock 70 kDa protein 1A/1B (Heat shock 70 kDa protein 1/2) (HSP70-1/HSP70-2) (HSP70.1/HSP70.2)	HSPA1A HSPA1 HSX70; HSPA1B	1.34	HEK293	5S-GlcNAc	24
Q14247	Src substrate cortactin (Amplaxin) (Oncogene EMS1)	CTTN EMS1	1.34	HEK293	5S-GlcNAc	12
P62158	Calmodulin (CaM)	CALM1 CALM CAM CAM1; CALM2 CAM2 CAMB; CALM3 CALML2 CAM3 CAMC CAMIII	1.33	HEK293	5S-GlcNAc	5
P14314	Glucosidase 2 subunit beta (80K-H protein) (Glucosidase II subunit beta) (Protein kinase C substrate 60.1 kDa protein heavy chain) (PKCSH)	PRKCSH G19P1	1.33	HEK293	5S-GlcNAc	8
P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	EEF1D EF1D	1.33	HEK293	5S-GlcNAc	24
P05455	Lupus La protein (La autoantigen) (La ribonucleoprotein) (Sjoegren syndrome type B antigen) (SS-B)	SSB	1.32	HEK293	5S-GlcNAc	24
P06733	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1 ENO1L1 MBPB1 MPB1	1.31	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 (PPIase FKBP4) (EC 5.2.1.8) (51 kDa FK506-binding protein) (FKBP51) (52 kDa FK506-binding protein) (52 kDa FKBP) (FKBP-52) (59 kDa immunophilin) (p59) (FK506-binding protein 4) (FKBP-4) (FKBP59) (HSP-binding immunophilin) (HBI) (Immunophilin FKBP52) (Rotamase) [Cleaved into: Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed]	FKBP4 FKBP52	1.31	HEK293	5S-GlcNAc	24
P08670	Vimentin	VIM	1.30	HEK293	5S-GlcNAc	8
Q07955	Serine/arginine-rich splicing factor 1 (Alternative-splicing factor 1) (ASF-1) (Splicing factor, arginine/serine-rich 1) (pre-mRNA-splicing factor SF2, P33 subunit)	SRSF1 ASF SF2 SF2P33 SFRS1 OK/SW-cl.3	1.30	HEK293	5S-GlcNAc	8
Q99878	Histone H2A type 1-J (Histone H2A/e)	HIST1H2AJ H2AFE	1.30	HEK293	5S-GlcNAc	8
O60814	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK H2BFT HIRIP1	1.30	HEK293	5S-GlcNAc	8
P23246	Splicing factor, proline- and glutamine-rich (100 kDa DNA-pairing protein) (hPOMp100) (DNA-binding p52/p100 complex, 100 kDa subunit) (Polypyrimidine tract-binding protein-associated-splicing factor) (PSF) (PTB-associated-splicing factor)	SFPQ PSF	1.30	HEK293	5S-GlcNAc	8

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8 HSC70 HSP73 HSPA10	1.30	HEK293	5S-GlcNAc	24
P61247	40S ribosomal protein S3a (v-fos transformation effector protein) (Fte-1)	RPS3A FTE1 MFTL	1.30	HEK293	5S-GlcNAc	24
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	1.30	HEK293	5S-GlcNAc	8
Q15233	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO NRB54	1.29	HEK293	5S-GlcNAc	8
Q15717	ELAV-like protein 1 (Hu-antigen R) (HuR)	ELAVL1 HUR	1.28	HEK293	5S-GlcNAc	8
P35637	RNA-binding protein FUS (75 kDa DNA-pairing protein) (Oncogene FUS) (Oncogene TLS) (POMp75) (Translocated in liposarcoma protein)	FUS TLS	1.28	HEK293	5S-GlcNAc	8

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P23528	Cofilin-1 (18 kDa phosphoprotein) (p18) (Cofilin, non-muscle isoform)	CFL1 CFL	1.27	HEK293	5S-GlcNAc	24
P67809	Nuclease-sensitive element-binding protein 1 (CCAAT-binding transcription factor I subunit A) (CBF-A) (DNA-binding protein B) (DBPB) (Enhancer factor I subunit A) (EFI-A) (Y-box transcription factor) (Y-box-binding protein 1) (YB-1)	YBX1 NSEP1 YB1	1.25	HEK293	5S-GlcNAc	8
P06454	Prothymosin alpha [Cleaved into: Prothymosin alpha, N-terminally processed; Thymosin alpha-1]	PTMA TMSA	1.24	HEK293	5S-GlcNAc	2
P43243	Matrin-3	MATR3 KIAA0723	1.23	HEK293	5S-GlcNAc	8
P31943	Heterogeneous nuclear ribonucleoprotein H (hnRNP H) [Cleaved into: Heterogeneous nuclear ribonucleoprotein H, N-terminally processed]	HNRNPH1 HNRPH HNRPH1	1.22	HEK293	5S-GlcNAc	8
P10809	60 kDa heat shock protein, mitochondrial (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1 HSP60	1.21	HEK293	5S-GlcNAc	8
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1 HNRPA2B1	1.21	HEK293	5S-GlcNAc	8

Appendix I: Table of volcano plot derived proteins showing increased turnover in HEK293 cells due to 5Thio-GlcNAc inhibition.

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q8N9T8	Protein KRI1 homolog	KRI1	23.34	HEK293	5S-GlcNAc	2
P07305	Histone H1.0 (Histone H1') (Histone H1(0)) [Cleaved into: Histone H1.0, N-terminally processed]	H1F0 H1FV	9.79	HEK293	5S-GlcNAc	2
Q9Y3C6	Peptidyl-prolyl cis-trans isomerase-like 1 (PPIase) (EC 5.2.1.8) (Rotamase PPIL1)	PPIL1 CYPL1 CGI-124 UNQ2425/PRO4984	6.36	HEK293	5S-GlcNAc	2
Q9H307	Pinin (140 kDa nuclear and cell adhesion-related phosphoprotein) (Desmosome-associated protein) (Domain-rich serine protein) (DRS protein) (DRSP) (Melanoma metastasis clone A protein) (Nuclear protein SDK3) (SR-like protein)	PNN DRS MEMA	4.53	HEK293	5S-GlcNAc	2

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P49327	Fatty acid synthase (EC 2.3.1.85) [Includes: [Acyl-carrier-protein] S-acetyltransferase (EC 2.3.1.38); [Acyl-carrier-protein] S-malonyltransferase (EC 2.3.1.39); 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41); 3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100); 3-hydroxyacyl-[acyl-carrier-protein] dehydratase (EC 4.2.1.59); Enoyl-[acyl-carrier-protein] reductase (EC 1.3.1.39); Oleoyl-[acyl-carrier-protein] hydrolase (EC 3.1.2.14)]	FASN FAS	3.78	HEK293	5S-GlcNAc	2
P35613	Basigin (5F7) (Collagenase stimulatory factor) (Extracellular matrix metalloproteinase inducer) (EMMPRIN) (Leukocyte activation antigen M6) (OK blood group antigen) (Tumor cell-derived collagenase stimulatory factor) (TCSF) (CD antigen CD147)	BSG UNQ6505/PRO21383	3.65	HEK293	5S-GlcNAc	8

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P11021	78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	HSPA5 GRP78	3.52	HEK293	5S-GlcNAc	24
P13667	Protein disulfide-isomerase A4 (EC 5.3.4.1) (Endoplasmic reticulum resident protein 70) (ER protein 70) (ERp70) (Endoplasmic reticulum resident protein 72) (ER protein 72) (ERp-72) (ERp72)	PDIA4 ERP70 ERP72	2.93	HEK293	5S-GlcNAc	24
Q6UXH1	Cysteine-rich with EGF-like domain protein 2	CRELD2 UNQ185/PRO211	2.53	HEK293	5S-GlcNAc	24
P55145	Mesencephalic astrocyte-derived neurotrophic factor (Arginine-rich protein) (Protein ARMET)	MANF ARMET ARP	2.40	HEK293	5S-GlcNAc	24
P30533	Alpha-2-macroglobulin receptor-associated protein (Alpha-2-MRAP) (Low density lipoprotein receptor-related protein-associated protein 1) (RAP)	LRPAP1 A2MRAP	2.18	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P14625	Endoplasmin (94 kDa glucose-regulated protein) (GRP-94) (Heat shock protein 90 kDa beta member 1) (Tumor rejection antigen 1) (gp96 homolog)	HSP90B1 GRP94 TRA1	2.02	HEK293	5S-GlcNAc	24
P11021	78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	HSPA5 GRP78	1.94	HEK293	5S-GlcNAc	12
P11021	78 kDa glucose-regulated protein (GRP-78) (Endoplasmic reticulum lumenal Ca(2+)-binding protein grp78) (Heat shock 70 kDa protein 5) (Immunoglobulin heavy chain-binding protein) (BiP)	HSPA5 GRP78	1.87	HEK293	5S-GlcNAc	8
Q15084	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	PDIA6 ERP5 P5 TXNDC7	1.76	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P30101	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	PDIA3 ERP57 ERP60 GRP58	1.53	HEK293	5S-GlcNAc	24
P27797	Calreticulin (CRP55) (Calregulin) (Endoplasmic reticulum resident protein 60) (ERp60) (HACBP) (grp60)	CALR CRTC	1.53	HEK293	5S-GlcNAc	24
P55145	Mesencephalic astrocyte-derived neurotrophic factor (Arginine-rich protein) (Protein ARMET)	MANF ARMET ARP	1.37	HEK293	5S-GlcNAc	12
P23284	Peptidyl-prolyl cis-trans isomerase B (PPIase B) (EC 5.2.1.8) (CYP-S1) (Cyclophilin B) (Rotamase B) (S-cyclophilin) (SCYLP)	PPIB CYPB	1.32	HEK293	5S-GlcNAc	24

Appendix J: Table of volcano plot derived proteins showing decreased turnover in HEK293 cells due to 5Thio-GlcNAc inhibition.

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
O00115	Deoxyribonuclease-2-alpha (EC 3.1.22.1) (Acid DNase) (Deoxyribonuclease II alpha) (DNase II alpha) (Lysosomal DNase II) (R31240_2)	DNASE2 DNASE2A DNL2	0.12	HEK293	5S-GlcNAc	24
P10599	Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphydryl protein) (SASP)	TXN TRDX TRX TRX1	0.12	HEK293	5S-GlcNAc	2
O75947	ATP synthase subunit d, mitochondrial (ATPase subunit d)	ATP5H My032	0.15	HEK293	5S-GlcNAc	2
Q92820	Gamma-glutamyl hydrolase (EC 3.4.19.9) (Conjugase) (GH) (Gamma-Glu-X carboxypeptidase)	GGH	0.17	HEK293	5S-GlcNAc	24
Q92542	Nicastrin	NCSTN KIAA0253 UNQ1874/PRO4317	0.19	HEK293	5S-GlcNAc	24
P36551	Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial (COX) (Coprogen oxidase) (Coproporphyrinogenase) (EC 1.3.3.3)	CPOX CPO CPX	0.22	HEK293	5S-GlcNAc	2
P15586	N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) (Glucosamine-6-sulfatase) (G6S)	GNS	0.24	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P13473	Lysosome-associated membrane glycoprotein 2 (LAMP-2) (Lysosome-associated membrane protein 2) (CD107 antigen-like family member B) (CD antigen CD107b)	LAMP2	0.26	HEK293	5S-GlcNAc	24
Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10 (PPIase FKBP10) (EC 5.2.1.8) (65 kDa FK506-binding protein) (65 kDa FKBP) (FKBP-65) (FK506-binding protein 10) (FKBP-10) (Immunophilin FKBP65) (Rotamase)	FKBP10 FKBP65 PSEC0056	0.28	HEK293	5S-GlcNAc	24
Q8IV08	Phospholipase D3 (PLD 3) (EC 3.1.4.4) (Choline phosphatase 3) (HindIII K4L homolog) (Hu-K4) (Phosphatidylcholine-hydrolyzing phospholipase D3)	PLD3	0.29	HEK293	5S-GlcNAc	12
Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10 (PPIase FKBP10) (EC 5.2.1.8) (65 kDa FK506-binding protein) (65 kDa FKBP) (FKBP-65) (FK506-binding protein 10) (FKBP-10) (Immunophilin FKBP65) (Rotamase)	FKBP10 FKBP65 PSEC0056	0.32	HEK293	5S-GlcNAc	12
P61916	Epididymal secretory protein E1 (Human epididymis-specific protein 1) (He1) (Niemann-Pick disease type C2 protein)	NPC2 HE1	0.33	HEK293	5S-GlcNAc	24
P32322	Pyrroline-5-carboxylate reductase 1, mitochondrial (P5C reductase 1) (P5CR 1) (EC 1.5.1.2)	PYCR1	0.34	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q9NZM5	Glioma tumor suppressor candidate region gene 2 protein (p60)	GLTSCR2	0.39	HEK293	5S-GlcNAc	8
Q00610	Clathrin heavy chain 1 (Clathrin heavy chain on chromosome 17) (CLH-17)	CLTC CLH17 CLTCL2 KIAA0034	0.42	HEK293	5S-GlcNAc	24
P35268	60S ribosomal protein L22 (EBER-associated protein) (EAP) (Epstein-Barr virus small RNA-associated protein) (Heparin-binding protein HBp15)	RPL22	0.44	HEK293	5S-GlcNAc	12
Q86U42	Polyadenylate-binding protein 2 (PABP-2) (Poly(A)-binding protein 2) (Nuclear poly(A)-binding protein 1) (Poly(A)-binding protein II) (PABII) (Polyadenylate-binding nuclear protein 1)	PABPN1 PAB2 PABP2	0.45	HEK293	5S-GlcNAc	12
P33993	DNA replication licensing factor MCM7 (EC 3.6.4.12) (CDC47 homolog) (P1.1-MCM3)	MCM7 CDC47 MCM2	0.45	HEK293	5S-GlcNAc	24
Q9H773	dCTP pyrophosphatase 1 (EC 3.6.1.12) (Deoxycytidine-triphosphatase 1) (dCTPase 1) (RS21C6) (XTP3-transactivated gene A protein)	DCTPP1 XTP3TPA CDA03	0.46	HEK293	5S-GlcNAc	24
O95347	Structural maintenance of chromosomes protein 2 (SMC protein 2) (SMC-2) (Chromosome-associated protein E) (hCAP-E) (XCAP-E homolog)	SMC2 CAPE SMC2L1 PRO0324	0.46	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q96AY3	Peptidyl-prolyl cis-trans isomerase FKBP10 (PPIase FKBP10) (EC 5.2.1.8) (65 kDa FK506-binding protein) (65 kDa FKBP) (FKBP-65) (FK506-binding protein 10) (FKBP-10) (Immunophilin FKBP65) (Rotamase)	FKBP10 FKBP65 PSEC0056	0.47	HEK293	5S-GlcNAc	8
P62424	60S ribosomal protein L7a (PLA-X polypeptide) (Surfeit locus protein 3)	RPL7A SURF-3 SURF3	0.47	HEK293	5S-GlcNAc	12
P15586	N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) (Glucosamine-6-sulfatase) (G6S)	GNS	0.47	HEK293	5S-GlcNAc	12
O75976	Carboxypeptidase D (EC 3.4.17.22) (Metallocarboxypeptidase D) (gp180)	CPD	0.48	HEK293	5S-GlcNAc	8
Q9BRK5	45 kDa calcium-binding protein (Cab45) (Stromal cell-derived factor 4) (SDF-4)	SDF4 CAB45 PSEC0034	0.49	HEK293	5S-GlcNAc	12
Q99460	26S proteasome non-ATPase regulatory subunit 1 (26S proteasome regulatory subunit RPN2) (26S proteasome regulatory subunit S1) (26S proteasome subunit p112)	PSMD1	0.50	HEK293	5S-GlcNAc	24
P46778	60S ribosomal protein L21	RPL21	0.50	HEK293	5S-GlcNAc	12
P05388	60S acidic ribosomal protein P0 (60S ribosomal protein L10E)	RPLP0	0.50	HEK293	5S-GlcNAc	8
Q9UNX3	60S ribosomal protein L26-like 1	RPL26L1 RPL26P1	0.51	HEK293	5S-GlcNAc	12
P18206	Vinculin (Metavinculin) (MV)	VCL	0.52	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P33993	DNA replication licensing factor MCM7 (EC 3.6.4.12) (CDC47 homolog) (P1.1-MCM3)	MCM7 CDC47 MCM2	0.52	HEK293	5S-GlcNAc	8
Q9BYG3	MKI67 FHA domain-interacting nucleolar phosphoprotein (Nucleolar phosphoprotein Nopp34) (Nucleolar protein interacting with the FHA domain of pKI-67) (hNIFK)	NIFK MKI67IP NOPP34	0.54	HEK293	5S-GlcNAc	8
P62750	60S ribosomal protein L23a	RPL23A	0.55	HEK293	5S-GlcNAc	12
O75955	Flotillin-1	FLOT1	0.55	HEK293	5S-GlcNAc	24
P29966	Myristoylated alanine-rich C-kinase substrate (MARCKS) (Protein kinase C substrate, 80 kDa protein, light chain) (80K-L protein) (PKCSL)	MARCKS MACS PRKCSL	0.55	HEK293	5S-GlcNAc	24
Q14566	DNA replication licensing factor MCM6 (EC 3.6.4.12) (p105MCM)	MCM6	0.55	HEK293	5S-GlcNAc	24
Q96PK6	RNA-binding protein 14 (Paraspeckle protein 2) (PSP2) (RNA-binding motif protein 14) (RRM-containing coactivator activator/modulator) (Synaptotagmin-interacting protein) (SYT-interacting protein)	RBM14 SIP	0.55	HEK293	5S-GlcNAc	12

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P36957	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial (EC 2.3.1.61) (2-oxoglutarate dehydrogenase complex component E2) (OGDC-E2) (Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex) (E2K)	DLST DLTS	0.55	HEK293	5S-GlcNAc	24
P13010	X-ray repair cross-complementing protein 5 (EC 3.6.4.-) (86 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 2) (ATP-dependent DNA helicase II 80 kDa subunit) (CTC box-binding factor 85 kDa subunit) (CTC85) (CTCBF) (DNA repair protein XRCC5) (Ku80) (Ku86) (Lupus Ku autoantigen protein p86) (Nuclear factor IV) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining))	XRCC5 G22P2	0.56	HEK293	5S-GlcNAc	12
Q03252	Lamin-B2	LMNB2 LMN2	0.56	HEK293	5S-GlcNAc	24
P23396	40S ribosomal protein S3 (EC 4.2.99.18)	RPS3 OK/SW-cl.26	0.56	HEK293	5S-GlcNAc	8

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P68104	Elongation factor 1-alpha 1 (EF-1-alpha-1) (Elongation factor Tu) (EF-Tu) (Eukaryotic elongation factor 1 A-1) (eEF1A-1) (Leukocyte receptor cluster member 7)	EEF1A1 EEF1A EF1A LENG7	0.56	HEK293	5S-GlcNAc	24
P20700	Lamin-B1	LMNB1 LMN2 LMNB	0.56	HEK293	5S-GlcNAc	24
P05141	ADP/ATP translocase 2 (ADP,ATP carrier protein 2) (ADP,ATP carrier protein, fibroblast isoform) (Adenine nucleotide translocator 2) (ANT 2) (Solute carrier family 25 member 5) [Cleaved into: ADP/ATP translocase 2, N-terminally processed]	SLC25A5 ANT2	0.56	HEK293	5S-GlcNAc	12
Q13263	Transcription intermediary factor 1-beta (TIF1-beta) (E3 SUMO-protein ligase TRIM28) (EC 6.3.2.-) (KRAB-associated protein 1) (KAP-1) (KRAB-interacting protein 1) (KRIP-1) (Nuclear corepressor KAP-1) (RING finger protein 96) (Tripartite motif-containing protein 28)	TRIM28 KAP1 RNF96 TIF1B	0.57	HEK293	5S-GlcNAc	24
Q16891	MICOS complex subunit MIC60 (Cell proliferation-inducing gene 4/52 protein) (Mitochondrial inner membrane protein) (Mitofilin) (p87/89)	IMMT HMP MIC60 MINOS2 PIG4 PIG52	0.57	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	0.57	HEK293	5S-GlcNAc	12
Q02878	60S ribosomal protein L6 (Neoplasm-related protein C140) (Tax-responsive enhancer element-binding protein 107) (TaxREB107)	RPL6 TXREB1	0.57	HEK293	5S-GlcNAc	12
P62244	40S ribosomal protein S15a	RPS15A OK/SW-cl.82	0.57	HEK293	5S-GlcNAc	8
P05387	60S acidic ribosomal protein P2 (Renal carcinoma antigen NY-REN-44)	RPLP2 D11S2243E RPP2	0.57	HEK293	5S-GlcNAc	8
P06748	Nucleophosmin (NPM) (Nucleolar phosphoprotein B23) (Nucleolar protein NO38) (Numatrin)	NPM1 NPM	0.58	HEK293	5S-GlcNAc	24
P05388	60S acidic ribosomal protein P0 (60S ribosomal protein L10E)	RPLP0	0.58	HEK293	5S-GlcNAc	12
P14868	Aspartate--tRNA ligase, cytoplasmic (EC 6.1.1.12) (Aspartyl-tRNA synthetase) (AspRS) (Cell proliferation-inducing gene 40 protein)	DARS PIG40	0.58	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P42704	Leucine-rich PPR motif-containing protein, mitochondrial (130 kDa leucine-rich protein) (LRP 130) (GP130)	LRPPRC LRP130	0.58	HEK293	5S-GlcNAc	12
P40227	T-complex protein 1 subunit zeta (TCP-1-zeta) (Acute morphine dependence-related protein 2) (CCT-zeta-1) (HTR3) (Tcp20)	CCT6A CCT6 CCTZ	0.58	HEK293	5S-GlcNAc	24
P13010	X-ray repair cross-complementing protein 5 (EC 3.6.4.-) (86 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 2) (ATP-dependent DNA helicase II 80 kDa subunit) (CTC box-binding factor 85 kDa subunit) (CTC85) (CTCBF) (DNA repair protein XRCC5) (Ku80) (Ku86) (Lupus Ku autoantigen protein p86) (Nuclear factor IV) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining))	XRCC5 G22P2	0.59	HEK293	5S-GlcNAc	24
P67936	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4	0.59	HEK293	5S-GlcNAc	8
P39019	40S ribosomal protein S19	RPS19	0.59	HEK293	5S-GlcNAc	12
Q08211	ATP-dependent RNA helicase A (RHA) (EC 3.6.4.13) (DEAH box protein 9) (Leukophysin) (LKP) (Nuclear DNA helicase II) (NDH II)	DHX9 DDX9 LKP NDH2	0.60	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q01844	RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein)	EWSR1 EWS	0.60	HEK293	5S-GlcNAc	24
P61247	40S ribosomal protein S3a (v-fos transformation effector protein) (Fte-1)	RPS3A FTE1 MFTL	0.60	HEK293	5S-GlcNAc	12
P31948	Stress-induced-phosphoprotein 1 (STI1) (Hsc70/Hsp90-organizing protein) (Hop) (Renal carcinoma antigen NY-REN-11) (Transformation-sensitive protein IEF SSP 3521)	STIP1	0.60	HEK293	5S-GlcNAc	24
P84103	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3 SFRS3 SRP20	0.60	HEK293	5S-GlcNAc	8
Q9Y3Y2	Chromatin target of PRMT1 protein (Friend of PRMT1 protein) (Small arginine- and glycine-rich protein) (SRAG)	CHTOP C1orf77 FOP HT031 PP7704	0.60	HEK293	5S-GlcNAc	24
P11177	Pyruvate dehydrogenase E1 component subunit beta, mitochondrial (PDHE1-B) (EC 1.2.4.1)	PDHB PHE1B	0.61	HEK293	5S-GlcNAc	24
O14979	Heterogeneous nuclear ribonucleoprotein D-like (hnRNP D-like) (hnRNP DL) (AU-rich element RNA-binding factor) (JKT41-binding protein) (Protein laAUF1)	HNRNPDL HNRPDL JKTBP	0.61	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P35268	60S ribosomal protein L22 (EBER-associated protein) (EAP) (Epstein-Barr virus small RNA-associated protein) (Heparin-binding protein HBp15)	RPL22	0.61	HEK293	5S-GlcNAc	24
Q14566	DNA replication licensing factor MCM6 (EC 3.6.4.12) (p105MCM)	MCM6	0.61	HEK293	5S-GlcNAc	8
P08107	Heat shock 70 kDa protein 1A/1B (Heat shock 70 kDa protein 1/2) (HSP70-1/HSP70-2) (HSP70.1/HSP70.2)	HSPA1A HSPA1 HSX70; HSPA1B	0.61	HEK293	5S-GlcNAc	24
P08865	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGr1-Ag) (NEM/1CHD4)	RPSA LAMBR LAMR1	0.61	HEK293	5S-GlcNAc	12
P05388	60S acidic ribosomal protein P0 (60S ribosomal protein L10E)	RPLP0	0.61	HEK293	5S-GlcNAc	24
P39023	60S ribosomal protein L3 (HIV-1 TAR RNA-binding protein B) (TARBP-B)	RPL3 OK/SW-cl.32	0.61	HEK293	5S-GlcNAc	8
P49368	T-complex protein 1 subunit gamma (TCP-1-gamma) (CCT-gamma) (hTRiC5)	CCT3 CCTG TRIC5	0.61	HEK293	5S-GlcNAc	24
P60866	40S ribosomal protein S20	RPS20	0.61	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62899	60S ribosomal protein L31	RPL31	0.61	HEK293	5S-GlcNAc	8
P17987	T-complex protein 1 subunit alpha (TCP-1-alpha) (CCT-alpha)	TCP1 CCT1 CCTA	0.61	HEK293	5S-GlcNAc	24
O95202	LETM1 and EF-hand domain-containing protein 1, mitochondrial (Leucine zipper-EF-hand-containing transmembrane protein 1)	LETM1	0.61	HEK293	5S-GlcNAc	24
P22102	Trifunctional purine biosynthetic protein adenosine-3 [Includes: Phosphoribosylamine--glycine ligase (EC 6.3.4.13) (Glycinamide ribonucleotide synthetase) (GARS) (Phosphoribosylglycinamide synthetase); Phosphoribosylformylglycinamidine cyclo-ligase (EC 6.3.3.1) (AIR synthase) (AIRS) (Phosphoribosyl-aminoimidazole synthetase); Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2) (5'-phosphoribosylglycinamide transformylase) (GAR transformylase) (GART)]	GART PGFT PRGS	0.62	HEK293	5S-GlcNAc	24
P45880	Voltage-dependent anion-selective channel protein 2 (VDAC-2) (hVDAC2) (Outer mitochondrial membrane protein porin 2)	VDAC2	0.62	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P45973	Chromobox protein homolog 5 (Antigen p25) (Heterochromatin protein 1 homolog alpha) (HP1 alpha)	CBX5 HP1A	0.62	HEK293	5S-GlcNAc	24
P09429	High mobility group protein B1 (High mobility group protein 1) (HMG-1)	HMGB1 HMG1	0.62	HEK293	5S-GlcNAc	24
P18621	60S ribosomal protein L17 (60S ribosomal protein L23) (PD-1)	RPL17	0.62	HEK293	5S-GlcNAc	8
P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A (Acidic nuclear phosphoprotein pp32) (pp32) (Leucine-rich acidic nuclear protein) (LANP) (Mapmodulin) (Potent heat-stable protein phosphatase 2A inhibitor I1PP2A) (Putative HLA-DR-associated protein I) (PHAPI)	ANP32A C15orf1 LANP MAPM PHAP1	0.62	HEK293	5S-GlcNAc	24
P46013	Antigen KI-67	MKI67	0.62	HEK293	5S-GlcNAc	12
P13639	Elongation factor 2 (EF-2)	EEF2 EF2	0.62	HEK293	5S-GlcNAc	8
P83731	60S ribosomal protein L24 (60S ribosomal protein L30)	RPL24	0.62	HEK293	5S-GlcNAc	8
Q96I99	Succinyl-CoA ligase [GDP-forming] subunit beta, mitochondrial (EC 6.2.1.4) (GTP-specific succinyl-CoA synthetase subunit beta) (Succinyl-CoA synthetase beta-G chain) (SCS-betaG)	SUCLG2	0.62	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9 GRP75 HSPA9B mt-HSP70	0.63	HEK293	5S-GlcNAc	8
P07954	Fumarate hydratase, mitochondrial (Fumarase) (EC 4.2.1.2)	FH	0.63	HEK293	5S-GlcNAc	24
Q99879	Histone H2B type 1-M (Histone H2B.e) (H2B/e)	HIST1H2BM H2BFE	0.63	HEK293	5S-GlcNAc	12
P05387	60S acidic ribosomal protein P2 (Renal carcinoma antigen NY-REN-44)	RPLP2 D11S2243E RPP2	0.63	HEK293	5S-GlcNAc	24
P38159	RNA-binding motif protein, X chromosome (Glycoprotein p43) (Heterogeneous nuclear ribonucleoprotein G) (hnRNP G) [Cleaved into: RNA-binding motif protein, X chromosome, N-terminally processed]	RBMX HNRPG RBMXP1	0.63	HEK293	5S-GlcNAc	24
P20700	Lamin-B1	LMNB1 LMN2 LMNB	0.63	HEK293	5S-GlcNAc	8
Q13526	Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1 (EC 5.2.1.8) (Peptidyl-prolyl cis-trans isomerase Pin1) (PPIase Pin1) (Rotamase Pin1)	PIN1	0.63	HEK293	5S-GlcNAc	24
O75390	Citrate synthase, mitochondrial (EC 2.3.3.1) (Citrate (Si)-synthase)	CS	0.63	HEK293	5S-GlcNAc	24
P67936	Tropomyosin alpha-4 chain (TM30p1) (Tropomyosin-4)	TPM4	0.63	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9 GRP75 HSPA9B mt-HSP70	0.63	HEK293	5S-GlcNAc	12
P29692	Elongation factor 1-delta (EF-1-delta) (Antigen NY-CO-4)	EEF1D EF1D	0.64	HEK293	5S-GlcNAc	8
P54819	Adenylate kinase 2, mitochondrial (AK 2) (EC 2.7.4.3) (ATP-AMP transphosphorylase 2) (ATP:AMP phosphotransferase) (Adenylate monophosphate kinase) [Cleaved into: Adenylate kinase 2, mitochondrial, N-terminally processed]	AK2 ADK2	0.64	HEK293	5S-GlcNAc	24
Q99878	Histone H2A type 1-J (Histone H2A/e)	HIST1H2AJ H2AFE	0.64	HEK293	5S-GlcNAc	8
P46060	Ran GTPase-activating protein 1 (RanGAP1)	RANGAP1 KIAA1835 SD	0.64	HEK293	5S-GlcNAc	24
P54727	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	RAD23B	0.64	HEK293	5S-GlcNAc	24
P14618	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	PKM OIP3 PK2 PK3 PKM2	0.64	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P13639	Elongation factor 2 (EF-2)	EEF2 EF2	0.64	HEK293	5S-GlcNAc	24
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8 HSC70 HSP73 HSPA10	0.65	HEK293	5S-GlcNAc	8
P09651	Heterogeneous nuclear ribonucleoprotein A1 (hnRNP A1) (Helix-destabilizing protein) (Single-strand RNA-binding protein) (hnRNP core protein A1) [Cleaved into: Heterogeneous nuclear ribonucleoprotein A1, N-terminally processed]	HNRNPA1 HNRPA1	0.65	HEK293	5S-GlcNAc	24
Q71DI3	Histone H3.2 (Histone H3/m) (Histone H3/o)	HIST2H3A; HIST2H3C H3F2 H3FM; HIST2H3D	0.65	HEK293	5S-GlcNAc	24
P26583	High mobility group protein B2 (High mobility group protein 2) (HMG-2)	HMGB2 HMG2	0.65	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P12956	X-ray repair cross-complementing protein 6 (EC 3.6.4.-) (EC 4.2.99.-) (5'-deoxyribose-5-phosphate lyase Ku70) (5'-dRP lyase Ku70) (70 kDa subunit of Ku antigen) (ATP-dependent DNA helicase 2 subunit 1) (ATP-dependent DNA helicase II 70 kDa subunit) (CTC box-binding factor 75 kDa subunit) (CTC75) (CTCBF) (DNA repair protein XRCC6) (Lupus Ku autoantigen protein p70) (Ku70) (Thyroid-lupus autoantigen) (TLAA) (X-ray repair complementing defective repair in Chinese hamster cells 6)	XRCC6 G22P1	0.65	HEK293	5S-GlcNAc	24
P08865	40S ribosomal protein SA (37 kDa laminin receptor precursor) (37LRP) (37/67 kDa laminin receptor) (LRP/LR) (67 kDa laminin receptor) (67LR) (Colon carcinoma laminin-binding protein) (Laminin receptor 1) (LamR) (Laminin-binding protein precursor p40) (LBP/p40) (Multidrug resistance-associated protein MGr1-Ag) (NEM/1CHD4)	RPSA LAMBR LAMR1	0.65	HEK293	5S-GlcNAc	24
Q9Y5J7	Mitochondrial import inner membrane translocase subunit Tim9	TIMM9 TIM9 TIM9A TIMM9A	0.65	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	0.65	HEK293	5S-GlcNAc	8
P18621	60S ribosomal protein L17 (60S ribosomal protein L23) (PD-1)	RPL17	0.65	HEK293	5S-GlcNAc	24
P48643	T-complex protein 1 subunit epsilon (TCP-1-epsilon) (CCT-epsilon)	CCT5 CCTE KIAA0098	0.65	HEK293	5S-GlcNAc	24
P61247	40S ribosomal protein S3a (v-fos transformation effector protein) (Fte-1)	RPS3A FTE1 MFTL	0.66	HEK293	5S-GlcNAc	24
P62701	40S ribosomal protein S4, X isoform (SCR10) (Single copy abundant mRNA protein)	RPS4X CCG2 RPS4 SCAR	0.66	HEK293	5S-GlcNAc	24
Q99878	Histone H2A type 1-J (Histone H2A/e)	HIST1H2AJ H2AFE	0.66	HEK293	5S-GlcNAc	12
P25398	40S ribosomal protein S12	RPS12	0.66	HEK293	5S-GlcNAc	24
P35232	Prohibitin	PHB	0.66	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8 HSC70 HSP73 HSPA10	0.66	HEK293	5S-GlcNAc	12
P61758	Prefoldin subunit 3 (HIBBJ46) (Von Hippel-Lindau-binding protein 1) (VBP-1) (VHL-binding protein 1)	VBP1 PFDN3	0.66	HEK293	5S-GlcNAc	24
Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13	TIMM13 TIM13B TIMM13A TIMM13B	0.66	HEK293	5S-GlcNAc	12
P18669	Phosphoglycerate mutase 1 (EC 3.1.3.13) (EC 5.4.2.11) (EC 5.4.2.4) (BPG-dependent PGAM 1) (Phosphoglycerate mutase isozyme B) (PGAM-B)	PGAM1 PGAMA CDABP0006	0.66	HEK293	5S-GlcNAc	24
P46013	Antigen KI-67	MKI67	0.66	HEK293	5S-GlcNAc	8
O60814	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK H2BFT HIRIP1	0.67	HEK293	5S-GlcNAc	12
P38646	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	HSPA9 GRP75 HSPA9B mt-HSP70	0.67	HEK293	5S-GlcNAc	24
P09622	Dihydrolipoyl dehydrogenase, mitochondrial (EC 1.8.1.4) (Dihydrolipoamide dehydrogenase) (Glycine cleavage system L protein)	DLD GCSL LAD PHE3	0.67	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P08238	Heat shock protein HSP 90-beta (HSP 90) (Heat shock 84 kDa) (HSP 84) (HSP84)	HSP90AB1 HSP90B HSPC2 HSPCB	0.67	HEK293	5S-GlcNAc	24
Q99832	T-complex protein 1 subunit eta (TCP-1-eta) (CCT-eta) (HIV-1 Nef-interacting protein)	CCT7 CCTH NIP7-1	0.67	HEK293	5S-GlcNAc	24
P20042	Eukaryotic translation initiation factor 2 subunit 2 (Eukaryotic translation initiation factor 2 subunit beta) (eIF-2-beta)	EIF2S2 EIF2B	0.67	HEK293	5S-GlcNAc	24
P30084	Enoyl-CoA hydratase, mitochondrial (EC 4.2.1.17) (Enoyl-CoA hydratase 1) (Short-chain enoyl-CoA hydratase) (SCEH)	ECHS1	0.68	HEK293	5S-GlcNAc	24
P62805	Histone H4	HIST1H4A H4/A H4FA; HIST1H4B H4/I H4FI; HIST1H4C H4/G H4FG; HIST1H4D H4/B H4FB; HIST1H4E H4/J H4FJ; HIST1H4F H4/C H4FC; HIST1H4H H4/H H4FH; HIST1H4I H4/M H4FM; HIST1H4J H4/E H4FE; HIST1H4K H4/D H4FD; HIST1H4L H4/K H4FK; HIST2H4A H4/N H4F2 H4FN HIST2H4; HIST2H4B H4/O H4FO; HIST4H4	0.68	HEK293	5S-GlcNAc	24
Q9UQ80	Proliferation-associated protein 2G4 (Cell cycle protein p38-2G4 homolog) (hG4-1) (ErbB3-binding protein 1)	PA2G4 EBP1	0.68	HEK293	5S-GlcNAc	24
P20700	Lamin-B1	LMNB1 LMN2 LMNB	0.68	HEK293	5S-GlcNAc	12
P24534	Elongation factor 1-beta (EF-1-beta)	EEF1B2 EEF1B EF1B	0.68	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q86V81	THO complex subunit 4 (Tho4) (Ally of AML-1 and LEF-1) (Aly/REF export factor) (Transcriptional coactivator Aly/REF) (bZIP-enhancing factor BEF)	ALYREF ALY BEF THOC4	0.68	HEK293	5S-GlcNAc	24
Q99497	Protein DJ-1 (EC 3.4.-.-) (Oncogene DJ1) (Parkinson disease protein 7)	PARK7	0.69	HEK293	5S-GlcNAc	24
O60814	Histone H2B type 1-K (H2B K) (HIRA-interacting protein 1)	HIST1H2BK H2BFT HIRIP1	0.69	HEK293	5S-GlcNAc	24
Q99878	Histone H2A type 1-J (Histone H2A/e)	HIST1H2AJ H2AFE	0.69	HEK293	5S-GlcNAc	24
Q9UBC2	Epidermal growth factor receptor substrate 15-like 1 (Eps15-related protein) (Eps15R)	EPS15L1 EPS15R	0.69	HEK293	5S-GlcNAc	24
Q00839	Heterogeneous nuclear ribonucleoprotein U (hnRNP U) (Scaffold attachment factor A) (SAF-A) (p120) (pp120)	HNRNPU HNRPU SAFA U21.1	0.70	HEK293	5S-GlcNAc	12
P08107	Heat shock 70 kDa protein 1A/1B (Heat shock 70 kDa protein 1/2) (HSP70-1/HSP70-2) (HSP70.1/HSP70.2)	HSPA1A HSPA1 HSX70; HSPA1B	0.70	HEK293	5S-GlcNAc	8
P50454	Serpin H1 (47 kDa heat shock protein) (Arsenic-transactivated protein 3) (AsTP3) (Cell proliferation-inducing gene 14 protein) (Collagen-binding protein) (Colligin) (Rheumatoid arthritis-related antigen RA-A47)	SERPINH1 CBP1 CBP2 HSP47 SERPINH2 PIG14	0.70	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P84103	Serine/arginine-rich splicing factor 3 (Pre-mRNA-splicing factor SRP20) (Splicing factor, arginine/serine-rich 3)	SRSF3 SFRS3 SRP20	0.70	HEK293	5S-GlcNAc	24
P31942	Heterogeneous nuclear ribonucleoprotein H3 (hnRNP H3) (Heterogeneous nuclear ribonucleoprotein 2H9) (hnRNP 2H9)	HNRNPH3 HNRPH3	0.70	HEK293	5S-GlcNAc	24
P09012	U1 small nuclear ribonucleoprotein A (U1 snRNP A) (U1-A) (U1A)	SNRPA	0.70	HEK293	5S-GlcNAc	24
P63241	Eukaryotic translation initiation factor 5A-1 (eIF-5A-1) (eIF-5A1) (Eukaryotic initiation factor 5A isoform 1) (eIF-5A) (Rev-binding factor) (eIF-4D)	EIF5A	0.70	HEK293	5S-GlcNAc	24
O00151	PDZ and LIM domain protein 1 (C-terminal LIM domain protein 1) (Elfin) (LIM domain protein CLP-36)	PDLIM1 CLIM1 CLP36	0.70	HEK293	5S-GlcNAc	24
Q12906	Interleukin enhancer-binding factor 3 (Double-stranded RNA-binding protein 76) (DRBP76) (M-phase phosphoprotein 4) (MPP4) (Nuclear factor associated with dsRNA) (NFAR) (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Translational control protein 80) (TCP80)	ILF3 DRBF MPHOSPH4 NF90	0.71	HEK293	5S-GlcNAc	24
P68363	Tubulin alpha-1B chain (Alpha-tubulin ubiquitous) (Tubulin K-alpha-1) (Tubulin alpha-ubiquitous chain)	TUBA1B	0.71	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P60709	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	ACTB	0.71	HEK293	5S-GlcNAc	24
P10412	Histone H1.4 (Histone H1b) (Histone H1s-4)	HIST1H1E H1F4	0.71	HEK293	5S-GlcNAc	12
P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 (hnRNP A2/B1)	HNRNPA2B1 HNRPA2B1	0.71	HEK293	5S-GlcNAc	24
P16949	Stathmin (Leukemia-associated phosphoprotein p18) (Metablastin) (Oncoprotein 18) (Op18) (Phosphoprotein p19) (pp19) (Prosolin) (Protein Pr22) (pp17)	STMN1 C1orf215 LAP18 OP18	0.72	HEK293	5S-GlcNAc	24
Q99623	Prohibitin-2 (B-cell receptor-associated protein BAP37) (D-prohibitin) (Repressor of estrogen receptor activity)	PHB2 BAP REA	0.72	HEK293	5S-GlcNAc	24
P61604	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	HSPE1	0.72	HEK293	5S-GlcNAc	24
P24752	Acetyl-CoA acetyltransferase, mitochondrial (EC 2.3.1.9) (Acetoacetyl-CoA thiolase) (T2)	ACAT1 ACAT MAT	0.72	HEK293	5S-GlcNAc	24
P04075	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	ALDOA ALDA	0.72	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q9Y230	RuvB-like 2 (EC 3.6.4.12) (48 kDa TATA box-binding protein-interacting protein) (48 kDa TBP-interacting protein) (51 kDa erythrocyte cytosolic protein) (ECP-51) (INO80 complex subunit J) (Repressing pontin 52) (Reptin 52) (TIP49b) (TIP60-associated protein 54-beta) (TAP54-beta)	RUVBL2 INO80J TIP48 TIP49B CGI-46	0.72	HEK293	5S-GlcNAc	24
P35579	Myosin-9 (Cellular myosin heavy chain, type A) (Myosin heavy chain 9) (Myosin heavy chain, non-muscle IIa) (Non-muscle myosin heavy chain A) (NMMHC-A) (Non-muscle myosin heavy chain IIa) (NMMHC II-a) (NMMHC-IIA)	MYH9	0.72	HEK293	5S-GlcNAc	24
P43487	Ran-specific GTPase-activating protein (Ran-binding protein 1) (RanBP1)	RANBP1	0.73	HEK293	5S-GlcNAc	24
P19338	Nucleolin (Protein C23)	NCL	0.73	HEK293	5S-GlcNAc	24
P43243	Matrin-3	MATR3 KIAA0723	0.73	HEK293	5S-GlcNAc	24
P19338	Nucleolin (Protein C23)	NCL	0.73	HEK293	5S-GlcNAc	8
Q99879	Histone H2B type 1-M (Histone H2B.e) (H2B/e)	HIST1H2BM H2BFE	0.73	HEK293	5S-GlcNAc	24
P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	HNRNPC HNRPC	0.74	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P11142	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	HSPA8 HSC70 HSP73 HSPA10	0.74	HEK293	5S-GlcNAc	24
P61978	Heterogeneous nuclear ribonucleoprotein K (hnRNP K) (Transformation up-regulated nuclear protein) (TUNP)	HNRNPK HNRPK	0.74	HEK293	5S-GlcNAc	24
Q15233	Non-POU domain-containing octamer-binding protein (NonO protein) (54 kDa nuclear RNA- and DNA-binding protein) (55 kDa nuclear protein) (DNA-binding p52/p100 complex, 52 kDa subunit) (NMT55) (p54(nrb)) (p54nrb)	NONO NRB54	0.74	HEK293	5S-GlcNAc	24
P78371	T-complex protein 1 subunit beta (TCP-1-beta) (CCT-beta)	CCT2 99D8.1 CCTB	0.74	HEK293	5S-GlcNAc	24
P10809	60 kDa heat shock protein, mitochondrial (60 kDa chaperonin) (Chaperonin 60) (CPN60) (Heat shock protein 60) (HSP-60) (Hsp60) (HuCHA60) (Mitochondrial matrix protein P1) (P60 lymphocyte protein)	HSPD1 HSP60	0.74	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 (PPIase FKBP4) (EC 5.2.1.8) (51 kDa FK506-binding protein) (FKBP51) (52 kDa FK506-binding protein) (52 kDa FKBP) (FKBP-52) (59 kDa immunophilin) (p59) (FK506-binding protein 4) (FKBP-4) (FKBP59) (HSP-binding immunophilin) (HBI) (Immunophilin FKBP52) (Rotamase) [Cleaved into: Peptidyl-prolyl cis-trans isomerase FKBP4, N-terminally processed]	FKBP4 FKBP52	0.74	HEK293	5S-GlcNAc	24
P09874	Poly [ADP-ribose] polymerase 1 (PARP-1) (EC 2.4.2.30) (ADP-ribosyltransferase diphtheria toxin-like 1) (ARTD1) (NAD(+) ADP-ribosyltransferase 1) (ADPRT 1) (Poly[ADP-ribose] synthase 1)	PARP1 ADPRT PPOL	0.75	HEK293	5S-GlcNAc	24
P52272	Heterogeneous nuclear ribonucleoprotein M (hnRNP M)	HNRNPM HNRPM NAGR1	0.75	HEK293	5S-GlcNAc	24
Q9Y5L4	Mitochondrial import inner membrane translocase subunit Tim13	TIMM13 TIM13B TIMM13A TIMM13B	0.76	HEK293	5S-GlcNAc	24
P04406	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	GAPDH GAPD CDABP0047 OK/SW-cl.12	0.76	HEK293	5S-GlcNAc	24
P08670	Vimentin	VIM	0.77	HEK293	5S-GlcNAc	24

UNIPROT ENTRY	Protein names	Gene names	Fold Change	Sample	Treatment	Hr
P06733	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	ENO1 ENO1L1 MBPB1 MPB1	0.79	HEK293	5S-GlcNAc	24

Appendix Table K: O-GlcNAc mapped sites reported in the literature

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732452G07 product:transcription factor 4, full insert sequence	81914326	Q8CE98	666	S268	GGMLGNSSHIPQSSSYCSLHPHERLSYPSHSSADINSSLPPMSTFHRSGTNHYSTSSCTPP	(Trinidad, Barkan et al. 2012)
15 days embryo brain cDNA, RIKEN full-length enriched library, clone:M421005L02 product:ERC2 homolog	123788009	Q3UHT7	977	T7	BBBBBBBBBBBBBBBBBBBBBBBMYGSARTISNLEGSPSRSPRLPRSPRLGHRRTSSGGG	(Trinidad et al., 2012)
182 kDa tankyrase-1-binding protein	150387848	P58871.2	1720	S260	ECQEEHSKTPEERNLTSSPAMNGDLAKLACSEAPTDVSKTWVTSSADPVSEHGGSTSAVRL	(Alfaro et al. 2012)
26S protease regulatory subunit 8	49065820	P62196.1	406	T272	APSIIFMDEIDSIGSSRLEGGSGGDSEVQRTMLELLNQLDGFEATKNIKVIMATNRIDILD	(Trinidad et al., 2012)
3-beta-hydroxysteroid-Delta(8),Delta(7)-isomerase	18202339	P70245.3	230	T2	BBBBBBBBBBBBBBBBBBBBBBBBBBBMTTNTVPLHPYWPRHLKLDNFVPNDLPTSHIL	(Myers et al. 2011)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
5'-3' exoribonuclease 1	81861755	P97789.1	1719	S1668	AQSSQATPLQTNKPGSSEATKMTPQESPPASSSSSQAAQPVSSHVETASQGHVGSQPRSAP	(Alfaro et al. 2012)
60S acidic ribosomal protein P2	46397855	P99027.3	115	S74	SELNGKNIEDVIAQGVGKLASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEKKEESEE	(Alfaro et al. 2012)
60S acidic ribosomal protein P2	133061	P05387.1	115	S86	AQGIGKLASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEKKDEKKEESEESDDDMGFGLFDB	(Hahne et al. 2012)
78 kDa glucose-regulated protein	149169999	P11021.2	654	S637	SHQDADIEDFKAKKKELEEIVQPIISKLYGSAGPPPTGEEDTAEKDELBBBBBBBBBBBBB	(Hahne et al. 2012)(Hahne et al. 2012)
85 kDa calcium-independent phospholipase A2	149170355	P97819.2	752	T650	DMIRKGQGNKVKKLSIVVSLGTGKSPQVPVTCVDVFRPSNPWELAKTVFGAKELGKMVVDC	(Trinidad et al., 2012)
Abelson tyrosine-protein kinase 2	118582158	Q4JIM5.1	1182	T872	GAAPARERPKAKLLPRGATALPLRAPDPAITESDSPGVGVAGVAAAPKGKERNGGTRLGVA	(Alfaro et al. 2012)
Abl interactor 2	50400259	P62484.1	446	T297	VPTPSPPSVFPGHPVQFYSMNRPASRHTPPTIGGSLPYRRPPSITSQTSLQNQMNGGPFYN	(Alfaro et al. 2012)(Trinidad et al., 2012)
Acetyl-CoA carboxylase 1	81862571	Q5SWU9.1	2345	T1185	RAYIAYELNSVQHRQLKDNTCVVEFQFMLPTSHPNRGNIPTLNRMSFASNLNHYGMTHVAS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Actin, alpha cardiac muscle 1	54036667	P68035.1	377	S157	ETFNVPAMYVAIQAVLSLYASGRTTGIVLDSGDGVTHNVPIYEGYALPHAIMRLDLAGRDL	(Ramirez-Correa et al. 2008)
Actin, alpha cardiac muscle 1	54036667	P68035.1	377	S201	YALPHAIMRLDLAGRDLTDYLMKILTERGYSFVTTAEREIVRDIKEKLCYVALDFENEMAT	(Ramirez-Correa et al. 2008)
Actin, alpha cardiac muscle 1	54036667	P68035.1	377	S234	TTAEREIVRDIKEKLCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNERFRCPETLF	(Ramirez-Correa et al. 2008)
Actin, alpha cardiac muscle 1	54036667	P68035.1	377	S325	LYANNVLSGGTTMYPGIADRMQKEITALAPSTMKIKIIAPPERKYSVWIGGSILASLSTFQ	(Ramirez-Correa et al. 2008)
Actin, alpha cardiac muscle 1	54036667	P68035.1	377	S370	SVWIGGSILASLSTFQQMWISKQEYDEAGPSIVHRKCFBBBBBBBBBBBBBBBBBBBBBB	(Ramirez-Correa et al. 2008)
Actin, alpha cardiac muscle 1	54036667	P68035.1	377	S54	AGDDAPRAVFPSIVGRPRHQGVMVGMGQKDSYVGDEAQSKRGILTLKYPIEHGIITNWDDM	(Ramirez-Correa et al. 2008)
Actin, alpha skeletal muscle	61218045	P68134.1	377	S241	VRDIKEKLCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGM	(Trinidad et al., 2012)
Actin, alpha skeletal muscle	61218045	P68134.1	377	T91	QSKRGILTLKYPIEHGIITNWDDMEKIWHHTFYNELRVAPEEHPTLLTEAPLNPKANREKM	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Actin, aortic smooth muscle	51316973	P62737.1	377	S241	VRDIKEKLCYVALDFENEMATAASSSSLEKSYELPDGQVITIGNERFRCPETLFQPSFIGM	(Trinidad et al., 2012)
Actin, cytoplasmic 1	46397334	P60710.1	375	S239	VRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNERFRCPEALFQPSFLGM	(Trinidad et al., 2012)
Actin, cytoplasmic 1	46397334	P60710.1	375	S365	RKYSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCFBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Actin, cytoplasmic 1	46397334	P60710.1	375	T106	VTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAI	(Trinidad et al., 2012)
Actin, cytoplasmic 1	46397334	P60710.1	375	T89	QSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKM	(Trinidad et al., 2012)
Actin, cytoplasmic 1	46397334	P60710.1	375	S199	YALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMAT	(Trinidad et al., 2012)
Actin, cytoplasmic 2	54036677	P63260.1	375	S239	VRDIKEKLCYVALDFEQEMATAASSSSLEKSYELPDGQVITIGNERFRCPEALFQPSFLGM	(Trinidad et al., 2012)
Actin, cytoplasmic 2	54036677	P63260.1	375	S365	RKYSVWIGGSILASLSTFQQMWISKQEYDESGPSIVHRKCFBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Actin, cytoplasmic 2	54036677	P63260.1	375	T106	VTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKMTQIMFETFNTPAMYVAI	(Trinidad et al., 2012)
Actin, cytoplasmic 2	54036677	P63260.1	375	T89	QSKRGILTLKYPIEHGIVTNWDDMEKIWHHTFYNELRVAPEEHPVLLTEAPLNPKANREKM	(Trinidad et al., 2012)
Actin, cytoplasmic 2	54036677	P63260.1	375	S199	YALPHAILRLDLAGRDLTDYLMKILTERGYSFTTTAEREIVRDIKEKLCYVALDFEQEMAT	(Trinidad et al., 2012)
Actin-binding LIM protein 1	56404616	Q8K4G5.1	861	S496	SLGESPRTLSPTPSAEGYQDVRDRMIHRSTSQGSINSPVYSRHSYTPTTSRSPQHFHRPEL	(Chalkley et al. 2009)
Actin-binding LIM protein 1	56404616	Q8K4G5.1	861	S499	ESPRTLSPTPSAEGYQDVRDRMIHRSTSQGSINSPVYSRHSYTPTTSRSPQHFHRPELLSP	(Chalkley et al. 2009)
Actin-binding LIM protein 1	56404616	Q8K4G5.1	861	S734	KEEMEKESRERASLASRYDSPLHSASHAPSSKTSSLPGYGKNGLHRPVSTDFAQYNSYGDI	(Trinidad et al., 2012)
Actin-binding LIM protein 1	56404616	Q8K4G5.1	861	S506	PTPSAEGYQDVRDRMIHRSTSQGSINSPVYSRHSYTPTTSRSPQHFHRPELLSPGVHRWSP	(Trinidad et al., 2012)
Actin-binding LIM protein 1	56404616	Q8K4G5.1	861	S729	GQLILKEEMEKESRERASLASRYDSPLHSASHAPSSKTSSLPGYGKNGLHRPVSTDFAQYN	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Actin-binding LIM protein 1	56404616	Q8K4G5.1	861	T473	ERPDLITYEPFYTSGYEDKQERQSLGESPRTLSPTPSAEGYQDVRDRMIHRSTSQGSINSP	(Trinidad et al., 2012)
Actin-binding LIM protein 2	56404602	Q8BL65.1	612	S373	GDRQSYGEGDQDDRSYKQCRTSSPSSAGSVSLGHYTPTSRSPQHYSRPGSESGRSTPSLSV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Actin-binding LIM protein 2	56404602	Q8BL65.1	612	S381	GDQDDRSYKQCRTSSPSSAGSVSLGHYTPTSRSPQHYSRPGSESGRSTPSLSVHSDSRPPS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Actin-binding LIM protein 2	56404602	Q8BL65.1	612	S412	RSPQHYSRPGSESGRSTPSLSVHSDSRPPSSTYQQAPRHFHVPDTGVKDNIYRKPPIYKQH	(Alfaro et al. 2012)
Actin-binding LIM protein 2	56404602	Q8BL65.1	612	S511	DSQSLSLSSGTDQEPLQRMAGDSLYSRFPYSKPDTLPGPRKDGLDLRNANLAPCGADPDAS	(Trinidad et al., 2012)
Actin-binding LIM protein 2	56404602	Q8BL65.1	612	T363	YSPYISHSAVGDRQSYGEGDQDDRSYKQCRTSSPSSAGSVSLGHYTPTSRSPQHYSRPGSE	(Alfaro et al. 2012)
Actin-binding LIM protein 2	56404602	Q8BL65.1	612	S402	VSLGHYTPTSRSPQHYSRPGSESGRSTPSLSVHSDSRPPSSTYQQAPRHFHVPDTGVKDNI	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Actin-binding LIM protein 3	56404493	Q69ZX8.2	682	S383	LSPYSQDIYENLDLRQRRASSPGYIDSPTYSRQGMSPTFSRSPHYYRSGPESGRSSPYHSQ	(Chalkley et al. 2009)(Alfaro et al. 2012)(Trinidad et al., 2012)
Actin-binding LIM protein 3	56404493	Q69ZX8.2	682	S419	PTFSRSPHYYRSGPESGRSSPYHSQLDVRSSTPTSYQAPKHFHIPAGESNIYRKPPIYKRH	(Chalkley et al. 2009)(Trinidad et al., 2012)
Actin-binding LIM protein 3	56404493	Q69ZX8.2	682	S423	RSPHYYRSGPESGRSSPYHSQLDVRSSTPTSYQAPKHFHIPAGESNIYRKPPIYKRHGDLS	(Chalkley et al. 2009)(Trinidad et al., 2012)
Actin-binding LIM protein 3	56404493	Q69ZX8.2	682	S534	GGEEEDFDRSMHKLQSGIGRLILKEEMKARSSSYADPWTPPRSSTSSREALHTTGYEMSFN	(Chalkley et al. 2009)(Trinidad et al., 2012)
Actin-binding LIM protein 3	56404493	Q69ZX8.2	682	S546	KLQSGIGRLILKEEMKARSSSYADPWTPPRSSTSSREALHTTGYEMSFNGSPRSHYLADSD	(Chalkley et al. 2009)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Actin-binding LIM protein 3	56404493	Q69ZX8.2	682	S547	LQSGIGRLILKEEMKARSSSYADPWTPPRSSTSSREALHTTGYEMSFNGSPRSHYLADSDP	(Chalkley et al. 2009)
Actin-binding LIM protein 3	56404493	Q69ZX8.2	682	S580	SREALHTTGYEMSFNGSPRSHYLADSDPLISKSASLPAYRRNGLHRTPSADLFHYDSMNAV	(Trinidad et al., 2012)
Actin-binding LIM protein 3	56404493	Q69ZX8.2	682	S536	EEEDFDRSMHKLQSGIGRLILKEEMKARSSSYADPWTPPRSSTSSREALHTTGYEMSFNGS	(Trinidad et al., 2012)
Activated CDC42 kinase 1	161789026	O54967.2	1055	T833	GSRTPSPLVPPGSSPLPHRLSSSPGKTMPTTQSFASDPKYATPQVIQAPGPRAGPCILPIV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Activated CDC42 kinase 1	161789026	O54967.2	1055	T832	QGSRTPSPLVPPGSSPLPHRLSSSPGKTMPTTQSFASDPKYATPQVIQAPGPRAGPCILPI	(Alfaro et al. 2012)
Activated CDC42 kinase 1	161789026	O54967.2	1055	S835	RTPSPLVPPGSSPLPHRLSSSPGKTMPTTQSFASDPKYATPQVIQAPGPRAGPCILPIVRD	(Trinidad et al., 2012)
Activated spleen cDNA, RIKEN full-length enriched library, clone:F830206E03 product:zinc finger protein 281, full insert sequence	123790706	Q3U063	893	S691	MLQEYSKYLQQAFEKSTNAGFTLGHGFQFVSLSSPLHNHTLFPEKQIYTTSPLECGFGQSV	(Myers et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Activated spleen cDNA, RIKEN full-length enriched library, clone:F830206E03 product:zinc finger protein 281, full insert sequence	123790706	Q3U063	893	S889	VRTSVSDFSGYTNMMSDVSEPCSTRVKTPTSQSYRBBBBBBBBBBBBBBBBBBB BBBBBBB	(Myers et al. 2011)
Activated spleen cDNA, RIKEN full-length enriched library, clone:F830206E03 product:zinc finger protein 281, full insert sequence	123790706	Q3U063	893	T888	RVRTSVSDFSGYTNMMSDVSEPCSTRVKTPTSQSYRBBBBBBBBBBBBBBBBBBB BBBBBBB	(Myers et al. 2011)
Adaptin ear-binding coat-associated protein 1	62287163	Q9CR95.2	275	S162	QETEISKESQEMDNRPKLDLGFKEGQTIKLSIGNITAKKGGASKPRASGTGGLSLL PPPPG	(Trinidad et al., 2012)
Adaptin ear-binding coat-associated protein 1	62287163	Q9CR95.2	275	S202	GASKPRASGTGGLSLLPPPPGGKVTIPPPSSSVAISNHVTPPPIPKSNHGGNDSDI LLDLD	(Trinidad et al., 2012)
Adaptin ear-binding coat-associated protein 1	62287163	Q9CR95.2	275	S203	ASKPRASGTGGLSLLPPPPGGKVTIPPPSSSVAISNHVTPPPIPKSNHGGNDSDIL LDLDS	(Trinidad et al., 2012)
Adenomatous polyposis coli protein	12643510	Q61315.1	2845	S2765	QKGTEAKPGQSNPVSIAETAETCIAERTPFSSSSSSKHSSPSGTVAARVTPFNYN PSPRKS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Adenomatous polyposis coli protein	12643510	Q61315.1	2845	T2843	TNTKKRDSKTDITESSGAQSPKRHSGSYLVTSVBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Adenomatous polyposis coli protein	12643510	Q61315.1	2845	T865	SRGSLDSSRSEKDRSLERERGIGLSAYHPTTENAGTSSKRGLQITTTAAQIAKVMEEVSAI	(Trinidad et al., 2012)
Adenomatous polyposis coli protein	12643510	Q61315.1	2845	T881	ERERGIGLSAYHPTTENAGTSSKRGLQITTTAAQIAKVMEEVSAIHTSQDDRSSASTTEFH	(Trinidad et al., 2012)
Adipocyte plasma membrane-associated protein	24211474	Q9HDC9.2	416	T162	IARFGSGPCKTRDDEPVCGRPLGIRAGPNGTLFVADAYKGLFEVNPWKREVKLLLSSETPI	(Hahne et al. 2012)
Adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230003L08 product:Cytomatrix protein p110 homolog	123793589	Q3TRG3	405	T187	EVILDQKEKENIHLREELHRRSQLQPEPAKTKALQTVIEMKDTKIASLERNIRDLEDEVQM	(Trinidad et al., 2012)
Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430510H01 product:hypothetical protein, full insert sequence	123785415	Q3UY82	251	S103	EDMELSDVEDDGSKIIVEDRKEKPVEKPAVSTGVPTKSTESVSKASPCAPPSVPTTAAPLL	(Myers et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Adult male olfactory brain cDNA, RIKEN full-length enriched library, clone:6430510H01 product:hypothetical protein, full insert sequence	123785415	Q3UY82	251	T104	DMELSDVEDDGSKIIVEDRKEKPVEKPAVSTGVPTKSTESVSKASPCAPPSVPTTAAPLLP	(Myers et al. 2011)
Adult pancreas islet cells cDNA, RIKEN full-length enriched library, clone:C820001M09 product:hypothetical protein, full insert sequence	123791232	Q3UFK1	184	S182	NLDRLLSDLEELNSSIQKLHLADAQDVPNASSSBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Alpha-1-antichymotrypsin	112874	P01011.2	423	S118	SLGAHNTTLTEILKGLKFNLTETSEAEIHQSFQHLLRTLNQSSDELQLSMGNAMFVKEQLS	(Hahne et al. 2012)
Alpha-1-antichymotrypsin	112874	P01011.2	423	S273	MMSLHHLTIPYFRDEELSCTVVELKYTGNASALFILPDQDKMEEVEAMLLPETLKRWRDSL	(Hahne et al. 2012)
Alpha-1-antichymotrypsin	112874	P01011.2	423	T108	LSISTALAFLSLGAHNTTLTEILKGLKFNLTETSEAEIHQSFQHLLRTLNQSSDELQLSMG	(Hahne et al. 2012)
Alpha-2-macroglobulin receptor-associated protein	231539	P30533.1	357	S139	ARLIRNLNVILAKYGLDGKKDARQVTSNSLSGTQEDGLDDPRLEKLWHKAKTSGKFSGEEL	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Alpha-adducin	10719868	Q9QYC0.2	735	S557	VMMDRSLVQGELVTASKAIIEKEYQPHVIVSTTGPNPFNTLTDRELEEYRREVERKQKGSE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Alpha-adducin	10719868	Q9QYC0.2	735	T17	BBBBBBBBBBBBBBMNGDTRAAVVTSPPPTTAPHKERYFDRVDENNPEYLRERNMAPDLRQ	(Alfaro et al. 2012)(Trinidad et al., 2012)
Alpha-adducin	10719868	Q9QYC0.2	735	S542	QDIKTAGPQSQVLCGVMMDRSLVQGELVTASKAIIEKEYQPHVIVSTTGPNPFNTLTDREL	(Trinidad et al., 2012)
Alpha-adducin	10719868	Q9QYC0.2	735	T11	BBBBBBBBBBBBBBBBBBBMNGDTRAAVVTSPPPTTAPHKERYFDRVDENNPEYLRERNM	(Alfaro et al. 2012)
Alpha-adducin	10719868	Q9QYC0.2	735	T16	BBBBBBBBBBBBBBMNGDTRAAVVTSPPPTTAPHKERYFDRVDENNPEYLRERNMAPDLR	(Alfaro et al. 2012)
Alpha-adducin	10719868	Q9QYC0.2	735	T540	NLQDIKTAGPQSQVLCGVMMDRSLVQGELVTASKAIIEKEYQPHVIVSTTGPNPFNTLTDR	(Alfaro et al. 2012)
Alpha-adducin	10719868	Q9QYC0.2	735	T558	MMDRSLVQGELVTASKAIIEKEYQPHVIVSTTGPNPFNTLTDRELEEYRREVERKQKGSEE	(Alfaro et al. 2012)
Alpha-adducin	10719868	Q9QYC0.2	735	T559	MDRSLVQGELVTASKAIIEKEYQPHVIVSTTGPNPFNTLTDRELEEYRREVERKQKGSEEN	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Alpha-adducin	10719868	Q9QYC0.2	735	S12	BBBBBBBBBBBBBBBBBBMNGDTRAAVVTSPPPTTAPHKERYFDRVDENNPEYLRERNMA	(Trinidad et al., 2012)
alpha-crystallin A chain	27805855	NP_776714.1	173	S162	SLSADGMLTFSGPKIPSGVDAGHSERAIPVSREEKPSSAPSSBBBBBBBBBBBBBBBBBBB	(Roquemore et al. 1992)
Alpha-internexin	94730353	P46660.2	504	S55	LSARLSGPGGSGSFRSQSLSRSNVASTAACSSASSLGLGLAYRRLPASDGLDLSQAAARTN	(Alfaro et al. 2012)
Alpha-internexin	94730353	P46660.2	504	S72	SLSRSNVASTAACSSASSLGLGLAYRRLPASDGLDLSQAAARTNEYKIIRTNEKEQLQGLN	(Trinidad et al., 2012)
Alpha-synuclein	13432217	O55042.2	140	T72	SKTKEGVVHGVTTVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGNIAAATGFVKKDQMGK	(Alfaro et al. 2012)(Trinidad et al., 2012)
Alpha-synuclein	13432217	O55042.2	140	T53	KQGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTKEQVTNVGGAVVTGVTAVAQKTVE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Alpha-synuclein	13432217	O55042.2	140	T64	KEGVLYVGSKTKEGVVHGVTTVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGNIAAATGF	(Alfaro et al. 2012)
Alpha-synuclein	586067	P37840.1	140	S87	EKTKEQVTNVGGAVVTGVTAVAQKTVEGAGSIAAATGFVKKDQLGKNEEGAPQEGILEDMP	(Wang et al. 2009)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Alpha-synuclein	13432217	O55042.2	140	T59	AAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGNIA	(Trinidad et al., 2012)
Alpha-synuclein	13432217	O55042.2	140	T54	QGVAEAAGKTKEGVLYVGSKTKEGVVHGVTTVAEKTKEQVTNVGGAVVTGVTAVAQKTVEG	(Trinidad et al., 2012)
Alsin	30580358	Q920R0.2	1651	T404	DLHSPPTTSTSALNSLVVSCASAVGVRVAATYEAGALSLKKVMNFYSTAPCETAAQSGSAS	(Trinidad et al., 2012)
Amyloid beta (A4) protein (CDNA, RIKEN full-length enriched library, clone:M5C1069M13 product:amyloid beta (A4) protein, full insert sequence)	81886292	Q6GR78	695	T292	YEEATERTTSTATTTTTTTESVEEVVRVPTTAASTPDAVDKYLETPGDENEHAHFQKAKER	(Trinidad et al., 2012)
Amyloid beta A4 precursor protein-binding family B member 1	341940602	Q9QXJ1.3	710	S666	MFWCEPNAASLSEAVQAACMLRYQKCLDARSQTSTSCLPAPPAESVARRVGWTVRRGVQSL	(Trinidad et al., 2012)
Amyloid beta A4 protein	30581015	P12023.3	770	T651	WHPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFGHDSGF	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Amyloid beta A4 protein	30581015	P12023.3	770	T652	HPFGVDSVPANTENEVEPVDARPAADRGLTTRPGSGLTNIKTEEISEVKMDAEFGHDSGFE	(Trinidad et al., 2012)
Amyloid-like protein 1	416630	Q03157.1	653	S277	SFPQPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPRPTDGVDVYFGMPGEI	(Trinidad et al., 2012)
Amyloid-like protein 1	416630	Q03157.1	653	T280	QPVDDYFVEPPQAEEEEEEEEERAPPPSSHTPVMVSRVTPTPRPTDGVDVYFGMPGEIGEH	(Trinidad et al., 2012)
AN1-type zinc finger protein 2B	81902379	Q91X58.1	257	T167	EGHQTSRAGLAAISRAQGLASTSTAPSPSRTLPSSSSPSRATPQLPTRTASPVIALQNGLS	(Alfaro et al. 2012)
AN1-type zinc finger protein 2B	81902379	Q91X58.1	257	S159	PLDHECSGEGHQTSRAGLAAISRAQGLASTSTAPSPSRTLPSSSSPSRATPQLPTRTASPV	(Trinidad et al., 2012)
Angiomotin	158936747	Q8VHG2.3	1126	T196	DLKQGHVRSLSERLMQMSLATSGVKAHPPVTSAPLSPPQPNDLYKNATSSSEFYKAQGPPP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Angiomotin	158936747	Q8VHG2.3	1126	S183	LTPGKMHQDEGLRDLKQGHVRSLSERLMQMSLATSGVKAHPPVTSAPLSPPQPNDLYKNAT	(Trinidad et al., 2012)
Angiomotin	158936747	Q8VHG2.3	1126	T275	FKGVPSQSVVCKSQEPGHFYSEHRLNQPGRTEGQLMRYQHPPEYGAARATQDISSLSLSAR	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Ankyrin repeat and KH domain-containing protein 1	74750718	Q8IWZ3.1	2542	S1817	SIHANFSSGVGTTAASSKNAFPLGAPTLVTSQATTLSTFQPANKLNKNVPTNVRSSFPVSL	(Zhao et al. 2011)
Ankyrin repeat and KH domain-containing protein 1	74750718	Q8IWZ3.1	2542	T1816	KSIHANFSSGVGTTAASSKNAFPLGAPTLVTSQATTLSTFQPANKLNKNVPTNVRSSFPVS	(Zhao et al. 2011)
Ankyrin repeat and KH domain-containing protein 1	74750718	Q8IWZ3.1	2542	T1820	ANFSSGVGTTAASSKNAFPLGAPTLVTSQATTLSTFQPANKLNKNVPTNVRSSFPVSLPLA	(Zhao et al. 2011)
Ankyrin repeat and sterile alpha motif domain-containing protein 1B	341940603	Q8BIZ1.3	1259	S440	PCNGCRNLGFPMLAQESYPKKRNFPMEMEPSASLDTFPSENENFLCELVDTAVTKKPCSLE	(Trinidad et al., 2012)
Ankyrin repeat and sterile alpha motif domain-containing protein 1B	341940603	Q8BIZ1.3	1259	S442	NGCRNLGFPMLAQESYPKKRNFPMEMEPSASLDTFPSENENFLCELVDTAVTKKPCSLEIA	(Trinidad et al., 2012)
Ankyrin repeat domain-containing protein 17	160017861	Q99NH0.2	2603	T1822	PDKEIDELIPKNRLKSSTANSKIGSSAPTTTAANSSLMGIKMTTVALSSTSQTATALTVPA	(Alfaro et al. 2012)(Trinidad et al., 2012)
Ankyrin repeat domain-containing protein 17	160017861	Q99NH0.2	2603	T1821	DPDKEIDELIPKNRLKSSTANSKIGSSAPTTTAANSSLMGIKMTTVALSSTSQTATALTVP	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Ankyrin repeat domain-containing protein 17	160019013	O75179.3	2603	T1830	IDELIPKNRLKSSSANSKIGSSAPTTTAANTSLMGIKMTTVALSSTSQTATALTVPAISSA	(Hahne et al. 2012)
Ankyrin repeat domain-containing protein 17	160017861	Q99NH0.2	2603	S2193	SQPPKMEAPAIRPPSHATAAPHKTPAPVQSSSASVLNVNHIKRPHSVPSSVQLPSTLSTQS	(Trinidad et al., 2012)
Ankyrin repeat domain-containing protein 17	160017861	Q99NH0.2	2603	S2382	PLGGAPLGGAPTAANFNRQHFSPLSLLTPCSSASNESPAQSVSSGVRAPSPAPSSVPLGSE	(Alfaro et al. 2012)
Ankyrin repeat domain-containing protein 17	160017861	Q99NH0.2	2603	S2388	LGGAPTAANFNRQHFSPLSLLTPCSSASNESPAQSVSSGVRAPSPAPSSVPLGSEKPSSVS	(Alfaro et al. 2012)
Ankyrin repeat domain-containing protein 17	160017861	Q99NH0.2	2603	T1834	RLKSSTANSKIGSSAPTTTAANSSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKN	(Alfaro et al. 2012)
Ankyrin repeat domain-containing protein 17	160017861	Q99NH0.2	2603	T2379	PGAPLGGAPLGGAPTAANFNRQHFSPLSLLTPCSSASNESPAQSVSSGVRAPSPAPSSVPL	(Trinidad et al., 2012)
Ankyrin repeat domain-containing protein 40	818895223	Q5SUE8.1	363	T199	GAFPRDHSSLALVQNGDISAPSAILRTPESTKPGPVCQPPVSQNRSLFSVPSKPPVSLEPQ	(Alfaro et al. 2012)(Trinidad et al., 2012)
Ankyrin-1	116241246	P16157.3	1881	S1162	VTVEPRRRKFHRPIGLRIPLPPSWTDNPRDSGEGDTTSLRLLCSVIGGTDQAQWEDITGTT	(Wang et al. 2009)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Ankyrin-1	116241246	P16157.3	1881	S794	SSDGTTPLAIAKRLGYISVTDVLKVVTDETSFVLVSDKHRMSFPETVDEILDVSEDEGEEL	(Wang et al. 2009)
Ankyrin-1	116241246	P16157.3	1881	S960	RHNGLRVVIPPRTCAAPTRITCRLVKPQKLSTPPPLAEEEGLASRIIALGPTGAQFLSPVI	(Wang et al. 2009)
Ankyrin-1	116241246	P16157.3	1881	S288	LLDRGAQIETKTKDELTPLHCAARNGHVRISEILLDHGAPIQAKTKNGLSPIHMAAQGDHL	(Wang et al. 2009)
Ankyrin-2	223634791	Q8C8R3.2	3898	S1337	IEARLRCFCMTDDKVDKTLEQQENFSEVARSRDVEVLEGKPIYVDCFGNLVPLTKSGQHHI	(Trinidad et al., 2012)
Ankyrin-2	223634791	Q8C8R3.2	3898	S2024	GHTVTQREVTQRETQRIESQTAKRGQRFQVSAATESRRFRSTTITVGLRMEDPVRERFERT	(Trinidad et al., 2012)
Ankyrin-2	223634791	Q8C8R3.2	3898	T2905	ENSDPQIISPYENVPSSSFFSAEPSKIQTDTCHSTVVHSPEVYSVIIRSSPEDVVVTNSSN	(Trinidad et al., 2012)
Ankyrin-2	223634791	Q8C8R3.2	3898	T2931	IQTDTCHSTVVHSPEVYSVIIRSSPEDVVVTNSSNRTVSGEESHCESHDLETESEQKSALW	(Alfaro et al. 2012)
Ankyrin-2	223634791	Q8C8R3.2	3898	T2903	TDENSDPQIISPYENVPSSSFFSAEPSKIQTDTCHSTVVHSPEVYSVIIRSSPEDVVVTNS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Ankyrin-2	223634791	Q8C8R3.2	3898	T3682	KESESSDHPPMVSEEDISVGYSTFQDCLPKTEGDSPAAALSPQMHQEPVQQDFSGKTQDQQ	(Trinidad et al., 2012)
Ankyrin-2	223634791	Q8C8R3.2	3898	T3759	ATAVPDSLCKTPEDISTPPEGTKPCLQTPVTSERGSPIVQEPEEASEPKEESSPRKTSLVI	(Trinidad et al., 2012)
AP-2 complex subunit alpha-2	341940231	P17427.2	938	T126	LFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIANVGSREMAEAFAGEIPKILV	(Trinidad et al., 2012)
AP2-associated protein kinase 1	115503759	Q3UHJ0.2	959	S648	TPPSSPKTQRAGHRRILSDVTHSAVFGVPASKSTQLLQAAAAEASLNKSKSATTTPSGSPR	(Trinidad et al., 2012)
AP2-associated protein kinase 1	115503759	Q3UHJ0.2	959	T360	PAKLPEPVKASEAAVKKTQPKARLTDPIPTTETSIAPRQRPKAGQTQPNPGILPIQPALTP	(Alfaro et al. 2012)
AP2-associated protein kinase 1	115503759	Q3UHJ0.2	959	T578	QQQQQQLMAQQAALQQKTAVVVPQSQAQPATAPQAAAAQEPGQIQAPVRQQPKVQTTPPPT	(Trinidad et al., 2012)
Aquaporin-1	267412	P29972.3	269	S236	FSNHWIFWVGPFIGGALAVLIYDFILAPRSSDLTDRVKVWTSGQVEEYDLDADDINSRVEM	(Wang et al. 2009)
Arachidonate 5-lipoxygenase-activating protein	120267	P20292.2	161	T152	LFLMSVAGIFNYYLIFFFGSDFENYIKTISTTISPLLLIPBBBBBBBBBBBBBBBBBBBB	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
ARF GTPase-activating protein GIT1	81910752	Q68FF6.1	770	S570	LQPFHSTELEDDAIYSVHVPAGLYRIRKGVSASSVPFTPSSPLLSCSQEGSRHASKLSRHG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Arf-GAP domain and FG repeat-containing protein 1	90110041	Q8K2K6.2	561	S302	GGSAGSVNANFAHFDNFPKSSSADFGTFSTSQSHQTASTVSKVSTNKAGLQTADKYAALAN	(Alfaro et al. 2012)(Trinidad et al., 2012)
Arf-GAP domain and FG repeat-containing protein 1	90110041	Q8K2K6.2	561	S367	FSAGQGGDQGSGFGTTGKAPVGSVVSVPSHSSASSDKYAALAELDSVFSSAATSSNAYTPT	(Alfaro et al. 2012)(Trinidad et al., 2012)
Arf-GAP domain and FG repeat-containing protein 1	26007019	P52594.2	562	S362	NLDNIFSAGQGGDQGSGFGTTGKAPVGSVVSVPSQSSASSDKYAALAELDSVFSSAATSSN	(Zhao et al. 2011)
Arf-GAP domain and FG repeat-containing protein 1	26007019	P52594.2	562	S365	NIFSAGQGGDQGSGFGTTGKAPVGSVVSVPSQSSASSDKYAALAELDSVFSSAATSSNAYT	(Zhao et al. 2011)
Arf-GAP domain and FG repeat-containing protein 1	26007019	P52594.2	562	S367	FSAGQGGDQGSGFGTTGKAPVGSVVSVPSQSSASSDKYAALAELDSVFSSAATSSNAYTST	(Zhao et al. 2011)
Arf-GAP domain and FG repeat-containing protein 1	26007019	P52594.2	562	S368	SAGQGGDQGSGFGTTGKAPVGSVVSVPSQSSASSDKYAALAELDSVFSSAATSSNAYTSTS	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Arf-GAP domain and FG repeat-containing protein 1	26007019	P52594.2	562	S370	GQGGDQGSGFGTTGKAPVGSVVSVPSQSSASSDKYAALAELDSVFSSAATSSNAYTSTSNA	(Zhao et al. 2011)
Arf-GAP domain and FG repeat-containing protein 1	90110041	Q8K2K6.2	561	T298	PQTTGGSAGSVNANFAHFDNFPKSSSADFGTFSTSQSHQTASTVSKVSTNKAGLQTADKYA	(Alfaro et al. 2012)
Arf-GAP domain and FG repeat-containing protein 1	90110041	Q8K2K6.2	561	S138	RDPQKVKEFLQEKYEKKRWYVPPEQAKVVASVHASISGSSASSTSSTPEVKPLKSLLGESA	(Alfaro et al. 2012)
Arf-GAP domain and FG repeat-containing protein 1	90110041	Q8K2K6.2	561	S146	FLQEKYEKKRWYVPPEQAKVVASVHASISGSSASSTSSTPEVKPLKSLLGESAPALHLNKG	(Alfaro et al. 2012)
Arf-GAP domain and FG repeat-containing protein 1	90110041	Q8K2K6.2	561	S300	TTGGSAGSVNANFAHFDNFPKSSSADFGTFSTSQSHQTASTVSKVSTNKAGLQTADKYAAL	(Alfaro et al. 2012)
Arf-GAP domain and FG repeat-containing protein 1	90110041	Q8K2K6.2	561	S362	NLDNIFSAGQGGDQGSGFGTTGKAPVGSVVSVPSHSSASSDKYAALAELDSVFSSAATSSN	(Trinidad et al., 2012)
Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3	81902092	Q8VHH5.1	910	T473	YMQNIHGKEIDLLRTTVKVPGKRLPRATPTTAPGTSPRANGLAMERSNTQLGGATGAPHSA	(Trinidad et al., 2012)
Armadillo repeat-containing X-linked protein 2	84027757	Q6A058.2	784	T328	SPGAAVHPVAAQSTGVVVPPRAVQYSGAAVTSGGAAVPSGGAATPRAAASTQRTASTEVMQ	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Armadillo repeat-containing X-linked protein 2	84027757	Q6A058.2	784	T93	IDLGPGFSPPNPVDIEIMNKAQGEASNLATTVAEEVAPAAPSPKVQNGAESKVQELNGAKT	(Trinidad et al., 2012)
Armadillo repeat-containing X-linked protein 5	84027759	Q3UZB0.1	606	T106	KVKKKKDKTNARVMAQAKTELPAGPALVPHTKSDALPTSVVITVTKSEVKIDTGIEASLKG	(Trinidad et al., 2012)
Ataxin-1	292494974	P54254.2	791	S81	GIRGHGGGRHGSAGTSGEHGLQGMGLHKALSAGLDYSPPSAPRSVPTANTLPTVYPPPQSG	(Trinidad et al., 2012)
Ataxin-1-like	206557835	P0C7T6.1	687	S40	ECLPPKKRDLPVTSEDMGRTTSCSTNHTPSSDASEWSRGVVVAGQSQTGARVSLGGDGTEA	(Alfaro et al. 2012)
Ataxin-2	52000657	O70305.1	1285	S187	PQPPAPATGRKPGGGLLSSPGAAPASAAVTSASVVPAPAAPVASSSAAAGGGRPGLGRGRN	(Alfaro et al. 2012)
Ataxin-2	52000657	O70305.1	1285	T186	QPQPPAPATGRKPGGGLLSSPGAAPASAAVTSASVVPAPAAPVASSSAAAGGGRPGLGRGR	(Alfaro et al. 2012)
Ataxin-2	52000657	O70305.1	1285	S745	AKDSRLQDQRQNSPAGSKENVKASETSPSFSKADNKGMSPVVSEHRKQIDDLKKFKNDFRL	(Trinidad et al., 2012)
Ataxin-2	52000657	O70305.1	1285	T852	NCTSGSSKTNSPSISPSMLSNAEHKRGPEVTSQGVQTSSPACKQEKDDREEKKDTTEQVRK	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Ataxin-2-like protein	52000729	Q8WWM7.2	1075	S475	YPPRSPKSAAPAPISASCPEPPIGSAVPTSSASIPVTSSVSDPGVGSISPASPKISLAPTD	(Hahne et al. 2012)
Ataxin-2-like protein	52000729	Q8WWM7.2	1075	S496	PIGSAVPTSSASIPVTSSVSDPGVGSISPASPKISLAPTDVKELSTKEPGRTLEPQELARI	(Hahne et al. 2012)
Ataxin-2-like protein	52000711	Q7TQH0.1	1049	S687	VKKSTLNPNAKEFNPTKPLLSVNKSTSTPTSPGPRTHSTPSIPVLTAGQSGLYSPQYISYI	(Trinidad et al., 2012)
Ataxin-2-like protein	52000711	Q7TQH0.1	1049	T267	DDYDLESDMSNGWDPNEMFKFNEENYGVKTTYDSSLSSYTVPLEKDNSEEFRQRELRAAQL	(Trinidad et al., 2012)
Ataxin-2-like protein	52000711	Q7TQH0.1	1049	T686	QVKKSTLNPNAKEFNPTKPLLSVNKSTSTPTSPGPRTHSTPSIPVLTAGQSGLYSPQYISY	(Trinidad et al., 2012)
ataxin-2-like protein isoform B	27262645	NP_663760.1	1062	S684	VKKSTLNPNAKEFNPTKPLLSVNKSTSTPTSPGPRTHSTPSIPVLTAGQSGLYSPQYISYI	(Wang et al. 2010)
Atf2 protein	81910601	Q640L6	389	T174	GIPGPSSPQPVQSEAKMRLKAALTQQHPPVTNGDTVKGHGSGLVRTQSEESRPQSLQQPAT	(Trinidad et al., 2012)
AT-hook DNA-binding motif-containing protein 1	81892397	Q6PAL7.1	1594	S800	GGGWAPHHGHPGGQAGRNCGFQGTEARAFASTGLESGASGRGSYYAGAPSGQTELSQERQN	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
ATP synthase subunit beta, mitochondrial	20455479	P56480.2	529	S128	EVAQHLGESTVRTIAMDGTEGLVRGQKVLDSGAPIKIPVGPETLGRIMNVIGEPIDERGPI	(Trinidad et al., 2012)
ATP synthase subunit f, mitochondrial	20141252	P56135.3	88	S32	ASLVPLKEKKLMEVKLGELPSWIMMRDFTPSGIAGAFRRGYDRYYNKYINVRKGSISGISM	(Trinidad et al., 2012)
ATP synthase subunit g, mitochondrial	52782750	Q9CPQ8.1	103	S23	BBBBBBBBMAKFIRNFAEKAPSMVAAAVTYSKPRLATFWHYAKVELVPPTPAEIPTAIQSV	(Trinidad et al., 2012)
ATP synthase-coupling factor 6, mitochondrial	2829840	P97450.1	108	T89	GPVDIGPEYQQDLDRELYKLKQMYGKGEMDTFPTFKFDDPKFEVIDKPQSBBBBBBBBBBB	(Trinidad et al., 2012)
ATP8A1 protein	121942137	Q32M35	1149	S1087	IKRTAFKTLVDEVQELEAKSQDPGAVVLGKSLTERAQLLKNVFKKNHVNLYRSESLQQNLL	(Zhao et al. 2011)
ATP8A1 protein	121942137	Q32M35	1149	T1089	RTAFKTLVDEVQELEAKSQDPGAVVLGKSLTERAQLLKNVFKKNHVNLYRSESLQQNLLHG	(Zhao et al. 2011)
AT-rich interactive domain-containing protein 3B	152013359	Q8IVW6.2	561	T416	LRKGDGAPVTTVPVPNRLAVPVTLASQQAGTRTAALEQLRERLESGEPAEKKASRLSEEEQ	(Hahne et al. 2012)
Band 3 anion transport protein	114787	P02730.3	911	S162	ANQLLDRFIFEDQIRPQDREELLRALLLKHSHAGELEALGGVKPAVLTRSGDPSQPLLPQH	(Wang et al. 2009)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Band 3 anion transport protein	114787	P02730.3	911	S224	SLETQLFCEQGDGGTEGHSPSGILEKIPPDSEATLVLVGRADFLEQPVLGFVRLQEAAELE	(Wang et al. 2009)
Band 3 anion transport protein	114787	P02730.3	911	S745	VAALFGMPWLSATTVRSVTHANALTVMGKASTPGAAAQIQEVKEQRISGLLVAVLVGLSIL	(Wang et al. 2009)
Band 4.1-like protein 1	134047752	Q9Z2H5.2	879	S721	FESVKAETMTVSSLAIRKKIEPEAMLQSRVSAADSTQVDGGTPMVKDFMTTPPCITTETIS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Band 4.1-like protein 1	134047752	Q9Z2H5.2	879	S792	KGAAAMIPGPQTVATEIRSLSPIIGKDVLTSTYGATAETLSTSTTTHVTKTVKGGFSETRI	(Alfaro et al. 2012)
Band 4.1-like protein 1	134047752	Q9Z2H5.2	879	T773	PCITTETISTTMENSLKSGKGAAAMIPGPQTVATEIRSLSPIIGKDVLTSTYGATAETLST	(Trinidad et al., 2012)
Band 4.1-like protein 1	134047752	Q9Z2H5.2	879	T776	TTETISTTMENSLKSGKGAAAMIPGPQTVATEIRSLSPIIGKDVLTSTYGATAETLSTSTT	(Trinidad et al., 2012)
Band 4.1-like protein 1	134047752	Q9Z2H5.2	879	T793	GAAAMIPGPQTVATEIRSLSPIIGKDVLTSTYGATAETLSTSTTTHVTKTVKGGFSETRIE	(Alfaro et al. 2012)
Band 4.1-like protein 1	134047752	Q9Z2H5.2	879	T797	MIPGPQTVATEIRSLSPIIGKDVLTSTYGATAETLSTSTTTHVTKTVKGGFSETRIEKRII	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Band 4.1-like protein 1	134047752	Q9Z2H5.2	879	T800	GPQTVATEIRSLSPIIGKDVLTSTYGATAETLSTSTTTHVTKTVKGGFSETRIEKRIIITG	(Alfaro et al. 2012)
Band 4.1-like protein 1	134047752	Q9Z2H5.2	879	T746	LQSRVSAADSTQVDGGTPMVKDFMTTPPCITTETISTTMENSLKSGKGAAAMIPGPQTVAT	(Trinidad et al., 2012)
Band 4.1-like protein 3	20138079	Q9WV92.1	929	S797	SHEEEQASTIRTSEGLEQKSHFESSTVRVESTSVGSISPGGAKLEISTKEVPVVHTETKTI	(Alfaro et al. 2012)
Band 4.1-like protein 3	20138079	Q9WV92.1	929	T822	TVRVESTSVGSISPGGAKLEISTKEVPVVHTETKTITYESSQVDPGADLEPGVLMSAQTIT	(Trinidad et al., 2012)
Band 4.1-like protein 3	20138079	Q9WV92.1	929	S470	RSSSKRYTMSRSLDGASVSENHEIYMKDSVSAAEVGTGQYATTKGISQTNLITTVTPEKKA	(Trinidad et al., 2012)
Band 4.1-like protein 3	20138079	Q9WV92.1	929	S832	SISPGGAKLEISTKEVPVVHTETKTITYESSQVDPGADLEPGVLMSAQTITSETTSTTTTT	(Trinidad et al., 2012)
Basement membrane-specific heparan sulfate proteoglycan core protein	1172451	Q05793.1	3707	T1746	PLPSSAQQRHQGSELHFPSVQPSDAGVYICTCRNLIHTSNSRAELLVAEAPSKPIMVTVEE	(Trinidad et al., 2012)
BCL-6 corepressor isoform b	183396785	NP_001116856.1	1703	S365	PSPRPSPRVHLPTQPAADTYSEFHKHYARISTSPSVALSKPYMTVSSEFPAARLSNGKYPK	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Beta-actin-like protein 2	81895966	Q8BFZ3.1	376	S240	VRDVKEKLCYVALDFEQEMVTAAASSSLERSYELPDGQVITIGNERFRCPEAIFQPSFLGI	(Trinidad et al., 2012)
Beta-glucuronidase	146345377	P08236.2	651	T276	YQISVKGSNLFKLEVRLLDAENKVVANGTGTQGQLKVPGVSLWWPYLMHERPAYLYSLEVQ	(Hahne et al. 2012)
Beta-synuclein	81879780	Q91ZZ3.1	133	S53	KQGVTEAAEKTKEGVLYVGSKTSGVVQGVASVAEKTKEQASHLGGAVFSGAGNIAAATGLV	(Alfaro et al. 2012)
Beta-synuclein	81879780	Q91ZZ3.1	133	T27	BBBBMDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSKTSGVVQGVASVAEK	(Alfaro et al. 2012)
Beta-synuclein	81879780	Q91ZZ3.1	133	T58	EAAEKTKEGVLYVGSKTSGVVQGVASVAEKTKEQASHLGGAVFSGAGNIAAATGLVKKEEF	(Alfaro et al. 2012)
Beta-synuclein	81879780	Q91ZZ3.1	133	S71	GSKTSGVVQGVASVAEKTKEQASHLGGAVFSGAGNIAAATGLVKKEEFPTDLKPEEVAQEA	(Trinidad et al., 2012)
beta-synuclein	77404215	NP_542955.2	134	T27	BBBBMDVFMKGLSMAKEGVVAAAEKTKQGVTEAAEKTKEGVLYVGSKTKEGVVQGVASVAE	(Wang et al. 2010)
Bnc2 protein	123779664	Q2TBA4	1021	S437	SRNRHSANPNPRLHMPMLRNNRDKDLIRATSGAATPVIASTKSNLTLTSPGRPPMGFTTPP	(Myers et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Brain acid soluble protein 1	66773932	Q91XV3.3	226	S169	APEEGEAKKTEAPAAAGPEAKSDAAPAASDSKPSSAEPAPSSKETPAASEAPSSAAKAPAP	(Alfaro et al. 2012)
brain-specific angiogenesis inhibitor 1-associated protein 2	123856885	CAM22926.1	482	S460	PDYGTSSRAFPTQTAGTFKQRPYSVAVPAFSQGLDDYGARSVSSGSGTLVSTVBBBBBBB	(Trinidad et al., 2012)
brain-specific angiogenesis inhibitor 1-associated protein 2	123856885	CAM22926.1	482	S480	RPYSVAVPAFSQGLDDYGARSVSSGSGTLVSTVBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Brain-specific angiogenesis inhibitor 3	48428046	Q80ZF8.1	1522	S1399	PQEHMQNLPFEPRTAVKNFMASELDDNVGLSRSETGSTISMSSLERRKSRYSDLDFEKVMH	(Trinidad et al., 2012)
bromodomain PHD finger transcription factor	123241371	CAM20630.1	289	T225	TGSPVTMAGKVITKLPLPANSKIVAVNVPATQGGMVQVQQKVLGIIPSTTGPSQQTFTSFQ	(Trinidad et al., 2012)
bromodomain-containing protein 4 isoform long	197187331	NP_490597.1	1362	S1215	KTPVAPKKDLKIKNMGSWASLVQKHPTTPSSTAKSSSDSFEQFRRAAREKEERERKALKAQA	(Wang et al. 2010)
C2 domain-containing protein 2-like	46577418	Q80X80.2	706	T438	EQGSPRNLGTPTSSTPRPSITPTKKIELDRTIMPDGTVVTTVTTVQSRPRVDGKLDSPSRS	(Alfaro et al. 2012)(Trinidad et al., 2012)
C2 domain-containing protein 2-like	46577418	Q80X80.2	706	T447	TPTSSTPRPSITPTKKIELDRTIMPDGTVVTTVTTVQSRPRVDGKLDSPSRSPSKVEVTEK	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
C2 domain-containing protein 2-like	46577418	Q80X80.2	706	S420	GPGKSLSPAATVTAELHYEQGSPRNLGTPTSSTPRPSITPTKKIELDRTIMPDGTVVTTVT	(Trinidad et al., 2012)
C2 domain-containing protein 2-like	46577418	Q80X80.2	706	T450	SSTPRPSITPTKKIELDRTIMPDGTVVTTVTTVQSRPRVDGKLDSPSRSPSKVEVTEKMTT	(Trinidad et al., 2012)
CAD protein	344239768	EGV95871.1	2225	S2131	LRYVAPPSLRMPPSVRDFVASRGTKQEEFESIEEALPDTDVLYMTRIQKERFGSTQEYEAC	(Trinidad et al., 2012)
Cadherin-20	81917936	Q9Z0M3.1	801	T715	NPREAQAGAAPKTRQDMLPEIESLSRYVPQTCAVSSTVHSYVLAKLYEADMDLWAPPFDSL	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase II, delta	81910166	Q5SVJ0	666	S327	RRKLKGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLLNKKADGVKPQTN	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase II, delta	81910166	Q5SVJ0	666	T320	CLKKFNARRKLKGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLLNKKAD	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase II, delta	81910166	Q5SVJ0	666	T321	LKKFNARRKLKGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLLNKKADG	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase II, delta	81910166	Q5SVJ0	666	T325	NARRKLKGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLLNKKADGVKPQ	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Calcium/calmodulin-dependent protein kinase II, delta	81910166	Q5SVJ0	666	T328	RKLKGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLLNKKADGVKPQTNS	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase type 1D	56404603	Q8BW96.2	385	T352	LQLGSSLDSSNASVSSNLSLASQKDCLAPSTLCSFLSSSSGVAGVGAERRPRPTTVTTGHT	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase type II subunit alpha	124056467	P11798.2	478	T253	QQIKAGAYDFPSPEWDTVTPEAKDLINKMLTINPSKRITAAEALKHPWISHRSTVASCMHR	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase type II subunit alpha	124056467	P11798.2	478	T306	TVASCMHRQETVDCLKKFNARRKLKGAILTTMLATRNFSGGKSGGNKKNDGVKESSESTNT	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase type II subunit beta	94730394	P28652.2	542	T325	NARRKLKGAILTTMLATRNFSVGRQTTAPATMSTAASGTTMGLVEQAKSLLNKKADGVKPQ	(Alfaro et al. 2012)
Calcium/calmodulin-dependent protein kinase type II subunit delta	81911483	Q6PHZ2.1	499	T307	TVASMMHRQETVDCLKKFNARRKLKGAILTTMLATRNFSAAKSLLKKPDGVKESTESSNTT	(Trinidad et al., 2012)
Calcium/calmodulin-dependent protein kinase type IV	2499586	Q16566.1	473	S137	IFETPTEISLVLELVTGGELFDRIVEKGYYSERDAADAVKQILEAVAYLHENGIVHRDLKP	(Dias et al. 2009)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Calcium/calmodulin-dependent protein kinase type IV	2499586	Q16566.1	473	S189	GIVHRDLKPENLLYATPAPDAPLKIADFGLSKIVEHQVLMKTVCGTPGYCAPEILRGCAYG	(Dias et al. 2009)
Calcium/calmodulin-dependent protein kinase type IV	2499586	Q16566.1	473	S356	LKAAVKAVVASSRLGSASSSHGSIQESHKASRDPSPIQDGNEDMKAIPEGEKIQGDGAQAA	(Dias et al. 2009)
Calcium/calmodulin-dependent protein kinase type IV	266411	P08414.2	469	T5	BBBBBBBBBBBBBBBBBBBBBBBBBMLKVTVPSCPSSPCSSVTASTENLVPDYWIDGSNR	(Trinidad et al., 2012)
Calcium-responsive transactivator	81875472	Q8BW22.1	402	T48	QQTIQKMLDENHHLIQCILDYQSKGKTAECTQYQQILHRNLVYLATIADSNQNMQSLLPAP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Calmodulin-regulated spectrin-associated protein 1	166991293	A2AHC3.1	1581	T559	LSNVNIEDEDEELVAIIRTDVSPPSPQMPRTSPQAPGLVASIRSPQRQADTLESKPDSFYL	(Trinidad et al., 2012)
Calmodulin-regulated spectrin-associated protein 3	612136936	Q80VC9.1	1252	S379	SSSPVFNFRHPLLSPGGPQSPLRGSTGSLKSSPSMSHMEALGKAWNRQLSRPLSQAVSFST	(Trinidad et al., 2012)
Calnexin	543920	P27824.2	592	S74	DSKPDTTAPPSSPKVTYKAPVPTGEVYFADSFDRGTLSGWILSKAKKDDTDDEIAKYDGKW	(Hahne et al. 2012)
Calnexin	543920	P27824.2	592	T66	DDVIEEVEDSKPDTTAPPSSPKVTYKAPVPTGEVYFADSFDRGTLSGWILSKAKKDDTDDE	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
CaM kinase-like vesicle-associated protein	115311320	Q3UHL1.2	512	T457	GSVTPATDRSATPATDGRATPATEESTVPATQSSALPAAKAAATPEPAVAQPDSTALEGAT	(Alfaro et al. 2012)
cAMP-regulated phosphoprotein 21	344248594	EGW04698.1	628	T377	TALTSSVASGSPGCMPYAENGMGGQVPPSSTSYILLPLETATGIPPGSILLNPHTGQPFVN	(Trinidad et al., 2012)
CAP-Gly domain-containing linker protein 1	81879884	Q922J3.1	1391	T150	RPSKLTRKVQAEDEANGLQAAPGRTASPLSTAAATMVSSSPATPSNIPHKPSQSTAKEPSA	(Alfaro et al. 2012)
CAP-Gly domain-containing linker protein 1	81879884	Q922J3.1	1391	T154	LTRKVQAEDEANGLQAAPGRTASPLSTAAATMVSSSPATPSNIPHKPSQSTAKEPSATPQI	(Trinidad et al., 2012)
Carbonic anhydrase 1	115449	P00915.2	261	S130	STNEHGSEHTVDGVKYSAELHVAHWNSAKYSSLAEAASKADGLAVIGVLMKVGEANPKLQK	(Wang et al. 2009)
Carbonic anhydrase 1	115449	P00915.2	261	S218	SSLDFWTYPGSLTHPPLYESVTWIICKESISVSSEQLAQFRSLLSNVEGDNAVPMQHNNRP	(Wang et al. 2009)
Casein kinase I isoform delta	47116753	Q9DC28.2	415	S382	TANTSPRPVSGMERERKVSMRLHRGAPVNVSSSDLTGRQDTSRMSTSQIPGRVASSGLQSV	(Trinidad et al., 2012)
Casein kinase II subunit alpha'	107200047	O54833.1	350	T347	KEAMEHPYFYPVVKEQSQPCAENTVLSSGLTAARBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
casein kinase II subunit alpha	88319941	NP_777060.2	391	S347	EAMEHPYFYTVVKDQARMGSSSMPGGSTPVSSANMMSGISSVPTPSPLGPLAGSPVIAAAN	(Tarrant et al. 2012)
Caskin-1	61212969	Q6P9K8.2	1431	S824	ALGGPHGPATAKVKPTPQLLPPTDRPMSPRSLPQSPTHRGFAYVLPQPVEGEVGPPAPGPA	(Trinidad et al., 2012)
Catalase	115702	P04040.3	527	S114	YFEVTHDITKYSKAKVFEHIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWD	(Wang et al. 2009)
Catalase	115702	P04040.3	527	S254	NANGEAVYCKFHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSWTFYIQVM	(Wang et al. 2009)
Catenin alpha-3	78099216	Q65CL1.2	895	T719	AEIEIWDDTSNDIIVLAKKMCMIMMEMTDFTRGKGPLKHTTDVIYAAKMISESGSRMDVLA	(Trinidad et al., 2012)
Catenin beta-1	399310	Q02248.1	781	S23	BBBBBBBBMATQADLMELDMAMEPDRKAAVSHWQQQSYLDSGIHSGATTTAPSLSGKGNPE	(Trinidad et al., 2012)
Catenin delta-2	20177853	O35927.1	1247	T447	IDPIYEDRVYQKPPMRSLSQSQGDPLPPAHTGTFRTSTAPSSPGVDSVPLQRTGSQHGPQN	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Catenin delta-2	20177853	O35927.1	1247	S319	YAAPRGSSPKQSPSRLAKSYSTSSPINIVVSSAGLSPIRVTSPPTVQSTISSSPIHQLSST	(Alfaro et al. 2012)(Trinidad et al., 2012)
Catenin delta-2	20177853	O35927.1	1247	S320	AAPRGSSPKQSPSRLAKSYSTSSPINIVVSSAGLSPIRVTSPPTVQSTISSSPIHQLSSTI	(Alfaro et al. 2012)(Trinidad et al., 2012)
Catenin delta-2	20177853	O35927.1	1247	S437	LRALQSPEHHIDPIYEDRVYQKPPMRSLSQSQGDPLPPAHTGTFRTSTAPSSPGVDSVPLQ	(Alfaro et al. 2012)
Catenin delta-2	20177853	O35927.1	1247	S453	DRVYQKPPMRSLSQSQGDPLPPAHTGTFRTSTAPSSPGVDSVPLQRTGSQHGPQNAAAATF	(Chalkley et al. 2009)
Catenin delta-2	20177853	O35927.1	1247	S340	TSSPINIVVSSAGLSPIRVTSPPTVQSTISSSPIHQLSSTIGTYATLSPTKRLVHASEQYS	(Alfaro et al. 2012)
Catenin delta-2	20177853	O35927.1	1247	S370	SSPIHQLSSTIGTYATLSPTKRLVHASEQYSKHSQELYATATLQRPGSLAAGSRASYSSQH	(Trinidad et al., 2012)
Catenin delta-2	20177853	O35927.1	1247	T329	QSPSRLAKSYSTSSPINIVVSSAGLSPIRVTSPPTVQSTISSSPIHQLSSTIGTYATLSPT	(Alfaro et al. 2012)
Catenin delta-2	20177853	O35927.1	1247	T337	SYSTSSPINIVVSSAGLSPIRVTSPPTVQSTISSSPIHQLSSTIGTYATLSPTKRLVHASE	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Catenin delta-2	20177853	O35927.1	1247	T1140	TDYESAGNNATYHGTKGEHTSRKDTMTAQNTGVSTLYRNSYGAPAEDIKQNQVSTQPVPQE	(Trinidad et al., 2012)
Catenin delta-2	20177853	O35927.1	1247	T268	HLPDAPPAAAALYYSSSTLPAPPRGGSPLTTTQGGSPTKLQRGGSAPEGAAYAAPRGSSPK	(Trinidad et al., 2012)
Catenin delta-2	20177853	O35927.1	1247	T454	RVYQKPPMRSLSQSQGDPLPPAHTGTFRTSTAPSSPGVDSVPLQRTGSQHGPQNAAAATFQ	(Trinidad et al., 2012)
Cathepsin L1	115741	P07711.2	333	T223	NGGLDSEESYPYEATEESCKYNPKYSVANDTGFVDIPKQEKALMKAVATVGPISVAIDAGH	(Hahne et al. 2012)
CCR4-NOT transcription complex subunit 1	166216087	Q6ZQ08.2	2375	T1040	TPGSIALAQAQAQAQVPAKAPLAGQVNTMVTTSTTTTVAKTVTVTKPTGVSFKKDVPPSIN	(Alfaro et al. 2012)(Trinidad et al., 2012)
CCR4-NOT transcription complex subunit 1	166216087	Q6ZQ08.2	2375	T1037	SITTPGSIALAQAQAQAQVPAKAPLAGQVNTMVTTSTTTTVAKTVTVTKPTGVSFKKDVPP	(Alfaro et al. 2012)(Trinidad et al., 2012)
CCR4-NOT transcription complex subunit 1	166216087	Q6ZQ08.2	2375	T1041	PGSIALAQAQAQAQVPAKAPLAGQVNTMVTTSTTTTVAKTVTVTKPTGVSFKKDVPPSINT	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
CCR4-NOT transcription complex subunit 1	166216087	Q6ZQ08.2	2375	T1054	QVPAKAPLAGQVNTMVTTSTTTTVAKTVTVTKPTGVSFKKDVPPSINTTNIDTLLVATDQT	(Alfaro et al. 2012)(Trinidad et al., 2012)
CCR4-NOT transcription complex subunit 1	166216087	Q6ZQ08.2	2375	S1042	GSIALAQAQAQAQVPAKAPLAGQVNTMVTTSTTTTVAKTVTVTKPTGVSFKKDVPPSINTT	(Trinidad et al., 2012)
CCR4-NOT transcription complex subunit 1	166216087	Q6ZQ08.2	2375	T1043	SIALAQAQAQAQVPAKAPLAGQVNTMVTTSTTTTVAKTVTVTKPTGVSFKKDVPPSINTTN	(Alfaro et al. 2012)
CCR4-NOT transcription complex subunit 1	166216087	Q6ZQ08.2	2375	T1050	QAQAQVPAKAPLAGQVNTMVTTSTTTTVAKTVTVTKPTGVSFKKDVPPSINTTNIDTLLVA	(Trinidad et al., 2012)
CCR4-NOT transcription complex subunit 2	46395846	Q8C5L3.2	540	T113	GLPMRGMSNNTPQLNRSLSQGTQLPSHVTPTTGVPTMSLHTPPSPSRGILPMNPRNMMNHS	(Myers et al. 2011)
CCR4-NOT transcription complex subunit 2	46395846	Q8C5L3.2	540	T114	LPMRGMSNNTPQLNRSLSQGTQLPSHVTPTTGVPTMSLHTPPSPSRGILPMNPRNMMNHSQ	(Alfaro et al. 2012)
CCR4-NOT transcription complex subunit 2	46395846	Q8C5L3.2	540	T118	GMSNNTPQLNRSLSQGTQLPSHVTPTTGVPTMSLHTPPSPSRGILPMNPRNMMNHSQVGQG	(Myers et al. 2011)
CCR4-NOT transcription complex subunit 2	46395846	Q8C5L3.2	540	T111	ALGLPMRGMSNNTPQLNRSLSQGTQLPSHVTPTTGVPTMSLHTPPSPSRGILPMNPRNMMN	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
CCR4-NOT transcription complex subunit 4	46395844	Q8BT14.2	575	S316	GNGDNSQQISNSDTPSPPPGLSKSNPVIPISSSNHSARSPFEGAVTESQSLFSDNFRHPNP	(Alfaro et al. 2012)(Trinidad et al., 2012)
CCR4-NOT transcription complex subunit 4	46395844	Q8BT14.2	575	T331	SPPPGLSKSNPVIPISSSNHSARSPFEGAVTESQSLFSDNFRHPNPIPSGLPPFPSSPQTP	(Trinidad et al., 2012)
CD99 antigen	119049	P14209.1	185	T41	LFGLLGVLVAAPDGGFDLSDALPDNENKKPTAIPKKPSAGDDFDLGDAVVDGENDDPRPPN	(Hahne et al. 2012)
CDKN2A-interacting protein	32747859 1	Q9NXV6.3	580	S331	VELPLLSSKPSSETASSGLTSKTSSEASVSSSVAKNSSSSGTSLLTPKSSSSTNTSLLTSK	(Hahne et al. 2012)
CDKN2A-interacting protein	32747859 1	Q9NXV6.3	580	T359	VSSSVAKNSSSSGTSLLTPKSSSSTNTSLLTSKSTSQVAASLLASKSSSQTSGSLVSKSTS	(Hahne et al. 2012)
Cell cycle checkpoint protein RAD1	81882021	Q9QWZ1.1	280	T232	DYPKDSDLVEAFHCDKTQVNRYKLSLLKPSTKALALSCKVSIRTDNRGFLSLQYMIRNEDG	(Alfaro et al. 2012)
Centrosomal protein of 170 kDa	14395529 9	Q6A065.2	1588	T1047	TSSVPHSAISDIMSSDQETYSCKSHGRTPLTSADEHNIHSKLEGGKATKSKTSPVASGSTS	(Trinidad et al., 2012)
Chromodomain-helicase-DNA-binding protein 8	12377825 8	Q09XV5.1	2582	T2524	HHHHHHPHPHHHHHHHPGLRTTGYPSSPATTTSGTALRLPTLQPEDDDEEEDEEDDDLSQG	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Chromosome transmission fidelity protein 8 homolog isoform 2	298351629	P0CG14.1	533	S339	TMTRVPGPIGPNTGPSSRGLGLPGPNPSPMSRAPGPMGPNSAHFSRPGGPMGVNAGVFPRG	(Trinidad et al., 2012)
Chromosome transmission fidelity protein 8 homolog isoform 2	298351629	P0CG14.1	533	S381	HFSRPGGPMGVNAGVFPRGTGSGGLNPNAFSQSSGTLASNPGTFQRSAGLQGSNQAVFPRA	(Alfaro et al. 2012)
Chromosome transmission fidelity protein 8 homolog isoform 2	298351629	P0CG14.1	533	S297	LNLRMAGPQGLDLAPILRAAGLLGTNSVSFSQASGNMGTNPPTMTRVPGPIGPNTGPSSRG	(Trinidad et al., 2012)
Citrate synthase like (Adult male testis cDNA, RIKEN full-length enriched library, clone:4922505I09 product:1700007H16Rik protein (Citrate synthase), full insert sequence)	81895308	Q80X68	466	T454	FGVSRALGVLSQLIWSRALGFPLERPKSMSTDALMKFVNSESGBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
C-Jun-amino-terminal kinase-interacting protein 1	17433097	Q9WVI9.2	707	S362	FDCLSSPERAEPPGGGWRGSLGEPPPPPRASLSSDTSALSYDSVKYTLVVDEHAQLELVSL	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Clathrin coat assembly protein AP180	2492687	Q61548.1	901	T310	QHLNTLEGKKPGNNEGSGAPSPLSKSSPATTVTSPNSTPAKTIDTSPPVDIFATASAAAPV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Clathrin coat assembly protein AP180	2492687	Q61548.1	901	S303	SLMETLEQHLNTLEGKKPGNNEGSGAPSPLSKSSPATTVTSPNSTPAKTIDTSPPVDIFAT	(Trinidad et al., 2012)
Clathrin coat assembly protein AP180	2492687	Q61548.1	901	T309	EQHLNTLEGKKPGNNEGSGAPSPLSKSSPATTVTSPNSTPAKTIDTSPPVDIFATASAAAP	(Trinidad et al., 2012)
clathrin coat assembly protein AP180	13994177	NP_113916.1	915	T310	QHLNTLEGKKPGNNEGSGAPSPLSKSSPATTVTSPNSTPAKTIDTSPPVDIFATASAAAPV	(Graham et al. 2011)
Clathrin interactor 1	41017053	Q99KN9.2	631	S328	AAHYTGDKASPDQNASTHTPQSSAKPSVPSSKSSGDLVDLFDGSSQSAGGSADLFGGFADF	(Alfaro et al. 2012)
Clathrin interactor 1	344245303	EGW01407.1	625	S320	TPQSSAKVQPSVPNSKSSGDLVDLFDGNSQSTGGSTDLFGGFADFGSAAASGSFPYQATSG	(Trinidad et al., 2012)
Claudin-12	30923399	Q9ET43.2	244	S241	YSHAPGMHTYSQPYSSRSRLSAIEIDIPVVSHSTBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
CLIP-associating protein 2	77416393	Q8BRT1.1	1286	S459	GRVRAKLSTPLVAVGNAKTDSRGRSRTKMVSQSQPGSRSGSPGRVLTTTALSTVSSGAQRV	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
CLIP-associating protein 2	77416393	Q8BRT1.1	1286	S531	KIPRSQGCSREASPSRLSVARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLGPGYGI	(Trinidad et al., 2012)
CLIP-associating protein 2	77416393	Q8BRT1.1	1286	T476	KTDSRGRSRTKMVSQSQPGSRSGSPGRVLTTTALSTVSSGAQRVLVNSASAQKRSKIPRSQ	(Trinidad et al., 2012)
Coiled-coil-helix-coiled-coil-helix domain-containing protein 6, mitochondrial	384872322	Q91VN4.2	273	S220	DTFYKEQQGRIQEKNAELYKLSSQQFHEAASKAESTIKPRRVEPVCSGLQAQILRCYRDHL	(Trinidad et al., 2012)
Collagen alpha-1(XII) chain	146345397	Q99715.2	3063	T1749	IYEVSITAIYPDESESDDLIGSERTLPILTTQAPKSGPRNLQVYNATSNSLTVKWDPASGR	(Hahne et al. 2012)
Connector enhancer of kinase suppressor of ras 2	50400458	Q80YA9.1	1032	S329	SMLTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQDLYIPPPPPAE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Connector enhancer of kinase suppressor of ras 2	50400458	Q80YA9.1	1032	S328	QSMLTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQDLYIPPPPA	(Trinidad et al., 2012)
Connector enhancer of kinase suppressor of ras 2	50400458	Q80YA9.1	1032	T332	TSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQDLYIPPPPAEPYI	(Trinidad et al., 2012)
Connector enhancer of kinase suppressor of ras 2	50400458	Q80YA9.1	1032	T336	ALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQDLYIPPPPAEPYIPRDE	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Coronin-1B	12229769	Q9WUM3.1	484	S421	SLREAYVPSKQRDLKVSRRNVLSDSRPASYSRSGASTATAVTDVPSGNLAGAGEAGKLEEV	(Alfaro et al. 2012)(Trinidad et al., 2012)
CREB-regulated transcription coactivator 1	68565578	Q68ED7.1	630	T417	VGLPQGGPLLPSASLTRGPQLPPLSVTVPSTLPQSPTENPGQSPMGIDATSAPALQYRTSA	(Alfaro et al. 2012)
C-type mannose receptor 2	341940996	Q64449.3	1479	S624	WLSGDEVIYTHWNRDQPGYRRGGCVALATGSAMGLWEVKNCTSFRARYICRQSLGTPVTPE	(Trinidad et al., 2012)
C-type mannose receptor 2	341940996	Q64449.3	1479	T622	FRWLSGDEVIYTHWNRDQPGYRRGGCVALATGSAMGLWEVKNCTSFRARYICRQSLGTPVT	(Trinidad et al., 2012)
cyclic AMP-dependent transcription factor ATF-1	4885073	NP_005162.1	271	S189	QILVPSNQVVVQTASGDMQTYQIRTTPSATSLPQTVVMTSPVTLTSQTTKTDDPQLKREIR	(Wang et al. 2010)
Cyclic AMP-dependent transcription factor ATF-2	6920063	P16951.2	487	T272	GIPGPSSPQPVQSEAKMRLKAALTQQHPPVTNGDTVKGHGSGLVRTQSEESRPQSLQQPAT	(Alfaro et al. 2012)
cyclic AMP-responsive element-binding protein 1 isoform A	82546874	NP_598589.2	327	S40	QQSGDAAVTEAENQQMTVQAQPQIATLAQVSMPAAHATSSAPTVTLVQLPNGQTVQVHGVI	(Rexach et al. 2012)
Cyclin-dependent kinase 12	308153421	Q9NYV4.2	1490	S608	ASSTSTLPPSTHSKTSAVSSQANSQPPVQVSVKTQVSVTAAIPHLKTSTLPPLPLPPLLPG	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Cyclin-dependent kinase 12	166234056	Q14AX6.2	1484	T1359	HPNRTYGNTDGPETGFSSADTDERSSGPALTESLVQTPVKNRTFSGSVSHLGESNSYQGTG	(Trinidad et al., 2012)
Cyclin-dependent kinase 12	166234056	Q14AX6.2	1484	S589	QPPLPPPQPPFSQVPVSSTSILPSSPHPRTSTLSSQTNSQPPVQVSMKTQVSITAAIPHLK	(Trinidad et al., 2012)
Cyclin-dependent kinase 12	166234056	Q14AX6.2	1484	T588	LQPPLPPPQPPFSQVPVSSTSILPSSPHPRTSTLSSQTNSQPPVQVSMKTQVSITAAIPHL	(Trinidad et al., 2012)
cyclin-dependent kinase 12 isoform 2	157817073	NP_055898.1	1481	S597	PPSQPAFSQVPASSTSTLPPSTHSKTSAVSSQANSQPPVQVSVKTQVSVTAAIPHLKTSTL	(Wang et al. 2010)
cyclin-dependent kinase 12 isoform 2	157817073	NP_055898.1	1481	T592	QQPPLPPSQPAFSQVPASSTSTLPPSTHSKTSAVSSQANSQPPVQVSVKTQVSVTAAIPHL	(Wang et al. 2010)
Cysteine-rich protein 2	47605547	Q9DCT8.1	208	T88	YATLFGPKGVNIGGAGSYIYEKPQTEAPQVTGPIEVPVVRTEERKTSGPPKGPSKASSVTT	(Alfaro et al. 2012)(Trinidad et al., 2012)
Cysteine-rich with EGF-like domain protein 2	74738218	Q6UXH1.1	353	S202	YQGPLCTDCMDGYFSSLRNETHSICTACDESCKTCSGLTNRDCGECEVGWVLDEGACVDVD	(Hahne et al. 2012)
Cytochrome b-c1 complex subunit 1, mitochondrial	341941780	Q9CZ13.2	480	T217	LHATAFQGTPLAQAVEGPSENVRRLSRTDLTDYLNRHYKAPRMVLAAAGGVEHQQLLDLAQ	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Cytochrome c oxidase subunit 5A, mitochondrial	166897986	P12787.2	146	S100	MNTLVGYDLVPEPKIIDAALRACRRLNDFASAVRILEVVKDKAGPHKEIYPYVIQELRPTL	(Trinidad et al., 2012)
Cytoplasmic dynein 1 light intermediate chain 1	73919260	Q8R1Q8.1	523	S412	LLAKQPPTAAGRPVDASPRVPGGSPRTPNRSVSSNVASVSPIPAGSKKIDPNMKAGATSEG	(Trinidad et al., 2012)
Cytoplasmic FMR1-interacting protein 2	81862370	Q5SQX6.2	1253	T1252	NKYMKSVETDSSTVEHVRCFQPPIHQSLATTCBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Death-inducer obliterator 1	152031593	Q8C9B9.4	2256	T1288	PPPPPLPEPPVLKILSSLKPGSTSTVTAPTTAAITTTASPVTAATSKTASPLEHILQTLFG	(Alfaro et al. 2012)(Myers et al. 2011)
Death-inducer obliterator 1	152031593	Q8C9B9.4	2256	S1279	TSTTPPGSPPPPPPLPEPPVLKILSSLKPGSTSTVTAPTTAAITTTASPVTAATSKTASPL	(Alfaro et al. 2012)
Death-inducer obliterator 1	152031593	Q8C9B9.4	2256	T1280	STTPPGSPPPPPPLPEPPVLKILSSLKPGSTSTVTAPTTAAITTTASPVTAATSKTASPLE	(Myers et al. 2011)
Death-inducer obliterator 1	152031593	Q8C9B9.4	2256	T1282	TPPGSPPPPPPLPEPPVLKILSSLKPGSTSTVTAPTTAAITTTASPVTAATSKTASPLEHI	(Alfaro et al. 2012)
Death-inducer obliterator 1	152031593	Q8C9B9.4	2256	T1284	PGSPPPPPPLPEPPVLKILSSLKPGSTSTVTAPTTAAITTTASPVTAATSKTASPLEHILQ	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Death-inducer obliterator 1	152031593	Q8C9B9.4	2256	T1287	PPPPPPLPEPPVLKILSSLKPGSTSTVTAPTTAAITTTASPVTAATSKTASPLEHILQTLF	(Myers et al. 2011)
Dedicator of cytokinesis protein 4	32469672	P59764.1	1978	T1806	SWSLDSGKEAKNMSDSGKLISPPVPPRPTQTASPARHTTSVSPSPAGRSPLKGSVQSFTPS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Dedicator of cytokinesis protein 7	122065171	Q8R1A4.3	2130	S190	SDEAPDGSSYQDEQDDLKRRSMSIDDTPRGSWACSIFDLKNSLPDALLPNLLDRTPNEEID	(Trinidad et al., 2012)
Dematin	22653706	Q9WV69.1	405	S110	RSRECSLSPKSTSPPPSPEVWAESRTLGIISQASTPRTTGTPRTSLPHFHHPETTRPDSNI	(Alfaro et al. 2012)(Trinidad et al., 2012)
Dematin	22653706	Q9WV69.1	405	S285	EEMEKSLPIRRKTRSLPDRTPFHTSLHSGTSKSSSLPSYGRTTLSRLQSTEFSPSGSEAGS	(Chalkley et al. 2009)(Trinidad et al., 2012)
Dematin	22653706	Q9WV69.1	405	S18	BBBBBBBBBBBBBMERLQKQPLTSPGSVSSSRDSSVPGSPSSIVAKMDNQVLGYKDLAAIP	(Trinidad et al., 2012)
Dematin	22653706	Q9WV69.1	405	S287	MEKSLPIRRKTRSLPDRTPFHTSLHSGTSKSSSLPSYGRTTLSRLQSTEFSPSGSEAGSPG	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Deubiquitinating protein VCIP135	42559967	Q8CDG3.1	1220	T1072	PRARETLAVRKHNTGTDFSNSSIKTEPPVFTAASSNSELIRIAPGVVTMRDGRQIDPDVVE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Deubiquitinating protein VCIP135	42559967	Q8CDG3.1	1220	S1075	RETLAVRKHNTGTDFSNSSIKTEPPVFTAASSNSELIRIAPGVVTMRDGRQIDPDVVEAQR	(Trinidad et al., 2012)
Dihydropyrimidinase-like 2	74714004	Q86U75	619	S613	QHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDELBBBBBBBBBBBBBBBBBBBBBBB	(Hahne et al. 2012)
Dihydropyrimidinase-related protein 1	3122030	P97427.1	572	S495	MGRFIPRKPFPEHLYQRVRIRSKVFGLHSVSRGMYDGPVYEVPATPKHAAPAPSAKSSPSK	(Trinidad et al., 2012)
Dihydropyrimidinase-related protein 2	94730376	O08553.2	572	S507	FVYKRIKARSRLAELRGVPRGLYDGPVCEVSVTPKTVTPASSAKTSPAKQQAPPVRNLHQS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Dihydropyrimidinase-related protein 5	21362536	Q9EQF6.1	564	T520	TPYLGDVAIVVHPGKKEMGTPLADTPTRPVTRHGGMRDLHESSFSLSGSQIDDHVPKRASA	(Trinidad et al., 2012)
Diphosphoinositol polyphosphate phosphohydrolase 1	68565939	Q9JI46.1	168	T159	LQCHKPVQASYFETLRQGYPANNGTPVVPTTYSSSVSGIRBBBBBBBBBBBBBBBBBBBB	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Disabled homolog 2-interacting protein	116247769	Q3UHC7.1	1189	S793	SPVGPDALPADGQVPATQLLAGWPARAAPVSLAGLATVRRAVPTPTTPGTSEGAPGRPQLL	(Trinidad et al., 2012)
Disks large homolog 2	59797879	Q91XM9.1	852	T341	GTLEYKTSLPPIPPGRYSPIPKHMLGEDDYTRPPEPVYSTVNKLCDKPASPRHYSPVECDK	(Trinidad et al., 2012)
Disks large homolog 2	59797879	Q91XM9.1	852	S349	LPPIPPGRYSPIPKHMLGEDDYTRPPEPVYSTVNKLCDKPASPRHYSPVECDKSFLLSTPY	(Trinidad et al., 2012)
Disks large-associated protein 1	71153506	Q9D415.3	992	T531	VRAIEKGCSQDDECVSLRSSSPPRTTTTVRTIQSSTGVIKLSSAVEVSSCITTYKKTPPPV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Disks large-associated protein 1	71153506	Q9D415.3	992	T386	AMGDEDSGDSDTSPKPSPKVAARRESYLKATQPSLTELTTLKISNEHSPKLQIRSHSYLRA	(Trinidad et al., 2012)
Disks large-associated protein 1	71153506	Q9D415.3	992	T525	MRSHSYVRAIEKGCSQDDECVSLRSSSPPRTTTTVRTIQSSTGVIKLSSAVEVSSCITTYK	(Trinidad et al., 2012)
Disks large-associated protein 1	71153506	Q9D415.3	992	T526	RSHSYVRAIEKGCSQDDECVSLRSSSPPRTTTTVRTIQSSTGVIKLSSAVEVSSCITTYKK	(Trinidad et al., 2012)
Disks large-associated protein 1	71153506	Q9D415.3	992	T528	HSYVRAIEKGCSQDDECVSLRSSSPPRTTTTVRTIQSSTGVIKLSSAVEVSSCITTYKKTP	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Disks large-associated protein 1	71153506	Q9D415.3	992	S535	EKGCSQDDECVSLRSSSPPRTTTTVRTIQSSTGVIKLSSAVEVSSCITTYKKTPPPVPPRT	(Trinidad et al., 2012)
Disks large-associated protein 1	71153506	Q9D415.3	992	T527	SHSYVRAIEKGCSQDDECVSLRSSSPPRTTTTVRTIQSSTGVIKLSSAVEVSSCITTYKKT	(Trinidad et al., 2012)
Disks large-associated protein 2	71151789	Q8BJ42.2	1059	T633	RSTAAVSYTNYKKTPPPVPPRTTSKPLISVTAQSSTESTQDAYQDSRAQRMSPWPQDSRGG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Disks large-associated protein 2	71151789	Q8BJ42.2	1059	S355	HIPHCYPEALQSPFGDLSLKTSKSNNDVKCSACEGLALTPDTRYMKRSSWSTLTVSQAKEA	(Trinidad et al., 2012)
Disks large-associated protein 2	71151789	Q8BJ42.2	1059	S811	VQADLELEGFPGHVSMEDKGLQFGSSFQRHSEPSTPTQYGALRTVRTQGLFSYREDYRTQV	(Trinidad et al., 2012)
Disks large-associated protein 3	71151790	Q6PFD5.1	977	S410	GKDGEIPCRRMRSGSYIKAMGDEESGDSDGSPKTSPKALARRFASRRSSSVDTARINCCVP	(Trinidad et al., 2012)
Disks large-associated protein 3	71151790	Q6PFD5.1	977	S414	EIPCRRMRSGSYIKAMGDEESGDSDGSPKTSPKALARRFASRRSSSVDTARINCCVPPRIH	(Trinidad et al., 2012)
Disks large-associated protein 3	71151790	Q6PFD5.1	977	T750	APTYSVFRTVHTQGQWAYREGYPLPYEPPATDGSPGPTPVPAPGPGSGRRDSWMERGSRSL	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Disks large-associated protein 3	71151790	Q6PFD5.1	977	T757	RTVHTQGQWAYREGYPLPYEPPATDGSPGPTPVPAPGPGSGRRDSWMERGSRSLPDSGRTS	(Trinidad et al., 2012)
Disks large-associated protein 4	205831576	B1AZP2.1	992	T547	IQAGCSQEEDSVSLQSLSPPPSTGSLSNSRTLPSSSCLVAYKKTPPPVPPRTTSKPFISVT	(Trinidad et al., 2012)
Disks large-associated protein 4	205831576	B1AZP2.1	992	S278	ISGHMLKTTKNTTTELTAPPPPPAPPATCPSLGVGTDTNYVKRGSWSTLTLSHAHEVCQKT	(Trinidad et al., 2012)
Double-stranded RNA-binding protein Staufen homolog 2	73919459	Q8CJ67.1	570	T435	TNNTPKGILHLSPDVYQEMEASRHRVTSGTTLSYLSPKDMNQPSSSFFSVSPSSTSSATVA	(Trinidad et al., 2012)
Drebrin-like protein	51315842	Q62418.2	436	T282	RQEWESAGQQAPHPREIFKQKERAMSTTSVTSSQPGKLRSPFLQKQLTQPETSYGREPTAP	(Trinidad et al., 2012)
Dynactin subunit 1	341940511	O08788.3	1281	S1254	TDFATFPSSAFLRAKEEQQDDTVYMGKVTFSCAAGLGQRHRLVLTQEQLHQLHSRLISBBB	(Trinidad et al., 2012)
Dynactin subunit 4	78100038	Q8CBY8.1	467	S211	HTIHVVDKYSLGTRLQRPRAGASISTLAGLSLREGEDQKEVKIEPAQAVAEVEPLPEDYYT	(Trinidad et al., 2012)
Dystonin	30315937	Q91ZU6.1	7389	S2023	MVNSYMDAHTGQRLLLYDGDLDEAVSMLLESCGAELGADTSTRESLSVLTIPDAFPDCALS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Dystrophin	341940506	P11531.3	3678	T2427	EDLRSEWEAVNHLLRELRTKQPDRAPGLSTTGASASQTVTLVTQSVVTKETVISKLEMPSS	(Trinidad et al., 2012)
E1A-binding protein p400	341941110	Q8CHI8.3	3072	S2599	IAGVPAATFQSINKRLASPVAPGTLTTSGGSAPAQVVHTQQRAVGSPATATTDLVSMTTTQ	(Myers et al. 2011)
E1A-binding protein p400	341941110	Q8CHI8.3	3072	S2662	RAVTSVTASAVVTTNLTPVQTPTRSLVTQVSQATGVQLPGKTITPAAHFQLLRQQQQQQQQ	(Trinidad et al., 2012)
E1A-binding protein p400	341941110	Q8CHI8.3	3072	T954	PEHSLDLGISGRKRKASTSLTDDEVEDEEETIEEEEAHEGLVDHHTELTNLAKEAELPLID	(Trinidad et al., 2012)
E1A-binding protein p400	341941110	Q8CHI8.3	3072	S2624	TTSGGSAPAQVVHTQQRAVGSPATATTDLVSMTTTQGVRAVTSVTASAVVTTNLTPVQTPT	(Trinidad et al., 2012)
E1A-binding protein p400	341941110	Q8CHI8.3	3072	S2940	TQQITTQGPQQKVAYAAQPALKTQFLTTPISQAQKLAGTQQVQTQIQVAKLPQVVQQQTPV	(Trinidad et al., 2012)
E3 SUMO-protein ligase RanBP2	341941873	Q9ERU9.2	3053	S1307	IRFKTPEEAALFKCKFEEAQNILKALGTNTSTAPNHTLRIVKESATQDNKDICKADGGNLN	(Alfaro et al. 2012)(Myers et al. 2011)
E3 SUMO-protein ligase RanBP2	341941873	Q9ERU9.2	3053	T1138	NMGPNQQKNFGFHRSDDMFAFHGPGKSVFTTAASELANKSHETDGGSAHGDEEDDGPHFEP	(Myers et al. 2011)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
E3 SUMO-protein ligase RanBP2	83305554	P49792.2	3224	S1890	KFGHVDQENSPSFMFQGSSNTEFKSTKEGFSIPVSADGFKFGISEPGNQEKKSEKPLENGT	(Hahne et al. 2012)
E3 SUMO-protein ligase RanBP2	341941873	Q9ERU9.2	3053	S1731	QEKTPSFAFQGGSNTEFKSIKDGFSFCIPVSADGFKFGIQEKGNQEKKSEKHLENDPSFQA	(Trinidad et al., 2012)
E3 SUMO-protein ligase RanBP2	341941873	Q9ERU9.2	3053	T1306	AIRFKTPEEAALFKCKFEEAQNILKALGTNTSTAPNHTLRIVKESATQDNKDICKADGGNL	(Myers et al. 2011)
E3 SUMO-protein ligase RanBP2	83305554	P49792.2	3224	S1894	VDQENSPSFMFQGSSNTEFKSTKEGFSIPVSADGFKFGISEPGNQEKKSEKPLENGTGFQA	(Hahne et al. 2012)
E3 ubiquitin-protein ligase NEDD4	321724366	P46935.3	887	T375	SGHIDVQTHLAEEFNTRLAVCGNPATSQPVTSSNHSSRGGSLQTCIFEEQPTLPVLLPTSS	(Alfaro et al. 2012)
E3 ubiquitin-protein ligase NEDD4-like	739212005	Q8CFI0.2	1004	T482	DGASGSATNSNNHLVEPQIRRPRSLSSPTVTLSAPLEGAKDSPIRRAVKDTLSNPQSPQPS	(Trinidad et al., 2012)
E3 ubiquitin-protein ligase SH3RF1	189046785	Q69ZI1.2	892	T512	FERCQDGWYKGTSMHTSKIGVFPGNYVAPVTRAVTNASQAKVSMSTAGQASRGVTMVSPST	(Alfaro et al. 2012)(Trinidad et al., 2012)
E3 ubiquitin-protein ligase SH3RF1	189046785	Q69ZI1.2	892	S526	HTSKIGVFPGNYVAPVTRAVTNASQAKVSMSTAGQASRGVTMVSPSTAGGPTQKPQGNGVA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
E3 ubiquitin-protein ligase SH3RF1	189046785	Q69ZI1.2	892	T527	TSKIGVFPGNYVAPVTRAVTNASQAKVSMSTAGQASRGVTMVSPSTAGGPTQKPQGNGVAG	(Trinidad et al., 2012)
E3 ubiquitin-protein ligase TRIM33	56404945	Q99PP7.2	1142	S650	RHSAPQYSMMQPHLQRQHSNPGHAGPFPVVSAHNPINPTSPTTATMANANRGPTSPSVTAI	(Trinidad et al., 2012)
E3 ubiquitin-protein ligase UBR4	147742910	A2AN08.1	5180	S2577	SKAVQCLNTSSKEGKDLDPEVFQRLVITARSIAVTRPNNLVHFTESKLPQMETEGADEGKE	(Trinidad et al., 2012)
Early growth response protein 1	119243	P08046.2	533	S117	GEPSEQPYEHLTTESFSDIALNNEKAMVETSYPSQTTRLPPITYTGRFSLEPAPNSGNTLW	(Myers et al. 2011)(Trinidad et al., 2012)
ELKS/Rab6-interacting/CAST family member 1	51827912	Q99MI1.1	1120	S134	MTAMGSSPNIASSGVASDTIAFGEHHLPPVSMASTVPHSLRQARDNTIMDLQTQLKEVLRE	(Alfaro et al. 2012)
Endophilin-A2	10720273	Q62419.1	368	T284	EFKPRPREPFELGELEQPNGGFPCAPAPKITASSSFRSSDKPIRMPSKSMPPLDQPSCKAL	(Trinidad et al., 2012)
Endoplasmic reticulum resident protein 44	31077035	Q9BS26.1	406	S385	KLHREFHHGPDPTDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLLRDRDELBBBBBBBB	(Hahne et al. 2012)(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Endoplasmic reticulum resident protein 44	31077035	Q9BS26.1	406	S386	LHREFHHGPDPTDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLLRDRDELBBBBBBBBB	(Hahne et al. 2012)(Hahne et al. 2012)
Endoplasmic reticulum resident protein 44	31077035	Q9BS26.1	406	S381	LHSGKLHREFHHGPDPTDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLLRDRDELBBBBB	(Hahne et al. 2012)
Endoplasmic reticulum resident protein 44	31077035	Q9BS26.1	406	S380	DLHSGKLHREFHHGPDPTDTAPGEQAQDVASSPPESSFQKLAPSEYRYTLLRDRDELBBBB	(Hahne et al. 2012)
Endoplasmic reticulum-Golgi intermediate compartment protein 3	37999823	Q9Y282.1	383	S136	QRLDKDGIPVSSEAERHELGKVEVTVFDPDSLDPDRCESCYGAEAEDIKCCNTCEDVREAY	(Hahne et al. 2012)
ENH1	123779629	Q2Q7P0	591	S115	SAAAKSEPVSVQKGEPKEVVKPVPITSPAVSKVTSTTNMAYNKAPRPFGSVSSPKVTSIPS	(Trinidad et al., 2012)
ENH1	123779629	Q2Q7P0	591	T110	TLQRASAAAKSEPVSVQKGEPKEVVKPVPITSPAVSKVTSTTNMAYNKAPRPFGSVSSPKV	(Trinidad et al., 2012)
ENH1	123779629	Q2Q7P0	591	T531	VACGKPIRNNVFHLEDGEPYCETDYYALFGTICRGCEFPIEAGDMFLEALGYTWHDTCFVC	(Trinidad et al., 2012)
Epsin-1	118572643	Q80VP1.3	575	S416	PSSNGTAVGGFDTEPDEFSDFDRLRTALPTSGSSTGELELLAGEVPARSPGAFDMSGVGGS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Equilibrative nucleoside transporter 1	9296956	Q99808.3	456	S63	MTATQYFTNRLDMSQNVSLVTAELSKDAQASAAPAAPLPERNSLSAIFNNVMTLCAMLPLL	(Hahne et al. 2012)(Wang et al. 2009)
Erlin-2	38257366	O94905.1	339	T108	TSGGVMIYFDRIEVVNFLVPNAVYDIVKNYTADYDKALIFNKIHHELNQFCSVHTLQEVYI	(Hahne et al. 2012)
Erlin-2	38257366	O94905.1	339	T336	MDSAGSVSKQFEGLADKLSFGLEDEPLETATKENBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Hahne et al. 2012)
Erythrocyte membrane protein band 4.2	215274164	P16452.3	691	S82	FLPALKKVALTAQTGEQPSKINRTQATFPISSLGDRKWWSAVVEERDAQSWTISVTTPADA	(Wang et al. 2009)
Estrogen receptor	119599	P19785.1	599	T50	GNELEPLNRPQLKMPMERALGEVYVDNSKPTVFNYPEGAAYEFNAAAAAAAAASAPVYGQS	(Cheng et al. 2001)
Estrogen receptor	119599	P19785.1	599	T575	LEMLDAHRLHAPASRMGVPPEEPSQTQLATTSSTSAHSLQTYYIPPEAEGFPNTIBBBBBB	(Cheng et al. 2001)
ETS-related transcription factor Elf-2	68052252	Q9JHC9.1	593	T376	LNCSRAEKGVARVVNITSPTHDGSSRSPTTTAPVSAAAAPRTVRVAMQVPVVMTSLGQKIS	(Myers et al. 2011)(Trinidad et al., 2012)
ETS-related transcription factor Elf-2	68052252	Q9JHC9.1	593	S502	CQLQAKSNLTGSGSINIVGTPLAVRALTPVSIAHGTPVMRLSVPAQQASGQTPPRVISALL	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
ETS-related transcription factor Elf-2	68052252	Q9JHC9.1	593	T375	PLNCSRAEKGVARVVNITSPTHDGSSRSPTTTAPVSAAAAPRTVRVAMQVPVVMTSLGQKI	(Myers et al. 2011)
Eukaryotic translation initiation factor 2 subunit 1	61226505	Q6ZWX6.3	315	T220	KIRADIEVACYGYEGIDAVKEALRAGLNCSTETMPIKINLIAPPRYVMTTTTLERTEGLSV	(Trinidad et al., 2012)
eukaryotic translation initiation factor 4 gamma 1 isoform 1	38201621	NP_886553.2	1599	S61	VVFSTPQATQMNTPSQPRQHFYPSRAQPPSSAASRVQSAAPARPGPAAHVYPAGSQVMMIP	(Wang et al. 2010)
Eukaryotic translation initiation factor 4 gamma 3	48428276	O43432.2	1585	T295	PPSPTTVSSVARSTIAAPTSSALSSQPIFTTAIDDRCELSSPREDTIPIPSLTSCTETSDP	(Hahne et al. 2012)
Eukaryotic translation initiation factor 4 gamma 3	48428276	O43432.2	1585	S284	TAIVSIAELPLPPSPTTVSSVARSTIAAPTSSALSSQPIFTTAIDDRCELSSPREDTIPIP	(Hahne et al. 2012)
Eukaryotic translation initiation factor 4 gamma 3	48428276	O43432.2	1585	T250	EKPKPDPVLKSPSPVLRLVLSGEKKEQEGQTSETTAIVSIAELPLPPSPTTVSSVARSTIA	(Hahne et al. 2012)
Eukaryotic translation initiation factor 4E transporter	34194015 1	Q9EST3.2	983	S416	PSEDHAENKVDILEMLQKAKVDLKPLLSSLSANKEKLKESSHSGVVLSVEEVEAGLKGLKV	(Alfaro et al. 2012)
Exosome complex exonuclease RRP44	16623153 3	Q9CSH3.4	958	S200	QVILITNDRKNKEKAVQEGIPAFTCEEYVKSLTANPELIDRLAYLSDEMNEIESGKIIFSE	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Extracellular glycoprotein lacritin	33301325	Q9GZZ8.1	138	S86	TTTTAQETSAAAVQGTAKVTSSRQELNPLKSIVEKSILLTEQALAKAGKGMHGGVPGGKQF	(Hahne et al. 2012)
F-box only protein 41	517013977	Q6NS60.3	873	T387	GRGGGGSASGPGVRGPGRMREHHAGSAVPSTYAVSRHGSSPSTGASSRVPAASQSSGCYDS	(Trinidad et al., 2012)
FERM domain-containing protein 4A	109940080	Q8BIE6.2	1020	S934	AVSDELRQWYQRSTASHKEHSRLSHTSSTSSDSGSQYSTSSQSTFVAHSRVTRMPQMCKAT	(Trinidad et al., 2012)
Fibroblast growth factor receptor substrate 3	71152060	Q91WJ0.3	492	S439	PEPPRQLNYIQVELKGWGTARPKGPQNPSVSGAPGPTPHPVRSSDSYAVIDLKKTAAMSDL	(Alfaro et al. 2012)(Trinidad et al., 2012)
Filaggrin-2	187471178	Q2VIS4.2	2362	S371	RSCSQSSSQRGYGSKQCGQPQNCGRQQRMGSSHSSCCGPYGSGATQSSGCGQQRMSSCGHS	(Trinidad et al., 2012)
Forkhead box protein K1	118572324	P85037.1	733	S562	ANSANGYILTSQGAAGGSHDAAGAAVLDLGSEARGLEEKPTIAFATIPAAGGVIQTVASQM	(Hahne et al. 2012)
Forkhead box protein K2	341941094	Q3UCQ1.3	651	S540	GDHREVRVKVEPVPAISPATLGAASRIIQTSQGTPVQTVTIVQQAPLGQHQLPIKTVTQNG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Forkhead box protein K2	341941094	Q3UCQ1.3	651	S415	SREGSPAPLEPEPGASQPKLAVIQEARFAQSAPGSPLSSQPVLITVQRQLPPAIKPVTYTV	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Forkhead box protein P1	17433011	P58462.1	705	T446	SVTLSKSASEASPQSLPHTPTTPTAPLTPVTQGPSVITTTSMHTVGPIRRRYSDKYNVPIS	(Alfaro et al. 2012)
Formin-2	166214936	Q9JL04.2	1578	T263	GLDQFLLGPRSEAEKDTVQALPVRPDLPETTKSLVPEHPPSSGSHLTSETPGYATAPSAVT	(Trinidad et al., 2012)
formin-binding protein 4	158534059	NP_056123.2	1017	S797	TTVVTSQSSVDSTISSSSSTKGIKRKATEISTAVVQRSATIGSSPVLYSQSAIATGHQAAG	(Wang et al. 2010)
Fructose-bisphosphate aldolase A	113607	P05064.2	364	S354	AQEEYIKRALANSLACQGKYTPSGQSGAAASESLFISNHAYBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
G protein-regulated inducer of neurite outgrowth 1	97051843	Q3UNH4.2	932	T343	AVSSGEGGSVSVRMAETVSARQPEGMFPAKTDSTSSNSTGPSGRADPVSLRNSELVSPVKP	(Alfaro et al. 2012)(Trinidad et al., 2012)
G protein-regulated inducer of neurite outgrowth 1	97051843	Q3UNH4.2	932	S655	KAESQTSAKTVPQAPDKATSSLRQSDGTPYSSAQPQRDTRSIGSLPEREPSASTSQKDLAA	(Trinidad et al., 2012)
G protein-regulated inducer of neurite outgrowth 1	97051843	Q3UNH4.2	932	T607	PGKVETPSLQKEQPQLSEKTDPSRKVDPPTTVEPVSLGKADSASPSPRKAESQTSAKTVPQ	(Trinidad et al., 2012)
Gametogenetin-binding protein 2	818625005	Q5SV77.1	696	S659	LDESECTSDEEIFISQDEIQSFMANNQSFYSNREQYRQHLKEKFNKYCRLNDHKRPVCSGW	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Gamma-synuclein	13431905	Q9Z0F7.1	123	S67	VMYVGTKTKENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVANKTVEEAENIVVTTGVVRK	(Alfaro et al. 2012)
Gamma-synuclein	122066261	Q63544.2	123	S67	VMYVGTKTKGERGTSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEEAENIVVTTGVVRK	(Wang et al. 2010)
Gamma-synuclein	90110074	O76070.2	127	S54	QGVTEAAEKTKEGVMYVGAKTKENVVQSVTSVAEKTKEQANAVSEAVVSSVNTVATKTVEE	(Hahne et al. 2012)
Gelsolin	28381362	P13020.3	780	S48	CALSPSHAATTSRGRAQERAPQSRVSEARPSTMVVEHPEFLKAGKEPGLQIWRVEKFDLVP	(Trinidad et al., 2012)
Gephyrin	341940739	Q8BUV3.2	769	T236	EDKGVQCEEEEEEKKDSGVASTEDSSSSHITAAALAAKIPDSIISRGVQVLPRDTASLSTT	(Trinidad et al., 2012)
Glucocorticoid modulatory element-binding protein 2	22001626	Q9UKD1.1	530	T408	QSAQLALGPGVPVPQLTSVPLGKVVSTLPSTVLGKGSLQAPPASSPASPLLGGYTVLASSG	(Hahne et al. 2012)
glucocorticoid modulatory element-binding protein 2	6912568	NP_036516.1	530	T404	QVLTQSAQLALGPGVPVPQLTSVPLGKVVSTLPSTVLGKGSLQAPPASSPASPLLGGYTVL	(Wang et al. 2010)
Glucocorticoid receptor	121073	P06537.1	783	S43	DEVPSSLLGRGRGSVMDLYKTLRGGATVKVSASSPSVAAASQADSKQQRILLDFSKGSASN	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Glutamate [NMDA] receptor subunit epsilon-2	14549168	Q01097.3	1482	S1030	IDGLYDCDNPPFTTQPRSISKKPLDIGLPSSKHSQLSDLYGKFSFKSDRYSGHDDLIRSDV	(Trinidad et al., 2012)
Glutamate receptor delta-2 subunit	25090501	Q61625.1	1007	T929	SIDLTPLDIDTLPTRQALEQISDFRNTHITTTTFIPEQIQTLSRTLSAKAASGFAFGSVPE	(Trinidad et al., 2012)
Glutamate receptor delta-2 subunit	25090501	Q61625.1	1007	T981	GFAFGSVPEHRTGPFRHRAPNGGFFRSPIKTMSSIPYQPTPTLGLNLGNDPDRGTSIBBBB	(Trinidad et al., 2012)
Glutamate receptor, ionotropic kainate 3	385178634	B1AS29.1	919	S907	KHKPQPPMMVKTDAVINMHTFNDRRLPGKDSMSCSTSLAPVFPBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Glutamine and serine-rich protein 1	308153569	Q2KHR3.3	1735	S1272	AYKSVSTPLTTLDATSDKKKKTEALQVATTSPTANTTGTATTSSTTVGAVKQEPLHSTSYA	(Zhao et al. 2011)
Glutamine and serine-rich protein 1	308153569	Q2KHR3.3	1735	T1270	QDAYKSVSTPLTTLDATSDKKKKTEALQVATTSPTANTTGTATTSSTTVGAVKQEPLHSTS	(Zhao et al. 2011)
Glutamine and serine-rich protein 1	308153569	Q2KHR3.3	1735	T1271	DAYKSVSTPLTTLDATSDKKKKTEALQVATTSPTANTTGTATTSSTTVGAVKQEPLHSTSY	(Zhao et al. 2011)
Glutamine and serine-rich protein 1	308153569	Q2KHR3.3	1735	T1274	KSVSTPLTTLDATSDKKKKTEALQVATTSPTANTTGTATTSSTTVGAVKQEPLHSTSYAVN	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Glutamine and serine-rich protein 1	308153569	Q2KHR3.3	1735	T1277	STPLTTLDATSDKKKKTEALQVATTSPTANTTGTATTSSTTVGAVKQEPLHSTSYAVNILE	(Zhao et al. 2011)
Glutamine and serine-rich protein 1	308153569	Q2KHR3.3	1735	T1278	TPLTTLDATSDKKKKTEALQVATTSPTANTTGTATTSSTTVGAVKQEPLHSTSYAVNILEN	(Zhao et al. 2011)
Glutamine synthetase	145559476	P15105.6	373	T258	VCEDFGVIATFDPKPIPGNWNGAGCHTNFSTKAMREENGLKCIEEAIDKLSKRHQYHIRAY	(Trinidad et al., 2012)
Glutathione S-transferase omega-1	6016173	P78417.2	241	S13	BBBBBBBBBBBBBBBBBMSGESARSLGKGSAPPGPVPEGSIRIYSMRFCPFAERTRLVLK	(Wang et al. 2009)
Glyceraldehyde-3-phosphate dehydrogenase	120702	P16858.2	333	S208	AITATQKTVDGPSGKLWRDGRGAAQNIIPASTGAAKAVGKVIPELNGKLTGMAFRVPTPNV	(Alfaro et al. 2012)
Glyceraldehyde-3-phosphate dehydrogenase	122065190	P04797.3	333	T227	GRGAAQNIIPASTGAAKAVGKVIPELNGKLTGMAFRVPTPNVSVVDLTCRLEKPAKYDDIK	(Park et al. 2009)
Golgi reassembly-stacking protein 2	51316074	Q99JX3.3	451	T426	PPSDPVMTTAKADASSLTVDVTSPASKVPTTVEDRVSDCTPAVEKPVSDADASEPSBBBBB	(Alfaro et al. 2012)
Golgin subfamily A member 3	81175171	P55937.3	1487	T207	PATKMKLFSTLDPELMLNPENLPRASTVAVTKEYSFLRTSVPRGPKVGSLGLLAHSKEKKN	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Golgin subfamily A member 5	32469790	Q9QYE6.2	729	S158	NSSQKEPTGRVEVKKEKGRAPVSPSSPSGVSSVNTSVTTTKAMGGNAGSQSPGVNSSDSVP	(Trinidad et al., 2012)
Granulins	77416865	P28799.2	593	T532	AQPATFLARSPHVGVKDVECGEGHFCHDNQTCCRDNRQGWACCPYRQGVCCADRRHCCPAG	(Hahne et al. 2012)
GRB2-associated-binding protein 1	46396021	Q9QYY0.2	695	T322	GTAGVETQMRHVSISYDIPPTPGNTYQIPRTFPESTLGQSSKLDTIPDIPPPRPPKPHPTH	(Trinidad et al., 2012)
GTPase-activating Rap/Ran-GAP domain-like protein 3	123785528	Q3V0G7.1	1038	S905	YKIPLRNLVGRSIERPLKSPLVSKVITPPTSIGLGVAAIPVTHSLSLSRMEIKEIASRTRR	(Alfaro et al. 2012)
Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	51317303	P62874.3	340	S136	APSGNYVACGGLDNICSIYNLKTREGNVRVSRELAGHTGYLSCCRFLDDNQIVTSSGDTTC	(Trinidad et al., 2012)
Heat shock 70 kDa protein 12A	33112324	Q8K0U4.1	675	S20	BBBBBBBBBBBMADKEAGGGDAGPRETAPTSTYSSPARSLGDTGITPLSPSHILNDADPVS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Heat shock protein beta-1	19855073	P04792.2	205	S187	LSPEGTLTVEAPMPKLATQSNEITIPVTFESRAQLGGPEAAKSDETAAKBBBBBBBBBBBB	(Hahne et al. 2012)(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Heat shock protein beta-1	19855073	P04792.2	205	S176	PGVDPTQVSSSLSPEGTLTVEAPMPKLATQSNEITIPVTFESRAQLGGPEAAKSDETAAKB	(Hahne et al. 2012)
helicase SRCAP	146219843	NP_006653.2	3230	S2416	KAPERPGTRVSERLRGARAETQGANHTPVISAHQTRSTTTPPRCSPARERVPRPAPRPRPT	(Wang et al. 2010)
Hemoglobin subunit alpha	57013850	P69905.2	142	S134	HCLLVTLAAHLPAEFTPAVHASLDKFLASVSTVLTSKYRBBBBBBBBBBBBBBBBBBBBB	(Wang et al. 2009)
Hemoglobin subunit alpha	122441	P01942.2	142	S53	AEYGAEALERMFASFPTTKTYFPHFDVSHGSAQVKGHGKKVADALASAAGHLDDLPGALSA	(Trinidad et al., 2012)
Hemoglobin subunit alpha	57013850	P69905.2	142	S36	ADKTNVKAAWGKVGAHAGEYGAEALERMFLSFPTTKTYFPHFDLSHGSAQVKGHGKKVADA	(Wang et al. 2009)
Hemoglobin subunit alpha	57013850	P69905.2	142	S4	BBBBBBBBBBBBBBBBBBBBBBBBBMVLSPADKTNVKAAWGKVGAHAGEYGAEALERMF	(Wang et al. 2009)
Hemoglobin subunit beta	56749856	P68871.2	147	S50	NVDEVGGEALGRLLVVYPWTQRFFESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLD	(Wang et al. 2009)
Hemoglobin subunit beta	56749856	P68871.2	147	S73	FESFGDLSTPDAVMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPEN	(Wang et al. 2009)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Hemoglobin subunit beta	56749856	P68871.2	147	T85	VMGNPKVKAHGKKVLGAFSDGLAHLDNLKGTFATLSELHCDKLHVDPENFRLLGNVLVCVL	(Wang et al. 2009)
Hepatocyte growth factor-regulated tyrosine kinase substrate	71152119	O14964.1	777	S315	TYTSYPKAEPMPSASSAPPASSLYSSPVNSSAPLAEDIDPELARYLNRNYWEKKQEEARKS	(Hahne et al. 2012)(Hahne et al. 2012)
Heterogeneous nuclear ribonucleoprotein A3	30316201	Q8BG05.1	379	S367	SGQQQSNYGPMKGGSFGGRSSGSPYGGGYGSGGGSGGYGSRRFBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Histone deacetylase complex subunit SAP130	74717977	Q9H0E3.1	1048	T695	SPRPSILRKKPATDGAKPKSEIHVSMATPVTVSMETVSNQNNDQPTIAVPPTAQQPPPTIP	(Hahne et al. 2012)
Histone deacetylase complex subunit SAP130	143585771	Q8BIH0.2	1057	T320	SRPTLSIQHPPSAAISIQRPAQSRDVTTRITLPSHPALGTPKQQLHTMAQKTIFSTGTPVA	(Myers et al. 2011)
histone H2A	603553	CAA58539.1	130	T102	RDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQGGVLPNIQAVLLPKKTESHHKAKGKBB	(Sakabe et al. 2010)
histone H2B	510991	CAA41051.1	126	S37	SAPAPKKGSKKAVTKAQKKDGKKRKRSRKESYSIYVYKVLKQVHPDTGISSKAMGIMNSFV	(Sakabe et al. 2010)
histone H2B type 2-E	4504277	NP_003519.1	126	S113	HYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSKBBBBBBBBBBBBBBBBB	(Fujiki et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
histone H2B type 2-E	4504277	NP_003519.1	126	S124	EIQTAVRLLLPGELAKHAVSEGTKAVTKYTSSKBBBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Fujiki et al. 2011)
histone H2B type 2-E	4504277	NP_003519.1	126	S92	IMNSFVNDIFERIAGEASRLAHYNKRSTITSREIQTAVRLLLPGELAKHAVSEGTKAVTKY	(Fujiki et al. 2011)
histone H3	1894787	CAA58540.1	136	T33	RTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQKSTELLI	(Fong et al. 2012)
histone H4	4504321	NP_003486.1	103	S48	RHRKVLRDNIQGITKPAIRRLARRGGVKRISGLIYEETRGVLKVFLENVIRDAVTYTEHAK	(Sakabe et al. 2010)
homeodomain interacting protein kinase 1	162770931	CAP58492.1	1210	T1001	GPGRPAADGIGTRTIIVPPLKTQLGDCTVATQASGLLSSKTKPVASVSGQSSGCCITPTGY	(Trinidad et al., 2012)
homeodomain interacting protein kinase 1	162770931	CAP58492.1	1210	T151	CGLKRKSEEVESNGSVQIIEEHPPLMLQNRTVVGAAATTTTVTTKSSSSSGEGDYQLVQHE	(Trinidad et al., 2012)
Homeodomain-interacting protein kinase 2	13627157	Q9QZR5.2	1196	S1009	VLVECDSLGPAISASHHSSSFKSKSSSTVTSTSGHSSGSSSGAIAYRQQRPGPHFQQQQPL	(Alfaro et al. 2012)
Homer protein homolog 1	38605093	Q9Z2Y3.2	366	S185	DVTQNSEPRAEPTQNALPFPHSAGDRTQALSHASSAISKHWEAELATLKGNNAKLTAALLE	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Homer protein homolog 1	38605093	Q9Z2Y3.2	366	S249	NVKQWKQQLAAYQEEAERLHKRVTELECVSSQANAVHSHKTELNQTVQELEETLKVKEEEI	(Trinidad et al., 2012)
Host cell factor 1	160332311	P51610.2	2035	T629	PVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTK	(Zhao et al. 2011)(Hahne et al. 2012)(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T652	SSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGK	(Zhao et al. 2011)(Hahne et al. 2012)(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T658	STRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGKVMSVVQ	(Zhao et al. 2011)(Hahne et al. 2012)(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T592	SSAPTVLSVPAGTTIVKTMAVTPGTTTLPATVKVASSPVMVSNPATRMLKTAAAQVGTSVS	(Hahne et al. 2012)(Hahne et al. 2012)(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	160332311	P51610.2	2035	T642	TAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLVKSPISVPG	(Zhao et al. 2011)(Hahne et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	S623	VKVASSPVMVSNPATRMLKTAAAQVGTSVSSAANTSTRPIITVHKSGTVTVAQQAQVVTTV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	S685	GGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPVTQIIQTKGP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T490	TIQVLPTVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLVTMRPASQAGKAPVTVTSLP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T515	AVLKVTGPQATTGTPLVTMRPASQAGKAPVTVTSLPASVRMVVPTQSAQGTVIGSNPQMSG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T651	VSSAANTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSALISNLG	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	341940790	Q61191.2	2045	T652	SSAANTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSALISNLGK	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T779	TILGISSVSPSTTKPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T831	TKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLKGAPGQPGTILRTVPMGGVRLVTPVT	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	160332311	P51610.2	2035	T801	TIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVT	(Hahne et al. 2012)(Hahne et al. 2012)(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	S473	VGITLLPQAAPAPPTTTTIQVLPTVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLVTM	(Hahne et al. 2012)(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	S789	STTKPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVP	(Hahne et al. 2012)(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	160332311	P51610.2	2035	T476	TLLPQAAPAPPTTTTIQVLPTVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLVTMRPA	(Hahne et al. 2012)(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T634	NPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLV	(Hahne et al. 2012)(Hahne et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	S622	TVKVASSPVMVSNPATRMLKTAAAQVGTSVSSAANTSTRPIITVHKSGTVTVAQQAQVVTT	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T1238	VQLALPSVRVGLSGPSSKDMPTGRQPETYHTYTTNTPTTTRSIMVAGELGAARVVPTSTYE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T495	PTVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLVTMRPASQAGKAPVTVTSLPASVRM	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T579	LAAAAAATQKIPPSSAPTVLSVPAGTTIVKTVAVTPGTTTLPATVKVASSPVMVSNPATRM	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	341940790	Q61191.2	2045	T588	KIPPSSAPTVLSVPAGTTIVKTVAVTPGTTTLPATVKVASSPVMVSNPATRMLKTAAAQVG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T801	TIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVT	(Alfaro et al. 2012)(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T808	ITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLKGA	(Myers et al. 2011)(Trinidad et al., 2012)
Host cell factor 1	160332311	P51610.2	2035	S562	AQGTVIGSSPQMSGMAALAAAAAATQKIPPSSAPTVLSVPAGTTIVKTMAVTPGTTTLPAT	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	S563	QGTVIGSSPQMSGMAALAAAAAATQKIPPSSAPTVLSVPAGTTIVKTMAVTPGTTTLPATV	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	S620	PATVKVASSPVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVV	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	S622	TVKVASSPVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTT	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	160332311	P51610.2	2035	S623	VKVASSPVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTTV	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	S628	SPVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVT	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	S638	RMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLVKSPI	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	S727	VTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVS	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	S742	TKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTTTIIKTI	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T566	VIGSSPQMSGMAALAAAAAATQKIPPSSAPTVLSVPAGTTIVKTMAVTPGTTTLPATVKVA	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T619	LPATVKVASSPVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQV	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T625	VASSPVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVG	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	160332311	P51610.2	2035	T627	SSPVMVSNPATRMLKTAAAQVGTSVSSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVGGV	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T651	VSSATNTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLVKSPISVPGGSALISNLG	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T694	VKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKL	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T726	AVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSV	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T737	TQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTTT	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T738	QIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTTTI	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T739	IIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTTTII	(Zhao et al. 2011)
Host cell factor 1	160332311	P51610.2	2035	T746	LPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTTTIIKTIPMSA	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	341940790	Q61191.2	2045	T1148	STATTAMSSMGTGQQRDTRRTTNTPTVVRITVAPGALERVQGTVKPQCQTQQTNMTTTTMT	(Alfaro et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	T642	TAAAQVGTSVSSAANTSTRPIITVHKSGTVTVAQQAQVVTTVVGGVTKTITLVKSPISVPG	(Alfaro et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	S1497	TSSSAITTTVSSTLTRAVTTVTQSTPVPGPSVPPPEELQVSPGPRQQLPPRQLLQSASTAL	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	S427	LQKYDIPATAATATSPTPNPVPSVPANPPKSPAPAAAAPAVQPLTQVGITLLPQAAPAPPT	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	S471	TQVGITLLPQAAPAPPTTTTIQVLPTVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLV	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	S775	GTKPTILGISSVSPSTTKPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMT	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	S788	PSTTKPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAV	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T588	KIPPSSAPTVLSVPAGTTIVKTMAVTPGTTTLPATVKVASSPVMVSNPATRMLKTAAAQVG	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	160332311	P51610.2	2035	T712	KVMSVVQTKPVQTSAVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQAS	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T784	SSVSPSTTKPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKI	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T871	QPGTILRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVSTSLAGAGGHS	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	S1188	AAQGSKSQCQTRQTSATSTTMTVMATGAPCSAGPLLGPSMAREPGGRSPAFVQLAPLSSKV	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T1143	ETGTTNTATTAMSSVGANHQRDARRACAAGTPAVIRISVATGALEAAQGSKSQCQTRQTSA	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T446	PVPSVPANPPKSPAPAAAAPAVQPLTQVGITLLPQAAPAPPTTTTIQVLPTVPGSSISVPT	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T457	SPAPAAAAPAVQPLTQVGITLLPQAAPAPPTTTTIQVLPTVPGSSISVPTAARTQGVPAVL	(Hahne et al. 2012)
Host cell factor 1	160332311	P51610.2	2035	T587	QKIPPSSAPTVLSVPAGTTIVKTMAVTPGTTTLPATVKVASSPVMVSNPATRMLKTAAAQV	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	160332311	P51610.2	2035	T808	ITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLKGA	(Hahne et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	T1241	ALPSVRVGLSGPSSKDMPTGRQPETYHTYTTNTPTTTRSIMVAGELGAARVVPTSTYESLQ	(Alfaro et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	T1246	RVGLSGPSSKDMPTGRQPETYHTYTTNTPTTTRSIMVAGELGAARVVPTSTYESLQASSPS	(Alfaro et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	T405	ANTNSLEVSWGAVATADSYLLQLQKYDIPATAATATSPTPNPVPSVPANPPKSPAPAAAAP	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T496	TVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLVTMRPASQAGKAPVTVTSLPASVRMV	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T787	SPSTTKPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITA	(Alfaro et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	T800	KTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGV	(Alfaro et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	T861	TQVVLKGAPGQPGTILRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	160332311	P51610.2	2035	T1243	PLSSKVRLSSPSIKDLPAGRHSHAVSTAAMTRSSVGAGEPRMAPVCESLQGGSPSTTVTVT	(Hahne et al. 2012)
Host cell factor 1	341940790	Q61191.2	2045	S518	KVTGPQATTGTPLVTMRPASQAGKAPVTVTSLPASVRMVVPTQSAQGTVIGSNPQMSGMAA	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	S563	QGTVIGSNPQMSGMAALAAAAAAATQKIPPSSAPTVLSVPAGTTIVKTVAVTPGTTTLPATV	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	S620	PATVKVASSPVMVSNPATRMLKTAAAQVGTSVSSAANTSTRPIITVHKSGTVTVAQQAQVV	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	S806	AIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLK	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T1138	PCETHETGTTSTATTAMSSMGTGQQRDTRRTTNTPTVVRITVAPGALERVQGTVKPQCQTQ	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T1247	VGLSGPSSKDMPTGRQPETYHTYTTNTPTTTRSIMVAGELGAARVVPTSTYESLQASSPSS	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T517	LKVTGPQATTGTPLVTMRPASQAGKAPVTVTSLPASVRMVVPTQSAQGTVIGSNPQMSGMA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Host cell factor 1	341940790	Q61191.2	2045	T587	QKIPPSSAPTVLSVPAGTTIVKTVAVTPGTTTLPATVKVASSPVMVSNPATRMLKTAAAQV	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T784	SSVSPSTTKPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKI	(Trinidad et al., 2012)
Host cell factor 1	341940790	Q61191.2	2045	T870	GQPGTILRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVSTSLAGAGAH	(Trinidad et al., 2012)
host cell factor 1	213385315	NP_001132979.1	2034	T1148	STATTAMSSMGTGQQRDARRATNTPTVVRITVAPGALERAQGTVKPPCQTQQTNMTSTTMT	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	S1150	ATTAMSSVGANHQRDARRACAAGTPAVIRISVATGALEAAQGSKSQCQTRQTSATSTTMTV	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	S685	GGVTKTITLVKSPISVPGGSALISNLGKVMSVVQTKPVQTSAVTGQASTGPVTQIIQTKGP	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	S806	AIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLK	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	T1239	VQLAPLSSKVRLSSPSIKDLPAGRHSHAVSTAAMTRSSVGAGEPRMAPVCESLQGGSPSTT	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
host cell factor 1	98986457	NP_005325.2	2035	T490	TIQVLPTVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLVTMRPASQAGKAPVTVTSLP	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	T495	PTVPGSSISVPTAARTQGVPAVLKVTGPQATTGTPLVTMRPASQAGKAPVTVTSLPAGVRM	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	T579	LAAAAAATQKIPPSSAPTVLSVPAGTTIVKTMAVTPGTTTLPATVKVASSPVMVSNPATRM	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	T726	AVTGQASTGPVTQIIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSV	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	T739	IIQTKGPLPAGTILKLVTSADGKPTTIITTTQASGAGTKPTILGISSVSPSTTKPGTTTII	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	T779	TILGISSVSPSTTKPGTTTIIKTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTG	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	T800	KTIPMSAIITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGV	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	T808	ITQAGATGVTSSPGIKSPITIITTKVMTSGTGAPAKIITAVPKIATGHGQQGVTQVVLKGA	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
host cell factor 1	98986457	NP_005325.2	2035	T861	TQVVLKGAPGQPGTILRTVPMGGVRLVTPVTVSAVKPAVTTLVVKGTTGVTTLGTVTGTVS	(Wang et al. 2010)
host cell factor 1	98986457	NP_005325.2	2035	S563	QGTVIGSSPQMSGMAALAAAAAATQKIPPSSAPTVLSVPAGTTIVKTMAVTPGTTTLPATV	(Wang et al. 2010)
Hypoxia up-regulated protein 1	10720185	Q9Y4L1.1	999	S612	SSLFGGGTTPDAKENGTDTVQEEEESPAEGSKDEPGEQVELKEEAEAPVEDGSQPPPPEPK	(Hahne et al. 2012)
Hypoxia up-regulated protein 1	10720185	Q9Y4L1.1	999	S833	KLCQGLFFRVEERKKWPERLSALDNLLNHSSMFLKGARLIPEMDQIFTEVEMTTLEKVINE	(Hahne et al. 2012)
Hypoxia up-regulated protein 1	10720185	Q9Y4L1.1	999	T590	FETLVEDSAEEESTLTKLGNTISSLFGGGTTPDAKENGTDTVQEEEESPAEGSKDEPGEQV	(Hahne et al. 2012)
Hypoxia up-regulated protein 1	10720185	Q9Y4L1.1	999	T598	AEEESTLTKLGNTISSLFGGGTTPDAKENGTDTVQEEEESPAEGSKDEPGEQVELKEEAEA	(Hahne et al. 2012)
Hypoxia up-regulated protein 1	10720185	Q9Y4L1.1	999	S583	LDRVESVFETLVEDSAEEESTLTKLGNTISSLFGGGTTPDAKENGTDTVQEEEESPAEGSK	(Hahne et al. 2012)
Hypoxia up-regulated protein 1	10720185	Q9Y4L1.1	999	T864	MFLKGARLIPEMDQIFTEVEMTTLEKVINETWAWKNATLAEQAKLPATEKPVLLSKDIEAK	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Inositol polyphosphate 1-phosphatase	51704296	P49442.2	396	T394	ANKGGLIAYRSRNRLDTFLSRLIQNLGPVKTQABBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Insulin receptor substrate 2	341940841	P81122.2	1321	S425	PLSRSHTLSAGCGGRPSKVTLAPAGGALQHSRSMSMPVAHSPPAATSPGSLSSSSGHGSGS	(Trinidad et al., 2012)
Insulin receptor substrate 2	341940841	P81122.2	1321	S303	DSVVAQNIHETILEAMKALKELFEFRPRSKSQSSGSSATHPISVPGARRHHHLVNLPPSQT	(Trinidad et al., 2012)
Insulin receptor substrate 2	341940841	P81122.2	1321	T1144	QPPDPHRGAKVIRADPQGGRRRHSSETFSSTTTVTPVSPSFAHNSKRHNSASVENVSLRKS	(Trinidad et al., 2012)
Integrin beta-1	218563324	P05556.2	798	S588	FNCDRSNGLICGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGQICNGRGICECGVC	(Hahne et al. 2012)
Interferon regulatory factor 2-binding protein-like	34395561	Q8K3X4.1	775	S159	RYGLSAAAAAAAAAAAVEQRSRFEYPPPPVSLGSSSHAARLPNGLGGPNGFPKPAPEEGPP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Intermediate filament family orphan 1	81897957	Q8BXL9.1	562	T175	PAAVCPPSARVLGSPSRSPAGPLASSAACHTSSSTSTSTAFSSSTRFMPGTIWSFSHARRL	(Alfaro et al. 2012)
Intermediate filament family orphan 1	81897957	Q8BXL9.1	562	S170	PLSSRPAAVCPPSARVLGSPSRSPAGPLASSAACHTSSSTSTSTAFSSSTRFMPGTIWSFS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
IQ motif and SEC7 domain-containing protein 1	110279022	Q8R0S2.2	961	S886	RESVAEVQEMEKHRIESELEKQKGVVRPSMSQCSSLKKESGNGTLSRACLDDSYASGEGLK	(Trinidad et al., 2012)
KAT8 regulatory NSL complex subunit 3	147646956	A2RSY1.1	903	T858	LLTNGSLAKLASSLPGLAQISNQASGLKVPTTITLTLRGQPSRITTLSPMGSGATPSEEPN	(Myers et al. 2011)
keratin, type I cytoskeletal 18	4557888	NP_000215.1	430	S31	MSFTTRSTFSTNYRSLGSVQAPSYGARPVSSAASVYAGAGGSGSRISVSRSTSFRGGMGSG	(Wang et al. 2010)
Keratin, type II cytoskeletal 1	238054406	P04264.6	644	S517	EGEESRMSGECAPNVSVSVSTSHTTISGGGSRGGGGGGYGSGGSSYGSGGGSYGSGGGGG	(Hahne et al. 2012)
Keratin, type II cytoskeletal 1	126302559	P04104.4	637	S530	RMSGECTPNVSVSVSTSHTSMSGSSSRGGGSGGGRYGGGGSYGGGSGGGSYGGSSGGGGSG	(Trinidad et al., 2012)
Keratin, type II cytoskeletal 1	126302559	P04104.4	637	S598	GGGSYGGGSGGGSSGSHRGGSGGGGGSSGGSYGGSSGGGRGGSSSGGGGVKSSGSSTVKFV	(Trinidad et al., 2012)
Keratin, type II cytoskeletal 2 epidermal	123796763	Q3TTY5.1	707	S130	RGFGGGQGFGGSGGFGGGSGFGGGQGFGGGSRFGGGSGFGGGGFGGGSFGGGRFGGGPGGF	(Trinidad et al., 2012)
Keratin, type II cytoskeletal 2 epidermal	123796763	Q3TTY5.1	707	S592	GSTYGSGGRSSGSRGSGSGSGGGGYSSGGGSRGGSGGGYGSGGGSRGGSGGGYGSGGGSGS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Keratin, type II cytoskeletal 2 epidermal	123796763	Q3TTY5.1	707	S596	GSGGRSSGSRGSGSGSGGGGYSSGGGSRGGSGGGYGSGGGSRGGSGGGYGSGGGSGSGGGY	(Trinidad et al., 2012)
Keratin, type II cytoskeletal 2 epidermal	123796763	Q3TTY5.1	707	S118	SSFGGSSGFGGGRGFGGGQGFGGSGGFGGGSGFGGGQGFGGGSRFGGGSGFGGGGFGGGSF	(Trinidad et al., 2012)
Keratin, type II cytoskeletal 2 epidermal	123796763	Q3TTY5.1	707	S581	SYGGRGGGGGGGSTYGSGGRSSGSRGSGSGSGGGGYSSGGGSRGGSGGGYGSGGGSRGGSG	(Trinidad et al., 2012)
Keratin, type II cytoskeletal 2 epidermal	123796763	Q3TTY5.1	707	S632	SGGGSRGGSGGGYGSGGGSGSGGGYSSGGGSRGGSGGGGVSSGGGSRGGSSSGGGSRGGSS	(Trinidad et al., 2012)
Keratin, type II cytoskeletal 2 epidermal	123796763	Q3TTY5.1	707	S647	GGGSGSGGGYSSGGGSRGGSGGGGVSSGGGSRGGSSSGGGSRGGSSSGGGGYSSGGGSRGG	(Trinidad et al., 2012)
Keratin, type II cytoskeletal 2 epidermal	123796763	Q3TTY5.1	707	S678	RGGSSSGGGSRGGSSSGGGGYSSGGGSRGGSSSGGAGSSSEKGGSGSGEGCGSGVTFSFRB	(Trinidad et al., 2012)
Kinase suppressor of Ras 2	147647674	Q3UVC0.2	959	T212	VCPPEPSPWIRTHLSQSPRVQTKCPQHFCPTSPTPGTPVYTQVDRLTVDAYPNLCPPPPPL	(Trinidad et al., 2012)
La-related protein 4B	134034151	Q6A0A2.2	741	T51	GKDSSHLMNGPISQTTSQTRSLPALTQVPTTKVSELNPNAKVWGTHMLHLEASSAAVGVNA	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
La-related protein 4B	134034151	Q6A0A2.2	741	T632	PSPVHLPEDPKVAEKQRETQSVDRLPSTPTTTACKSVQVNGAATELRKPSYAEICQRTSKD	(Trinidad et al., 2012)
Large structural phosphoprotein	130702	P08318.1	1048	S921	KGRGSRVGVPSLKPTLGGKAVVGRPPSVPVSGSAPGRLSGSSRAASTTPTYPAVTTVYPPS	(Greis et al. 1994)
Large structural phosphoprotein	130702	P08318.1	1048	S952	GSAPGRLSGSSRAASTTPTYPAVTTVYPPSSTAKSSVSNAPPVASPSILKPGASAALQSRR	(Greis et al. 1994)
Latrophilin-3	122065423	Q80TS3.3	1537	S1536	RGSSDGFIVPPNKDGASPEGTSKGPAHLVTSLBBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Leucine zipper protein 1	970721777	Q8R4U7.2	1068	T952	SKRDLKCSEDPPTGIGRNMEATNAYTQRPCTDFLELEQPRSQPSEQGARRVGNSGDAPELS	(Trinidad et al., 2012)
Leucine-rich repeat transmembrane neuronal protein 4	68052334	Q80XG9.2	590	T368	ICAGPKHIQGEKVSDAVETYNICSDVQVVNTERSHLAPQTPQKPPFIPKPTIFKPDAVPAT	(Trinidad et al., 2012)
Leucine-rich repeat-containing protein 7	50400980	Q80TE7.2	1490	S904	RKDHMKEPTETPGPFSPGVPWEYHDPTPNRSLGNVFSQIHCRPDSSKGVIAISKSTERLSP	(Trinidad et al., 2012)
Leucine-rich repeat-containing protein 7	50400980	Q80TE7.2	1490	S995	LENYASGSDHLGSHERPDKFLGPEHGMSSMSRSQSVPMLDDEMLMYGSSKGPPQQKASMTK	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
LIM and calponin homology domains-containing protein 1	152032557	Q3UH68.2	1057	T506	VSSFPNDPSPMKYLRQQSLPPPKFTATVETTIARTSVPESIASAGTGSPSKIITPNTVPML	(Alfaro et al. 2012)
LINE-1 type transposase domain-containing protein 1	74745406	Q5T7N2.1	865	S559	VHKTQEEEETAVPTSQGTGTPCLTLCLASPSKSLEMSHDEHKKHSHTNLSISTGVTKLKKT	(Hahne et al. 2012)
Lipid phosphate phosphatase-related protein type 3	81894536	Q7TPB0.1	716	T370	EKTSLGSLKRASVDVDLLAPRSPMGKEGMVTFSNTLPRVSTPSLDDPARRHMTIHVPLDAS	(Trinidad et al., 2012)
Lipid phosphate phosphatase-related protein type 4	167008975	Q7TME0.2	766	T413	DASSLTNLKRANADVEIITPRSPMGKESMVTFSNTLPRANTPSVEDPVRRNASIHASMDSA	(Trinidad et al., 2012)
Lipoma-preferred partner homolog	81895958	Q8BFW7.1	613	S11	BBBBBBBBBBBBBBBBBBBMSHPSWLPPKSTGEPLGHVPARMETTHSFGNPSISVSTQQP	(Trinidad et al., 2012)
Liprin-alpha-2	42558981	Q8BSS9.2	1257	S545	KVSLAEEIEKLRSELDQMKMRTGSLIEPTISRTHIDTSTELRYSVGSLVDSQSDYRTTKVI	(Trinidad et al., 2012)
Liprin-alpha-2	42558981	Q8BSS9.2	1257	S558	ELDQMKMRTGSLIEPTISRTHIDTSTELRYSVGSLVDSQSDYRTTKVIRRPRRGRMGVRRD	(Trinidad et al., 2012)
Liprin-alpha-3	42558958	P60469.1	1043	S368	RMQMEIDQLRGRPPSSYSRSLPGSALELRYSQAPTLPSGAPLDPYGAGSGRAGKRGRWSGA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Lysine-specific demethylase 3B	308153456	Q7LBC6.2	1761	T433	NKEAGKTLEQVGQGIVASAAVVTTASSTPNTVRISDTGLAAGTVPEKQKGSRSQASGENSR	(Hahne et al. 2012)
Lysine-specific demethylase 3B	97054042	Q6ZPY7.2	1562	S455	QPPKLSREEPSNPFLAFVEKVEHSPFSSFVSQASGSSSSATSVTSKATASWPESHSSAESA	(Trinidad et al., 2012)
Lysine-specific demethylase 3B	97054042	Q6ZPY7.2	1562	T497	VTSKATASWPESHSSAESAPLAKKKPLFITTDSSKLVSGVLGSALSTGSPSLSAVGNGRSS	(Trinidad et al., 2012)
Lysine-specific demethylase 6A	122066655	O70546.2	1401	S554	LNGPTVDSSLPTNSVSGQQPQLPLTRMPSVSQPGVHTACPRQTLANGPFSAGHVPCSTSRT	(Trinidad et al., 2012)
Lysosomal alpha-glucosidase	317373572	P10253.4	952	T153	GQPWCFFPPSYPSYKLENLSSSEMGYTATLTRTTPTFFPKDILTLRLDVMMETENRLHFTI	(Hahne et al. 2012)
Lysosomal alpha-mannosidase	118574274	O00754.3	1011	S371	AQQAKGSSVHVLYSTPACYLWELNKANLTWSVKHDDFFPYADGPHQFWTGYFSSRPALKRY	(Hahne et al. 2012)
MAGUK p55 subfamily member 2	27734429	Q9WV34.1	552	S549	SLVNSNLERTFRELQTAMEKLRTEPQWVPVSWVYBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Malate dehydrogenase, mitochondrial	146345457	P08249.3	338	S276	SATLSMAYAGARFVFSLVDAMNGKEGVVECSFVQSKETECTYFSTPLLLGKKGLEKNLGIG	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
MAP/microtubule affinity-regulating kinase 3	81175182	Q03141.2	753	S495	IAPASPMLGNAGNPNKADIPERKKSPAVPSSNTASGGMTRRNTYVCSERCAADRHSVIQNG	(Trinidad et al., 2012)
MAP7 domain-containing protein 2	158705866	A2AG50.1	781	S307	ISAMGDAGKGAMAGGEPSQMEKMKKGRVATSAASGGHGSPLRRCEPPEDISKRLSSPVKSK	(Trinidad et al., 2012)
Mastermind-like domain-containing protein 1	167008903	P0C6A2.1	803	S253	CSQVAGTSLPIMPSSTGMSYSIPSSSKQIVSSSSSTAQAQVKNQVQNMLPVTMPPLSVPQW	(Alfaro et al. 2012)
Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1	52782720	Q6RHR9.1	1471	T1093	GNTVTLRIIPGDESSNATLLTNAEKIATITTTHAPSQQGTQETRTTTKPKQDSQFEFKGPQ	(Alfaro et al. 2012)
Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1	52782720	Q6RHR9.1	1471	T1094	NTVTLRIIPGDESSNATLLTNAEKIATITTTHAPSQQGTQETRTTTKPKQDSQFEFKGPQA	(Alfaro et al. 2012)
Membrane-associated guanylate kinase, WW and PDZ domain-containing protein 1	52782720	Q6RHR9.1	1471	S1098	LRIIPGDESSNATLLTNAEKIATITTTHAPSQQGTQETRTTTKPKQDSQFEFKGPQAAQEQ	(Trinidad et al., 2012)
Membrane-associated phosphatidylinositol transfer protein 1	81882145	O35954.1	1243	T1226	PVDFLRKQSQLLRSRGPSQVDREGPGTPPTTLARGKTRSISLKLDSEEBBBBBBBBBBBBBB	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Metabotropic glutamate receptor 5	158705917	Q3UVX5.2	1203	S1058	AGRTDDDAPSLHSETAARSSSSQGSLMEQISSVVTRFTANITELNSMMLSTAAAPGPPGTP	(Trinidad et al., 2012)
Metal transporter CNNM1	308153679	Q0GA42.5	951	T808	FVKITRQQYQNALTACHMDSSPQSPDMEAFTDGDSTKAPTTRGTPQTPKDDPVLTLLSNRT	(Trinidad et al., 2012)
methyl CpG binding protein 2	149029883	EDL84995.1	492	T443	EEKMPRAGSLESDGCPKEPAKTQPMVAAAATTTTTTTTTVAEKYKHRGEGERKDIVSSSMP	(Wang et al. 2010)
Methyl-CpG-binding protein 2	12585281	Q9Z2D6.1	484	T434	QDLSSSICKEEKMPRGGSLESDGCPKEPAKTQPMVATTTTVAEKYKHRGEGERKDIVSSSM	(Alfaro et al. 2012)(Trinidad et al., 2012)
Methyl-CpG-binding protein 2	12585281	Q9Z2D6.1	484	T441	CKEEKMPRGGSLESDGCPKEPAKTQPMVATTTTVAEKYKHRGEGERKDIVSSSMPRPNREE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Methylcytosine dioxygenase TET3	239938841	Q8BG87.3	1668	S1083	KLSTPEKIKQEALELAGVTTDPGLSLKGGLSQQSLKPSLKVEPQNHFSSFKYSGNAVVESY	(Trinidad et al., 2012)
Methylcytosine dioxygenase TET3	239938841	Q8BG87.3	1668	S1252	NHHPIPHHQQPAYPGPKEYLLPKVPQLHPASRDPSPFAQSSSCYNRSIKQEPIDPLTQAES	(Trinidad et al., 2012)
MFLJ00139 protein	81888762	Q5DU62	992	T317	GFVQTELKPPSTSQVHVGSSAGPKLPTSTVTTTSVTSKALTHVTNSSPTGWSSPAQSSPAN	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
MFLJ00139 protein	81888762	Q5DU62	992	T318	FVQTELKPPSTSQVHVGSSAGPKLPTSTVTTTSVTSKALTHVTNSSPTGWSSPAQSSPANF	(Trinidad et al., 2012)
MFLJ00139 protein	81888762	Q5DU62	992	T319	VQTELKPPSTSQVHVGSSAGPKLPTSTVTTTSVTSKALTHVTNSSPTGWSSPAQSSPANFN	(Trinidad et al., 2012)
microtubule-actin crosslinking factor 1	123244263	CAM20961.1	5333	T448	LQDELVTLRLECTNLYRKGHFSSLELVPPSTLTTTHLKAEPLNKTTHSSSTSWFRKPMTRT	(Trinidad et al., 2012)
Microtubule-associated protein 1A	122065442	Q9QYR6.2	2776	T2186	SPAEPRSAPCGSLAFSGDRALALVPGTPTRTRHDEYLEVTKAPSLDSSLPQLPSPSSPGAP	(Trinidad et al., 2012)
Microtubule-associated protein 1A	122065442	Q9QYR6.2	2776	S877	DQSVASLTAPQTEETGKSSLLLDTVTSIPSSRTEATQGLDYVPSAGTISPTSSLEEDKGFK	(Trinidad et al., 2012)
Microtubule-associated protein 1B	341940933	P14873.2	2464	T2027	LGDCSYSYETTEKITSFPESESYSYETSTKTTRSPDTSAYCYETMEKITKTPQASTYSYET	(Alfaro et al. 2012)
Microtubule-associated protein 2	341940935	P20357.2	1828	T777	LPPTTPAVEKMPCFPIESKEEEDKAEQAKVTGGQTIQVETSSESPFPAKEYYKNGTVMAPD	(Trinidad et al., 2012)
Microtubule-associated protein 4	269849673	P27816.3	1152	S797	PSKDVKPKPIADAKAPEKRASPSKPASAPASRSGSKSTQTVAKTTTAAAVASTGPSSRSPS	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Microtubule-associated protein 6	205830863	Q7TSJ2.2	906	T705	KDSVPLAPAKAQSPLLPEPLKNQSPVVPASTKDQSFPTPAPRKDPGPVIPEPEKDRAPTVP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Microtubule-associated protein 6	205830863	Q7TSJ2.2	906	T425	AHAQGTGPEGGKGRAVADALNRQIREEVASTVSSSYRNEFRAWTDIKPVKPIKAKPQYKPP	(Alfaro et al. 2012)
Microtubule-associated protein 6	205830863	Q7TSJ2.2	906	S182	TQYQKDFRAWPLPRRGDHPWIPKPVQIPATSQPSQPVLGVPKRRPQSQERGPMQLSADARD	(Alfaro et al. 2012)
Microtubule-associated protein 6	205830863	Q7TSJ2.2	906	S294	QEGGPAAGKASGADQRDTRRKAGPAWMVTRSEGHEEKPLPPAQSQTQEGGPAAGKASGADQ	(Trinidad et al., 2012)
Microtubule-associated protein 6	205830863	Q7TSJ2.2	906	S386	QEGGPAAGKASGADERDTRRKAGPAWMVRRSEGHEQTPAAHAQGTGPEGGKGRAVADALNR	(Trinidad et al., 2012)
Microtubule-associated protein 6	205830863	Q7TSJ2.2	906	S704	NKDSVPLAPAKAQSPLLPEPLKNQSPVVPASTKDQSFPTPAPRKDPGPVIPEPEKDRAPTV	(Alfaro et al. 2012)
microtubule-associated protein tau isoform 2	6754638	NP_005901.2	441	S208	APKTPPSSGEPPKSGDRSGYSSPGSPGTPGSRSRTPSLPTPPTREPKKVAVVRTPPKSPSS	(Yuzwa et al. 2012)
microtubule-associated protein tau isoform 2	6754638	NP_005901.2	441	S400	KIETHKLTFRENAKAKTDHGAEIVYKSPVVSGDTSPRHLSNVSSTGSIDMVDSPQLATLAD	(Yuzwa et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
microtubule-associated protein tau isoform 2	6754638	NP_005901.2	441	T123	PHTEIPEGTTAEEAGIGDTPSLEDEAAGHVTQARMVSKSKDGTGSDDKKAKGADGKTKIAT	(Yuzwa et al. 2011)
Microtubule-associated serine/threonine-protein kinase 4	34194105	Q811L6.3	2618	S2165	NSASWQHGSSPSHTLKKEPGTKAAAAEPSTSLHDTPRSATATTTAIATTTTTTSAGHSDCS	(Alfaro et al. 2012)
Misshapen-like kinase 1	341940992	Q9JM52.3	1308	S685	PNPPSWVRPDNEAPPKVPQRTSSIATALNTSGAGGSRPAQAVRASNPDLRRSDPGWERSDS	(Trinidad et al., 2012)
Mitochondrial antiviral-signaling protein	81170679	Q8VCF0.1	503	T298	QAKAATCFSTTLTNSVTTSSVPSPRLVPVKTMSSKLPLSSKSTAAMTSTVLTNTAPSKLPS	(Trinidad et al., 2012)
Mitochondrial antiviral-signaling protein	81170679	Q8VCF0.1	503	T373	SVAKAPANTIPPERNSKQAKETPEGPATKVTTGGNQTGPNSSIRSLHSGPEMSKPGVLVSQ	(Trinidad et al., 2012)
Mitochondrial import receptor subunit TOM70	342187059	Q9CZW5.2	611	S94	RRRRRREAGGRGDASGLKRNSERKTPEGRASPALGSGHHDGSGDSLEMSSLDRAQAAKNKG	(Trinidad et al., 2012)
MKIAA0044 protein	81893777	Q6ZQK4	458	S62	VKSGKGPKEGQDTAETEIASRKNSLTVVQSSTSTKIKVPIPQPVVVPVKKDKRQNSSRFNA	(Trinidad et al., 2012)
MKIAA0429 protein	81893719	Q6ZQB7	773	T594	STIPRNSDISQSYRRMFQAKRPASTAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
MKIAA0757 protein	81865711	Q80TS6	534	S421	SALSKCQNCGLSCSSSLCQRCDSVLVCPSASKPSAFPSKASVHDSLAHGAPMREKYVGHQT	(Trinidad et al., 2012)
MKL/myocardin-like protein 2	32363198	P59759.1	1080	T214	LSPDQPASQESQGSAASPSEPKVSASPPPVTASTPAQFTSVSPAVPEFLKTPLTADQPPTR	(Alfaro et al. 2012)(Trinidad et al., 2012)
MKL/myocardin-like protein 2	32363198	P59759.1	1080	S245	ASTPAQFTSVSPAVPEFLKTPLTADQPPTRSTAPVLPTNTVSSAKSGPMLVKQSHPKNPND	(Alfaro et al. 2012)(Trinidad et al., 2012)
MKL/myocardin-like protein 2	32363198	P59759.1	1080	T858	QNGPSLASKPSSPPPPQQFVVQHSLFATPITKTKDPPRYEEAIKQTRSTQPALPEVSSVHS	(Alfaro et al. 2012)
Msx2-interacting protein	37999864	Q62504.2	3644	T2899	NASPVISSVKTDRPSLEKPEPIHLSVSTPVTQGGTVKVLTQGINTPPVLVHNQLVLTPSIV	(Myers et al. 2011)(Trinidad et al., 2012)
Msx2-interacting protein	37999864	Q62504.2	3644	T2896	QTYNASPVISSVKTDRPSLEKPEPIHLSVSTPVTQGGTVKVLTQGINTPPVLVHNQLVLTP	(Myers et al. 2011)
Msx2-interacting protein	37999864	Q62504.2	3644	S2786	ENSRFHPGSMSVIDDRPADTGSGAGLRVNTSEGVVLLSYSGQKTEGPQRISAKISQIPPAS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
msx2-interacting protein	14790190	NP_055816.2	3664	S2811	ENSRFHPGSMPVIDDRPADAGSGAGLRVNTSEGVVLLSYSGQKTEGPQRISAKISQIPPAS	(Wang et al. 2010)
msx2-interacting protein	14790190	NP_055816.2	3664	T2924	NASPVISSVKADRPSLEKPEPIHLSVSTPVTQGGTVKVLTQGINTPPVLVHNQLVLTPSIV	(Wang et al. 2010)
Multiple coagulation factor deficiency protein 2	49036425	Q8NI22.1	146	T98	SPQELQLHYFKMHDYDGNNLLDGLELSTAITHVHKEEGSEQAPLMSEDELINIIDGVLRDD	(Hahne et al. 2012)
Multiple inositol polyphosphate phosphatase 1	68565617	Q9UNW1.1	487	T244	MEFGPPTVNDKLMRFFDHCEKFLTEVEKNATALYHVEAFKTGPEMQNILKKVAATLQVPVN	(Hahne et al. 2012)
Myc proto-oncogene protein	127619	P01106.1	439	T58	EENFYQQQQQSELQPPAPSEDIWKKFELLPTPPLSPSRRSGLCSPSYVAVTPFSLRGDNDG	(Chou et al. 1995)
Myelin basic protein	17378829	P04370.2	250	S172	QRSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFSGDRGAPKRGSGKDSHTRTTHYGSL	(Trinidad et al., 2012)
Myelin basic protein	17378829	P04370.2	250	S201	DSIGRFFSGDRGAPKRGSGKDSHTRTTHYGSLPQKSQHGRTQDENPVVHFFKNIVTPRTPP	(Trinidad et al., 2012)
Myelin basic protein	17378829	P04370.2	250	T211	RGAPKRGSGKDSHTRTTHYGSLPQKSQHGRTQDENPVVHFFKNIVTPRTPPPSQGKGGRDS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Myelin basic protein	17378829	P04370.2	250	S151	QEDPTAASGGLDVMASQKRPSQRSKYLATASTMDHARHGFLPRHRDTGILDSIGRFFSGDR	(Trinidad et al., 2012)
Myelin proteolipid protein	41019154	P60202.2	277	S114	ALLLAEGFYTTGAVRQIFGDYKTTICGKGLSATVTGGQKGRGSRGQHQAHSLERVCHCLGK	(Trinidad et al., 2012)
Myelin proteolipid protein	41019154	P60202.2	277	T118	AEGFYTTGAVRQIFGDYKTTICGKGLSATVTGGQKGRGSRGQHQAHSLERVCHCLGKWLGH	(Trinidad et al., 2012)
myocyte-specific enhancer factor 2D	5174545	NP_005911.1	521	S275	KVIPAKSPPPPTHSTQLGAPSRKPDLRVITSQAGKGLMHHLTEDHLDLNNAQRLGVSQSTH	(Wang et al. 2010)
Myosin light chain 3	127151	P16409.2	200	T164	TYEDFVEGLRVFDKEGNGTVMGAELRHVLATLGERLTEDEVEKLMAGQEDSNGCINYEAFV	(Ramirez-Correa et al. 2008)
Myosin light chain 3	127151	P16409.2	200	T93	FQLFDRTPKGEMKITYGQCGDVLRALGQNPTQAEVLRVLGKPKQEELNSKMMDFETFLPML	(Ramirez-Correa et al. 2008)
Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	127167	P08733.2	166	S15	BBBBBBBBBBBBBBBBMSPKKAKKRLEGGSSNVFSMFEQTQIQEFKEAFTIMDQNRDGFID	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1038	LDDLQAEEDKVNTLTKSKVKLEQQVDDLEGSLEQEKKVRMDLERAKRKLEGDLKLTQESIM	(Ramirez-Correa et al. 2008)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Myosin-6	127741	P02563.2	1938	S1148	ELEEELEAERTARAKVEKLRSDLTRELEEISERLEEAGGATSVQIEMNKKREAEFQKMRRD	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1159	ARAKVEKLRSDLTRELEEISERLEEAGGATSVQIEMNKKREAEFQKMRRDLEEATLQHEAT	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1200	AEFQKMRRDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKLELD	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1308	RAKLQTENGELARQLEEKEALIWQLTRGKLSYTQQMEDLKRQLEEEGKAKNALAHALQSAR	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1336	KLSYTQQMEDLKRQLEEEGKAKNALAHALQSARHDCDLLREQYEEEMEAKAELQRVLSKAN	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1470	AAALDKKQRNFDKILAEWKQKYEESQSELESSQKEARSLSTELFKLKNAYEESLEHLETFK	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1471	AALDKKQRNFDKILAEWKQKYEESQSELESSQKEARSLSTELFKLKNAYEESLEHLETFKR	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1597	NQIKAEIERKLAEKDEEMEQAKRNHLRVVDSLQTSLDAETRSRNEALRVKKKMEGDLNEME	(Ramirez-Correa et al. 2008)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Myosin-6	127741	P02563.2	1938	S1711	LLQAELEELRAVVEQTERSRKLAEQELIETSERVQLLHSQNTSLINQKKKMDADLSQLQTE	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S172	RGKKRSEAPPHIFSISDNAYQYMLTDRENQSILITGESGAGKTVNTKRVIQYFASIAAIGD	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1777	QECRNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNMEQTIKDLQHRLDEAEQIALK	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S179	APPHIFSISDNAYQYMLTDRENQSILITGESGAGKTVNTKRVIQYFASIAAIGDRSKKDNP	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S1916	AEEQANTNLSKFRKVQHELDEAEERADIAESQVNKLRAKSRDIGAKQKMHDEEBBBBBBB	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S196	TDRENQSILITGESGAGKTVNTKRVIQYFASIAAIGDRSKKDNPNANKGTLEDQIIQANPA	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S392	MKFKQKQREEQAEPDGTEDADKSAYLMGLNSADLLKGLCHPRVKVGNEYVTKGQSVQQVYY	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S622	GWLEKNKDPLNETVVGLYQKSSLKLMATLFSTYASADTGDSGKGKGGKKKGSSFQTVSALH	(Ramirez-Correa et al. 2008)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Myosin-6	127741	P02563.2	1938	S626	KNKDPLNETVVGLYQKSSLKLMATLFSTYASADTGDSGKGKGGKKKGSSFQTVSALHRENL	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S644	LKLMATLFSTYASADTGDSGKGKGGKKKGSSFQTVSALHRENLNKLMTNLRTTHPHFVRCI	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S749	FRQRYRILNPAAIPEGQFIDSGKGAEKLLGSLDIDHNQYKFGHTKVFFKAGLLGLLEEMRD	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	S880	MANMKEEFGRVKDALEKSEARRKELEEKMVSLLQEKNDLQLQVQAEQDNLADAEERCDQLI	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	T1189	SVQIEMNKKREAEFQKMRRDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLE	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	T1600	KAEIERKLAEKDEEMEQAKRNHLRVVDSLQTSLDAETRSRNEALRVKKKMEGDLNEMEIQL	(Ramirez-Correa et al. 2008)
Myosin-6	127741	P02563.2	1938	T1606	KLAEKDEEMEQAKRNHLRVVDSLQTSLDAETRSRNEALRVKKKMEGDLNEMEIQLSQANRI	(Ramirez-Correa et al. 2008)
Myotubularin-related protein 1	11133678	Q9Z2C4.1	669	T667	EDLQREMATRTISSSSERGSSPTHSATPVHTSVBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	45476974	Q9CWS0.3	285	S261	GHVLLHRTPEEYPESAKVYEKLKDHLLIPVSNSEMEKVDGLLTCCSVFINKKIDSBBBBBB	(Trinidad et al., 2012)
N(G),N(G)-dimethylarginine dimethylaminohydrolase 2	45476968	Q99LD8.1	285	S261	TPFLLHRGGGDLPNSQEALQKLSDVTLVPVSCSELEKAGAGLSSLCLVLSTRPHCBBBBBB	(Trinidad et al., 2012)
N-acetylglucosamine-6-sulfatase	232126	P15586.3	552	S280	NVFAPRNKNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVDDLVEKLVKRL	(Hahne et al. 2012)
N-acetylglucosamine-6-sulfatase	232126	P15586.3	552	S281	VFAPRNKNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVDDLVEKLVKRLE	(Hahne et al. 2012)
N-acetylglucosamine-6-sulfatase	232126	P15586.3	552	T278	FQNVFAPRNKNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRWQTLLSVDDLVEKLVK	(Hahne et al. 2012)
N-acetylglucosamine-6-sulfatase	232126	P15586.3	552	T407	TILDIAGYDLNKTQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTDPTCPSLSPGVSQ	(Hahne et al. 2012)
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9, mitochondrial precursor	254692859	NP_079634.2	377	S156	VINLIGREWETRNFDFEDVFVNIPRAIAQASKEAGVERFIHVSHLNASMKSSSKSLRSKAV	(Hu et al. 2009)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	32363403	Q9DCS9.3	176	S25	BBBBBBMPDSWDKDVYPEPPSRTPAPSPQTSLPNPITYLTKAYDLVVDWPVTLVREFIERQ	(Trinidad et al., 2012)
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	47117242	Q8K3J1.1	212	T150	EAICPAQAITIEAEPRADGSRRTTRYDIDMTKCIYCGFCQEACPVDAIVEGPNFEFSTETH	(Trinidad et al., 2012)
Netrin receptor DCC	2497302	P70211.1	1447	T1330	SVSEGPTTQQQPMLPPAQPEHPSSEEAPSRTIPTACVRPTHPLRSFANPLLPPPMSAIEPK	(Trinidad et al., 2012)
Netrin receptor UNC5B	54036592	Q8K1S3.1	945	T418	VAVLMAVGVIVYRRNCRDFDTDITDSSAALTGGFHPVNFKTARPNNPQLLHPSAPPDLTAS	(Trinidad et al., 2012)
Neural cell adhesion molecule 1	205830666	P13595.3	1115	T882	TLTSSIAPPATTVPDSNSVPAGQATPSKGVTASSSSPASAPKVAPLVDLSDTPTSAPSASN	(Trinidad et al., 2012)
Neural cell adhesion molecule 1	205830666	P13595.3	1115	S911	VTASSSSPASAPKVAPLVDLSDTPTSAPSASNLSSTVLANQGAVLSPSTPASAGETSKAPP	(Trinidad et al., 2012)
Neural cell adhesion molecule 1	205830666	P13595.3	1115	T980	TPTPAGAASPLAAVAAPATDAPQAKQEAPSTKGPDPEPTQPGTVKNPPEAATAPASPKSKA	(Trinidad et al., 2012)
Neural proliferation differentiation and control protein 1	341941179	Q64322.2	332	T136	LALKEKEAGHSRLTAQPLLEAAQKLLEPAATLGFSQWGQRLEPGLPSTHGTSSPIPHTSLS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Neurobeachin	32171509	Q9EPN1.1	2936	T1797	HAILPMQFHSFDRSVVVPVKKPPPGSLAVTTVGATAAGSGLPTGSTSSIFAAPGATPKSMI	(Alfaro et al. 2012)(Trinidad et al., 2012)
Neurobeachin	32171509	Q9EPN1.1	2936	S1704	SILDGAELEPAAGPDAMSELLSTLSSEVKKSQESLTEHPSEMLKPAPSISSISQTKGINVK	(Trinidad et al., 2012)
Neurobeachin	32171509	Q9EPN1.1	2936	T1276	DAGSIISDTERSDDGKESGKEIRKIQTTATTQAVQGRSSTQQDRDLRVDLGFRGMPMTEEQ	(Alfaro et al. 2012)
Neurobeachin	32171509	Q9EPN1.1	2936	T1796	AHAILPMQFHSFDRSVVVPVKKPPPGSLAVTTVGATAAGSGLPTGSTSSIFAAPGATPKSM	(Alfaro et al. 2012)
Neuroblast differentiation-associated protein AHNAK	160332335	Q09666.2	5890	S5611	ISLGEGHLSVKGSGGEWKGPQVSSALNLDTSKFAGGLHFSGPKVEGGVKGGQIGLQAPGLS	(Hahne et al. 2012)
neuroblast differentiation-associated protein AHNAK isoform 1	61743954	NP_001611.1	5890	S5603	SGGVSAPDISLGEGHLSVKGSGGEWKGPQVSSALNLDTSKFAGGLHFSGPKVEGGVKGGQI	(Wang et al. 2010)
Neurofilament heavy polypeptide	83305012	P16884.4	1072	S54	LHYALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVSASPSRFRGAASSTDSLDTLSNGPEG	(Dong et al. 1996)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
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Neurofilament heavy polypeptide	83305012	P16884.4	1072	S56	YALSRKAGAGGTRSAAGSSSGFHSWARTSVSSVSASPSRFRGAASSTDSLDTLSNGPEGCV	(Dong et al. 1996)
Neurofilament heavy polypeptide	94730399	P19246.3	1090	S39	ALLGAPFAPLHGGGSLHYSLSRKAGPGGTRSAAGSSSGFHSWARTSVSSVSASPSRFRGAA	(Trinidad et al., 2012)
Neurofilament heavy polypeptide	94730399	P19246.3	1090	S431	RKLLEGEECRIGFGPSPFSLTEGLPKIPSISTHIKVKSEEMIKVVEKSEKETVIVEGQTEE	(Trinidad et al., 2012)
Neurofilament heavy polypeptide	94730399	P19246.3	1090	S56	YSLSRKAGPGGTRSAAGSSSGFHSWARTSVSSVSASPSRFRGAASSTDSLDTLSNGPEGCV	(Trinidad et al., 2012)
Neurofilament light polypeptide	97536879	P08551.5	543	S48	YVETPRVHISSVRSGYSTARSAYSSYSAPVSSSLSVRRSYSSSSGSLMPSLENLDLSQVAA	(Chalkley et al. 2009)(Trinidad et al., 2012)
Neurofilament light polypeptide	97536879	P08551.5	543	S414	DIEIAAYRKLLEGEETRLSFTSVGSITSGYSQSSQVFGRSAYSGLQSSSYLMSARSFPAYY	(Chalkley et al. 2009)
Neurofilament light polypeptide	1709260	P19527.3	542	S27	BBBBMSSFSYEPYFSTSYKRRYVETPRVHISSVRSGYSTARSAYSSYSAPVSSSLSVRRSY	(Dong et al. 1993)
Neurofilament light polypeptide	1709260	P19527.3	542	S34	FSYEPYFSTSYKRRYVETPRVHISSVRSGYSTARSAYSSYSAPVSSSLSVRRSYSSSSGSL	(Dong et al. 1996)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Neurofilament light polypeptide	1709260	P19527.3	542	S48	YVETPRVHISSVRSGYSTARSAYSSYSAPVSSSLSVRRSYSSSSGSLMPSLENLDLSQVAA	(Dong et al. 1996)
Neurofilament light polypeptide	1709260	P19527.3	542	T21	BBBBBBBBBBMSSFSYEPYFSTSYKRRYVETPRVHISSVRSGYSTARSAYSSYSAPVSSSL	(Dong et al. 1993)
Neurofilament light polypeptide	97536879	P08551.5	543	S423	LLEGEETRLSFTSVGSITSGYSQSSQVFGRSAYSGLQSSSYLMSARSFPAYYTSHVQEEQT	(Trinidad et al., 2012)
Neurofilament light polypeptide	97536879	P08551.5	543	S27	BBBBMSSFGYDPYFSTSYKRRYVETPRVHISSVRSGYSTARSAYSSYSAPVSSSLSVRRSY	(Trinidad et al., 2012)
Neurofilament light polypeptide	97536879	P08551.5	543	S405	DLLNVKMALDIEIAAYRKLLEGEETRLSFTSVGSITSGYSQSSQVFGRSAYSGLQSSSYLM	(Trinidad et al., 2012)
Neurofilament light polypeptide	97536879	P08551.5	543	S41	STSYKRRYVETPRVHISSVRSGYSTARSAYSSYSAPVSSSLSVRRSYSSSSGSLMPSLENL	(Trinidad et al., 2012)
Neurofilament light polypeptide	97536879	P08551.5	543	S430	RLSFTSVGSITSGYSQSSQVFGRSAYSGLQSSSYLMSARSFPAYYTSHVQEEQTEVEETIE	(Trinidad et al., 2012)
Neurofilament medium polypeptide	146345468	P08553.4	848	T430	RKLLEGEETRFSTFSGSITGPLYTHRQPSVTISSKIQKTKVEAPKLKVQHKFVEEIIEETK	(Chalkley et al. 2009)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Neurofilament medium polypeptide	146345468	P08553.4	848	S37	SLGNPSAYRRVTETRSSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLAYSSAM	(Chalkley et al. 2009)
Neurofilament medium polypeptide	146345468	P08553.4	848	S46	RVTETRSSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLAYSSAMLSSAESSLD	(Chalkley et al. 2009)
Neurofilament medium polypeptide	146345468	P08553.4	848	T845	VEEHEETFEEKLVSTKKVEKVTSHAIVKEVTQGDBBBBBBBBBBBBBBBBBBBBBBBBBB	(Alfaro et al. 2012)
Neurofilament medium polypeptide	128150	P12839.4	846	S34	TLDSLGNPSAYRRVPTETRSSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLAY	(Dong et al. 1996)
Neurofilament medium polypeptide	128150	P12839.4	846	T19	BBBBBBBBBBBBMSYTLDSLGNPSAYRRVPTETRSSFSRVSGSPSSGFRSQSWSRGSPSTV	(Dong et al. 1996)
Neurofilament medium polypeptide	128150	P12839.4	846	T431	RKLLEGEETRFSTFSGSITGPLYTHRQPSVTISSKIQKTKVEAPKLKVQHKFVEEIIEETK	(Dong et al. 1993)
Neurofilament medium polypeptide	128150	P12839.4	846	T48	PTETRSSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLAYSSAMLSSAESSLDF	(Dong et al. 1993)
Neurofilament medium polypeptide	146345468	P08553.4	848	S28	BBBMSYTLDSLGNPSAYRRVTETRSSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSALA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Neurofilament medium polypeptide	146345468	P08553.4	848	S414	DLLNVKMALDIEIAAYRKLLEGEETRFSTFSGSITGPLYTHRQPSVTISSKIQKTKVEAPK	(Trinidad et al., 2012)
Neurofilament medium polypeptide	146345468	P08553.4	848	S32	SYTLDSLGNPSAYRRVTETRSSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLA	(Trinidad et al., 2012)
Neurofilament medium polypeptide	146345468	P08553.4	848	S49	ETRSSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLAYSSAMLSSAESSLDFSQ	(Trinidad et al., 2012)
Neurofilament medium polypeptide	146345468	P08553.4	848	T47	VTETRSSFSRVSGSPSSGFRSQSWSRGSPSTVSSSYKRSALAPRLAYSSAMLSSAESSLDF	(Trinidad et al., 2012)
Neuromodulin	128101	P06837.1	227	T166	KATTDNSPSSKAEDGPAKEEPKQADVPAAVTDAAATTPAAEDAATKAAQPPTETAESSQAE	(Trinidad et al., 2012)
Neuron navigator 1	147704603	Q8CH77.2	1875	T543	DASKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSALKVAGKPEGKATDKGKLAVK	(Trinidad et al., 2012)
Neuron navigator 1	147704603	Q8CH77.2	1875	T617	DRLSDAKKPPSGIARPSTSGSFGYKKPPPATGTATVMQTGSSATLSKIQKSSGIPVKPVNG	(Trinidad et al., 2012)
Neuron navigator 3	147704669	Q80TN7.2	2359	S1210	KLREPTKIGSGRSSPVTVNQTDKEKEKVAVSDSESVSLSGSPKSSPTSASACGTQGLRQPG	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Neuron navigator 3	147704669	Q80TN7.2	2359	S1084	KPPSGIGRSTASSSFGYKKPSGVGASTMITSSGATITSGSATLGKIPKSAAIGGKSNAGRK	(Trinidad et al., 2012)
Neuronal PAS domain-containing protein 3	38605073	Q9QZQ0.1	925	T804	NSLLYTGDLEALQRLQAGNVVLPLVHRVTGTLAATSTAAQRVYTTGTIRYAPAEVTLAMQG	(Trinidad et al., 2012)
Neuronal PAS domain-containing protein 3	38605073	Q9QZQ0.1	925	T810	GDLEALQRLQAGNVVLPLVHRVTGTLAATSTAAQRVYTTGTIRYAPAEVTLAMQGNLLPNA	(Trinidad et al., 2012)
Neuronal PAS domain-containing protein 3	38605073	Q9QZQ0.1	925	S809	TGDLEALQRLQAGNVVLPLVHRVTGTLAATSTAAQRVYTTGTIRYAPAEVTLAMQGNLLPN	(Trinidad et al., 2012)
Neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adapter 1	81892618	Q6PFX7.1	833	T468	AAHPAPAALLPGPPKDKAVSYTMVYSAVKVTTHSVLPAGPPLGVGEPKTEEISVLHGMLCA	(Alfaro et al. 2012)(Trinidad et al., 2012)
Neurotrimin	27151644	Q99PJ0.2	344	S246	KVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSAEFQWFKDDKRLVEGKKGVKVENRPF	(Trinidad et al., 2012)
novel protein (9030409G11Rik)	220939463	CAX15670.1	261	T258	DINSPRHRTHSLWRQSRPSSEEPTQPYCTVTRGSBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
nuclear envelope pore membrane protein POM 121C	150378545	NP_001092885.1	987	T693	SAPATSSQPTLTFSNTSTPTFNIPFGSSAKSPLPSYPGANPQPAFGAAEGQPPGAAKPALT	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nuclear factor 1 A-type	14194972	Q02780.1	532	T362	GWHEVEPGLPSPSTLKKSEKSGFSSPSPSQTSSLGTAFTQHHRPVITGPRASPHATPSTLH	(Alfaro et al. 2012)
Nuclear factor related to kappa-B-binding protein	81885823	Q6PIJ4.1	1296	T1270	TAQQLQQLQQQGQATQVRIQTVPASHLQQGTASGSSKAVSTVVVTTAPSPKQAPEQQBBBB	(Alfaro et al. 2012)(Myers et al. 2011)(Trinidad et al., 2012)
Nuclear factor related to kappa-B-binding protein	81885823	Q6PIJ4.1	1296	S1172	ASGATSTPISIGTGAPTVRQVPVNTTVVSTSQSGKLPTRITVPLSVISQPMKGKSVVTAPI	(Alfaro et al. 2012)(Myers et al. 2011)
Nuclear factor related to kappa-B-binding protein	81885823	Q6PIJ4.1	1296	S221	RYLKVLREVKEECGDTALSSDEEDLSSWLPSSPARSPSPAVPLRVVPTLSTTDMKTADKIE	(Trinidad et al., 2012)
Nuclear factor related to kappa-B-binding protein	81885823	Q6PIJ4.1	1296	S222	YLKVLREVKEECGDTALSSDEEDLSSWLPSSPARSPSPAVPLRVVPTLSTTDMKTADKIEL	(Trinidad et al., 2012)
Nuclear factor related to kappa-B-binding protein	81885823	Q6PIJ4.1	1296	T1171	VASGATSTPISIGTGAPTVRQVPVNTTVVSTSQSGKLPTRITVPLSVISQPMKGKSVVTAP	(Trinidad et al., 2012)
Nuclear fragile X mental retardation-interacting protein 2	74713454	Q7Z417.1	695	S396	LNKTIQNSSVSPTSSSSSSSSTGETQTQSSSRLSQVPMSALKSVTSANFSNGPVLAGTDGN	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
nuclear mitotic apparatus protein 1	71361682	NP_006176.2	2115	S1844	IINITMTKKLDVEEPDSANSSFYSTRSAPASQASLRATSSTQSLARLGSPDYGNSALLSLP	(Wang et al. 2010)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S1017	SGLSNPVSLTPFQFGVSNLGQEEKKEELPKSSSAGFSFGTGVINSTPAPANTIVTSENKSS	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S1023	VSLTPFQFGVSNLGQEEKKEELPKSSSAGFSFGTGVINSTPAPANTIVTSENKSSFNLGTI	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S1113	SFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGKKADNEEPKCQPVFSFGNSEQTKD	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S534	SSQALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTFSVPVAKTAELSGSSS	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S543	QMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTFSVPVAKTAELSGSSSTLEPIISSS	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S544	MTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTFSVPVAKTAELSGSSSTLEPIISSSA	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S891	LVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTST	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S892	VQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTG	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S893	QNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGN	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S894	NKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNF	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S895	KADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFK	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S897	DSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFG	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S900	KCLACESAKPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQG	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S908	KPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSS	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S909	PGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSD	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S910	GTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDS	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S911	TKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSG	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S912	KSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGS	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S915	FKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGSINP	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	T1026	TPFQFGVSNLGQEEKKEELPKSSSAGFSFGTGVINSTPAPANTIVTSENKSSFNLGTIETK	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	T890	CLVQNKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTS	(Zhao et al. 2011)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S1115	GNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGKKADNEEPKCQPVFSFGNSEQTKDEN	(Hahne et al. 2012)
Nuclear pore complex protein Nup153	206729891	P49790.2	1475	S947	TLTSTGNFKFGDQGGFKIGVSSDSGSINPMSEGFKFSKPIGDFKFGVSSESKPEEVKKDSK	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
nuclear pore complex protein Nup153	24430146	NP_005115.2	1475	S1113	SFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGKKADNEEPKCQPVFSFGNSEQTKD	(Wang et al. 2010)
nuclear pore complex protein Nup153	24430146	NP_005115.2	1475	S534	SSQALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTFSVPVAKTAELSGSSS	(Wang et al. 2010)
nuclear pore complex protein Nup153	24430146	NP_005115.2	1475	S544	MTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTFSVPVAKTAELSGSSSTLEPIISSSA	(Wang et al. 2010)
nuclear pore complex protein Nup153	24430146	NP_005115.2	1475	S908	KPGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSS	(Wang et al. 2010)
nuclear pore complex protein Nup153	24430146	NP_005115.2	1475	S909	PGTKSGFKGFDTSSSSSNSAASSSFKFGVSSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSD	(Wang et al. 2010)
nuclear pore complex protein Nup153	24430146	NP_005115.2	1475	T1156	EPKCQPVFSFGNSEQTKDENSSKSTFSFSMTKPSEKESEQPAKATFAFGAQTSTTADQGAA	(Wang et al. 2010)
Nuclear pore complex protein Nup214	206558312	Q80U93.2	2085	T1091	TSATKVIPQGADSTMLATKTVKHGAPGPSHTVAAPQAAAAAALRRQMASQAPAMSTLTEST	(Alfaro et al. 2012)(Myers et al. 2011)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	S1202	LKPSGPTPASGQLSSGDKASGTAKIETAVTSTPSASGQFSKPFSFSPSGTGFNFGIITPTP	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	S1205	SGPTPASGQLSSGDKASGTAKIETAVTSTPSASGQFSKPFSFSPSGTGFNFGIITPTPSSN	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	S1207	PTPASGQLSSGDKASGTAKIETAVTSTPSASGQFSKPFSFSPSGTGFNFGIITPTPSSNFT	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	S1904	FGSGNTGRGGGFFSGLGGKPSQDAANKNPFSSASGGFGSTATSNTSNLFGNSGAKTFGGFA	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	S1905	GSGNTGRGGGFFSGLGGKPSQDAANKNPFSSASGGFGSTATSNTSNLFGNSGAKTFGGFAS	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	S1907	GNTGRGGGFFSGLGGKPSQDAANKNPFSSASGGFGSTATSNTSNLFGNSGAKTFGGFASSS	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	S1912	GGGFFSGLGGKPSQDAANKNPFSSASGGFGSTATSNTSNLFGNSGAKTFGGFASSSFGEQK	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	T1198	LINSLKPSGPTPASGQLSSGDKASGTAKIETAVTSTPSASGQFSKPFSFSPSGTGFNFGII	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	T1201	SLKPSGPTPASGQLSSGDKASGTAKIETAVTSTPSASGQFSKPFSFSPSGTGFNFGIITPT	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	T1203	KPSGPTPASGQLSSGDKASGTAKIETAVTSTPSASGQFSKPFSFSPSGTGFNFGIITPTPS	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	T1913	GGFFSGLGGKPSQDAANKNPFSSASGGFGSTATSNTSNLFGNSGAKTFGGFASSSFGEQKP	(Zhao et al. 2011)
Nuclear pore complex protein Nup214	205831380	P35658.2	2090	T1568	KKEPVLAQPAVSNSGTAASSTSLVALSAEATPATTGVPDARTEAVPPASSFSVPGQTAVTA	(Hahne et al. 2012)
Nuclear pore complex protein Nup214	206558312	Q80U93.2	2085	S1362	LLFPSSLAGETLGSFSGLRVGQAEDSTKPVSKASSTNLAGAQPAKPSGVSFPNTSVLGKPV	(Myers et al. 2011)
Nuclear pore complex protein Nup214	206558312	Q80U93.2	2085	S504	AGSPSVFSFGPSSFKSSASVTGEPPLYPTGSDSSRAAPGSGTSTFSFAPPSKGSLASTPAV	(Myers et al. 2011)
Nuclear pore complex protein Nup214	206558312	Q80U93.2	2085	S513	GPSSFKSSASVTGEPPLYPTGSDSSRAAPGSGTSTFSFAPPSKGSLASTPAVAPVATSAAP	(Myers et al. 2011)
Nuclear pore complex protein Nup214	206558312	Q80U93.2	2085	T1124	APQAAAAAALRRQMASQAPAMSTLTESTLKTVPQVVNVQELRSNPSPPSAAMGSAVQHSAA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nuclear pore complex protein Nup214	206558312	Q80U93.2	2085	S1167	NPSPPSAAMGSAVQHSAAKTPHAVLTPVANSQAKQGSLINSFKPSGPTAASCQLSSGDKAV	(Trinidad et al., 2012)
Nuclear pore complex protein Nup214	206558312	Q80U93.2	2085	S652	PLPASSSSMPLKSSVSPSPAAGRSTQTAPSSAPSTGQKSPRVNPPVPKSGSSQAKALQPPV	(Trinidad et al., 2012)
nuclear pore complex protein Nup214	33946327	NP_005076.3	2090	S1056	PSLLPHAAPFAKSHLVHGSSPGVMGTSVATSASKIIPQGADSTMLATKTVKHGAPSPSHPI	(Wang et al. 2010)
nuclear pore complex protein Nup214	33946327	NP_005076.3	2090	S1354	SSLAGETLGSFSGLRVGQADDSTKPTNKASSTSLTSTQPTKTSGVPSGFNFTAPPVLGKHT	(Wang et al. 2010)
nuclear pore complex protein Nup214	33946327	NP_005076.3	2090	T1201	SLKPSGPTPASGQLSSGDKASGTAKIETAVTSTPSASGQFSKPFSFSPSGTGFNFGIITPT	(Wang et al. 2010)
nuclear pore complex protein Nup214	33946327	NP_005076.3	2090	T580	SSGFKPTLESTPVPSVSAPNIAMKPSFPPSTSAVKVNLSEKFTAAATSTPVSSSQSAPPMS	(Wang et al. 2010)
nuclear pore complex protein Nup98-Nup96 isoform 4	56549645	NP_624358.2	1726	T184	TAAPTGTTIKFNPPTGTDTMVKAGVSTNISTKHQCITAMKEYESKSLEELRLEDYQANRKG	(Wang et al. 2010)
nuclear pore complex protein Nup98-Nup96 isoform 4	56549645	NP_624358.2	1726	T568	RPATRVRPKALQTTGTAKSHLFDGLDDDEPSLANGAFMPKKSIKKLVLKNLNNSNLFSPVN	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nuclear receptor coactivator 1	54036169	P70365.2	1447	T401	LSPQDDSNSGMSIPRINPSVNPGISPAHGVTRSSTLPPSNNNMVSARVNRQQSSDLNSSSS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Nuclear receptor coactivator 2	341942241	Q61026.3	1462	T964	NNSTGMIGSSTSRPSMPSGEWAPQSPAVRVTCAATTGAMNRPVQGGMIRNPTASIPMRANS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Nuclear receptor coactivator 2	341942241	Q61026.3	1462	S185	MNKSVYSILHVGDHTEFVKNLLPKSMVNGGSWSGEPPRRSSHTFNCRMLVKPLPDSEEEGH	(Trinidad et al., 2012)
Nuclear receptor coactivator 2	341942241	Q61026.3	1462	S179	YNQEELMNKSVYSILHVGDHTEFVKNLLPKSMVNGGSWSGEPPRRSSHTFNCRMLVKPLPD	(Trinidad et al., 2012)
Nuclear receptor coactivator 5	28380077	Q91W39.1	579	T521	AGSARNMGPRPGAPSQGLFGQPSSRLAPASTMASQRPVSSTGINFDNPSVQKALDTLIQSG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Nuclear receptor corepressor 1	126437781	Q60974.1	2453	S1496	SVLRSTLHEAPKAQLSPGLYDDSSARRTPVSYQNTISRGSPMMNRTSDVSSSKSASHERKS	(Alfaro et al. 2012)(Chalkley et al. 2009)(Myers et al. 2011)
Nuclear receptor corepressor 1	126437781	Q60974.1	2453	S1900	RSRSAAVSEQQQLEQKNLEVEKRSVQCVCTSSALPSGKAQPHASVVYSEAGKDKGPPPKSR	(Alfaro et al. 2012)(Myers et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nuclear receptor corepressor 1	12643781	Q60974.1	2453	T1899	LRSRSAAVSEQQQLEQKNLEVEKRSVQCVCTSSALPSGKAQPHASVVYSEAGKDKGPPPKS	(Alfaro et al. 2012)(Myers et al. 2011)
nuclear receptor corepressor 1 isoform 1	225384661	NP_006302.2	2440	S1487	SVLRSTLHEAPKAQLSPGIYDDTSARRTPVSYQNTMSRGSPMMNRTSDVTISSNKSTNHER	(Wang et al. 2010)
Nuclear receptor corepressor 2	341942242	Q9WU42.3	2472	T2089	PHLRPLPESQPSSSPLLQTAPGIKGHQRVVTLAQHISEVITQDYTRHHPQQLSGPLPAPLY	(Alfaro et al. 2012)
Nuclear receptor corepressor 2	341942242	Q9WU42.3	2472	S1944	GHAFLTKPPAREPASSPSKSSEPRSLAPPSSSHTAIARTPAKNLAPHHASPDPPAPTSASD	(Alfaro et al. 2012)
Nucleobindin-1	90110780	Q02818.4	461	T47	LLLLLRAVLAVPLERGAPNKEETPATESPDTGLYYHRYLQEVIDVLETDGHFREKLQAANA	(Hahne et al. 2012)(Hahne et al. 2012)
Nucleobindin-1	90110780	Q02818.4	461	S44	PLLLLLLLRAVLAVPLERGAPNKEETPATESPDTGLYYHRYLQEVIDVLETDGHFREKLQA	(Hahne et al. 2012)
Nucleobindin-1	17380463	Q02819.2	459	S406	RSQDRLEAQKRELQQAVLQMEQRKQQLQEQSAPPSKPDGQLQFRADTDDAPVPAPAGDQKD	(Trinidad et al., 2012)
Nucleobindin-1	17380463	Q02819.2	459	S338	DRLVTLEEFLASTQRKEFGDTGEGWKTVEMSPAYTEEELKRFEEELAAREAELNARAQRLS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nucleobindin-1	17380463	Q02819.2	459	S410	RLEAQKRELQQAVLQMEQRKQQLQEQSAPPSKPDGQLQFRADTDDAPVPAPAGDQKDVPAS	(Trinidad et al., 2012)
Nucleoporin 153	81873329	Q80WR0	1462	S1046	GVNNPPNAAIDTTATSENKSGFNFGTLDTKSVSVTPFTYKTTEAKKEDAPATKGGFTFGKV	(Myers et al. 2011)
Nucleoporin 153	81873329	Q80WR0	1462	S1102	TFGKVGSSSLPSSSMFVLGRTEEKQQEPVTSTSLVFGKKADSEEPKCQPVFSFGNSEQTKD	(Myers et al. 2011)
Nucleoporin 153	81873329	Q80WR0	1462	T1044	GAGVNNPPNAAIDTTATSENKSGFNFGTLDTKSVSVTPFTYKTTEAKKEDAPATKGGFTFG	(Myers et al. 2011)
Nucleoporin 153	81873329	Q80WR0	1462	T627	KILREGSVLDILKTPGFASPKVDSPALQPTTTSSIVYTRPAISTFSSSGIEYGESLKAGSS	(Myers et al. 2011)
Nucleoporin 153	81873329	Q80WR0	1462	T628	ILREGSVLDILKTPGFASPKVDSPALQPTTTSSIVYTRPAISTFSSSGIEYGESLKAGSSW	(Myers et al. 2011)
Nucleoporin NUP188 homolog	158563956	Q6ZQH8.2	1759	T1524	SRKMLQHYLQNKNGDGLPSAVTPRAQRPSTTTTTTTTTTALATPAGCSSKQPTADTEASEQ	(Alfaro et al. 2012)(Trinidad et al., 2012)
Nucleoporin NUP188 homolog	158563956	Q6ZQH8.2	1759	T1526	KMLQHYLQNKNGDGLPSAVTPRAQRPSTTTTTTTTTTALATPAGCSSKQPTADTEASEQRA	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Nucleoporin NUP188 homolog	158563956	Q6ZQH8.2	1759	T1527	MLQHYLQNKNGDGLPSAVTPRAQRPSTTTTTTTTTTALATPAGCSSKQPTADTEASEQRAL	(Alfaro et al. 2012)(Trinidad et al., 2012)
Nucleoporin NUP188 homolog	158563956	Q6ZQH8.2	1759	S1522	LHSRKMLQHYLQNKNGDGLPSAVTPRAQRPSTTTTTTTTTTALATPAGCSSKQPTADTEAS	(Myers et al. 2011)
Nucleoporin NUP188 homolog	158563956	Q6ZQH8.2	1759	T1525	RKMLQHYLQNKNGDGLPSAVTPRAQRPSTTTTTTTTTTALATPAGCSSKQPTADTEASEQR	(Alfaro et al. 2012)
Nucleoporin NUP53	97180265	Q8R4R6.2	325	S297	IRTLGTPTQSGSTPRVSTMRPLATAYKASTSDYQVISDRQTPKKDESLVSRAMEYMFGWBB	(Myers et al. 2011)(Trinidad et al., 2012)
Nucleoporin NUP53	97180265	Q8R4R6.2	325	S53	PTSPKTGANAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGSPPQPVVPAHK	(Myers et al. 2011)(Trinidad et al., 2012)
Nucleoporin NUP53	97180265	Q8R4R6.2	325	T264	SIMIGVKPCIDKNVMENSDRGVLSSPSLAFTTPIRTLGTPTQSGSTPRVSTMRPLATAYKA	(Trinidad et al., 2012)
Nucleoprotein TPR	215274208	P12270.3	2363	S1679	TTPASGERGIASTSDPPTANIKPTPVVSTPSKVTAAAMAGNKSTPRASIRPMVTPATVTNP	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
nucleoprotein TPR	114155142	NP_003283.2	2363	S1676	TLKTTPASGERGIASTSDPPTANIKPTPVVSTPSKVTAAAMAGNKSTPRASIRPMVTPATV	(Wang et al. 2010)
Nucleosome-remodeling factor subunit BPTF	215274183	Q12830.3	3046	T1712	NLSNDFIDENGLPINKNENVNGESKRKTVITEVTTMTSTVATESKTVIKVEKGDKQTVVSS	(Hahne et al. 2012)
Nucleosome-remodeling factor subunit BPTF	215274183	Q12830.3	3046	T1715	NDFIDENGLPINKNENVNGESKRKTVITEVTTMTSTVATESKTVIKVEKGDKQTVVSSTEN	(Hahne et al. 2012)
Nucleosome-remodeling factor subunit BPTF	215274183	Q12830.3	3046	T2088	TTSPTSSTTSTISPAQKVMVAPISGSVTTGTKMVLTTKVGSPATVTFQQNKNFHQTFATWV	(Hahne et al. 2012)
Nucleosome-remodeling factor subunit BPTF	215274183	Q12830.3	3046	T1757	TVIKVEKGDKQTVVSSTENCAKSTVTTTTTTVTKLSTPSTGGSVDIISVKEQSKTVVTTTV	(Hahne et al. 2012)
Nucleosome-remodeling factor subunit BPTF	215274183	Q12830.3	3046	T1759	IKVEKGDKQTVVSSTENCAKSTVTTTTTTVTKLSTPSTGGSVDIISVKEQSKTVVTTTVTD	(Hahne et al. 2012)
NudC domain-containing protein 2	67461063	Q8WVJ2.1	157	T146	DQMQRKLTLERFQKENPGFDFSGAEISGNYTKGGPDFSNLEKBBBBBBBBBBBBBBBBBBB	(Hahne et al. 2012)
Numb-like protein	341942226	O08919.3	604	T285	GPAQPGHVSPTPATTSPGEKGEAGTPVAAGTTAAAIPRRHAPLEQLVRQGSFRGFPALSQK	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
nup155	288965	CAA79848.1	1390	S525	PPKKFVLLSAQGSLMFHKLRPVDQLRHLLVSNVGGDGEEIERFFKLHQEDQACATCLILAC	(Wells et al. 2002)
Nup98 protein	81884398	Q68G59	1209	S426	EDVDAMDQRFGHIPSKGETVQEICSPRLPISASHSSKSRSIVGGLLQSKFASETFLSPSAS	(Myers et al. 2011)
Osteoclast-like cell cDNA, RIKEN full-length enriched library, clone:I420023H06 product:vimentin, full insert sequence	123793818	Q3TWV0	466	S49	GTSSRSSSNRSYVTTSTRTYSLGSALRPSTSRSLYSSSPGGAYVTRSSAVRLRSSVPGVRL	(Myers et al. 2011)
Oxidation resistance protein 1	294862498	Q4KMM3.3	866	S343	DPRARDQGNDSASTAPRSTEESLSEDAFTESELSPIREELLSSEPRQEKSSDASSESVQTV	(Trinidad et al., 2012)
Oxidation resistance protein 1	294862498	Q4KMM3.3	866	T190	SPLSPTSSEAEFDKTTTPDVAHPKEAPPASTVSGIRPARVVSSTSEEEEAFTEKFLKINCK	(Trinidad et al., 2012)
Oxysterol-binding protein 2	81889379	Q5QNQ6.1	908	T140	NGTRSVSIIKASPELAMPSPLQSTVGSLPVTKPESKLVPKTQSFLRQGQAKISVGTPVSGI	(Alfaro et al. 2012)
P140 gene	123241708	CAM27400.1	1174	S516	LYKAGAGGPLYGDGYGFRLPPSSPQKLADVSAPSGGPPPPHSPYSGPPSRGSPVRQSFRKD	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
P140 gene	123241708	CAM27400.1	1174	S568	PVRQSFRKDSGSSSVFAESPGGKARSTGSASTAGAPPSELFPGPGERSLVGFGPPVPAKDT	(Trinidad et al., 2012)
P140 gene	123241708	CAM27400.1	1174	S662	SEKVEGSNGAATPSAPVCGSGSKSSGATPVSGPPPPSASSTPAGQPTAVSRLQMQLHLRGL	(Trinidad et al., 2012)
P140 gene	123241708	CAM27400.1	1174	T1057	VPRYRTEKPSKSPPPPPPRRSFPSSHGLTTTRTGEVVVTSKKDSVFIKKAESEELEVQKPQ	(Trinidad et al., 2012)
Paired amphipathic helix protein Sin3a	37999759	Q96ST3.2	1273	S277	PAKVSKPSQLQAHTPASQQTPPLPPYASPRSPPVQPHTPVTISLGTAPSLQNNQPVEFNHA	(Hahne et al. 2012)
Paired amphipathic helix protein Sin3a	308153557	Q60520.3	1274	S251	QPPPQHPSQPSSQSAPTPAQPAPQPTAAKVSKPSQLQAHTPASQQTPPLPPYASPRSPPVQ	(Myers et al. 2011)
PDZ and LIM domain protein 5	341942252	Q8CI51.4	591	S115	SAAAKSEPVSVQKGEPKEVVKPVPITSPAVSKVTSTTNMAYNKAPRPFGSVSSPKVTSIPS	(Alfaro et al. 2012)
PDZ and LIM domain protein 5	341942252	Q8CI51.4	591	T110	TLQRASAAAKSEPVSVQKGEPKEVVKPVPITSPAVSKVTSTTNMAYNKAPRPFGSVSSPKV	(Alfaro et al. 2012)
PDZ and LIM domain protein 5	317373590	Q96HC4.5	596	S115	SAAPKPEPVPVQKGEPKEVVKPVPITSPAVSKVTSTNNMAYNKAPRPFGSVSSPKVTSIPS	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
PDZ and LIM domain protein 5 isoform a	197383077	NP_006448.3	596	T110	TLQRASAAPKPEPVPVQKGEPKEVVKPVPITSPAVSKVTSTNNMAYNKAPRPFGSVSSPKV	(Wang et al. 2010)
PDZ and LIM domain protein 7 isoform 4	47157328	NP_998801.1	222	S89	GSLTHIEAQNKIRACGERLSLGLSRAQPVQSKPQKASAPAADPPRYTFAPSVSLNKTARPF	(Wang et al. 2010)
Peptidyl-prolyl cis-trans isomerase FKBP10	23396594	Q96AY3.1	582	S296	DAVQLETLELPPGCVRRAGAGDFMRYHYNGSLMDGTLFDSSYSRNHTYNTYIGQGYIIPGM	(Hahne et al. 2012)
Peptidyl-prolyl cis-trans isomerase FKBP11	23396601	Q9NYL4.1	201	T37	LLPLHLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFGDTLHIHYTGS	(Hahne et al. 2012)
Perilipin-3	68565612	Q9DBG5.1	437	S76	YTSTKENYPHVRTVCDVAEKGVKTLTTAAVSTAQPILSKLEPQIATASEYAHRGLDRLQES	(Trinidad et al., 2012)
Perilipin-3	68565612	Q9DBG5.1	437	T6	BBBBBBBBBBBBBBBBBBBBBBBBMSSNGTDAPAEAQAAMEEPVVQPSVVDRVAGLPLIS	(Trinidad et al., 2012)
Perilipin-3	68565612	Q9DBG5.1	437	S2	BBBBBBBBBBBBBBBBBBBBBBBBBBBBMSSNGTDAPAEAQAAMEEPVVQPSVVDRVAGL	(Trinidad et al., 2012)
Perilipin-3	68565612	Q9DBG5.1	437	T128	RGLDRLQESLPILQQPTEKVLADTKELVSSTVSGAQEMVSSSVSSAKETVATRVTGAVDVT	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
perilipin-4	122937195	NP_001073869.1	1357	S704	TAKTVLTGTKDTVTTGLMGAVNVAKGTVQTSVDTTKTVLTGTKDTVCSGVTGAANVAKGAI	(Wang et al. 2010)
Peroxiredoxin-2	2507169	P32119.5	198	S112	THLAWINTPRKEGGLGPLNIPLLADVTRRLSEDYGVLKTDEGIAYRGLFIIDGKGVLRQIT	(Wang et al. 2009)
Peroxiredoxin-6	3219774	O08709.3	224	T152	KDDNNMPVTARVVFIFGPDKKLKLSILYPATTGRNFDEILRVVDSLQLTGTKPVATPVDWK	(Myers et al. 2011)
PERQ amino acid-rich with GYF domain-containing protein 2	122064904	Q6Y7W8.2	1291	T681	SQQQQQLALLLQQFQALKMRMSDQNIIPSVTRSVSVPDTGSIWELQPAASQPAVWEGGSVW	(Trinidad et al., 2012)
PH and SEC7 domain-containing protein 3	160419228	Q2PFD7.2	1037	S245	LPEEAQAHRSQITNYRRQGPLRVPESACPVSSSSAGSHNPVDRVGALREQRSDLGREHPRG	(Alfaro et al. 2012)
PHD finger protein 21A	90167365	Q6ZPK0.2	659	S286	APAPPPMLAAPQLIQRPVMLTKFTPTTLPTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIV	(Myers et al. 2011)
PHD finger protein 21A	90167365	Q6ZPK0.2	659	T132	QPQQQQQQQQQHAQQSAAAPPSLTASQKTVTTASMITTKTLPLVLKAATATMPASVVGQRP	(Trinidad et al., 2012)
PHD finger protein 21A	90167365	Q6ZPK0.2	659	T133	PQQQQQQQQQHAQQSAAAPPSLTASQKTVTTASMITTKTLPLVLKAATATMPASVVGQRPT	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
PHD finger protein 21A	74731224	Q96BD5.1	680	T130	QYHHHHAQQSAAASPNLTASQKTVTTASMITTKTLPLVLKAATATMPASVVGQRPTIAMVT	(Hahne et al. 2012)
PHD finger protein 21A	74731224	Q96BD5.1	680	T131	YHHHHAQQSAAASPNLTASQKTVTTASMITTKTLPLVLKAATATMPASVVGQRPTIAMVTA	(Hahne et al. 2012)
PHD finger protein 21A	90167365	Q6ZPK0.2	659	T282	NIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTLPTSQNSIHPVRVVNGQTATIAKTFPMAQL	(Trinidad et al., 2012)
Phosphatase and actin regulator 1	97180283	Q2M3X8.1	580	S337	PSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHSSDGITKAGPMGLPEIRQVPT	(Alfaro et al. 2012)(Trinidad et al., 2012)
Phosphatase and actin regulator 4	147720081	Q501J7.2	694	T231	TSAATTAATDMTKTVKSFVGPTPAPAPAPRTLPAAPASANTAATTTAPAKQPPIPPPKPAQ	(Trinidad et al., 2012)
Phosphatase and actin regulator 4	147720081	Q501J7.2	694	T194	QPLLPPKRPLSSSCEAKEVPAGSTARSVSSTSGSTTVTSAATTAATDMTKTVKSFVGPTPA	(Trinidad et al., 2012)
Phosphatidylinositol 4,5-bisphosphate 5-phosphatase A	341941251	P59644.2	1003	S117	APLSIAGEQKRPPPPHSSNRAAKSVGQLVVSAAAASKPPPVASVSILAPKSLGQLVISASA	(Alfaro et al. 2012)
Phosphatidylinositol-binding clathrin assembly protein	44888257	Q7M6Y3.1	660	S453	SATLDAVEDAIPSLNPFLTKSSGDVHLPIASDVSTFTTRTPTHEMFVGFSPSPVAQPHSSA	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Phosphatidylinositol-binding clathrin assembly protein	44888257	Q7M6Y3.1	660	T355	QAALEEEQARLKALKEQRLKELAKKPHTSLTTAASPVSTSAGGIMTAPAIDIFSTPSSSNS	(Alfaro et al. 2012)
Phosphatidylinositol-binding clathrin assembly protein	44888257	Q7M6Y3.1	660	T356	AALEEEQARLKALKEQRLKELAKKPHTSLTTAASPVSTSAGGIMTAPAIDIFSTPSSSNST	(Alfaro et al. 2012)
Phosphatidylinositol-binding clathrin assembly protein	116242714	Q13492.2	652	T370	EQRLKELAKKPHTSLTTAASPVSTSAGGIMTAPAIDIFSTPSSSNSTSKLPNDLLDLQQPT	(Hahne et al. 2012)
Phosphoglycerate mutase 1	20178035	Q9DBJ1.3	254	S189	TIARALPFWNEEIVPQIKEGKRVLIAAHGNSLRGIVKHLEGLSEEAIMELNLPTGIPIVYE	(Trinidad et al., 2012)
Phosphoglycerate mutase 2	6093745	O70250.3	253	S189	TIARALPFWNEEIAPKIKAGQRVLIAAHGNSLRGIVKHLEGMSDQAIMELNLPTGIPIVYE	(Trinidad et al., 2012)
Plakophilin-4	57013004	Q68FH0.1	1190	S1087	PRSEYDRTQPPMQYYNSQGDTTHKGLYPGSSKPSPIYISSYSSPAREQNRRLQHQQLYYQD	(Alfaro et al. 2012)(Trinidad et al., 2012)
Plakophilin-4	57013004	Q68FH0.1	1190	S226	QTLVQPSVANRAMRRVSSVPSRAQSPSYVTSTGVSPSRGSLRTSLGSGFGSPSVTDSRPLN	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Plakophilin-4	57013004	Q68FH0.1	1190	T225	GQTLVQPSVANRAMRRVSSVPSRAQSPSYVTSTGVSPSRGSLRTSLGSGFGSPSVTDSRPL	(Alfaro et al. 2012)(Trinidad et al., 2012)
Plakophilin-4	57013004	Q68FH0.1	1190	T180	NSYSDSGYQEAGSFHNSQTVNKADSRQHPFTGSTSNHVVRTSRAEGQTLVQPSVANRAMRR	(Trinidad et al., 2012)
Plakophilin-4	57013004	Q68FH0.1	1190	T183	SDSGYQEAGSFHNSQTVNKADSRQHPFTGSTSNHVVRTSRAEGQTLVQPSVANRAMRRVSS	(Trinidad et al., 2012)
Plakophilin-4	57013004	Q68FH0.1	1190	S182	YSDSGYQEAGSFHNSQTVNKADSRQHPFTGSTSNHVVRTSRAEGQTLVQPSVANRAMRRVS	(Trinidad et al., 2012)
Plakophilin-4	57013004	Q68FH0.1	1190	T1152	KTLDAYRLYLQSPRSYEDPYCDDRVHFPASTDYSTQYGLKSTTNYVDFYSTKRPSYRAEQY	(Trinidad et al., 2012)
Plasma cell-induced resident endoplasmic reticulum protein	74730663	Q8WU39.1	189	S41	LLGAWAIPGGLGDRAPLTATAPQLDDEEMYSAHMPAHLRCDACRAVAYQMWQNLAKAETKL	(Hahne et al. 2012)
pleckstrin homology domain-containing family A member 5 isoform 1	19923493	NP_061885.2	1116	S382	EYESGSACPAQTVHYRPINLSSSENKIVNVSLADLRGGNRPNTGPLYTEADRVIQRTNSMQ	(Wang et al. 2010)
Plectin	122065897	Q9QXS1.2	4691	T2762	LAEENQRLRERLQRLEEEHRAALAHSEIATTQAASTKALPNGRDAPDGPSVEAEPEYTFEG	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Plexin-A2	251757336	P70207.2	1894	S1610	RLNTLMHYQVSDRSVVALVPKQTSSYNIPASASISRTSISRYDSSFRYTGSPDSLRSRVPM	(Trinidad et al., 2012)
Pogo transposable element with ZNF domain	46577037	Q8BZH4.2	1409	T358	PSLGQSPGPVVVSNNSSAQRTSGPESSVKVTSSIPVFDLQDGGRKICPRCNAQFRVTEALR	(Myers et al. 2011)(Trinidad et al., 2012)
Pogo transposable element with ZNF domain	46577037	Q8BZH4.2	1409	T310	QTSNPKLAPSFPSPPAVSIASFVTVKRPGVTGENSNEVAKLVNTLNTVPSLGQSPGPVVVS	(Myers et al. 2011)
Pogo transposable element with ZNF domain	46577037	Q8BZH4.2	1409	S359	SLGQSPGPVVVSNNSSAQRTSGPESSVKVTSSIPVFDLQDGGRKICPRCNAQFRVTEALRG	(Trinidad et al., 2012)
pogo transposable element with ZNF domain isoform 2	46397394	NP_997054.1	1357	S244	LGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVTVKRPGVTGENSNEVAKLVNTLNTI	(Wang et al. 2010)
Polyhomeotic-like protein 3	341941266	Q8CHP6.2	981	T238	AAQVQNLTLRSQKLGVLSSSQNGSPKSAGQTQSLTICHNKTTVTSSKISQRDPSPESKKGG	(Chalkley et al. 2009)(Myers et al. 2011)(Trinidad et al., 2012)
Polyhomeotic-like protein 3	341941266	Q8CHP6.2	981	T762	RPLLDNQVVNSVCVQPELQNNTKHADNSSDTEIEDMMAEETLEEMDSELLKCEFCGKMGYP	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Polyhomeotic-like protein 3	341941266	Q8CHP6.2	981	T772	SVCVQPELQNNTKHADNSSDTEIEDMMAEETLEEMDSELLKCEFCGKMGYPNEFLRSKRFC	(Trinidad et al., 2012)
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 1	29840778	O88704.1	910	T792	QQQQQQQQQQQQQPQTPGSSTPKNEVHKSTQALHNTNLTKEVRPLSASQPSLPHEVSTLI	(Trinidad et al., 2012)
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 2	29840777	O88703.1	863	T763	APPGPLPPAASPGPPAASPPAAPSSPRAPRTSPYGVPGSPATRVGPALPARRLSRASRPLS	(Trinidad et al., 2012)
Potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 4	29840776	O70507.2	1186	T1138	GGGSGSSGGLGPPGRPYGAIPGQHVTLPRKTSSGSLPPPLSLFGARAASSGGPPLTTAAPQ	(Trinidad et al., 2012)
Potassium-transporting ATPase alpha chain 1	20137339	Q64436.3	1033	T626	GLVSMIDPPRATVPDAVLKCRTAGIRVIMVTGDHPITAKAIAASVGIISEGSETVEDIAAR	(Trinidad et al., 2012)
PPAR gamma	643611	AAA62110.1	475	T54	EDHSHSFDIKPFTTVDFSSISAPHYEDIPFTRADPMVADYKYDLKLQEYQSAIKVEPASPP	(Ji et al. 012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Prelamin-A/C	125962	P02545.1	664	T623	QPADKASASGSGAQVGGPISSGSSASSVTVTRSYRSVGGSGGGSFGDNLVTRS YLLGNSSP	(Hahne et al. 2012)
Pre-mRNA 3'-end-processing factor FIP1	81881579	Q9D824.1	581	S261	AEFTSPPSLFKTGLPPSRNSTSSQSQTSTASRKASSSVGKWQDRYGRAESPDLR RLPGAID	(Trinidad et al., 2012)
Pre-mRNA 3'-end-processing factor FIP1	81881579	Q9D824.1	581	T204	YFNYGFNEDTWKAYCEKQKRIRMGLEVIPVTSTTNKITVQQGRTGNSEKEAALPS TKAEFT	(Alfaro et al. 2012)
Pre-mRNA 3'-end-processing factor FIP1	81881579	Q9D824.1	581	T229	EVIPVTSTTNKITVQQGRTGNSEKEAALPSTKAEFTSPPSLFKTGLPPSRNSTSSQ SQTST	(Alfaro et al. 2012)
Pre-mRNA-processing factor 19	55976619	Q9UMS4.1	504	T169	GLIVPQAVPSSQPSVVGAGEPMDLGELVGMTPEIIQKLQDKATVLTTERKKRGKT VPEELV	(Hahne et al. 2012)
Prickle-like protein 2	341942184	Q80Y24.3	845	S479	PKRSSSMALKGHGGSFIQECREDYYPGRLMSQESYSDMSSQSFNETRGSIPVPK YEEEEEE	(Trinidad et al., 2012)
Prickle-like protein 2	341942184	Q80Y24.3	845	T752	EDYDQFMRQRSFQESLGQGSRRDLYSQCPRTVSDLALQNAFGERWGPYFTEY DWCSTCSSS	(Trinidad et al., 2012)
Proactivator polypeptide	134218	P07602.2	524	S216	RSKPQPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMAD ICKNYIS	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Proactivator polypeptide	134218	P07602.2	524	T217	SKPQPKDNGDVCQDCIQMVTDIQTAVRTNSTFVQALVEHVKEECDRLGPGMADICKNYISQ	(Hahne et al. 2012)
Probable JmjC domain-containing histone demethylation protein 2C	341941046	Q69ZK6.3	2350	S1250	SLSSAETSYSLSNTISASTPFECTSSKSVVSQAVAQAKDCTVSTAVPGTLACSKTGSAVQP	(Alfaro et al. 2012)(Myers et al. 2011)
Probable JmjC domain-containing histone demethylation protein 2C	85541650	Q15652.2	2540	S655	SKLNTSVDTHKIKSSPSPEVVKPKITHSPDSVKSKATYVNSQATGERRLANKIEHELSRCS	(Hahne et al. 2012)
Probable JmjC domain-containing histone demethylation protein 2C	341941046	Q69ZK6.3	2350	S911	KDVDRSVSEIYKMKHSVPQSLPQSNYFTTLSNSVVNEPPRSYPSKEVSNIYTEKQNNNLSA	(Myers et al. 2011)
Procollagen galactosyltransferase 1	74715064	Q8NBJ5.1	622	S383	DRRERMLRALQAQEIECRLVEAVDGKAMNTSQVEALGIQMLPGYRDPYHGRPLTKGELGCF	(Hahne et al. 2012)
ProSAP-interacting protein 1	296439742	A2AHG0.1	700	S295	SQHLAPLSASTSHINRIGTAGYSSGSSGGGSGYQDLGTSDSGRASSKSGSSSSMGRSGHLG	(Trinidad et al., 2012)
ProSAP-interacting protein 1	296439742	A2AHG0.1	700	T75	RDPLLAFAPRPSELGPPDPRLTMGSVGSGVTHAQEFPMKSVGTRTGGGGNQGSFPGPRSGG	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Proteasomal ubiquitin receptor ADRM1	20141265	Q16186.2	407	T225	LGSSGPPGSSSSSSSRSQSAAVTPSSTTSSTRATPAPSAPAAASATSPSPAPSSGNGASTA	(Hahne et al. 2012)(Hahne et al. 2012)
Proteasomal ubiquitin receptor ADRM1	20141265	Q16186.2	407	T222	ASLLGSSGPPGSSSSSSSRSQSAAVTPSSTTSSTRATPAPSAPAAASATSPSPAPSSGNGA	(Hahne et al. 2012)
Proteasomal ubiquitin receptor ADRM1	146345361	Q9JKV1.2	407	S213	LGALTGPGLASLLGSSGPPASSSSSSSRSQSAAVTPSSSTSSARATPAPSAPAAASATSPS	(Trinidad et al., 2012)
Proteasomal ubiquitin receptor ADRM1	146345361	Q9JKV1.2	407	S221	LASLLGSSGPPASSSSSSSRSQSAAVTPSSSTSSARATPAPSAPAAASATSPSPAPSSGNG	(Trinidad et al., 2012)
Proteasome subunit alpha type-5	38258905	P28066.3	241	S198	RAIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNATNIELATVQPGQNFHM	(Wang et al. 2009)
Protein 4.1	90101808	P11171.4	864	S491	STIGFKLPSYRAAKKLWKVCVEHHTFFRLTSTDTIPKSKFLALGSKFRYSGRTQAQTRQAS	(Wang et al. 2009)
protein AF-10 isoform b	57546899	NP_001009569.1	1011	S269	DKHKQKHKKQPEPSPALVPSLTVTTEKTYTSTSNNSISGSLKRLEDTTARFTNANFQEVSA	(Wang et al. 2010)
Protein AF-17	344249169	EGW05273.1	976	S399	NRGKEGVTGPTASLPGAQLAGFTATAASPFSGGSLVSSGLGGLASRTFGPSGSLPSLSLES	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T2700	MSSVGIQTISDCSVQTEPEQLPRVSPAIHITAATDPKVEIVRYISAPEKTGRGESLACQTE	(Vosseller et al. 2006)(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1707	PTPIILTDQGMDLTSLAVEARKYGLALDPVSGRQSTAVQPLVINLNAQEQTHTFLATATTV	(Vosseller et al. 2006)(Alfaro et al. 2012)(Chalkley et al. 2009)
Protein bassoon	341940634	O88737.4	3942	T2945	HLPLAGQVPSQLYAASLLQRGLAGPTTVPATKASLLRELDRDLRLVEHESTKLRKKQAELD	(Alfaro et al. 2012)(Chalkley et al. 2009)(Vosseller et al. 2006)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T1395	LKLHSSPVSSTLTSKEVGMTFSQGPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYG	(Chalkley et al. 2009)(Vosseller et al. 2006)(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2318	KPAAAKASGAGGPPRPELPAGVAREEPFSTTAPAVIKEAPVAPAPGPAPAPPPGQKPAGEA	(Chalkley et al. 2009)(Vosseller et al. 2006)(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2027	AGLNYHAQRLGQLFQGPGRDSAVDLSSLKHSYSLGFADGRYLGQGLQYGSFTDLRHPTDLL	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S2029	LNYHAQRLGQLFQGPGRDSAVDLSSLKHSYSLGFADGRYLGQGLQYGSFTDLRHPTDLLSH	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2058	YSLGFADGRYLGQGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDHRYGPRGDAVGFQ	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2067	YLGQGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDHRYGPRGDAVGFQEASLAQYSA	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2091	LPLRRYSSVSNIYSDHRYGPRGDAVGFQEASLAQYSATTAREISRMCAALNSMDQYGGRHG	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S2141	NSMDQYGGRHGSGSGGPDLVQYQPQHGPGLSAPQGLAPLRSGLLGNPTYPEGQPSPGNLAQ	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2188	TYPEGQPSPGNLAQYGPAASQATAVRQLLPSTATVRAADGMIYSTINTPIAATLPITTQPA	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1537	AEFSTQTPSLTLSSDIPRSPGPPSPMVAQGTQTPHRPSTPRLVWQQSSQEAPIMVITLASD	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1962	SVTDTALPGQSSGPFYSPRDPEPPEPLTFRTQGVVGPGPHEEQRPYPQGLPGRLYSSMSDT	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T2703	VGIQTISDCSVQTEPEQLPRVSPAIHITAATDPKVEIVRYISAPEKTGRGESLACQTEPDG	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2068	LGQGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDHRYGPRGDAVGFQEASLAQYSAT	(Chalkley et al. 2009)(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2070	QGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDHRYGPRGDAVGFQEASLAQYSATTA	(Chalkley et al. 2009)(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1517	PSTPSESPTFSPGKLGPRATAEFSTQTPSLTLSSDIPRSPGPPSPMVAQGTQTPHRPSTPR	(Chalkley et al. 2009)(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T2317	GKPAAAKASGAGGPPRPELPAGVAREEPFSTTAPAVIKEAPVAPAPGPAPAPPPGQKPAGE	(Chalkley et al. 2009)(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2295	RYPAPRFPIASSVPPAEGPVYLGKPAAAKASGAGGPPRPELPAGVAREEPFSTTAPAVIKE	(Alfaro et al. 2012)(Chalkley et al. 2009)
Protein bassoon	341940634	O88737.4	3942	T1354	SPTQLAAPVSFSTSTSSDSSGGRVIPDVRVTQHFAKEPQDPLKLHSSPVSSTLTSKEVGMT	(Alfaro et al. 2012)(Chalkley et al. 2009)
Protein bassoon	341940634	O88737.4	3942	T1666	GALPAENISLCRISSVPGTSRVEPGPRPPGTAVVDLRTAVKPTPIILTDQGMDLTSLAVEA	(Alfaro et al. 2012)(Chalkley et al. 2009)
Protein bassoon	341940634	O88737.4	3942	S1373	SGGRVIPDVRVTQHFAKEPQDPLKLHSSPVSSTLTSKEVGMTFSQGPGSPATTASPTRGYM	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S1418	GPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQPPTTANYGSQTEELPHAPSGPP	(Chalkley et al. 2009)(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	S1472	HAPSGPPGSGRAPREKPLSGGDSEVGAPQPSRGYSYFTGSSPPLSPSTPSESPTFSPGKLG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1987	PLTFRTQGVVGPGPHEEQRPYPQGLPGRLYSSMSDTNLAEAGLNYHAQRLGQLFQGPGRDS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2096	YSSVSNIYSDHRYGPRGDAVGFQEASLAQYSATTAREISRMCAALNSMDQYGGRHGSGSGG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2122	LAQYSATTAREISRMCAALNSMDQYGGRHGSGSGGPDLVQYQPQHGPGLSAPQGLAPLRSG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2694	AATARAMSSVGIQTISDCSVQTEPEQLPRVSPAIHITAATDPKVEIVRYISAPEKTGRGES	(Chalkley et al. 2009)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T1394	PLKLHSSPVSSTLTSKEVGMTFSQGPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSY	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1506	SYFTGSSPPLSPSTPSESPTFSPGKLGPRATAEFSTQTPSLTLSSDIPRSPGPPSPMVAQG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1683	GTSRVEPGPRPPGTAVVDLRTAVKPTPIILTDQGMDLTSLAVEARKYGLALDPVSGRQSTA	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1824	GPRGRPREAKFARYNLPNQVTPLARRDILITQMGTAQGVGLKPGPVPEPGAEPHRATPAEL	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2099	VSNIYSDHRYGPRGDAVGFQEASLAQYSATTAREISRMCAALNSMDQYGGRHGSGSGGPDL	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2189	YPEGQPSPGNLAQYGPAASQATAVRQLLPSTATVRAADGMIYSTINTPIAATLPITTQPAS	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T2488	LQLEQIQQLQQQLQLQLEEQKQRQKAPFPATCEAPSRGPPPAATELAQNGQYWPPLTHAAF	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2685	ATASSSTTAAATARAMSSVGIQTISDCSVQTEPEQLPRVSPAIHITAATDPKVEIVRYISA	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2941	PEEAHLPLAGQVPSQLYAASLLQRGLAGPTTVPATKASLLRELDRDLRLVEHESTKLRKKQ	(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T412	PKIVFSDASKEAGPRPPGSGPGPGPTPGAKTEPGARMGPGSGPGALAKTGGTASPKHGRAE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1934	ACCDMVYKFPFGSSCTGTFHPAPSAPDKSVTDTALPGQSSGPFYSPRDPEPPEPLTFRTQG	(Vosseller et al. 2006)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1407	TSKEVGMTFSQGPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQPPTTANYGSQT	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S1419	PGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQPPTTANYGSQTEELPHAPSGPPG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1423	ATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQPPTTANYGSQTEELPHAPSGPPGSGRA	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1655	GTDGPLALYGWGALPAENISLCRISSVPGTSRVEPGPRPPGTAVVDLRTAVKPTPIILTDQ	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1932	QLACCDMVYKFPFGSSCTGTFHPAPSAPDKSVTDTALPGQSSGPFYSPRDPEPPEPLTFRT	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1943	PFGSSCTGTFHPAPSAPDKSVTDTALPGQSSGPFYSPRDPEPPEPLTFRTQGVVGPGPHEE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1988	LTFRTQGVVGPGPHEEQRPYPQGLPGRLYSSMSDTNLAEAGLNYHAQRLGQLFQGPGRDSA	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S1990	FRTQGVVGPGPHEEQRPYPQGLPGRLYSSMSDTNLAEAGLNYHAQRLGQLFQGPGRDSAVD	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2177	APLRSGLLGNPTYPEGQPSPGNLAQYGPAASQATAVRQLLPSTATVRAADGMIYSTINTPI	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2316	LGKPAAAKASGAGGPPRPELPAGVAREEPFSTTAPAVIKEAPVAPAPGPAPAPPPGQKPAG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2787	QIVTPGALGRFEKKKPDPLEIGYQAHLPPESLSQLVSRQPPKSPQVLYSPVSPLSPHRLLD	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S3216	ETGYSGPAVSGSYEQGKAPEHPRGSDRSSVSQSPAPTYPSDSHYTSLEQNVPRNYVMIDDI	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1417	QGPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQPPTTANYGSQTEELPHAPSGP	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T2098	SVSNIYSDHRYGPRGDAVGFQEASLAQYSATTAREISRMCAALNSMDQYGGRHGSGSGGPD	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2662	QPVRRRRSRLSRHSDSGSDSKHDATASSSTTAAATARAMSSVGIQTISDCSVQTEPEQLPR	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T308	EAARATSVPGPTQATAPPEVGRVSPQPPLSTKPSTAEPRPPAGEAQGKSATTVPSGLGAGE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T3179	AAHQKPRQTSLADLEQKVPTNYEVIGSPAVTMSSAPPETGYSGPAVSGSYEQGKAPEHPRG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T3222	PAVSGSYEQGKAPEHPRGSDRSSVSQSPAPTYPSDSHYTSLEQNVPRNYVMIDDISELTKD	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1445	PSTSSTIHSYGQPPTTANYGSQTEELPHAPSGPPGSGRAPREKPLSGGDSEVGAPQPSRGY	(Chalkley et al. 2009)
Protein bassoon	341940634	O88737.4	3942	S1772	ASSVLMAQQKQPVVYGDPFQSRLDFGQGSGSPVCLAQVKQVEQAVQTAPYRGGPRGRPREA	(Chalkley et al. 2009)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S2352	VIKEAPVAPAPGPAPAPPPGQKPAGEAVAGSGSGVLSRPASEKEEASQEDRQRKQQEQLLQ	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	S3197	PTNYEVIGSPAVTMSSAPPETGYSGPAVSGSYEQGKAPEHPRGSDRSSVSQSPAPTYPSDS	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	T1384	TQHFAKEPQDPLKLHSSPVSSTLTSKEVGMTFSQGPGSPATTASPTRGYMTPTSPAGSERS	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	T1788	DPFQSRLDFGQGSGSPVCLAQVKQVEQAVQTAPYRGGPRGRPREAKFARYNLPNQVTPLAR	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	T2514	PFPATCEAPSRGPPPAATELAQNGQYWPPLTHAAFIAVAGTEGPGQPREPVLHRGLPSSAS	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	T2524	RGPPPAATELAQNGQYWPPLTHAAFIAVAGTEGPGQPREPVLHRGLPSSASDMSLQTEEQW	(Vosseller et al. 2006)
Protein bassoon	341940634	O88737.4	3942	S1374	GGRVIPDVRVTQHFAKEPQDPLKLHSSPVSSTLTSKEVGMTFSQGPGSPATTASPTRGYMT	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1378	IPDVRVTQHFAKEPQDPLKLHSSPVSSTLTSKEVGMTFSQGPGSPATTASPTRGYMTPTSP	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S1386	HFAKEPQDPLKLHSSPVSSTLTSKEVGMTFSQGPGSPATTASPTRGYMTPTSPAGSERSPS	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1414	TFSQGPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQPPTTANYGSQTEELPHAP	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	S1460	TANYGSQTEELPHAPSGPPGSGRAPREKPLSGGDSEVGAPQPSRGYSYFTGSSPPLSPSTP	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1525	TFSPGKLGPRATAEFSTQTPSLTLSSDIPRSPGPPSPMVAQGTQTPHRPSTPRLVWQQSSQ	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1553	PRSPGPPSPMVAQGTQTPHRPSTPRLVWQQSSQEAPIMVITLASDASSQTRMVHASASTSP	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	S1566	GTQTPHRPSTPRLVWQQSSQEAPIMVITLASDASSQTRMVHASASTSPLCSPTDSQPTSHS	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1644	GPPGFPRAPSAGTDGPLALYGWGALPAENISLCRISSVPGTSRVEPGPRPPGTAVVDLRTA	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1917	EPAGALDLTGMRPESQLACCDMVYKFPFGSSCTGTFHPAPSAPDKSVTDTALPGQSSGPFY	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S1927	MRPESQLACCDMVYKFPFGSSCTGTFHPAPSAPDKSVTDTALPGQSSGPFYSPRDPEPPEP	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2017	SSMSDTNLAEAGLNYHAQRLGQLFQGPGRDSAVDLSSLKHSYSLGFADGRYLGQGLQYGSF	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2046	DSAVDLSSLKHSYSLGFADGRYLGQGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDH	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2074	YGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDHRYGPRGDAVGFQEASLAQYSATTAREIS	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2201	QYGPAASQATAVRQLLPSTATVRAADGMIYSTINTPIAATLPITTQPASVLRPMVRGGMYR	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	S2235	TPIAATLPITTQPASVLRPMVRGGMYRPYVSGGVTAVPLTSLTRVPMIAPRVPLGPAGLYR	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S3491	GEKLSSHDYSSRGKGYERERDTAERLQKAGSKPSSLSMAHGRARPPMRSQASEEESPVSPL	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S387	TQASTLMSVQPEADTQGQPSPSKGQPKIVFSDASKEAGPRPPGSGPGPGPTPGAKTEPGAR	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T1375	GRVIPDVRVTQHFAKEPQDPLKLHSSPVSSTLTSKEVGMTFSQGPGSPATTASPTRGYMTP	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1513	PPLSPSTPSESPTFSPGKLGPRATAEFSTQTPSLTLSSDIPRSPGPPSPMVAQGTQTPHRP	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	T1563	VAQGTQTPHRPSTPRLVWQQSSQEAPIMVITLASDASSQTRMVHASASTSPLCSPTDSQPT	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1654	AGTDGPLALYGWGALPAENISLCRISSVPGTSRVEPGPRPPGTAVVDLRTAVKPTPIILTD	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2550	AVAGTEGPGQPREPVLHRGLPSSASDMSLQTEEQWEAGRSGIKKRHSMPRLRDACEPESGP	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2719	QLPRVSPAIHITAATDPKVEIVRYISAPEKTGRGESLACQTEPDGQAQGVAGPQLIGPTAI	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T292	RSPRGPGATQSGPRQAEAARATSVPGPTQATAPPEVGRVSPQPPLSTKPSTAEPRPPAGEA	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T3822	QQQQQQQGLGQQAPQQAPSQARLQPQSQPTTRGTAPAASQPAGKPQPGPTTAPGPQPAGPP	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T3842	ARLQPQSQPTTRGTAPAASQPAGKPQPGPTTAPGPQPAGPPRAEQASSSKPPAAKAPQQGR	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	T3878	PAGPPRAEQASSSKPPAAKAPQQGRAPQAQTTPGPGPAGAKPGARPGGTPGAPASQPGAEG	(Alfaro et al. 2012)
Protein bassoon	341940634	O88737.4	3942	T3928	GAPASQPGAEGESVFSKILPGGAAEQAGKLTEAVSAFGKKFSSFWBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T609	SPQATKASPQATKASPQTTKASPQAKPLRATEPSKTSSSAQEKKTVTSAKAEPVPKPPPET	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T640	EPSKTSSSAQEKKTVTSAKAEPVPKPPPETTVPPGTPKAKSGVKRTDPATPVVKPVPEAPK	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1333	NAESAYMDPMKQNGGPLTPGTSPTQLAAPVSFSTSTSSDSSGGRVIPDVRVTQHFAKEPQD	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1411	VGMTFSQGPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQPPTTANYGSQTEELP	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1554	RSPGPPSPMVAQGTQTPHRPSTPRLVWQQSSQEAPIMVITLASDASSQTRMVHASASTSPL	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S1649	PRAPSAGTDGPLALYGWGALPAENISLCRISSVPGTSRVEPGPRPPGTAVVDLRTAVKPTP	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1650	RAPSAGTDGPLALYGWGALPAENISLCRISSVPGTSRVEPGPRPPGTAVVDLRTAVKPTPI	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S1916	EEPAGALDLTGMRPESQLACCDMVYKFPFGSSCTGTFHPAPSAPDKSVTDTALPGQSSGPF	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2112	GDAVGFQEASLAQYSATTAREISRMCAALNSMDQYGGRHGSGSGGPDLVQYQPQHGPGLSA	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2124	QYSATTAREISRMCAALNSMDQYGGRHGSGSGGPDLVQYQPQHGPGLSAPQGLAPLRSGLL	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2165	QHGPGLSAPQGLAPLRSGLLGNPTYPEGQPSPGNLAQYGPAASQATAVRQLLPSTATVRAA	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2658	ADWEQPVRRRRSRLSRHSDSGSDSKHDATASSSTTAAATARAMSSVGIQTISDCSVQTEPE	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2679	SDSKHDATASSSTTAAATARAMSSVGIQTISDCSVQTEPEQLPRVSPAIHITAATDPKVEI	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	S2819	SQLVSRQPPKSPQVLYSPVSPLSPHRLLDTSFASSERLNKAHVSPQKQFIADSTLRQQTLP	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S284	PLGKPEQERSPRGPGATQSGPRQAEAARATSVPGPTQATAPPEVGRVSPQPPLSTKPSTAE	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S2841	SPHRLLDTSFASSERLNKAHVSPQKQFIADSTLRQQTLPRPMKTLQRSLSDPKPLSPTAEE	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S3022	ITQRKESLAKDRGGRDYPPLRGLGEHRDYLSDSELNQLRLQGCTTPAGQYVDYPASAAVPA	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S3175	ADSRAAHQKPRQTSLADLEQKVPTNYEVIGSPAVTMSSAPPETGYSGPAVSGSYEQGKAPE	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S3214	PPETGYSGPAVSGSYEQGKAPEHPRGSDRSSVSQSPAPTYPSDSHYTSLEQNVPRNYVMID	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S3715	RHEARPHPQASPAPAMQKKGQPGYPSSADYSQSSRAPSAYHHASESKKGSRQAHTGPSALQ	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	S996	LDREPELEMESLTGSPEDRSRGEHSSTLPASTPSYTSGTSPTSLSSLEEDSDSSPSRRQRL	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein bassoon	341940634	O88737.4	3942	T1406	LTSKEVGMTFSQGPGSPATTASPTRGYMTPTSPAGSERSPSTSSTIHSYGQPPTTANYGSQ	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1673	ISLCRISSVPGTSRVEPGPRPPGTAVVDLRTAVKPTPIILTDQGMDLTSLAVEARKYGLAL	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1919	AGALDLTGMRPESQLACCDMVYKFPFGSSCTGTFHPAPSAPDKSVTDTALPGQSSGPFYSP	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T1921	ALDLTGMRPESQLACCDMVYKFPFGSSCTGTFHPAPSAPDKSVTDTALPGQSSGPFYSPRD	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2048	AVDLSSLKHSYSLGFADGRYLGQGLQYGSFTDLRHPTDLLSHPLPLRRYSSVSNIYSDHRY	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T2158	DLVQYQPQHGPGLSAPQGLAPLRSGLLGNPTYPEGQPSPGNLAQYGPAASQATAVRQLLPS	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T283	QPLGKPEQERSPRGPGATQSGPRQAEAARATSVPGPTQATAPPEVGRVSPQPPLSTKPSTA	(Trinidad et al., 2012)
Protein bassoon	341940634	O88737.4	3942	T3401	KQGMEQKISKFSPIEEAKDVESDLASYPPPTVSSSLTSRGRKFQDEITYGLKKNVYEQQRY	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein canopy homolog 3	74752319	Q9BT09.1	278	S156	MSETFETLHNLVHKGVKVVMDIPYELWNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQE	(Hahne et al. 2012)
Protein canopy homolog 3	74752319	Q9BT09.1	278	T155	GMSETFETLHNLVHKGVKVVMDIPYELWNETSAEVADLKKQCDVLVEEFEEVIEDWYRNHQ	(Hahne et al. 2012)
Protein CDV3	158563766	Q4VAA2.2	281	T178	WEEGGGGSGAEKSSGPWNKTAPVQAPPAPVTVTETPEPAMPSGVYRPPGARLTTTRKTPQG	(Alfaro et al. 2012)
Protein CREG1	59797902	O75629.1	220	T162	TNFCKKHGFDPQSPLCVHIMLSGTVTKVNETEMDIAKHSLFIRHPEMKTWPSSHNWFFAKL	(Hahne et al. 2012)
Protein EMSY	47605694	Q8BMB0.2	1264	T499	GTQATYTRPTVSPSLGRVATTPGAATYVKTTSGSIITVVPKSLATLGGKIISSNIVSGTTT	(Chalkley et al. 2009)(Alfaro et al. 2012)(Myers et al. 2011)
Protein EMSY	47605694	Q8BMB0.2	1264	S200	RTNSSSSSPVVLKEVPKAVVPVSKTITVPVSGSPKMSNIMQSIANSLPPHMSPVKITFTKP	(Alfaro et al. 2012)(Myers et al. 2011)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein EMSY	47605694	Q8BMB0.2	1264	T228	PVSGSPKMSNIMQSIANSLPPHMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNIL	(Alfaro et al. 2012)(Myers et al. 2011)(Trinidad et al., 2012)
Protein EMSY	47605694	Q8BMB0.2	1264	T247	PPHMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNILSKSHNYAAVTKLVPTSVIA	(Myers et al. 2011)(Trinidad et al., 2012)
Protein EMSY	47605660	Q7Z589.2	1322	S228	DEKPRKRRRTNSSSSSPVVLKEVPKAVVPVSKTITVPVSGSPKMSNIMQSIANSLPPHMSP	(Zhao et al. 2011)
Protein EMSY	47605694	Q8BMB0.2	1264	S192	DEKPRKRRRTNSSSSSPVVLKEVPKAVVPVSKTITVPVSGSPKMSNIMQSIANSLPPHMSP	(Vosseller et al. 2006)
Protein EMSY	47605694	Q8BMB0.2	1264	S231	GSPKMSNIMQSIANSLPPHMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNILSKS	(Myers et al. 2011)
Protein EMSY	47605694	Q8BMB0.2	1264	S500	TQATYTRPTVSPSLGRVATTPGAATYVKTTSGSIITVVPKSLATLGGKIISSNIVSGTTTK	(Myers et al. 2011)
Protein EMSY	47605694	Q8BMB0.2	1264	S520	PGAATYVKTTSGSIITVVPKSLATLGGKIISSNIVSGTTTKITTIPMTSKPNVIVVQKTTG	(Myers et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein EMSY	47605694	Q8BMB0.2	1264	S521	GAATYVKTTSGSIITVVPKSLATLGGKIISSNIVSGTTTKITTIPMTSKPNVIVVQKTTGK	(Alfaro et al. 2012)
Protein EMSY	47605694	Q8BMB0.2	1264	S525	YVKTTSGSIITVVPKSLATLGGKIISSNIVSGTTTKITTIPMTSKPNVIVVQKTTGKGTTI	(Trinidad et al., 2012)
Protein EMSY	47605694	Q8BMB0.2	1264	T232	SPKMSNIMQSIANSLPPHMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNILSKSH	(Trinidad et al., 2012)
Protein EMSY	47605694	Q8BMB0.2	1264	T234	KMSNIMQSIANSLPPHMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNILSKSHNY	(Trinidad et al., 2012)
Protein EMSY	47605694	Q8BMB0.2	1264	T235	MSNIMQSIANSLPPHMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNILSKSHNYA	(Alfaro et al. 2012)
Protein EMSY	47605694	Q8BMB0.2	1264	T246	LPPHMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNILSKSHNYAAVTKLVPTSVI	(Myers et al. 2011)
Protein EMSY	47605694	Q8BMB0.2	1264	T465	KPVTATLPTSSNSPIMVVSSNGAIMTTKLVTTPTGTQATYTRPTVSPSLGRVATTPGAATY	(Myers et al. 2011)
Protein EMSY	47605694	Q8BMB0.2	1264	T470	TLPTSSNSPIMVVSSNGAIMTTKLVTTPTGTQATYTRPTVSPSLGRVATTPGAATYVKTTS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein EMSY	47605694	Q8BMB0.2	1264	T1176	MTKCRESCSSPSAVGPPLTTRKIEAAGVPTTGQFMRIQNVGQKKAEESPTEIIIQAIPQYA	(Trinidad et al., 2012)
Protein EMSY	47605694	Q8BMB0.2	1264	T529	TSGSIITVVPKSLATLGGKIISSNIVSGTTTKITTIPMTSKPNVIVVQKTTGKGTTIQGLP	(Trinidad et al., 2012)
protein EMSY	19923559	NP_064578.2	1322	S236	RTNSSSSSPVVLKEVPKAVVPVSKTITVPVSGSPKMSNIMQSIANSLPPHMSPVKITFTKP	(Wang et al. 2010)
protein EMSY	19923559	NP_064578.2	1322	S557	GAATYVKTTSGSIITVVPKSLATLGGKIISSNIVSGTTTKITTIPMTSKPNVIVVQKTTGK	(Wang et al. 2010)
protein EMSY	19923559	NP_064578.2	1322	T271	MSNIMQSIANSLPPHMSPVKITFTKPSTQTTNTTTQKVIIVTTSPSSTFVPNILSKSHNYA	(Wang et al. 2010)
protein EMSY	19923559	NP_064578.2	1322	T501	KPVTATLPTSSNSPIMVVSSNGAIMTTKLVTTPTGTQATYTRPTVSPSIGRMAATPGAATY	(Wang et al. 2010)
protein EMSY	19923559	NP_064578.2	1322	T506	TLPTSSNSPIMVVSSNGAIMTTKLVTTPTGTQATYTRPTVSPSIGRMAATPGAATYVKTTS	(Wang et al. 2010)
protein EMSY	19923559	NP_064578.2	1322	S228	DEKPRKRRRTNSSSSSPVVLKEVPKAVVPVSKTITVPVSGSPKMSNIMQSIANSLPPHMSP	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein enabled homolog	30179826	Q03173.2	802	S362	AFHPVLPHYATVPRPLNKNSRPSSPVNTPSSQPPAAKSCAWPTSNFSPLPPSPPIMISSPP	(Alfaro et al. 2012)
Protein ERGIC-53	49035535	Q9D0F3.1	517	T385	QLNRQLDMILDEQRRYVSSLTEEISRRGAGTPGQPGQVSQQELDTVVKSQQEILRQVNEVK	(Myers et al. 2011)
Protein FAM117B	123784175	Q3U3E2.1	584	S51	AVGPPGGPGSRLQPMRATVPFQLKQQQQHGSPTRGGGGGGNNGGNGGASGPSGGGGSGGPR	(Trinidad et al., 2012)
Protein FAM135B	166233536	Q9DAI6.3	1403	T989	VNDTMTLNRRHNASLEAKHEAGTVCPTVTHTIASQVSRNQELKTGTSISGSHLNSTEAFTL	(Alfaro et al. 2012)
Protein FAM168A	46576553	Q8BGZ2.1	244	S97	AWPQNSSSCGTEGTFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPYSPSP	(Trinidad et al., 2012)
Protein FAM193A	119370317	Q8CGI1.2	1231	T706	LAPLPALSPSALSPASTPHLPNLAAPSFPKTATTAPGFVDTRKSFCPTPVAPPPSTTDGSI	(Alfaro et al. 2012)
Protein FAM193A	119370317	Q8CGI1.2	1231	T709	LPALSPSALSPASTPHLPNLAAPSFPKTATTAPGFVDTRKSFCPTPVAPPPSTTDGSISAP	(Trinidad et al., 2012)
protein FAM208A isoform a	163838631	NP_001106207.1	1512	S1124	AKGGNLPPVSPNDSGAKIASNPLERHVIPVSSSDFNNKHLLEPLCSDPLKDTNSDEQHSTS	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein KIAA1045	73621117	Q80TL4.2	400	S337	RGSTISEAECHHARHSWFCKRLTEAPSCSVSISHVGPIADSSPAASSSKSQEKALLPTEQE	(Trinidad et al., 2012)
protein lin-54 homolog isoform a	169234719	NP_919258.2	749	S238	QLINTTTQPSVLQTQQLKTVQIAKKPRTPTSGPVITKLIFAKPINSKAVTGQTTQVSPPVI	(Wang et al. 2010)
Protein lin-7 homolog A	59798463	Q8JZS0.2	233	T7	BBBBBBBBBBBBBBBBBBBBBBBMLKPSVTSAPTADMATLTVVQPLTLDRDVARAIELLE	(Trinidad et al., 2012)
Protein lunapark	81886094	Q7TQ95.1	425	T211	ASSSQGPPPQGPVSPGPAKDASAPGGPPERTVAPALPRRLGSPATSVPGMGLHPPGPPLAR	(Trinidad et al., 2012)
Protein phosphatase 1 regulatory subunit 12A	281185473	Q9DBR7.2	1029	T570	NSSINEGSTYHRSCSFGRRQDDLISCSVPSTTSTPTVTSAAGLQRSLPSSTSTAAKTPPGS	(Alfaro et al. 2012)(Trinidad et al., 2012)
protein 1 regulatory subunit 12A	41017262	O14974.1	1030	S402	DKTKPLASVTNANTSSTQAAPVAVTTPTVSSGQATPTSPIKKFPTTATKISPKEEERKDES	(Hahne et al. 2012)
Protein phosphatase 1 regulatory subunit 12A	41017262	O14974.1	1030	S409	SVTNANTSSTQAAPVAVTTPTVSSGQATPTSPIKKFPTTATKISPKEEERKDESPATWRLG	(Hahne et al. 2012)
Protein phosphatase 1 regulatory subunit 12A	41017262	O14974.1	1030	T408	ASVTNANTSSTQAAPVAVTTPTVSSGQATPTSPIKKFPTTATKISPKEEERKDESPATWRL	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein phosphatase 1 regulatory subunit 12A	41017262	O14974.1	1030	S578	TYHKSCSFGRRQDDLISSSVPSTTSTPTVTSAAGLQKSLLSSTSTTTKITTGSSSAGTQSS	(Hahne et al. 2012)
Protein phosphatase 1 regulatory subunit 12A	41017262	O14974.1	1030	T396	ESEAETDKTKPLASVTNANTSSTQAAPVAVTTPTVSSGQATPTSPIKKFPTTATKISPKEE	(Hahne et al. 2012)
Protein phosphatase 1 regulatory subunit 12A	41017262	O14974.1	1030	T397	SEAETDKTKPLASVTNANTSSTQAAPVAVTTPTVSSGQATPTSPIKKFPTTATKISPKEEE	(Hahne et al. 2012)
Protein phosphatase 1 regulatory subunit 12A	41017262	O14974.1	1030	T577	STYHKSCSFGRRQDDLISSSVPSTTSTPTVTSAAGLQKSLLSSTSTTTKITTGSSSAGTQS	(Hahne et al. 2012)
Protein phosphatase 1 regulatory subunit 12A	281185473	Q9DBR7.2	1029	S564	EDDLKKNSSINEGSTYHRSCSFGRRQDDLISCSVPSTTSTPTVTSAAGLQRSLPSSTSTAA	(Alfaro et al. 2012)
Protein phosphatase 1 regulatory subunit 12A	281185473	Q9DBR7.2	1029	S566	DLKKNSSINEGSTYHRSCSFGRRQDDLISCSVPSTTSTPTVTSAAGLQRSLPSSTSTAAKT	(Alfaro et al. 2012)
Protein phosphatase 1 regulatory subunit 12A	281185473	Q9DBR7.2	1029	S381	DESSCSSEEDEEDDSESEAETDKTKPMASVSNAHTSSTQAAPAAVTAPTLSSNQGTPTSPV	(Trinidad et al., 2012)
Protein phosphatase 1 regulatory subunit 12B	122065648	Q8BG95.2	976	T542	NRESAVNLVRSGSHTRQLWRDEAKGSETPQTIAPSTYTSTYLKRTPYKSQADSTAEKTADS	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein phosphatase 1 regulatory subunit 12B	122065648	Q8BG95.2	976	S772	HLLRTSRASGPDSENSETSTHATAAKEMDTSEKGEADLDDQSSNRLSVRERRRAKDRRRGT	(Trinidad et al., 2012)
Protein phosphatase 1 regulatory subunit 12B	122065648	Q8BG95.2	976	T764	RPSLYTGSHLLRTSRASGPDSENSETSTHATAAKEMDTSEKGEADLDDQSSNRLSVRERRR	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2930	EAGHFFYKSKNAFDYSGGTEAAVDLTSGRVSTGEVMDYSSKTTGPYPETRQVISGVGISTP	(Vosseller et al. 2006)(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2656	IDLRTIPKSEVKVTEKCMDLSASAMDVKRQTTANEVYRRQISAVQPSIINLSAASSLGTPV	(Chalkley et al. 2009)(Vosseller et al. 2006)(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	T2948	TEAAVDLTSGRVSTGEVMDYSSKTTGPYPETRQVISGVGISTPQYSTARMTPPPGPQYGVG	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T3873	TPQPSYQLPSQMMVIQQKPRQTTLYLEPKITSTYEVIRNQPLMIAPVSTDNTYAVSHLGSK	(Alfaro et al. 2012)(Chalkley et al. 2009)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2639	DRHQYKENGKLPLIGDAIDLRTIPKSEVKVTEKCMDLSASAMDVKRQTTANEVYRRQISAV	(Alfaro et al. 2012)(Chalkley et al. 2009)
Protein piccolo	94730407	Q9QYX7.3	5038	S2851	IIEDEEKPVDLTAGRRAVCCDMVYKLPFGRSCTAQQPATTLPEDRFGYRDDHYQYDRSGPY	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2953	DLTSGRVSTGEVMDYSSKTTGPYPETRQVISGVGISTPQYSTARMTPPPGPQYGVGSVLRS	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	S3874	PQPSYQLPSQMMVIQQKPRQTTLYLEPKITSTYEVIRNQPLMIAPVSTDNTYAVSHLGSKY	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3890	KPRQTTLYLEPKITSTYEVIRNQPLMIAPVSTDNTYAVSHLGSKYNSLDLRIGLEERSSMA	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S4283	AQNSEEESPLSPVGQPMGMARAAAGPLPPISADTRDQFGSSHSLPEVQQHMREESRTRGYD	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2352	PPPPPLPPATSPKPPTYPKRKLAAAAPVAPTAIVTAHADAIPTVEATAARRSNGLPATKIC	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2356	PLPPATSPKPPTYPKRKLAAAAPVAPTAIVTAHADAIPTVEATAARRSNGLPATKICAAAP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2364	KPPTYPKRKLAAAAPVAPTAIVTAHADAIPTVEATAARRSNGLPATKICAAAPPPVPPKPS	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	T2451	EIPVTTQKTTDTCPKPTGLPLTSNMSLNLVTSADYKLPSPTSPLSPHSNKSSPRYSKSLME	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2809	NGWTDSTISQGITDGEVVDLSTSKSHRTVVTMDESTSNVVTKIIEDEEKPVDLTAGRRAVC	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2859	VDLTAGRRAVCCDMVYKLPFGRSCTAQQPATTLPEDRFGYRDDHYQYDRSGPYGYRGIGGM	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2860	DLTAGRRAVCCDMVYKLPFGRSCTAQQPATTLPEDRFGYRDDHYQYDRSGPYGYRGIGGMK	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2941	AFDYSGGTEAAVDLTSGRVSTGEVMDYSSKTTGPYPETRQVISGVGISTPQYSTARMTPPP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2942	FDYSGGTEAAVDLTSGRVSTGEVMDYSSKTTGPYPETRQVISGVGISTPQYSTARMTPPPG	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	T3891	PRQTTLYLEPKITSTYEVIRNQPLMIAPVSTDNTYAVSHLGSKYNSLDLRIGLEERSSMAS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2238	KKETGDGIILEVLDAYKDKREESEAELTKISLPETGLAPTPSSQTKEQPGSPHSVSGEISG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2284	EQPGSPHSVSGEISGQEKPTYRSPSGGLPVSTHPSKSHPFFRSSSLDISAQPPPPPPPPP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2939	KNAFDYSGGTEAAVDLTSGRVSTGEVMDYSSKTTGPYPETRQVISGVGISTPQYSTARMTP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2958	RVSTGEVMDYSSKTTGPYPETRQVISGVGISTPQYSTARMTPPPGPQYGVGSVLRSSNGVV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2963	EVMDYSSKTTGPYPETRQVISGVGISTPQYSTARMTPPPGPQYGVGSVLRSSNGVVYSSVA	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	S3926	AVSHLGSKYNSLDLRIGLEERSSMASSPISSISADSFYADIDHHTSRNYVLIDDIGDITKG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3961	SFYADIDHHTSRNYVLIDDIGDITKGTAALSSAFSLHEKDLSKTDRLLRTTETRRSQEVTD	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S4554	AELQKVSLQQSPLVMSSVVEKGAHAHSGPTSAGSSSVPSPGQPGSPSVSKKKHGGSKPTDV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2285	QPGSPHSVSGEISGQEKPTYRSPSGGLPVSTHPSKSHPFFRSSSLDISAQPPPPPPPPPPP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2918	GMKPSMSDTNLAEAGHFFYKSKNAFDYSGGTEAAVDLTSGRVSTGEVMDYSSKTTGPYPET	(Alfaro et al. 2012)(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T3023	ATPIPSTFAITTQPGSIFSTTVRDLSGIHTTDAITSLSALHQSQPMPRSYFITTGASETDI	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	S2634	EPLALDRHQYKENGKLPLIGDAIDLRTIPKSEVKVTEKCMDLSASAMDVKRQTTANEVYRR	(Chalkley et al. 2009)
Protein piccolo	94730407	Q9QYX7.3	5038	S2815	TISQGITDGEVVDLSTSKSHRTVVTMDESTSNVVTKIIEDEEKPVDLTAGRRAVCCDMVYK	(Alfaro et al. 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3018	VYSSVATPIPSTFAITTQPGSIFSTTVRDLSGIHTTDAITSLSALHQSQPMPRSYFITTGA	(Alfaro et al. 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2806	GVTNGWTDSTISQGITDGEVVDLSTSKSHRTVVTMDESTSNVVTKIIEDEEKPVDLTAGRR	(Alfaro et al. 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T3740	LLKEREKRERAYLQGVAEDRDYMSDSEVSSTRPSRVESQHGIERPRTAPQTEFSQFIPPQT	(Alfaro et al. 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S1796	PSIESDPEGFEISPEKIIEVQKVYKLPTAVSLYSPTDEQSVMQKEGAQKALKSAEEMYEEM	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2261	EAELTKISLPETGLAPTPSSQTKEQPGSPHSVSGEISGQEKPTYRSPSGGLPVSTHPSKSH	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2446	KPAVPEIPVTTQKTTDTCPKPTGLPLTSNMSLNLVTSADYKLPSPTSPLSPHSNKSSPRYS	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	S2892	PEDRFGYRDDHYQYDRSGPYGYRGIGGMKPSMSDTNLAEAGHFFYKSKNAFDYSGGTEAAV	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3028	STFAITTQPGSIFSTTVRDLSGIHTTDAITSLSALHQSQPMPRSYFITTGASETDISVTSI	(Alfaro et al. 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3600	KTAKMMQRSMSDPKPLSPTADESSRAPFQYSEGFTAKGSQTTSGTQKKVKRTLPNPPPEEA	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3902	ITSTYEVIRNQPLMIAPVSTDNTYAVSHLGSKYNSLDLRIGLEERSSMASSPISSISADSF	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3965	DIDHHTSRNYVLIDDIGDITKGTAALSSAFSLHEKDLSKTDRLLRTTETRRSQEVTDFLAP	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3986	GTAALSSAFSLHEKDLSKTDRLLRTTETRRSQEVTDFLAPLQTSSRLHSYVKAEEDSMEDP	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S4099	LEKQAAKQLPAAILYQKQSKHKKALIDPKMSKFSPIQESRDLEPDYPTYLSSSTSSIGGIS	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S4182	KFMGSSLGSGLGTLGNTIRSALQDEADKPYSSGSRSRPSSRPSSVYGLDLSIKRDSSSSSL	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	S4243	RLKAQEAEALDVSFGHSSSSARTKPTSLPISQSRGRIPIVAQNSEEESPLSPVGQPMGMAR	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S4530	LELHEPPKVVDKAKSPGVDPKQLAAELQKVSLQQSPLVMSSVVEKGAHAHSGPTSAGSSSV	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S488	QPGLGKPSAQQPSKSISQTVTGRPLQAPPTSAAQAPAQGLSKTICPLCNTTELLLLHTPEKA	(Alfaro et al. 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S826	ATPQSQQPPKPPEQSRRFSLNLGGIADAPKSQPTTPQETVTGKLFGFGASIFSQASNLIST	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2368	YPKRKLAAAAPVAPTAIVTAHADAIPTVEATAARRSNGLPATKICAAAPPPVPPKPSSIPT	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2425	SIPTGLVFTHRPEASKPPIAPKPAVPEIPVTTQKTTDTCPKPTGLPLTSNMSLNLVTSADY	(Alfaro et al. 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2657	DLRTIPKSEVKVTEKCMDLSASAMDVKRQTTANEVYRRQISAVQPSIINLSAASSLGTPVT	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T3954	ISSISADSFYADIDHHTSRNYVLIDDIGDITKGTAALSSAFSLHEKDLSKTDRLLRTTETR	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	T3957	ISADSFYADIDHHTSRNYVLIDDIGDITKGTAALSSAFSLHEKDLSKTDRLLRTTETRRSQ	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T3990	LSSAFSLHEKDLSKTDRLLRTTETRRSQEVTDFLAPLQTSSRLHSYVKAEEDSMEDPYELK	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T4164	LLQDDITFGLRKNITDQQKFMGSSLGSGLGTLGNTIRSALQDEADKPYSSGSRSRPSSRPS	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T4235	RDSSSSSLRLKAQEAEALDVSFGHSSSSARTKPTSLPISQSRGRIPIVAQNSEEESPLSPV	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T703	TETLTDSPSSAAATSKPAILSSQVQAQAQVTTAPPLKTDSAKTSQSFPPTGDTITPLDSKA	(Alfaro et al. 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T881	SNLISTAGQQAPHPQTGPAAPSKQAPPPSQTLAAQGPPKSTGQHPSAPAKTTAVKKETKGP	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2169	SVIDYPEDIGVSLDRTITPESRTNADQIMISFPGIAPSITESVATKPERPQADTISTDLPI	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S2739	ESQVGIEHAVTSPLQLTTSKHTELQYRKPSSQAFPMIRDEAPINLSLGPSTQAVTLAVTKP	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	S2894	DRFGYRDDHYQYDRSGPYGYRGIGGMKPSMSDTNLAEAGHFFYKSKNAFDYSGGTEAAVDL	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3030	FAITTQPGSIFSTTVRDLSGIHTTDAITSLSALHQSQPMPRSYFITTGASETDISVTSIDI	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3500	TDPDTQSPPYMGATSPPKDKKRPTPLEIGYSSSHLRADPTVQLAPSPPKSPKVLYSPISPL	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S3743	EREKRERAYLQGVAEDRDYMSDSEVSSTRPSRVESQHGIERPRTAPQTEFSQFIPPQTQTE	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S4157	GISSRARLLQDDITFGLRKNITDQQKFMGSSLGSGLGTLGNTIRSALQDEADKPYSSGSRS	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	S472	AKPQPQQPTPAKPQPQQPGLGKPSAQQPSKSISQTVTGRPLQAPPTSAAQAPAQGLSKTIC	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2461	DTCPKPTGLPLTSNMSLNLVTSADYKLPSPTSPLSPHSNKSSPRYSKSLMETYVVITLPSE	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T2687	TANEVYRRQISAVQPSIINLSAASSLGTPVTMDSKTVAVVTCTDTTIYTTGTESQVGIEHA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein piccolo	94730407	Q9QYX7.3	5038	T2959	VSTGEVMDYSSKTTGPYPETRQVISGVGISTPQYSTARMTPPPGPQYGVGSVLRSSNGVVY	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T3980	IGDITKGTAALSSAFSLHEKDLSKTDRLLRTTETRRSQEVTDFLAPLQTSSRLHSYVKAEE	(Trinidad et al., 2012)
Protein piccolo	94730407	Q9QYX7.3	5038	T478	QPTPAKPQPQQPGLGKPSAQQPSKSISQTVTGRPLQAPPTSAAQAPAQGLSKTICPLCNTT	(Trinidad et al., 2012)
Protein PRRC1	74732288	Q96M27.1	445	T191	PSGTGLLPTPITQQASLTSLAQGTGTTSAITFPEEQEDPRITRGQDEASAGGIWGFIKGVA	(Hahne et al. 2012)
Protein PRRC1	74732288	Q96M27.1	445	S157	GPPISGFSVGSTYDITRGHAGRAPQTPLMPSFSAPSGTGLLPTPITQQASLTSLAQGTGTT	(Hahne et al. 2012)
Protein PRRC2B	308153415	Q5JSZ5.2	2229	S1990	PISLHTSLQAQAQLGLRGGLPVSQSQEIFSSLQPFRSQVYMHPSLSPPSTMILSGGTALKP	(Hahne et al. 2012)
Protein PRRC2C	205688689	Q3TLH4.2	2828	S2403	GQHQAQLSLGAGPAVSQAQELFSSSIQPYRSQPAFMQSSLSQPSVVLSGTAIHNFPAVQHQ	(Alfaro et al. 2012)
Protein PRRC2C	341942262	Q9Y520.4	2896	S2463	IYAPLQGQHQAQLSLGAGPAVSQAQELFSSSLQPYRSQPAFMQSSLSQPSVVLSGTAIHNF	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein PRRC2C	341942262	Q9Y520.4	2896	S2694	GSGIDIKPGTPPIAGRSTTPTSSPFRATSTSPNSQSSKMNSIVYQKQFQSAPATVRMTQPF	(Hahne et al. 2012)
Protein PRRC2C	341942262	Q9Y520.4	2896	T2693	FGSGIDIKPGTPPIAGRSTTPTSSPFRATSTSPNSQSSKMNSIVYQKQFQSAPATVRMTQP	(Hahne et al. 2012)
Protein PRRC2C	205688689	Q3TLH4.2	2828	T2177	VNNVPLPNTLPLPKRETIQQSSSLTSVPPTTFSLTFKMESARKAWENSPNLREKGSPVTST	(Alfaro et al. 2012)
protein PRRC2C	115298682	NP_055987.2	2817	T2243	VNNVPLPNTLPLPKRETIQQSSSLTSVPPTTFSLTFKMESARKAWENSPNVREKGSPVTST	(Wang et al. 2010)
protein PRRC2C	115298682	NP_055987.2	2817	S2694	GSGIDIKPGTPPIAGRSTTPTSSPFRATSTSPNSQSSKMNSIVYQKQFQSAPATVRMTQPF	(Wang et al. 2010)
Protein SCAF8	30580495	Q9UPN6.1	1271	T615	AEGGMIDQETVNTEWETVKSSEPVKETVQTTQSPTPVEKETVVTTQAEVFPPPVAMLQIPV	(Hahne et al. 2012)
Protein SCAF8	30580495	Q9UPN6.1	1271	T619	MIDQETVNTEWETVKSSEPVKETVQTTQSPTPVEKETVVTTQAEVFPPPVAMLQIPVAPAV	(Hahne et al. 2012)
Protein SMG7	81889396	Q5RJH6.1	1138	S949	LEKPSELMSHSSSFLSLTGFSVNQERYPNSSMFNEVYGKNLTTSSKAELNPSVASQETSLY	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein SON	296453022	P18583.4	2426	S244	LSVVSTSVISEQSEQSVAVMPEPSMTKILDSFAAAPVPTTTLVLKSSEPVVTMSVEYQMKS	(Hahne et al. 2012)
Protein SON	296453022	P18583.4	2426	T254	EQSEQSVAVMPEPSMTKILDSFAAAPVPTTTLVLKSSEPVVTMSVEYQMKSVLKSVESTSP	(Hahne et al. 2012)
Protein SON	338817942	Q9QX47.2	2444	S250	SEQSEQPMPGMLEPSMTKILDSFTAAPVPMSTAALKSPEPVVTMSVEYQKSVLKSLETMPP	(Trinidad et al., 2012)
Protein SON	338817942	Q9QX47.2	2444	T251	EQSEQPMPGMLEPSMTKILDSFTAAPVPMSTAALKSPEPVVTMSVEYQKSVLKSLETMPPE	(Trinidad et al., 2012)
Protein SON	338817942	Q9QX47.2	2444	S1092	MSAYERSMMSPMADRSMMSMGADRSMMSSYSAADRSMMSSYSAADRSMMSSYTDRSMMSMA	(Trinidad et al., 2012)
Protein sprouty homolog 2	13124565	Q9QXV8.1	315	T121	PPRLQPSQVHSSRAPLSRSISTVSSGSRSSTRTSTSSSSSEQRLLGPSFSHGPAAADGIIR	(Trinidad et al., 2012)
Protein sprouty-like 3	344236008	EGV92111.1	288	S40	QQILPIEQLRSTHASNDYVEQPPAPCKQALSSPSLIVQTHKSDWSLATMPTALPRSISQCH	(Trinidad et al., 2012)
Protein strawberry notch homolog 1	166233533	Q689Z5.2	1390	T124	LPTLGSTIVMTKTPPATTNRQTITLTKFIQTTANTRPSVSAPAVRNAMPAAPSKDQVQLKD	(Alfaro et al. 2012)(Myers et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein TANC1	166987402	Q0VGY8.2	1856	S1656	RLLAHASVAVDMAPPNQGGPVSCSDVRHPASLSSSGSSGSPSSSIKMSSSTSSLTSSSSVS	(Trinidad et al., 2012)
Protein TANC1	166987402	Q0VGY8.2	1856	S1658	LAHASVAVDMAPPNQGGPVSCSDVRHPASLSSSGSSGSPSSSIKMSSSTSSLTSSSSVSDG	(Trinidad et al., 2012)
Protein TANC1	166987402	Q0VGY8.2	1856	S1659	AHASVAVDMAPPNQGGPVSCSDVRHPASLSSSGSSGSPSSSIKMSSSTSSLTSSSSVSDGF	(Trinidad et al., 2012)
Protein TANC2	189029808	A2A690.1	1994	S1643	KAQIVRSNQPSSAVHSSTVIPTGAYGQVAHSMASKYQSSQGDMGVSQSRLVYQGSIGGIVG	(Trinidad et al., 2012)
Protein TANC2	189029808	A2A690.1	1994	S1724	GGLTKEDLPQRPSSAYRGGMRYSQTPQIGRSQSASYYPVCHSKLDLERSSSQLGSPDVSHL	(Trinidad et al., 2012)
Protein TANC2	189029808	A2A690.1	1994	T1956	PHGMLANGSRGDLLERVSQASSYPDVKVARTLPVAQAYQDNLYRQLSRDSRQGQTSPIKPK	(Trinidad et al., 2012)
Protein TANC2	189029808	A2A690.1	1994	S1651	QPSSAVHSSTVIPTGAYGQVAHSMASKYQSSQGDMGVSQSRLVYQGSIGGIVGDGRPVQHV	(Trinidad et al., 2012)
Protein transport protein Sec24B	218511774	O95487.2	1268	S347	VLSGSSGSSSTRTPPTANHPVEPVTSVTQPSELLQQKGVQYGEYVNNQASSAPTPLSSTSD	(Hahne et al. 2012)(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Protein transport protein Sec24B	218511774	O95487.2	1268	T327	LSCPVMQNVQPPKSSPVVSTVLSGSSGSSSTRTPPTANHPVEPVTSVTQPSELLQQKGVQY	(Zhao et al. 2011)
Protein unc-80 homolog	226698394	Q8BLN6.2	3261	S1433	LDENEDSKDSLHSSSHTIKSDAGAEEKKEGSPWSASEPSIEPEGLSNAGTEENYHRNMSWL	(Trinidad et al., 2012)
Protein unc-80 homolog	226698394	Q8BLN6.2	3261	S2923	CKSSLIAEFNSELKILKEAVHSGSAYQGKTSISTVGTSTSAYRLSLATMSRSNTGTGTVWE	(Trinidad et al., 2012)
Protein unc-80 homolog	226698394	Q8BLN6.2	3261	S2925	SSLIAEFNSELKILKEAVHSGSAYQGKTSISTVGTSTSAYRLSLATMSRSNTGTGTVWEQD	(Trinidad et al., 2012)
Protein WWC2	81911165	Q6NXJ0.1	1187	S520	LQEKGGYIPSGPITTIHENEVVKSPSQPGQSGLCGVGVTASSHTTPLTEASKSVASLSSRS	(Alfaro et al. 2012)
Protein WWC2	81911165	Q6NXJ0.1	1187	T528	PSGPITTIHENEVVKSPSQPGQSGLCGVGVTASSHTTPLTEASKSVASLSSRSSLSSLSPP	(Trinidad et al., 2012)
Protein YIF1B	160221314	Q9CX30.2	311	S27	BBBBMHATGLAAPAGTPRLRKWPSKRRVPVSQPGMADPHQFFDDTSSAPSRGYGGQPSPGG	(Trinidad et al., 2012)
Putative E3 ubiquitin-protein ligase UNKL	300669622	Q5FWH2.2	727	T459	DINIASLDKDLEEQDLGLTGPRSLAGSAPVTIPGSLPRSPSLHSSSSLSTSPLSSLSQSLS	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Putative E3 ubiquitin-protein ligase UNKL	300669622	Q5FWH2.2	727	S451	SALDLRLSDINIASLDKDLEEQDLGLTGPRSLAGSAPVTIPGSLPRSPSLHSSSSLSTSPL	(Trinidad et al., 2012)
Putative tyrosine-protein phosphatase auxilin	109818808	Q80TZ3.2	938	T588	ATGPAQAGQAGVEDVFHPSGPVSAQSTPRRTATSASASPTLRVGEGATFDPFGAPAKPPGQ	(Trinidad et al., 2012)
Putative tyrosine-protein phosphatase auxilin	109818808	Q80TZ3.2	938	S591	PAQAGQAGVEDVFHPSGPVSAQSTPRRTATSASASPTLRVGEGATFDPFGAPAKPPGQDLL	(Trinidad et al., 2012)
Putative tyrosine-protein phosphatase auxilin	109818808	Q80TZ3.2	938	T590	GPAQAGQAGVEDVFHPSGPVSAQSTPRRTATSASASPTLRVGEGATFDPFGAPAKPPGQDL	(Trinidad et al., 2012)
Pyruvate kinase isozymes M1/M2	146345448	P52480.4	531	S37	EAGTAFIQTQQLHAAMADTFLEHMCRLDIDSAPITARNTGIICTIGPASRSVEMLKEMIKS	(Trinidad et al., 2012)
Rabphilin-3A	21431839	P47708.2	681	T346	PPSDPGYPGAVAPAREERTGPAGGFQAAPHTAAPYSQAAPARQPPPAEEEEEEANSYDSDE	(Alfaro et al. 2012)(Trinidad et al., 2012)
Rabphilin-3A	21431839	P47708.2	681	S351	GYPGAVAPAREERTGPAGGFQAAPHTAAPYSQAAPARQPPPAEEEEEEANSYDSDEATTLG	(Trinidad et al., 2012)
RalBP1-associated Eps domain-containing protein 1	262527555	O54916.2	795	T258	DNWVSFADTPPTSALLTMHPASVQDQTTVRTVASAATANEIRRQSSSYEDPWKITDEQRQY	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
ranBP2-like and GRIP domain-containing protein 4	211059431	NP_872394.2	1758	S919	LLRPAANVTPTKGSSNTEFKSTKEGFSIPVSADGFKFGISEPGNQEKESEKPLENDTGFQA	(Wang et al. 2010)
Rap guanine nucleotide exchange factor 2	363548465	Q8CHG7.2	1496	S1165	TVDNFSDSGHSEISSRSSIVSNSSFDSVPVSLHDERRQRHSVSIVESNLGVGRMERRTLME	(Trinidad et al., 2012)
Rap guanine nucleotide exchange factor 2	363548465	Q8CHG7.2	1496	S1208	IVESNLGVGRMERRTLMEPDQYSLGSYAPVSESRGLYAAATVISSPSTEELSHDQGDRASL	(Trinidad et al., 2012)
Rap1 GTPase-activating protein	123229440	CAM19421.1	694	S489	FESFKRVIRSRSQSMDAMGLSNKKPNTVSTSHSGSFTPNNPDLAKAAGISLIVPGKSPTRK	(Trinidad et al., 2012)
Ras GTPase-activating protein SynGAP	150421677	Q9QUH6.2	1308	S892	NLAAVGDLLHSSQASLTAALGLRPAPAGRLSQGSGSSITAAGMRLSQMGVTTDGVPAQQLR	(Trinidad et al., 2012)
Ras GTPase-activating protein SynGAP	150421677	Q9QUH6.2	1308	S983	PPSSHHHHHHHHHHRGGEPPGDTFAPFHGYSKSEDLSTGVPKPPAASILHSHSYSDEFGPS	(Trinidad et al., 2012)
Ras GTPase-activating protein SynGAP	150421677	Q9QUH6.2	1308	T1134	PRQQSLSKEGSIGGSGGSGGGGGGGLKPSITKQHSQTPSTLNPTMPASERTVAWVSNMPHL	(Trinidad et al., 2012)
Ras GTPase-activating protein SynGAP	150421677	Q9QUH6.2	1308	S840	RPPLARSSPAYCTSSSDITEPEQKMLSVNKSVSMLDLQGDGPGGRLNSSSVSNLAAVGDLL	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Ras GTPase-activating protein SynGAP	150421677	Q9QUH6.2	1308	T1143	GSIGGSGGSGGGGGGGLKPSITKQHSQTPSTLNPTMPASERTVAWVSNMPHLSADIESAHI	(Trinidad et al., 2012)
Ras GTPase-activating protein SynGAP	150421677	Q9QUH6.2	1308	T900	LHSSQASLTAALGLRPAPAGRLSQGSGSSITAAGMRLSQMGVTTDGVPAQQLRIPLSFQNP	(Trinidad et al., 2012)
Ras GTPase-activating protein SynGAP	150421677	Q9QUH6.2	1308	T912	GLRPAPAGRLSQGSGSSITAAGMRLSQMGVTTDGVPAQQLRIPLSFQNPLFHMAADGPGPP	(Trinidad et al., 2012)
Ras GTPase-activating protein-binding protein 1	149165711	P97855.1	465	T266	DVAPAQEDLRTFSWASVTSKNLPPSGAVPVTGTPPHVVKVPASQPRPESKPDSQIPPQRPQ	(Trinidad et al., 2012)
ras-associated and pleckstrin homology domains-containing protein 1 isoform 1	47132519	NP_998754.1	1250	T784	HITQVAPPTPPPPPPIPAPLPPQAPPKPLVTIPAPTSTKTVAPVVTQAAPPTPTPPVPPAK	(Wang et al. 2010)
Ras-related GTP binding D	123858319	CAM22252.1	454	S43	EDGGEDEEEDELVGLAGYEDGPESSDAELDSGPEEGESRRNSWMPRSWCSEATRHECWEPG	(Trinidad et al., 2012)
Ras-related GTP binding D	123858319	CAM22252.1	454	S50	EEDELVGLAGYEDGPESSDAELDSGPEEGESRRNSWMPRSWCSEATRHECWEPGLWRSSHL	(Trinidad et al., 2012)
Ras-specific guanine nucleotide-releasing factor 2	81908500	P70392.2	1189	S763	SRTSSPVRARKLSLTSSLNSRIGALDLTNSSSSSSPTTTTHSPAASPPPHTAVLESAPADK	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Regulating synaptic membrane exocytosis protein 2	34395823	Q9EQZ7.1	1530	S1528	PPSSLVDPTLAPLTRRASQSSLESSTGPSYSRSBBBBBBBBBBBBBBBBBBBBBBBBBB	(Chalkley et al. 2009)(Alfaro et al. 2012)
Regulation of nuclear pre-mRNA domain-containing protein 2	81892071	Q6NXI6.1	1469	S417	EDMELSDVEDDGSKIIVEDRKEKPVEKPAVSTGVPTKSTESVSKASPCAPPSVPTTAAPPL	(Alfaro et al. 2012)(Trinidad et al., 2012)
Regulation of nuclear pre-mRNA domain-containing protein 2	81892071	Q6NXI6.1	1469	T418	DMELSDVEDDGSKIIVEDRKEKPVEKPAVSTGVPTKSTESVSKASPCAPPSVPTTAAPPLP	(Alfaro et al. 2012)(Trinidad et al., 2012)
Regulation of nuclear pre-mRNA domain-containing protein 2	74746888	Q5VT52.1	1461	S374	EESQSPTMESEKSATPEPVTDNRDVEDMELSDVEDDGSKIIVEDRKEKPAEKSAVSTSVPT	(Hahne et al. 2012)
Regulation of nuclear pre-mRNA domain-containing protein 2	74746888	Q5VT52.1	1461	T495	SVMKNTGVSPASRPSPGTPTSPSNLTSGLKTPAPATTTSHNPLANILSKVEITPESILSAL	(Hahne et al. 2012)
Regulation of nuclear pre-mRNA domain-containing protein 2	81892071	Q6NXI6.1	1469	S1010	QYPDSPHSVPHRSIFSSQSTLAAPAGHPPTSGVEKVLASTISTTSTIEFKNMLKNASRKPS	(Trinidad et al., 2012)
regulation of nuclear pre-mRNA domain-containing protein 2	183396804	NP_056018.2	1461	S399	EDMELSDVEDDGSKIIVEDRKEKPAEKSAVSTSVPTKPTENISKASSCTPVPVTMTATPPL	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
regulation of nuclear pre-mRNA domain-containing protein 2	183396804	NP_056018.2	1461	T400	DMELSDVEDDGSKIIVEDRKEKPAEKSAVSTSVPTKPTENISKASSCTPVPVTMTATPPLP	(Wang et al. 2010)
Reticulocalbin-1	2493462	Q15293.1	331	S55	RVLRAKPTVRKERVVRPDSELGERPPEDNQSFQYDHEAFLGKEDSKTFDQLTPDESKERLG	(Hahne et al. 2012)
Reticulon-1	61216668	Q8K0T0.1	780	T278	KLIKDHLFEESTFAPYIDELSDEQHRVSLVTAPVKITLTEIEPPLMTATQETIPEKQDLCL	(Trinidad et al., 2012)
Reticulon-3	134047901	Q9ES97.2	964	S146	AKGKDPLVLLDKKKLDSPQGTNKDRVDAPVSLATGIPCSHPSIPDSFPEQPAFLSKEIGPA	(Alfaro et al. 2012)(Trinidad et al., 2012)
Reticulon-3	134047901	Q9ES97.2	964	S206	AEEWVVKDQEPKNPNKVPDGEDRSALDFGQSKAEHICTYSLSPSELPVASVEKDSPESPFE	(Trinidad et al., 2012)
Reticulon-3	134047901	Q9ES97.2	964	T385	ELRSEIPVINLKTNPQQKMPVCSFNGSTPITKSTGDWTEAFTEGKPVRDYLSSTKEAGGNG	(Trinidad et al., 2012)
Reticulon-3	134047901	Q9ES97.2	964	T306	EMNDKLFPLRNKEAGRYPSSVLLGRQFSHTTAALEEVSRCVNDMHNFTNEILTWDLDPQAK	(Trinidad et al., 2012)
Reticulon-4	94730421	Q99P72.2	1162	T509	RKAQIITEKTSPKTSNPFLVAIHDSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEACES	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Rho GTPase-activating protein 32	206558298	Q811P8.2	2089	S1027	VLSSQSKAVPSGQSQTGAVTHDPPQDPVPVSSVSLIPPPPPPKNVARMLALALAESAQQAS	(Alfaro et al. 2012)
Rho GTPase-activating protein 32	206558298	Q811P8.2	2089	S1355	VGQVQEAPSIGLNNSHKVQGTAPAPERPPESRAMGDPAPIFLSDGTAAAQCPMGASAPQPG	(Trinidad et al., 2012)
Rho GTPase-activating protein 32	206558298	Q811P8.2	2089	S920	AFSPKIGRKLSKSPSMNISEPISVTLPPRVSEVIGTVSNTVAQNASPTSWDKSVEERDVIN	(Trinidad et al., 2012)
Rho GTPase-activating protein 32	206558298	Q811P8.2	2089	T1422	ESSRAPPLHLRAESFPGHSCGFAAPVPPTRTMESKMAAALHSSAADATSSSNYHSFVPSSA	(Trinidad et al., 2012)
Rho GTPase-activating protein 32	206558298	Q811P8.2	2089	S1918	HRQLCESKNGPPYPQGAGQLDYGSKGMPDTSEPSNYHNSGKYMTSGQGSLTLNHKEVRLPK	(Trinidad et al., 2012)
Rho GTPase-activating protein 32	206558298	Q811P8.2	2089	S2023	LHHTQNLERDPSVLYQYQTHSKRQSSMTVVSQYDNLEDYHSLPQHQRGGFGGAGMGAYVPS	(Trinidad et al., 2012)
Rho GTPase-activating protein 32	206558298	Q811P8.2	2089	T1012	GAAEEVELPGTEERPVLSSQSKAVPSGQSQTGAVTHDPPQDPVPVSSVSLIPPPPPPKNVA	(Trinidad et al., 2012)
Rho GTPase-activating protein 7	250090556	Q9R0Z9.2	1092	S174	MLTDLSEHQEVASVRSLSSTSSSVPTHAAHSGDATTPRTNSVISVCSSGHFVGNDDSFSSL	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
ribosomal RNA processing protein 1 homolog B	57863269	NP_055871.1	758	S731	KSILVSPTGPSRVAFDPEQKPLHGVLKTPTSSPASSPLVAKKPLTTTPRRRPRAMDFFBBB	(Wang et al. 2010)
RIKEN cDNA B630019K06 gene	81894508	Q7TNS5	333	S132	LEPRYAALAAEDCAAAARRFLLSSAAAAAASSASSPATRCKELGLAAAAAWEQQGRSLFVA	(Trinidad et al., 2012)
RIMS-binding protein 2	341942152	Q80U40.3	1072	T683	PPDMHSAGPGRRSPSPSRILPQPQGAPVSTTVAKAMAREAAQRVAESNRLEKRSLFLEQSS	(Alfaro et al. 2012)
RIMS-binding protein 2	341942152	Q80U40.3	1072	S681	LEPPDMHSAGPGRRSPSPSRILPQPQGAPVSTTVAKAMAREAAQRVAESNRLEKRSLFLEQ	(Alfaro et al. 2012)
RING finger and CCCH-type zinc finger domain-containing protein 2	73621224	P0C090.1	1187	S592	AGPSNFGTELNSLPPKSSPFLTRVPVYPQHSESIQYFQDPRTQIPFEVPQYPQTGYYPPPP	(Alfaro et al. 2012)(Trinidad et al., 2012)
RING finger and CCCH-type zinc finger domain-containing protein 2	73621224	P0C090.1	1187	S901	DVKRRVHLFEAQRRTKEEDPIIPFSDGPIISKWGAISRSSRTGYHTTDPVQATASQGSATK	(Trinidad et al., 2012)
RING finger and CCCH-type zinc finger domain-containing protein 2	73621224	P0C090.1	1187	T471	EKYRLRNKKMSATVRTFPLLNKVGVNSTVTTTAGNVISVIGSTETTGKIVASTNGISNTES	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
RNA-binding protein 14	73621447	Q8C2Q3.1	669	S244	RSPLRRSPPRASYVAPLTAQPATYRAQPSVSLGAAYRAQPSASLGVGYRTQPMAAQAASYR	(Alfaro et al. 2012)(Myers et al. 2011)(Trinidad et al., 2012)
RNA-binding protein 14	73621447	Q8C2Q3.1	669	S280	RAQPSASLGVGYRTQPMAAQAASYRAQPSVSLGAPYRGQLASPSSQSAAASSLGPYGGVQP	(Alfaro et al. 2012)(Myers et al. 2011)(Trinidad et al., 2012)
RNA-binding protein 14	73621447	Q8C2Q3.1	669	S256	YVAPLTAQPATYRAQPSVSLGAAYRAQPSASLGVGYRTQPMAAQAASYRAQPSVSLGAPYR	(Alfaro et al. 2012)(Trinidad et al., 2012)
RNA-binding protein 14	73621447	Q8C2Q3.1	669	S527	SYGAAAAYGAQPSATLAAPYRTQSSASLAASYAAQQHPQAAASYRGQPGSAYDGTGQPSAA	(Alfaro et al. 2012)
RNA-binding protein 14	73621447	Q8C2Q3.1	669	T231	QARQPTPPFFGRDRSPLRRSPPRASYVAPLTAQPATYRAQPSVSLGAAYRAQPSASLGVGY	(Trinidad et al., 2012)
RNA-binding protein 14 isoform 1	5454064	NP_006319.1	669	S244	RSPLRRSPPRASYVAPLTAQPATYRAQPSVSLGAAYRAQPSASLGVGYRTQPMTAQAASYR	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
RNA-binding protein 14 isoform 1	5454064	NP_006319.1	669	S254	ASYVAPLTAQPATYRAQPSVSLGAAYRAQPSASLGVGYRTQPMTAQAASYRAQPSVSLGAP	(Wang et al. 2010)
RNA-binding protein 14 isoform 1	5454064	NP_006319.1	669	S256	YVAPLTAQPATYRAQPSVSLGAAYRAQPSASLGVGYRTQPMTAQAASYRAQPSVSLGAPYR	(Wang et al. 2010)
RNA-binding protein 14 isoform 1	5454064	NP_006319.1	669	S280	RAQPSASLGVGYRTQPMTAQAASYRAQPSVSLGAPYRGQLASPSSQSAAASSLGPYGGAQP	(Wang et al. 2010)
RNA-binding protein 27	341942166	Q5SFM8.3	1060	S546	PNLIGLTSGDMDANPRAANIVIQTEPPVPVSVNSNVTRVVLEPESRKRAISGLEGPLTKKP	(Alfaro et al. 2012)
RNA-binding protein 27	124021005	Q9P2N5.2	1060	T552	TSGDMDVNPRAANIVIQTEPPVPVSINSNITRVVLEPDSRKRAMSGLEGPLTKKPWLGKQG	(Hahne et al. 2012)
RNA-binding protein 27	341942166	Q5SFM8.3	1060	T522	EAPSITSSGRSQYRQFFSRAQTQRPNLIGLTSGDMDANPRAANIVIQTEPPVPVSVNSNVT	(Trinidad et al., 2012)
RNA-binding protein 27	168229174	NP_061862.1	1060	S546	PNLIGLTSGDMDVNPRAANIVIQTEPPVPVSINSNITRVVLEPDSRKRAMSGLEGPLTKKP	(Wang et al. 2010)
RNA-binding protein 27	168229174	NP_061862.1	1060	S738	HLHQQQVLVAQSAPSTVHGGIQKMMSKPQTSGAYVLNKVPVKHRLGHAGGNQSDASHLLNQ	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Sal-like protein 2	296453020	Q9Y467.4	1007	S618	ETSKLQQLVEKIDRQGAVAVTSAASGAPTTSAPAPSSSASSGPNQCVICLRVLSCPRALRL	(Hahne et al. 2012)
Sal-like protein 2	296453020	Q9Y467.4	1007	S628	KIDRQGAVAVTSAASGAPTTSAPAPSSSASSGPNQCVICLRVLSCPRALRLHYGQHGGERP	(Hahne et al. 2012)
Sal-like protein 4	24212387	Q9UJQ4.1	1053	S1014	TNEISVIQSGGVPTLPVSLGATSVVNNATVSKMDGSQSGISADVEKPSATDGVPKHQFPHF	(Hahne et al. 2012)
SAP30-binding protein	110282994	Q02614.2	308	T233	AQKIEMDKLEKAKKERTKIEFVTGTKKGTTTNATATSTSTASTAVADAQKRKSKWDSAIPV	(Alfaro et al. 2012)(Trinidad et al., 2012)
SAP30-binding protein	110282994	Q02614.2	308	S239	DKLEKAKKERTKIEFVTGTKKGTTTNATATSTSTASTAVADAQKRKSKWDSAIPVTTIAQP	(Alfaro et al. 2012)
SAP30-binding protein	110282994	Q02614.2	308	T232	KAQKIEMDKLEKAKKERTKIEFVTGTKKGTTTNATATSTSTASTAVADAQKRKSKWDSAIP	(Alfaro et al. 2012)
Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	66774021	Q8R429.1	994	S210	LTGESVSVIKHTDPVPDPRAVNQDKKNMLFSGTNIAAGKAVGIVATTGVSTEIGKIRDQMA	(Trinidad et al., 2012)
Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	12643614	O55143.2	1044	S210	LTGESVSVIKHTDPVPDPRAVNQDKKNMLFSGTNIAAGKAMGVVVATGVNTEIGKIRDEMV	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
SCY1-like protein 2	81914354	Q8CFE4.1	930	S741	APIKQTKDLTDTLMENMSSLTSLSVSTPKISASSTFTPVPSTGLGMMFSTPIDNTKRNLTN	(Alfaro et al. 2012)(Trinidad et al., 2012)
Secretory carrier-associated membrane protein 1	47117239	Q8K021.1	338	T59	NVPPGLDEYNPFSDSRTPPPGSVKMPNVPNTQPAIMKPTEEHPAYTQITKEHALAQAELLK	(Alfaro et al. 2012)
Segment polarity protein dishevelled homolog DVL-1	341940468	P51141.2	695	S383	DPVRPIDPAAWLSHTAALTGALPRYGTSPCSSAITRTSSSSLTSSVPGAPQLEEAPLTVKS	(Alfaro et al. 2012)
Semaphorin-6D	81894127	Q76KF0.1	1073	S1018	LLSRQPSMNRGGYMPTPTGAKVDYIQGTPVSVHLQPSLSRQSSYTSNGTLPRTGLKRTPSL	(Trinidad et al., 2012)
Septin-9	56749655	Q80UG5.1	583	T151	STASAAGPSRFGLKRAEVLGHKTPEPVPRRTEITIVKPQESVLRRVETPASKIPEGSAVPA	(Trinidad et al., 2012)
serine/arginine repetitive matrix protein 2	118572613	NP_057417.3	2752	S2236	ARMSQVPAPVPLMSLRTAPAANLASRIPAASAAAMNLASARTPAIPTAVNLADSRTPAAAA	(Wang et al. 2010)
Serine/threonine-protein kinase DCLK1	20137987	Q9JLM8.1	756	T156	GESYVCGSIEPFKKLEYTKNVNPNWSVNVKTTSASRAVSSLATAKGGPSEVRENKDFIRPK	(Trinidad et al., 2012)
Serine/threonine-protein kinase LMTK3	81910384	Q5XJV6.1	1424	S1280	EDEDEDEEDEEAAGSRDPGRTREAPVPVVVSSADGDTVRPLRGLLKSPRAADEPEDSELER	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Serine/threonine-protein kinase LMTK3	81910384	Q5XJV6.1	1424	S535	APHTNPSNPFYEALSTPSVLPVISARSPSVSSEYYIRLEEHGSPPEPLFPNDWDPLDPGVP	(Trinidad et al., 2012)
Serine/threonine-protein kinase MARK1	341940936	Q8VHJ5.2	795	S531	RRNTYVCERSTDRYAALQNGRDSSLTEMSASSMSSAGSTVASAGPSARPRHQKSMSTSGHP	(Trinidad et al., 2012)
Serine/threonine-protein kinase MARK2	124056495	Q05512.3	776	T684	ETLRPHVVGSGGTDKDKEEFREAKPRSLRFTWSMKTTSSMEPNEMMREIRKVLDANSCQSE	(Trinidad et al., 2012)
Serine/threonine-protein kinase MRCK alpha	134034172	Q3UU96.2	1719	S1596	HIAHMGPGDGIQILKDLPMNPRPQESRTVFSGSVSIPSITKSRPEPGRSMSASSGLSARSS	(Trinidad et al., 2012)
Serine/threonine-protein kinase ULK2	78099276	Q9QY01.1	1037	T613	PRNSDWFFKTPLPTIIGSPTKTTAPFKIPKTQASSNLLALVTRHGPAESQSKDGNDPRECS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Serine/threonine-protein kinase ULK2	78099276	Q9QY01.1	1037	T727	RPMDVAPAGACGVMLALPAGTAASARAVLFTVGSPPHSATAPTCTHMVLRTRTTSVGSSSS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Serine/threonine-protein kinase WNK1	296453029	Q9H4A3.2	2382	S1849	SMAAPTAITEAGTQPQKGVSQVKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSED	(Zhao et al. 2011)
Serine/threonine-protein kinase WNK1	313104051	P83741.2	2377	S2301	YEGPGMARKFSAPGQLCVPMTSNLGGSTPISAASATSLGHFTKSMCPPQQYGFPPAPFGTQ	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Serine/threonine-protein kinase WNK1	313104051	P83741.2	2377	S1230	GLESLQGKDDYGFPGSQKLEGEFKQPIAVSSMPQQIGVPTSSLTQVVHSAGRRFIVSPVPE	(Alfaro et al. 2012)
Serine/threonine-protein kinase WNK1	313104051	P83741.2	2377	S1844	GPLSTMSSTTVTEAGTRLQKDGTEGHVTATSSGAGVVKMGRFQVSVTMDDAQKERKNRSED	(Alfaro et al. 2012)
Serine/threonine-protein kinase WNK1	313104051	P83741.2	2377	T2376	FQPVGTASLQNFNISNLQKSISNPPGSNLRTTBBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Alfaro et al. 2012)
Serine/threonine-protein kinase WNK1	313104051	P83741.2	2377	S1845	PLSTMSSTTVTEAGTRLQKDGTEGHVTATSSGAGVVKMGRFQVSVTMDDAQKERKNRSEDT	(Trinidad et al., 2012)
Serine/threonine-protein kinase WNK1	313104051	P83741.2	2377	T1841	PAVGPLSTMSSTTVTEAGTRLQKDGTEGHVTATSSGAGVVKMGRFQVSVTMDDAQKERKNR	(Trinidad et al., 2012)
Serine/threonine-protein kinase WNK1	313104051	P83741.2	2377	T1860	RLQKDGTEGHVTATSSGAGVVKMGRFQVSVTMDDAQKERKNRSEDTKSVHFESSTSESSVL	(Trinidad et al., 2012)
Serine/threonine-protein kinase WNK1	313104051	P83741.2	2377	T1945	DVPDSTHKAPTPEAKSDAGQPTKVGRFQVTTTANKVGRFSVSRTEDKVTELKKEGPVTSPP	(Trinidad et al., 2012)
Serine/threonine-protein kinase WNK2	126253823	Q3UH66.2	2149	T1698	ARDSGSPHKRPGQQDNSSPAKTVGRFSVVSTQDEWTLASPHSLRYSAPPDVYLDEIPSSPE	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Serine/threonine-protein kinase WNK3	126253824	Q80XP9.2	1789	S1193	AISHCGIQDSPAQSPNFQQTGSKILSNVAASQPAHISVFKKDLNVITSVPSELCLHEMSPD	(Trinidad et al., 2012)
Serine/threonine-protein phosphatase 6 regulatory ankyrin repeat subunit A	81908906	Q505D1.1	1053	T1009	ILATMMPVSSSSPLTSLTFNAINRYTNTSKTVSFEALPIMRNEASSYCSFNNIGGEQEYLY	(Trinidad et al., 2012)
Serum response factor	134876	P11831.1	508	S313	PSTSTTMQVSSGPSFPITNYLAPVSASVSPSAVSSANGTVLKSTGSGPVSSGGLMQLPTSF	(Chalkley et al. 2003)
SH3 and multiple ankyrin repeat domains protein 1	220019845	Q9WV48.1	2167	S1875	PWEEGPGPPPPPLPGPLSQPQASALATVKASIISELSSKLQQFGGSSTAGGALPWARGGSG	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 1	220019845	Q9WV48.1	2167	S2013	SASTRHLQGVEFEMRPPLLRRAPSPSLLPASDHKVSPAPRPSSLPILPSGPIYPGLFDIRS	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 1	342179357	D3YZU1.1	2167	S1067	GGSPDDPPPRLALGPQPSLRGWRGGGPSPTSGAPSPSHHSSSGGSSGPAQAPALRYFQLPP	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 1	342179357	D3YZU1.1	2167	S1137	PARSGRGRKGPLVKQTKVEGEPQKGSLPPASSPTSPALPRSEPPPAGPSEKNSIPIPTIII	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 1	342179357	D3YZU1.1	2167	S1891	LSQPQASALATVKASIISELSSKLQQFGGASTAGGALPWARGGSGGSTDSHHGGASYIPER	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
SH3 and multiple ankyrin repeat domains protein 1	22001985	Q9WV48.1	2167	S1891	LSQPQASALATVKASIISELSSKLQQFGGSSTAGGALPWARGGSGGSTDSHHGGASYIPER	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 1	22001985	Q9WV48.1	2167	S935	DRPYLAPPAMKFSRSLSVPGSEDIPPPPTTSPPEPPYSTPPAPSSSGRLTPSPRGGPFNPS	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 1	22001985	Q9WV48.1	2167	T1892	SQPQASALATVKASIISELSSKLQQFGGSSTAGGALPWARGGSGGSTDSHHGGASYIPERT	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 1	22001985	Q9WV48.1	2167	T1922	TAGGALPWARGGSGGSTDSHHGGASYIPERTSSLQRQRLSEDSQTSLLSKPSSSIFQNWPK	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	S404	TAELEELGLSLVDKASVRKKKDKPEEIVPASKPSRTAENVAIESRVATIKQRPTSRCFPAA	(Alfaro et al. 2012)(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	T1292	GKSVKPGEGLELPVGAKSANLAPRSPEVMSTVSGTRSTTVTFTVRPGTSQPITLQSRPPDY	(Alfaro et al. 2012)(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	T980	GPPLEEEEDREDGDTKPDHSPSTVPEGVPKTEGALQISAAPEPAVAPGRTIVAAGSVEEAV	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	T562	NCPRSPTPRVYGTIKPAFNQNPVVAKVPPATRSDTVATMMREKGMFYRRELDRFSLDSEDV	(Alfaro et al. 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	S1291	RGKSVKPGEGLELPVGAKSANLAPRSPEVMSTVSGTRSTTVTFTVRPGTSQPITLQSRPPD	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	T1302	ELPVGAKSANLAPRSPEVMSTVSGTRSTTVTFTVRPGTSQPITLQSRPPDYESRTSGPRRA	(Alfaro et al. 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	T485	GSPKGPFLGLPRGTMRRQKSIDSRIFLSGITEEERQFLAPPMLKFTRSLSMPDTSEDIPPP	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	T890	KGEAPKADLNKPLYIDTKMRPSVESGFPPVTRQNTRGPLRRQETENKYETDLGKDRRADDK	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	S1294	SVKPGEGLELPVGAKSANLAPRSPEVMSTVSGTRSTTVTFTVRPGTSQPITLQSRPPDYES	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	T1296	KPGEGLELPVGAKSANLAPRSPEVMSTVSGTRSTTVTFTVRPGTSQPITLQSRPPDYESRT	(Trinidad et al., 2012)
SH3 and multiple ankyrin repeat domains protein 2	341942027	Q80Z38.2	1476	T409	ELGLSLVDKASVRKKKDKPEEIVPASKPSRTAENVAIESRVATIKQRPTSRCFPAASDVNS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
SH3 and multiple ankyrin repeat domains protein 3	148841191	Q4ACU6.2	1805	T1136	LSVGAIEGSPPSADLPSLQPSRSIDERLLGTGATTGRDLLLPSPVSALKPLVGGPSLGPSG	(Trinidad et al., 2012)
Sickle tail protein	152061323	A2AQ25.1	1946	S357	PSRIPYGGSRPMAIPGNATIPRDRLSSLPVSRSISPSPSAILERRDVKPDEDMSSKNLVMF	(Trinidad et al., 2012)
Sickle tail protein	152061323	A2AQ25.1	1946	T1348	NADKSHIPLPTRSAEFSIHDVKTQDQDVPVTGYGQVVLRSKVGRHANMNMNEDGESTPSSP	(Trinidad et al., 2012)
Sickle tail protein	152061323	A2AQ25.1	1946	S1896	FQSPPHAGKGHHHLSFALQTQNGRAAPTTSSSSSPPSPASPTSLNQGARGIRTIHTPSLAS	(Trinidad et al., 2012)
Sickle tail protein	152061323	A2AQ25.1	1946	S1897	QSPPHAGKGHHHLSFALQTQNGRAAPTTSSSSSPPSPASPTSLNQGARGIRTIHTPSLASY	(Trinidad et al., 2012)
Sickle tail protein	152061323	A2AQ25.1	1946	T1070	QELDKIGGKSPPPPPPPPRRSYLPGSGLTTTRSGDVVYTGRSMSKVSSEDPGPTPQTRATK	(Trinidad et al., 2012)
Sickle tail protein	152061323	A2AQ25.1	1946	T1894	LKFQSPPHAGKGHHHLSFALQTQNGRAAPTTSSSSSPPSPASPTSLNQGARGIRTIHTPSL	(Trinidad et al., 2012)
Sickle tail-b	81894085	Q75UV8	1341	S357	PSRIPYGGSRPMAIPGNATIPRDRLSSLPVSRSISPSPSAILERRDVKPDEDMSSKNLVMF	(Vosseller et al. 2006)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Signal transducer and activator of transcription 3	48429227	P40763.2	770	T721	SQEHPEADPGSAAPYLKTKFICVTPTTCSNTIDLPMSPRTLDSLMQFGNNGEGAEPSAGGQ	(Hahne et al. 2012)
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	S1403	LDIHSKSQGGSSPLSRENSTFSINDAASHTSTMSSRHSASPVVFSSARSSPKEELHPTASS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	S1400	SLSLDIHSKSQGGSSPLSRENSTFSINDAASHTSTMSSRHSASPVVFSSARSSPKEELHPT	(Trinidad et al., 2012)
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	S1579	FPTTPTSRRALHRTLSDESIYSSQREHFFTSRASLLDQALPNDVLFSSTYPSLPKSLPLRR	(Trinidad et al., 2012)
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	S59	VHTDDFYMRRFRSQNGSLGSSVMAAVGPPRSEGPHHITSTPGVPKMGVRARIADWPPRKEN	(Trinidad et al., 2012)
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	T1402	SLDIHSKSQGGSSPLSRENSTFSINDAASHTSTMSSRHSASPVVFSSARSSPKEELHPTAS	(Alfaro et al. 2012)
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	S1114	QLQSPMTSRLNAGKGDGKMPPPERAANIPRSISSDGRPLERRLSPGSDIYVTVSSMALARS	(Trinidad et al., 2012)
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	S1387	ETEGHGMDRKAESSLSLDIHSKSQGGSSPLSRENSTFSINDAASHTSTMSSRHSASPVVFS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	S1440	SASPVVFSSARSSPKEELHPTASSQLAPSFSSSSSSSSGPRTFYPRQGATSKYLIGWKKPE	(Trinidad et al., 2012)
Signal-induced proliferation-associated 1-like protein 1	50401562	Q8C0T5.2	1782	T1404	DIHSKSQGGSSPLSRENSTFSINDAASHTSTMSSRHSASPVVFSSARSSPKEELHPTASSQ	(Trinidad et al., 2012)
Signal-induced proliferation-associated 1-like protein 2	341942122	Q80TE4.3	1722	S1079	DSEGTPCEYKTPFRRNTTWHRVPTPALQPVSRASPVPGTPDRLQCQPLLQQAQAAIPRSTS	(Trinidad et al., 2012)
Ski oncogene	68067481	Q60698.2	725	S384	RTLAGSSNKSLGCTHPRQRLSAFRPWSPAVSASEKETSPHLPALIRDSFYSYKSFETAVAP	(Trinidad et al., 2012)
SLAIN motif-containing protein 1	81890765	Q68FF7.1	579	T411	PQAQTADQQPNRTNGDKLRRSMPNLARMPSTAAASSNLSSPVTVRSSQSFDSSLHGAGSGV	(Trinidad et al., 2012)
SLIT-ROBO Rho GTPase-activating protein 1	122066214	Q91Z69.2	1062	S982	ELERQSTVKHAPDVVLDTLEQVKNSPTPATSTESLSPLHNVALRGSEPQIRRSTSSSSETM	(Alfaro et al. 2012)(Trinidad et al., 2012)
SLIT-ROBO Rho GTPase-activating protein 2	122065186	Q91Z67.2	1071	S990	LERQSSAKHTPDVVLDTLEPLKTSPVVAPTSEPSSPLHTQLLKDPEPAFQRSASTAGDIAC	(Alfaro et al. 2012)
Small conductance calcium-activated potassium channel protein 3	17366341	P58391.1	731	S113	HPLPQLAQLQSQLVHPGLLHSSPTAFRAPTSANSTAILHPSSRQGSQLNLNDHLLGHSPSS	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Sodium- and chloride-dependent glycine transporter 2	52783378	Q761V0.1	799	S56	DSPRAPRTSPEQDLPAEAPAATVQPPRVPRSASTGAQTFQSADARACEAQQSGVGFCNLSS	(Trinidad et al., 2012)
Sodium/potassium-transporting ATPase subunit alpha-1	55976751	Q8VDN2.1	1023	T617	GLISMIDPPRAAVPDAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAAR	(Trinidad et al., 2012)
Sodium/potassium-transporting ATPase subunit alpha-2	66773992	Q6PIE5.1	1020	S650	TAKAIAKGVGIISEGNETVEDIAARLNIPVSQVNPREAKACVVHGSDLKDMTSEQLDEILR	(Trinidad et al., 2012)
Sodium/potassium-transporting ATPase subunit alpha-2	66773992	Q6PIE5.1	1020	T614	GLMSMIDPPRAAVPDAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAAR	(Trinidad et al., 2012)
Sodium/potassium-transporting ATPase subunit alpha-2	66773992	Q6PIE5.1	1020	S559	KEMQDAFQNAYMELGGLGERVLGFCQLNLPSGKFPRGFKFDTDELNFPTEKLCFVGLMSMI	(Trinidad et al., 2012)
Sodium/potassium-transporting ATPase subunit alpha-3	52000687	Q6PIC6.1	1013	S643	TAKAIAKGVGIISEGNETVEDIAARLNIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQ	(Trinidad et al., 2012)
Sodium/potassium-transporting ATPase subunit alpha-3	52000687	Q6PIC6.1	1013	T607	GLMSMIDPPRAAVPDAVGKCRSAGIKVIMVTGDHPITAKAIAKGVGIISEGNETVEDIAAR	(Trinidad et al., 2012)
Sodium-coupled neutral amino acid transporter 3	52783422	Q9DCP2.1	505	T30	BMEIPRQTEMVELVPNGKHLEGLLPVGVPTTDTQRTEDTQHCGEGKGFLQKSPSKEPHFTD	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Solute carrier family 2, facilitated glucose transporter member 1	115502394	P11166.2	492	S465	IIFTVLLVLFFIFTYFKVPETKGRTFDEIASGFRQGGASQSDKTPEELFHPLGADSQVBBB	(Wang et al. 2009)
Sorbin and SH3 domain-containing protein 1	51701938	Q62417.2	1290	S1199	SRQGIFPITYVDVLKRPLVKTPVDYIDLPYSSSPSRSATVSPQQPQAQQRRVTPDRSQPSL	(Alfaro et al. 2012)(Trinidad et al., 2012)
Sorbin and SH3 domain-containing protein 1	51701938	Q62417.2	1290	S1200	RQGIFPITYVDVLKRPLVKTPVDYIDLPYSSSPSRSATVSPQQPQAQQRRVTPDRSQPSLD	(Trinidad et al., 2012)
Sorbin and SH3 domain-containing protein 2	205831244	Q3UTJ2.2	1180	S921	ASFPDVDTTSNYHAQDYGSALSLQDHESPRSYSSTLTDLGRSASRERRGTPEKEKLPAKAV	(Trinidad et al., 2012)
Sorbin and SH3 domain-containing protein 2	205831244	Q3UTJ2.2	1180	S368	KSEPAVGPLRGLGDQSSSRTSPGRADLPGSSSTFTKSFISSSPSSPSRAQGGDDSKMCPPL	(Trinidad et al., 2012)
Sorbin and SH3 domain-containing protein 2	205831244	Q3UTJ2.2	1180	S932	YHAQDYGSALSLQDHESPRSYSSTLTDLGRSASRERRGTPEKEKLPAKAVYDFKAQTSKEL	(Trinidad et al., 2012)
Sorbin and SH3 domain-containing protein 2	205831244	Q3UTJ2.2	1180	S934	AQDYGSALSLQDHESPRSYSSTLTDLGRSASRERRGTPEKEKLPAKAVYDFKAQTSKELSF	(Trinidad et al., 2012)
Sortilin-related receptor	341942117	O88307.3	2215	S1888	AVECIWTGPKNVVYGIFYATSFLDLYRNPKSVTTSLHNKTVIVSKDEQYLFLVRVLIPYQG	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Sortilin-related receptor	341942117	O88307.3	2215	T1890	ECIWTGPKNVVYGIFYATSFLDLYRNPKSVTTSLHNKTVIVSKDEQYLFLVRVLIPYQGPS	(Trinidad et al., 2012)
Spartin	50401611	Q8R1X6.1	671	T478	FTGKAIQKGASKLRERIQPEEKPVEVSPAVTRGLYIAKQATGGAAKVSQLLVDGVCTVANC	(Alfaro et al. 2012)(Trinidad et al., 2012)
Spectrin alpha chain, brain	122066202	P16546.4	2472	S324	LRKHEGLERDLAALEDKVKALCAEADRLQQSHPLSASQIQVKREELITNWEQIRTLAAERH	(Trinidad et al., 2012)
Spectrin alpha chain, brain	122066202	P16546.4	2472	T2425	MISRETENVKSSEEIESAFRALSSEGKPYVTKEELYQNLTREQADYCVSHMKPYVDGKGRE	(Trinidad et al., 2012)
Spectrin alpha chain, erythrocyte	308153675	P02549.5	2419	S1250	ALQRRHEGFERDLVPLGDKVTILGETAERLSESHPDATEDLQRQKMELNEAWEDLQGRTKD	(Wang et al. 2009)
Spectrin alpha chain, erythrocyte	308153675	P02549.5	2419	S1738	KLKEAYALFQFFQDLDDEESWIEEKLIRVSSQDYGRDLQGVQNLLKKHKRLEGELVAHEPA	(Wang et al. 2009)
Spectrin alpha chain, erythrocyte	308153675	P02549.5	2419	S844	PSATSTYLGKDLIASKKLLNRHRVILENIASHEPRIQEITERGNKMVEEGHFAAEDVASRV	(Wang et al. 2009)
spectrin beta 2, isoform CRA_a	149044856	EDL98042.1	2363	S2323	EMNTWIQAITSAISSDKHDTSASTQSTPASSRAQTLPTSVVTITSESSPGKREKDKEKDKE	(Wang et al. 2010)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Spectrin beta chain, brain 1	97537229	Q62261.2	2363	S2323	EMNTWIQAISSAISSDKHDTSASTQSTPASSRAQTLPTSVVTITSESSPGKREKDKEKDKE	(Vosseller et al. 2006)(Trinidad et al. 2012
Spectrin beta chain, brain 1	116242799	Q01082.2	2364	S2324	EMNTWIQAISSAISSDKHEVSASTQSTPASSRAQTLPTSVVTITSESSPGKREKDKEKDKE	(Hahne et al. 2012)(Hahne et al. 2012)
Spectrin beta chain, brain 1	97537229	Q62261.2	2363	S2337	SDKHDTSASTQSTPASSRAQTLPTSVVTITSESSPGKREKDKEKDKEKRFSLFGKKKBBBB	(Trinidad et al., 2012)
spectrin beta chain, brain 1 isoform 1	112382250	NP_003119.2	2364	S2324	EMNTWIQAISSAISSDKHEVSASTQSTPASSRAQTLPTSVVTITSESSPGKREKDKEKDKE	(Wang et al. 2010)
Spectrin beta chain, erythrocyte	215274269	P11277.5	2137	S1297	SVLLRDNLELQNFLQNCQELTLWINDKLLTSQDVSYDEARNLHNKWLKHQAFVAELASHEG	(Wang et al. 2009)
Spectrin beta chain, erythrocyte	215274269	P11277.5	2137	S1652	MLKRHLRQQRAVEDYGRNIKQLASRAQGLLSAGHPEGEQIIRLQGQVDKHYAGLKDVAEER	(Wang et al. 2009)
Spectrin beta chain, erythrocyte	215274269	P11277.5	2137	S1936	FRFFSMARDLLSWMESIIRQIETQERPRDVSSVELLMKYHQGINAEIETRSKNFSACLELG	(Wang et al. 2009)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Spectrin beta chain, erythrocyte	215274269	P11277.5	2137	S767	KNLQDAENFFQFQGDADDLKAWLQDAHRLLSGEDVGQDEGATRALGKKHKDFLEELEESRG	(Wang et al. 2009)
Spectrin beta chain, erythrocyte	215274269	P11277.5	2137	S671	KFFWEMDEAESWIKEKEQIYSSLDYGKDLTSVLILQRKHKAFEDELRGLDAHLEQIFQEAH	(Wang et al. 2009)
Splicing factor 1	341942283	Q64213.6	653	S328	GDPQSAQDKARMDKEYLSLMAELGEAPVPASVGSTSGPATTPLASAPRPAAPASNPPPPSL	(Alfaro et al. 2012)
Sprouty-related, EVH1 domain-containing protein 1	57013092	Q924S8.1	444	S166	GGDDDLQTTEEDTSRSLVKDHFFQQETVVTSEPYRSSDIRPLPFEDLNARRVYLQSQVSQI	(Trinidad et al., 2012)
SRC kinase signaling inhibitor 1	42559891	Q9QWI6.2	1250	S548	RCTRRALAALYGDGYGFRLPPSSPQKLADVSAPSGGPPPPHSPYSGPPSRGSPVRQSFRKD	(Alfaro et al. 2012)
Src substrate cortactin	341942067	Q60598.2	546	S345	DRMDKNASTFEEVVQVPSAYQKTVPIEAVTSKTSNIRANFENLAKEREQEDRRKAEAERAQ	(Trinidad et al., 2012)
STE20-like serine/threonine-protein kinase	94730572	O54988.2	1233	S1230	VFFKMTGESECLNPSAQSRISKFYPIPTLHSTGSBBBBBBBBBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Storkhead-box protein 2	166223488	Q499E5.2	926	T863	SSNQRATHSARLDSMDSSSITVDSGFNSPRTRESLASNTSSIVESNRRQNPALSPAHGGAG	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Stromal membrane-associated protein 2	81894445	Q7TN29.1	428	S180	EKKMEPVVFEKVKMPQKKEDAQLPRKSSPKSAAPVMDLLGLDAPVACSIANSKTSNALEKD	(Trinidad et al., 2012)
Stromal membrane-associated protein 2	81894445	Q7TN29.1	428	S197	KEDAQLPRKSSPKSAAPVMDLLGLDAPVACSIANSKTSNALEKDLDLLASVPSPSSVSRKA	(Trinidad et al., 2012)
Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial	52788305	Q9Z2I9.2	463	T253	AQKMGFPSNIVDSAAENMIKLYNLFLKYDATMVEINPMVEDSDGKVLCMDAKINFDSNSAY	(Trinidad et al., 2012)
Synapsin-1	73920802	O88935.2	706	T526	LGPPAGSPLPQRLPSPTAAPQQSASQATPVTQGQGRQSRPVAGGPGAPPAARPPASPSPQR	(Vosseller et al. 2006)(Alfaro et al. 2012)(Trinidad et al., 2012)
Synapsin-1	73920802	O88935.2	706	T87	AAPVASPAAPSPGSSGGGGFFSSLSNAVKQTTAAAAATFSEQVGGGSGGAGRGGAAARVLL	(Vosseller et al. 2006)(Alfaro et al. 2012)(Trinidad et al., 2012)
Synapsin-1	73920802	O88935.2	706	T575	AARPPASPSPQRQAGAPQATRQASISGPAPTKASGAPPGGQQRQGPPQKPPGPAGPTRQAS	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Synapsin-1	73920802	O88935.2	706	T650	QPRPSGPGPAGRPAKPQLAQKPSQDVPPPITAAAGGPPHPQLNKSQSLTNAFNLPEPAPPR	(Alfaro et al. 2012)
Synapsin-1	73920802	O88935.2	706	S432	DKQLIVELVVNKMTQALPRQPQRDASPGRGSHSQSSSPGALTLGRQTSQQPAGPPAQQRPP	(Trinidad et al., 2012)
Synapsin-1	73920802	O88935.2	706	S520	QQHLSGLGPPAGSPLPQRLPSPTAAPQQSASQATPVTQGQGRQSRPVAGGPGAPPAARPPA	(Alfaro et al. 2012)
Synapsin-1	73920802	O88935.2	706	S55	LQRPQPPPPPPSAASPGATPGSATASAERASTAAPVASPAAPSPGSSGGGGFFSSLSNAVK	(Alfaro et al. 2012)
Synapsin-1	73920802	O88935.2	706	T523	LSGLGPPAGSPLPQRLPSPTAAPQQSASQATPVTQGQGRQSRPVAGGPGAPPAARPPASPS	(Alfaro et al. 2012)
Synapsin-1	73920802	O88935.2	706	T618	QGPPQKPPGPAGPTRQASQAGPGPRTGPPTTQQPRPSGPGPAGRPAKPQLAQKPSQDVPPP	(Alfaro et al. 2012)
Synapsin-1	73920802	O88935.2	706	S518	QGQQHLSGLGPPAGSPLPQRLPSPTAAPQQSASQATPVTQGQGRQSRPVAGGPGAPPAARP	(Trinidad et al., 2012)
Synapsin-1	73920802	O88935.2	706	T262	MVRLHKKLGTEEFPLIDQTFYPNHKEMLSSTTYPVVVKMGHAHSGMGKVKVDNQHDFQDIA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Synapsin-1	73920802	O88935.2	706	T263	VRLHKKLGTEEFPLIDQTFYPNHKEMLSSTTYPVVVKMGHAHSGMGKVKVDNQHDFQDIAS	(Trinidad et al., 2012)
synapsin-1 isoform a	9507159	NP_062006.1	704	T524	LGPPAGSPLPQRLPSPTAAPQQSASQATPMTQGQGRQSRPVAGGPGAPPAARPPASPSPQR	(Cole et al. 1999)
synapsin-1 isoform a	9507159	NP_062006.1	704	T562	RPVAGGPGAPPAARPPASPSPQRQAGPPQATRQASISGPAPPKVSGASPGGQQRQGPPQKP	(Cole et al. 1999)
synapsin-1 isoform a	9507159	NP_062006.1	704	T576	PPASPSPQRQAGPPQATRQASISGPAPPKVSGASPGGQQRQGPPQKPPGPAGPIRQASQAG	(Cole et al. 1999)
synapsin-1 isoform a	9507159	NP_062006.1	704	T87	AAPVASPAAPSPGSSGGGGFFSSLSNAVKQTTAAAAATFSEQVGGGSGGAGRGGAAARVLL	(Cole et al. 1999)
Synapsin-2	73920803	Q64332.2	586	T95	APAPQPAPQPAPTPSVGSSFFSSLSQAVKQTAASAGLVDAPAPSAASRKAKVLLVVDEPHT	(Trinidad et al., 2012)
Synaptojanin-1	41018346	Q8CHC4.3	1574	S376	KLHSILKPQVQKFLDYGFFYFDGSEVQRCQSGTVRTNCLDCLDRTNSVQAFLGLEMLAKQL	(Trinidad et al., 2012)
Synaptojanin-1	41018346	Q8CHC4.3	1574	T378	HSILKPQVQKFLDYGFFYFDGSEVQRCQSGTVRTNCLDCLDRTNSVQAFLGLEMLAKQLEA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Synaptojanin-1	41018346	Q8CHC4.3	1574	S1341	VKINGISGVKQEPTLKSDPFEDLSLSVLAVSKAQPSVQISPVLTPDPKMLIQLPSASQSQV	(Trinidad et al., 2012)
Synaptopodin	48428644	Q8CC35.2	929	S397	TLCADDGQSPVPAEEVRSSILLIDKVSAPPSAASTFSREATPLSSSGPPAADLMSSSLLID	(Alfaro et al. 2012)(Trinidad et al., 2012)
Synaptopodin	48428644	Q8CC35.2	929	S403	GQSPVPAEEVRSSILLIDKVSAPPSAASTFSREATPLSSSGPPAADLMSSSLLIDMQPSTL	(Vosseller et al. 2006)
Synaptopodin	48428644	Q8CC35.2	929	S507	IQSPGTSQIEQSPMMGRRQFGEKAWAPPASSMADRSPQPQRHIMSRSPMVERRLLGQRSPV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Synaptopodin	48428644	Q8CC35.2	929	T551	SRSPMVERRLLGQRSPVLERRPLGNFTPPPTYAETLSTAPVASRVRSPPSYSTLYPSSDPK	(Alfaro et al. 2012)(Trinidad et al., 2012)
Synaptopodin	48428644	Q8CC35.2	929	T752	MEKYVIESSGHAELARCPSPTMSLPSSWKYTTNAPGGFRVASLSPARTPPASLYHGYLPEN	(Alfaro et al. 2012)(Trinidad et al., 2012)
Synaptopodin	48428644	Q8CC35.2	929	S393	SKPGTLCADDGQSPVPAEEVRSSILLIDKVSAPPSAASTFSREATPLSSSGPPAADLMSSS	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Synaptopodin	48428644	Q8CC35.2	929	T753	EKYVIESSGHAELARCPSPTMSLPSSWKYTTNAPGGFRVASLSPARTPPASLYHGYLPENG	(Trinidad et al., 2012)
Synergin gamma	62287604	Q5SV85.1	1306	S628	TQTQVKTPLNLEDLDMFSSVDCSGEKQVPFSATFSTAKSVSTRPQPAGSAAASAALASTKT	(Trinidad et al., 2012)
Synergin gamma	62287604	Q5SV85.1	1306	S646	SVDCSGEKQVPFSATFSTAKSVSTRPQPAGSAAASAALASTKTSSLADDFGEFNLFGEYSN	(Trinidad et al., 2012)
Syntaxin-binding protein 1	48429206	O08599.2	594	T512	IKDIMEDTIEDKLDTKHYPYISTRSSASFSTTAVSARYGHWHKNKAPGEYRSGPRLIIFIL	(Trinidad et al., 2012)
synuclein, alpha, isoform CRA_b	149037058	EDL91619.1	149	S72	SKTKEGVVHGVTTVAEKTKEQVTNVGGAVVTGVTAVAQKTVEGAGNIAAATGFVKKDQMGK	(Wang et al. 2010)
TAK1 binding protein	1401126	AAC12660.1	504	S395	FGYPLGEMSQPTPSPAPAAGGRVYPVSVPYSSAQSTSKTSVTLSLVMPSQGQMVNGAHSAS	(Pathak et al. 2012)
Target of Myb protein 1	25091403	O88746.1	492	T392	LEDDFDMFALTRGSSLADQRKGVKYEAPQTTDGLAGALDARQQSTGAIPATQARIMEDIEQ	(Trinidad et al., 2012)
TBC1 domain family member 10B	294862484	Q8BHL3.2	798	T162	PGPGTPTRTPSRMAPGALTAKPPLAPKPGTTVASGVTARGGVGQVAGGHEAATSASAGSVP	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
TBC1 domain family member 10B	294862484	Q8BHL3.2	798	T43	RRHGAPAAPSPPPRGSRAGSHLVVEPGPPVTTATSAPVELVAPGEARPACVPGSSQTSAST	(Alfaro et al. 2012)
TBC1 domain family member 9B	81862530	Q5SVR0.1	1263	S871	NRSAAVHRDPSLPYLEQYRIDASQFRELFASLTPWACGSHTPVLAGRMFRLLDQNKDSLIN	(Trinidad et al., 2012)
TBC1 domain family member 9B	81862530	Q5SVR0.1	1263	T873	SAAVHRDPSLPYLEQYRIDASQFRELFASLTPWACGSHTPVLAGRMFRLLDQNKDSLINFK	(Trinidad et al., 2012)
T-box brain protein 1	342187021	Q64336.2	681	S647	PSSIKSIDSSDSGIYEQAKRRRISPADTPVSESSSPLKSEVLAQRDCEKNCAKDIGGYYGF	(Alfaro et al. 2012)
T-box brain protein 1	342187021	Q64336.2	681	T397	IAVTAYQNTDITQLKIDHNPFAKGFRDNYDTIYTGCDMDRLTPSPNDSPRSQIVPGARYAM	(Trinidad et al., 2012)
T-cell surface glycoprotein CD3 epsilon chain	1345708	P07766.2	207	S55	NEEMGGITQTPYKVSISGTTVILTCPQYPGSEILWQHNDKNIGGDEDDKNIGSDEDHLSLK	(Hahne et al. 2012)
Teneurin-1	81869786	Q9WTS4.1	2731	T685	ETPLPICQEQCSGHGTFLLDTGVCSCDPKWTGSDCSTELCTMECGSHGVCSRGICQCEEGW	(Alfaro et al. 2012)
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	78099176	Q8CF89.2	502	S393	RNFGYPLGEMSQPTPTPAPGGRVYPVSVPYSSAQSTSKTSVTLSLVMPSQGQMVNGSHSAS	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	10720303	Q15750.1	504	S391	LVRNFGYPLGEMSQPTPSPAPAAGGRVYPVSVPYSSAQSTSKTSVTLSLVMPSQGQMVNGA	(Hahne et al. 2012)
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	10720303	Q15750.1	504	S401	EMSQPTPSPAPAAGGRVYPVSVPYSSAQSTSKTSVTLSLVMPSQGQMVNGAHSASTLDEAT	(Hahne et al. 2012)
TGF-beta-activated kinase 1 and MAP3K7-binding protein 1	78099176	Q8CF89.2	502	S394	NFGYPLGEMSQPTPTPAPGGRVYPVSVPYSSAQSTSKTSVTLSLVMPSQGQMVNGSHSAST	(Trinidad et al., 2012)
TGF-beta-activated kinase 1 and MAP3K7-binding protein 3	90108451	Q571K4.2	716	T385	LPYTASSLPKGSMKKIEITVEPSQRPGTAITRSPSPISNQPSPRNQHSLYTATTPPSSSPS	(Alfaro et al. 2012)(Trinidad et al., 2012)
TGF-beta-activated kinase 1 and MAP3K7-binding protein 3	90108451	Q571K4.2	716	S412	TAITRSPSPISNQPSPRNQHSLYTATTPPSSSPSRGISSQPKPPFSVNPVYITYTQPTGPS	(Alfaro et al. 2012)
Thioredoxin domain-containing protein 12	29839615	Q9CQU0.1	170	S134	SPDGGYIPRILFLDPSGKVRPEIINESGNPSYKYFYVSAEQVVQGMKEAQERLTGDAFREK	(Alfaro et al. 2012)
Thioredoxin domain-containing protein 5	29839560	Q8NBS9.2	432	S308	KGKRDLESLREYVESQLQRTETGATETVTPSEAPVLAAEPEADKGTVLALTENNFDDTIAE	(Hahne et al. 2012)(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Thioredoxin domain-containing protein 5	29839560	Q8NBS9.2	432	T306	QYKGKRDLESLREYVESQLQRTETGATETVTPSEAPVLAAEPEADKGTVLALTENNFDDTI	(Hahne et al. 2012)(Hahne et al. 2012)
Thioredoxin domain-containing protein 5	29839560	Q8NBS9.2	432	S183	GPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPELKQGLYELSASNFELHVAQGDHFIKFF	(Hahne et al. 2012)
Thioredoxin domain-containing protein 5	29839560	Q8NBS9.2	432	T167	PTLKLFKPGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPELKQGLYELSAS	(Hahne et al. 2012)
Thioredoxin domain-containing protein 5	29839560	Q8NBS9.2	432	T174	PGQEAVKYQGPRDFQTLENWMLQTLNEEPVTPEPEVEPPSAPELKQGLYELSASNFELHVA	(Hahne et al. 2012)
TNFAIP3-interacting protein 1	20139295	Q9WUU8.1	647	T103	SPPTSAPSLVSFDDLAELTGQDTKVQVHPATSTAATTTATATTGNSMEKPEPASKSPSNGA	(Trinidad et al., 2012)
TOM1-like protein 2	81910090	Q5SRX1.1	507	T187	DALSPIHTPQRSVPEMDPAATIPRSQTQPRTTAGTYSSPPPASYSTLQAPALSVTGPITAN	(Alfaro et al. 2012)(Trinidad et al., 2012)
TOM1-like protein 2	81910090	Q5SRX1.1	507	T188	ALSPIHTPQRSVPEMDPAATIPRSQTQPRTTAGTYSSPPPASYSTLQAPALSVTGPITANS	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
TOM1-like protein 2	81910090	Q5SRX1.1	507	S194	TPQRSVPEMDPAATIPRSQTQPRTTAGTYSSPPPASYSTLQAPALSVTGPITANSEQIARL	(Trinidad et al., 2012)
Traf2 and NCK-interacting protein kinase	158518420	P83510.2	1323	S539	EERSRLNRQSSPAMPHKVANRISDPNLPPRSESFSISGVQPARTPPMLRPVDPQIPQLVAV	(Alfaro et al. 2012)
Traf2 and NCK-interacting protein kinase	158518420	P83510.2	1323	T577	VQPARTPPMLRPVDPQIPQLVAVKSQGPALTASQSVHEQPTKGLSGFQEALNVTSHRVEMP	(Alfaro et al. 2012)
Trafficking kinesin-binding protein 1	81892481	Q6PD31.1	939	S444	SLTPSPMNIPGSNQSSAMNSLLSSCVSTPRSSFYGSDVSNVVLDNKTNSILLETEAADLGN	(Trinidad et al., 2012)
Trafficking kinesin-binding protein 1	81892481	Q6PD31.1	939	S696	FTFTTCRILHPSDELTRVTPSLNSAPAPACSSTSHLKSTPVATPCTPRRLSLAESFTNVRE	(Trinidad et al., 2012)
Trafficking kinesin-binding protein 1	81892481	Q6PD31.1	939	S924	LGCPSGIRRNRSFPTMVGSSVQMRAPVILTSGILMGAKLPKQTSLRBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Trafficking kinesin-binding protein 2	344243331	EGV99434.1	913	S718	SSGFPSLSSGSSGSSSSNTAVNSPAMSYRLSIGESITNRRDSTITFSSTRSLAKLLQERGI	(Trinidad et al., 2012)
Transcription factor 20	22096212	Q9EPQ8.2	1983	T725	KNGDNNSSNHNGEGNGPSSHSAVGPSFTGRTEPSKSPGSLRYSYKESFGSAVPRNVSGYPQ	(Myers et al. 2011)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Transcription factor E3	122066390	Q64092.2	572	S557	EGMVGGLSGGALSPLRAASDPLLSSVSPAVSKASSRRSSFSMEEESBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
Transcription factor HIVEP2	83308989	Q3UHF7.1	2430	S1271	SSYPLEHVAEHTGKKSADYPHAKEQTYPCYSGTSGLHSKNLPLKFPSDPGSKSTETPTEQL	(Chalkley et al. 2009)(Alfaro et al. 2012)(Trinidad et al., 2012)
Transcription factor HIVEP2	83308989	Q3UHF7.1	2430	S1316	PSDPGSKSTETPTEQLLREDFASENAGPLQSLPGTVVPVRIQTHVPSYGSVMYTSISQILG	(Trinidad et al., 2012)
Transcription factor HIVEP2	83308989	Q3UHF7.1	2430	S163	VASEDLFPFPMHGHSGGYPRKKISNLNPAYSQYSQKSIEQAEDAHKKEHKPKKPGKYICPY	(Trinidad et al., 2012)
Transcription factor HIVEP2	83308989	Q3UHF7.1	2430	T251	PCGFSFKTKSNLYKHRKSHAHAIKAGLVPFTESSVSKLDLEAGFIDVEAEIHSDGEQSTDT	(Trinidad et al., 2012)
Transcription factor HIVEP2	83308989	Q3UHF7.1	2430	S1049	MRRCSSEQMPCPHPTEVPEIRSKSFDYGNLSHAPVAGTSPSTLSPSRERKKCFLVRQASFS	(Trinidad et al., 2012)
Transcription factor HIVEP2	83308989	Q3UHF7.1	2430	S392	SHTVKQKLALRLSEKKGQDSEPSLNLLSPHSKGSTDSGYFSRSESAEQQISPPNTNAKSYE	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Transcription factor HIVEP3	187668011	A2A884.1	2348	T452	TSMLASTSTQPLLPLSSEDKPSLVPLSVPRTQVIEHITKLITINEAVVDTSEIDSVKPRRS	(Trinidad et al., 2012)
transcription factor MafK	4505075	NP_002351.1	156	T134	LDALRSKYEALQTFARTVARGPVAPSKVATTSVITIVKSTELSSTSVPFSAASBBBBBBBB	(Wang et al. 2010)
Transcription factor SOX-1	1711464	P53783.1	391	S332	AAAAASSGALGALGSLVKSEPSGSPPAPAHSRAPCPGDLREMISMYLPAGEGGDPAAAAAA	(Trinidad et al., 2012)
Transcription factor SOX-2	6094324	P48432.2	319	S248	YMNGSPTYSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRAPCQAGDLRDMISM	(Myers et al. 2011)(Trinidad et al., 2012)
Transcription factor SOX-2	1351091	P48431.1	317	S246	YMNGSPTYSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRAPCQAGDLRDMISM	(Hahne et al. 2012)
Transcription factor SOX-2	1351091	P48431.1	317	S249	GSPTYSMSYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRAPCQAGDLRDMISMYLP	(Hahne et al. 2012)
Transcription factor SOX-2	6094324	P48432.2	319	T258	SYSQQGTPGMALGSMGSVVKSEASSSPPVVTSSSHSRAPCQAGDLRDMISMYLPGAEVPEP	(Myers et al. 2011)
Transcription factor SOX-3	48429228	P41225.2	446	S389	AAAAAAMSLGPMGSVVKSEPSSPPPAIASHSQRACLGDLRDMISMYLPPGGDAADAASPLP	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Transcription factor SOX-3	48429228	P41225.2	446	S379	GQQPATAAAAAAAAAAMSLGPMGSVVKSEPSSPPPAIASHSQRACLGDLRDMISMYLPPGG	(Hahne et al. 2012)
Transcription factor Sp2	119367378	Q9D2H6.2	612	S186	QVIPGTNQAITTPSTSGHKPVPIKPAPVQKSSTTTTPVQSGANVVKLTGGGSNMTLTLPLN	(Myers et al. 2011)
transcription initiation factor TFIID subunit 4	110832843	NP_003176.2	1085	S528	APPVQISTVQAPGTPIIARQVTPTTIIKQVSQAQTTVQPSATLQRSPGVQPQLVLGGAAQT	(Wang et al. 2010)
transcription initiation factor TFIID subunit 4B	148792970	NP_005631.1	862	S489	GTAVTLSLPAVTFGETSGAAICLPSVKPVVSSAGTTSDKPVIGTPVQIKLAQPGPVLSQPA	(Wang et al. 2010)
Transcriptional activator Myb	341940978	P06876.2	636	S454	LIGHKLTPCRDQTVKTQKENSIFRTPAIKRSILESSPRTPTPFKHALAAQEIKYGPLKMLP	(Myers et al. 2011)
Transcriptional activator protein Pur-alpha	1172773	P42669.1	321	S17	BBBBBBBBBBBBBBMADRDSGSEQGGAALGSGGSLGHPGSGSGSGGGGGGGGGGGGGSGGGG	(Trinidad et al., 2012)
Transcriptional activator protein Pur-alpha	1172773	P42669.1	321	S6	BBBBBBBBBBBBBBBBBBBBBBBBMADRDSGSEQGGAALGSGGSLGHPGSGSGSGGGGGGG	(Trinidad et al., 2012)
Transcriptional activator protein Pur-alpha	1172773	P42669.1	321	S8	BBBBBBBBBBBBBBBBBBBBBBBMADRDSGSEQGGAALGSGGSLGHPGSGSGSGGGGGGGG	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Transcriptional repressor p66 alpha	50401041	Q8CHY6.2	629	S178	LRLEEAKLVLLKKLRQSQIQKEATAQKPTASSGSTVTTPPPLVRGTQNIPAGKTSLQTSST	(Trinidad et al., 2012)
Transcriptional repressor p66-beta	50401092	Q8VHR5.1	594	T256	LPSRPGAQGIEPQNMRTLQGHSVIRSATNTTLPHMLMSQRVIAPNPAQLQGQRGPPKPGIV	(Trinidad et al., 2012)
transcriptional repressor p66-beta	21218438	NP_065750.1	593	S584	AYLNTGIGGHKGPSLADRQREYLLDMIPPRSISQSISGQKBBBBBBBBBBBBBBBBBBBBB	(Wang et al. 2010)
Transducin-like enhancer protein 4	158518596	Q62441.4	773	T330	SSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGSNSTPGLRPVPGKPPGVDPLASSL	(Alfaro et al. 2012)
Transferrin receptor protein 1	108935939	P02786.2	760	S106	FFLIGFMIGYLGYCKGVEPKTECERLAGTESPVREEPGEDFPAARRLYWDDLKRKLSEKLD	(Hahne et al. 2012)
Transmembrane emp24 domain-containing protein 10	3915893	P49755.2	219	T55	GPRLVLAISFHLPINSRKCLREEIHKDLLVTGAYEISDQSGGAGGLRSHLKITDSAGHILY	(Hahne et al. 2012)
Transmembrane protein C15orf27 homolog	122065159	Q8BZB3.3	538	T400	SVDLPLKLSGNSTCASATSETTSHSTCGSVTRAQSASSQTLGSSTDCSTPREELLPSKPRS	(Trinidad et al., 2012)
Trinucleotide repeat-containing gene 6A protein	123791339	Q3UHK8.1	1896	T1623	GSSSSLNTTLPSTSAWSSIRASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHELW	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Trinucleotide repeat-containing gene 6A protein	123791339	Q3UHK8.1	1896	S1622	SGSSSSLNTTLPSTSAWSSIRASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHEL	(Alfaro et al. 2012)
Trinucleotide repeat-containing gene 6C protein	126253814	Q3UHC0.2	1690	S1002	EKKVDMDKRGLGMTDYNGMVTKPLGCRPPISKESSMDRPTFLDKLTLSFSNQDGGLVEEPT	(Trinidad et al., 2012)
Trinucleotide repeat-containing gene 6C protein	126253814	Q3UHC0.2	1690	T1453	TIQDVNRYLLKSGGKLSDIKSTWSSGPASHTQASLSHELWKVPRNTTAPTRPPPGLANPKP	(Trinidad et al., 2012)
Trinucleotide repeat-containing gene 6C protein	126253814	Q3UHC0.2	1690	S57	LVQSPSNQSALGAGGTNGNGGVARVWGVATSSSSGLAHCSVGGGDGKMDNMIGDGRSQNCW	(Trinidad et al., 2012)
Triple functional domain protein	257051075	Q0KL02.3	3102	T2452	RKAPGSTSGTSQDGNTKDARGNLGSLPLGKTRPGAVSPLNSPLSTTFPSPFGKEAFPPSSP	(Trinidad et al., 2012)
Tubby-related protein 4	20140819	Q9JIL5.1	1547	T943	CSQNTYTLPGPGSSATLRLTATEKKVPQPCTSATLNRLTVPRYSIPTGDPPPYPEIASQLA	(Trinidad et al., 2012)
Tubulin alpha-4A chain	55977478	P68368.1	448	S277	ALNVDLTEFQTNLVPYPRIHFPLATYAPVISAEKAYHEQLSVAEITNACFEPANQMVKCDP	(Trinidad et al., 2012)
Tubulin beta-2A chain	818859334	Q7TMM9.1	445	S168	SLGGGTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVVEPYNATLSVHQLVENTDE	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Tubulin beta-2A chain	81885934	Q7TMM9.1	445	S296	FMPGFAPLTSRGSQQYRALTVPELTQQMFDSKNMMAACDPRHGRYLTVAAIFRGRMSMKEV	(Trinidad et al., 2012)
Tubulin beta-2A chain	81885934	Q7TMM9.1	445	S172	GTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVVEPYNATLSVHQLVENTDETYSI	(Trinidad et al., 2012)
Tubulin beta-2B chain	81904211	Q9CWF2.1	445	S168	SLGGGTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVVEPYNATLSVHQLVENTDE	(Trinidad et al., 2012)
Tubulin beta-2B chain	81904211	Q9CWF2.1	445	S296	FMPGFAPLTSRGSQQYRALTVPELTQQMFDSKNMMAACDPRHGRYLTVAAIFRGRMSMKEV	(Trinidad et al., 2012)
Tubulin beta-2B chain	81904211	Q9CWF2.1	445	S172	GTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVVEPYNATLSVHQLVENTDETYCI	(Trinidad et al., 2012)
Tubulin beta-3 chain	20455323	Q9ERD7.1	450	T285	VNMVPFPRLHFFMPGFAPLTARGSQQYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVAT	(Trinidad et al., 2012)
Tubulin beta-4A chain	146345529	Q9D6F9.3	444	T285	VNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVAA	(Trinidad et al., 2012)
Tubulin beta-4B chain	55977481	P68372.1	445	T285	VNMVPFPRLHFFMPGFAPLTSRGSQQYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVAA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Tubulin beta-6 chain	68775966	Q922F4.1	447	S168	SLGGGTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVVEPYNATLSVHQLVENTDE	(Trinidad et al., 2012)
Tubulin beta-6 chain	68775966	Q922F4.1	447	T285	VNMVPFPRLHFFMPGFAPLTARGSQQYRALTVPELTQQMFDAKNMMAACDPRHGRYLTVAT	(Trinidad et al., 2012)
Tubulin beta-6 chain	68775966	Q922F4.1	447	S172	GTGSGMGTLLISKIREEYPDRIMNTFSVMPSPKVSDTVVEPYNATLSVHQLVENTDETYCI	(Trinidad et al., 2012)
Tubulin polymerization-promoting protein	57012946	Q7TQD2.1	218	S151	ELAKKRFKDKSSEEAVREVHRLIEGRAPVISGVTKAVSSPTVSRLTDTSKFTGSHKERFDQ	(Vosseller et al. 2006)
Tubulin polymerization-promoting protein	57012946	Q7TQD2.1	218	T154	KKRFKDKSSEEAVREVHRLIEGRAPVISGVTKAVSSPTVSRLTDTSKFTGSHKERFDQSGK	(Trinidad et al., 2012)
tumor protein D52-like 2	123234567	CAM21499.1	229	S164	SQAGQKTSAALSTMGSAISRKLGDMRAHPLSQSFSSYSIRHSISMPVMRNSATFKSFEDRV	(Trinidad et al., 2012)
tumor protein D52-like 2	123234572	CAM21504.1	160	S96	HCGELKRRLGLSTLGELKQNLSRSWHDVQVSTAYKKTQETLSQAGQKTSAALSTMGSAISR	(Trinidad et al., 2012)
tumor protein D52-like 2	123234567	CAM21499.1	229	T121	QNLSRSWHDVQVSTAYVKTSEKLGEWNEKVTQSDLYKKTQETLSQAGQKTSAALSTMGSAI	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Tyrosine-protein phosphatase non-receptor type 23	68053302	Q6PB44.2	1692	S655	QDNVLRALTEANVQYAAVRRVLSELDQKWNSTLQTLVASYEAYEDLMKKSQEGKDFYADLE	(Trinidad et al., 2012)
Tyrosine-protein phosphatase non-receptor type 23	68053302	Q6PB44.2	1692	T656	DNVLRALTEANVQYAAVRRVLSELDQKWNSTLQTLVASYEAYEDLMKKSQEGKDFYADLES	(Trinidad et al., 2012)
Ubiquitin carboxyl-terminal hydrolase 24	212288549	B1AY13.1	2617	S3	BBBBBBBBBBBBBBBBBBBBBBBBBBBMESEEEQHMTTLLCMGFSDPATIRKALRLAKND	(Trinidad et al., 2012)
Ubiquitin carboxyl-terminal hydrolase 8	44888442	Q80U87.2	1080	S218	LYTMMMDKNTSLIIMDARKIQDYQHSCILDSLSVPEEAISPGVTASWIEANLSDDSKDTWK	(Trinidad et al., 2012)
Ubiquitin-associated protein 2	74745207	Q5T6F2.1	1119	S492	QAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASKIPASAVE	(Zhao et al. 2011)
Ubiquitin-associated protein 2	74745207	Q5T6F2.1	1119	S494	KLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASKIPASAVEMP	(Zhao et al. 2011)
Ubiquitin-associated protein 2	74745207	Q5T6F2.1	1119	T486	LESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASKI	(Zhao et al. 2011)
Ubiquitin-associated protein 2	74745207	Q5T6F2.1	1119	T487	ESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPQPKHIKLAKRRIPPASKIP	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Ubiquitin-associated protein 2	74745207	Q5T6F2.1	1119	T1009	YSKGGYAGSSQAPNKSAGSGPGKGVSVSSSTTGLPDMTGSVYNKTQTFDKQGFHAGTPPPF	(Hahne et al. 2012)
Ubiquitin-associated protein 2	81879516	Q91VX2.1	1132	S401	ISNSQILDKLKPPGLSPFPAASSAQQNDTASPPATTAAWDLKPSAPQPSVLSRLDFKSQPE	(Alfaro et al. 2012)
Ubiquitin-associated protein 2-like	109940042	Q14157.2	1087	S445	HSPFTKRQAFTPSSTMMEVFLQEKSPAVATSTAAPPPPSSPLPSKSTSAPQMSPGSSDNQS	(Zhao et al. 2011)(Hahne et al. 2012)
Ubiquitin-associated protein 2-like	109940042	Q14157.2	1087	T446	SPFTKRQAFTPSSTMMEVFLQEKSPAVATSTAAPPPPSSPLPSKSTSAPQMSPGSSDNQSS	(Zhao et al. 2011)(Hahne et al. 2012)
Ubiquitin-associated protein 2-like	81895299	Q80X50.1	1107	S345	MENDSSNLDPSQAPSLAQPLVFSNSKQNAISQPASGSTFSHHSMVSMLGKGFGDVGEAKGG	(Alfaro et al. 2012)(Trinidad et al., 2012)
Ubiquitin-associated protein 2-like	109940042	Q14157.2	1087	S458	STMMEVFLQEKSPAVATSTAAPPPPSSPLPSKSTSAPQMSPGSSDNQSSSPQPAQQKLKQQ	(Hahne et al. 2012)(Hahne et al. 2012)
Ubiquitin-associated protein 2-like	109940042	Q14157.2	1087	T444	VHSPFTKRQAFTPSSTMMEVFLQEKSPAVATSTAAPPPPSSPLPSKSTSAPQMSPGSSDNQ	(Zhao et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Ubiquitin-associated protein 2-like	109940042	Q14157.2	1087	S439	PSDSAVHSPFTKRQAFTPSSTMMEVFLQEKSPAVATSTAAPPPPSSPLPSKSTSAPQMSPG	(Hahne et al. 2012)
Ubiquitin-associated protein 2-like	109940042	Q14157.2	1087	S453	AFTPSSTMMEVFLQEKSPAVATSTAAPPPPSSPLPSKSTSAPQMSPGSSDNQSSSPQPAQQ	(Hahne et al. 2012)
Ubiquitin-associated protein 2-like	81895299	Q80X50.1	1107	T297	EDWNEDLSETKIFTASNVSSVPLPAENVTITAGQRIDLAVLLGKTPSSMENDSSNLDPSQA	(Trinidad et al., 2012)
Ubiquitin-associated protein 2-like	81895299	Q80X50.1	1107	T377	PASGSTFSHHSMVSMLGKGFGDVGEAKGGSTTGSQFLEQFKTAQALAQLAAQHSQSGSTTT	(Trinidad et al., 2012)
Ubiquitin-associated protein 2-like	81895299	Q80X50.1	1107	T378	ASGSTFSHHSMVSMLGKGFGDVGEAKGGSTTGSQFLEQFKTAQALAQLAAQHSQSGSTTTS	(Trinidad et al., 2012)
ubiquitin-associated protein 2-like isoform a	188497758	NP_055662.3	1087	T782	VSSSLNSGSSLGLSLGSNSTVTASTRSSVATTSGKAPPNLPPGVPPLLPNPYIMAPGLLHA	(Wang et al. 2010)
ubiquitin-associated protein 2-like isoform a	188497758	NP_055662.3	1087	T783	SSSLNSGSSLGLSLGSNSTVTASTRSSVATTSGKAPPNLPPGVPPLLPNPYIMAPGLLHAY	(Wang et al. 2010)
UBX domain-containing protein 1	309134001	Q922Y1.1	297	T192	QRVREKIERDKAERAKKYGGSVGSRSSPPATDPGPVPSSPSQEPPTKREYDQCRIQVRLPD	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	146325019	Q8CGY8.2	1046	T1043	TMELERLYLQMWEHYAAGNKPDHMIKPVEVTESABBBBBBBBBBBBBBBBBBBBBBBBBBB	(Alfaro et al. 2012)
Uncharacterized protein C12orf35 homolog	156630980	Q5DTW7.2	1521	S291	QYAAEASKRLSALPYSCRYENQHVQNAQPVSKHLPMEVPQSSEVHSSEKKKDTYRGFKQQW	(Myers et al. 2011)
Uncharacterized protein C12orf35 homolog	156630980	Q5DTW7.2	1521	T232	LVDWTQYTSNELSYPEYRPPPKQYSYILPATTSLQVKNNQLPTYTQSLQSKHSVPLSSHQY	(Myers et al. 2011)
Uncharacterized protein C12orf35 homolog	156630980	Q5DTW7.2	1521	T233	VDWTQYTSNELSYPEYRPPPKQYSYILPATTSLQVKNNQLPTYTQSLQSKHSVPLSSHQYA	(Myers et al. 2011)
Uncharacterized protein C12orf35 homolog	156630980	Q5DTW7.2	1521	T491	LWKNQPSKTTEENVPKPLEEKQCNTSRISTTVVGSANPTNEVHVKSLCSGVGNSQKMMSSS	(Myers et al. 2011)
Uncharacterized protein C19orf47 homolog	81901667	Q8R3Y5.2	413	S354	ALPSRPGLQKKPDSLPKVSILQRLGKAAVVSEAQDSQVTSTKSKSSAEVKFAIKRTLVGPR	(Alfaro et al. 2012)
Uncharacterized protein C9orf172 homolog	292630634	A2AJA9.1	974	S497	RSYENLLGREVRDTRGSSPEGRRPPVVVNLSTSPRRYAALSLSETSLTEKGRAGESLGRNW	(Trinidad et al., 2012)
Unconventional myosin-IXa	205829208	Q8C170.2	2542	T1545	NEKEMMEQIRQQTDILEKERKAFKTIEQSRTEASVLAPSFYQPRQKVERPCSLYIQNTPSK	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
UPF0444 transmembrane protein C12orf23 homolog	81881684	Q9DAM7.1	115	T69	GGIFSVTKGAVGATIGGVAWIGGKSLEVTKTAVTTVPSMGIGLVKGGVSAVAGGVTAVGSA	(Alfaro et al. 2012)(Trinidad et al., 2012)
UPF0444 transmembrane protein C12orf23 homolog	81881684	Q9DAM7.1	115	T72	FSVTKGAVGATIGGVAWIGGKSLEVTKTAVTTVPSMGIGLVKGGVSAVAGGVTAVGSAVVN	(Alfaro et al. 2012)
UPF0444 transmembrane protein C12orf23 homolog	81881684	Q9DAM7.1	115	T73	SVTKGAVGATIGGVAWIGGKSLEVTKTAVTTVPSMGIGLVKGGVSAVAGGVTAVGSAVVNK	(Trinidad et al., 2012)
UPF0606 protein C11orf41	344238092	EGV94195.1	1830	S1516	IEETNVDRVHEPRGYGRARQVKGHSETSTLSSQPSIDEVRQQMHMLLEEAFSLASAGHAGQ	(Trinidad et al., 2012)
UPF0606 protein C11orf41	344238092	EGV94195.1	1830	S539	SSTKLQTLTAATSLSVLPASASKQVTALPSSTNVYDFPTMGGTRKPAATDVFWSSLSSETA	(Trinidad et al., 2012)
UPF0606 protein C11orf41	344238092	EGV94195.1	1830	S597	ETASLSTQSTISGLPWQTDHDLNTHTINSISWVPHPASATPPSGTTSAANAIQSQNFKEAG	(Trinidad et al., 2012)
UPF0606 protein C11orf41	344238092	EGV94195.1	1830	T143	SFSLAPDSPHSITPRTSIEHPTKVPLFHQITPADSSSGQSLGNVLNPFSHKTNHFPSRNAR	(Trinidad et al., 2012)
UPF0606 protein KIAA1549	327478575	Q68FD9.3	1940	S1658	YIGCPSDPDLPADVQTPSSTELGRYPGLPFSASQYIPPQPSIEEARQTMHSLLDDAFALVA	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
UV excision repair protein RAD23 homolog B	1709985	P54727.1	409	S135	TTVAQAPTPVPALAPTSTPASITPASATASSEPAPASAAKQEKPAEKPAETPVATSPTATD	(Hahne et al. 2012)(Hahne et al. 2012)
UV excision repair protein RAD23 homolog B	1709985	P54727.1	409	S141	PTPVPALAPTSTPASITPASATASSEPAPASAAKQEKPAEKPAETPVATSPTATDSTSGDS	(Hahne et al. 2012)(Hahne et al. 2012)
UV excision repair protein RAD23 homolog B	1709985	P54727.1	409	S134	TTTVAQAPTPVPALAPTSTPASITPASATASSEPAPASAAKQEKPAEKPAETPVATSPTAT	(Hahne et al. 2012)
Vascular endothelial zinc finger 1	81910197	Q5SXC4	518	S117	YHLRRHQSCHTGIKLVSRAKKTPTTVVPLISTIAGDSSRTSLVSTIAGILSTVTTSSSGTN	(Trinidad et al., 2012)
Vascular endothelial zinc finger 1	81910197	Q5SXC4	518	T111	KAFRDSYHLRRHQSCHTGIKLVSRAKKTPTTVVPLISTIAGDSSRTSLVSTIAGILSTVTT	(Trinidad et al., 2012)
Vascular endothelial zinc finger 1	81910197	Q5SXC4	518	T118	HLRRHQSCHTGIKLVSRAKKTPTTVVPLISTIAGDSSRTSLVSTIAGILSTVTTSSSGTNP	(Trinidad et al., 2012)
Vesicular inhibitory amino acid transporter	29428127	O35633.3	525	S185	AAVVCCYTGKILIACLYEENEDGEVVRVRDSYVAIANACCAPRFPTLGGRVVNVAQIIELV	(Trinidad et al., 2012)
Vimentin	138536	P20152.3	466	S49	GTSSRPSSNRSYVTTSTRTYSLGSALRPSTSRSLYSSSPGGAYVTRSSAVRLRSSVPGVRL	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
vimentin	76097693	ABA39528.1	466	S55	SSSRSYVTTSTRTYSLGSALRPSTSRSLYASSPGGVYATRSSAVRLRSSVPGVRLLQDSVD	(Wang et al. 2007)
vimentin	62414289	NP_003371.2	466	S34	RSVSSSSYRRMFGGPGTASRPSSSRSYVTTSTRTYSLGSALRPSTSRSLYASSPGGVYATR	(Wang et al. 2010)
vimentin	62414289	NP_003371.2	466	S7	BBBBBBBBBBBBBBBBBBBBBBBMSTRSVSSSSYRRMFGGPGTASRPSSSRSYVTTSTRT	(Wang et al. 2010)
vimentin	62414289	NP_003371.2	466	T33	TRSVSSSSYRRMFGGPGTASRPSSSRSYVTTSTRTYSLGSALRPSTSRSLYASSPGGVYAT	(Wang et al. 2010)
Visual cortex cDNA, RIKEN full-length enriched library, clone:K430313E02 product:calcium/calmodulin-dependent protein kinase II, beta, full insert sequence	123790599	Q3TY93	374	T178	TVASMMHRQETVECLKKFNARRKLKGAILTTMLATRNFSAAKSLLNKKADGVKPQTNSTKN	(Trinidad et al., 2012)
Voltage-dependent anion-selective channel protein 1	10720404	Q60932.3	296	S114	FTEKWNTDNTLGTEITVEDQLARGLKLTFDSSFSPNTGKKNAKIKTGYKREHINLGCDVDF	(Trinidad et al., 2012)
Voltage-dependent anion-selective channel protein 1	10720404	Q60932.3	296	T178	GPSIRGALVLGYEGWLAGYQMNFETSKSRVTQSNFAVGYKTDEFQLHTNVNDGTEFGGSIY	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Voltage-dependent calcium channel gamma-3 subunit	341940327	Q9JJV5.2	315	T260	RFRRRSSSRSTEPRSRDLSPISKGFHTIPSTDISMFTLSRDPSKLTMGTLLNSDRDHAFLQ	(Trinidad et al., 2012)
Voltage-dependent calcium channel gamma-8 subunit	20532015	Q8VHW2.1	423	T381	SERDRGSSAGFLTLHNAFPKEAASGVTVTVTGPPAAPAPAPAPPAPAAPAPGTLSKEAAAS	(Alfaro et al. 2012)
Voltage-dependent L-type calcium channel subunit beta-3	1705684	P54285.1	484	S464	QDLYQPHRQHTSGLPSANGHDPQDRLLAQDSEHDHNDRNWQRNRPWPKDSYBBBBBBBBB	(Trinidad et al., 2012)
Voltage-dependent N-type calcium channel subunit alpha-1B	6166049	O55017.1	2327	T1024	EKESNAVEGDKETRNHQPKEPHCDLEAIAVTGVGPLHMLPSTCLQKVDEQPEDADNQRNVT	(Trinidad et al., 2012)
Voltage-dependent P/Q-type calcium channel subunit alpha-1A	125987800	P97445.2	2368	S998	RRHRHGPPAHDDRERRHRRRKENQGSGVPVSGPNLSTTRPIQQDLGRQDLPLAEDLDNMKN	(Trinidad et al., 2012)
VPS10 domain-containing receptor SorCS2	341942055	Q9EPR5.2	1159	S1147	NEKEQEMTSPVSHSEDAQSTMQGNHSGVVLSINSREMHSYLVGBBBBBBBBBBBBBBBBBB	(Trinidad et al., 2012)
WASH complex subunit 7	143342666	Q3UMB9.2	1173	S19	BBBBBBBBBBBBMAVDTLSPDWDFDRVDDGSQKIHAEVQLKNYGRFLEEYTSQLRRIEDAL	(Trinidad et al., 2012)
WD repeat and FYVE domain-containing protein 3	81911628	Q6VNB8.1	3508	S3450	SVSDQPGRSAADHWVKDEGGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLK	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
WD repeat and FYVE domain-containing protein 3	81911628	Q6VNB8.1	3508	S3443	RGRVFSWSVSDQPGRSAADHWVKDEGGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQ	(Trinidad et al., 2012)
WD repeat and FYVE domain-containing protein 3	81911628	Q6VNB8.1	3508	S3446	VFSWSVSDQPGRSAADHWVKDEGGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEI	(Trinidad et al., 2012)
WD repeat and FYVE domain-containing protein 3	81911628	Q6VNB8.1	3508	T2268	LIEEAGLKCWQNHLAHEKKCISRGEALVPTTQSKLSRVSSGFGLSKLTGSRRNRKESGLHK	(Trinidad et al., 2012)
WD repeat and FYVE domain-containing protein 3	81911628	Q6VNB8.1	3508	T592	TNAGIFREFGGARCAHNIVKYPQCRQHALMTIQQLVLSPNGEDDMGTLLGLMHSAPPTELQ	(Trinidad et al., 2012)
WD repeat-containing protein 13	20140638	Q91V09.1	485	S140	RSVSRGSYQLQAQMNRAVYEDRPPGSVVPTSVAEASRAMAGDTSLSENYAFAGMYHVFDQH	(Alfaro et al. 2012)
WD repeat-containing protein 37	46577468	Q8CBE3.1	496	T165	SSFKTTTSRAICQLVKEYIGHRDGIWDVSVTRTQPIVLGTASADHTALLWSIETGKCLVKY	(Trinidad et al., 2012)
WW domain-binding protein 2	25091530	P97765.1	261	S20	BBBBBBBBBBBMALNKNHSEGGGVIVNNTESILMSYDHVELTFNDMKNVPEAFKGTKKGTV	(Trinidad et al., 2012)
WW domain-binding protein 2	25091530	P97765.1	261	S24	BBBBBBBMALNKNHSEGGGVIVNNTESILMSYDHVELTFNDMKNVPEAFKGTKKGTVYLTP	(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
YEATS domain-containing protein 2	85542166	Q3TUF7.2	1407	S600	KVQSPKAVTGGLGAFTKVIIKQEPGEAPHVSTTGAASQSAFPQYVTVKGGHMIAVSPQKQV	(Myers et al. 2011)
YEATS domain-containing protein 2	85542166	Q3TUF7.2	1407	T601	VQSPKAVTGGLGAFTKVIIKQEPGEAPHVSTTGAASQSAFPQYVTVKGGHMIAVSPQKQVI	(Myers et al. 2011)
YEATS domain-containing protein 2	85542166	Q3TUF7.2	1407	T602	QSPKAVTGGLGAFTKVIIKQEPGEAPHVSTTGAASQSAFPQYVTVKGGHMIAVSPQKQVIS	(Myers et al. 2011)
YEATS domain-containing protein 2	85542166	Q3TUF7.2	1407	S668	TQSPKIAPSKVVGVPVGSALPSTVKQAVAISSGQILVAKASSSVTKAVGPKQVVTQGVAKA	(Trinidad et al., 2012)
YLP motif-containing protein 1	342187348	Q9R0I7.2	1386	S636	QLTAPLPPASGSQNSQIPEKPRQALLPTPVSFGSTPPSPYHPPPQSEQVNSKPLNKVFSSE	(Alfaro et al. 2012)(Myers et al. 2011)
YTH domain family protein 1	28380041	Q9BYJ9.1	559	S198	GFHSDTLSKAPGMNSLEQGMVGLKIGDVSSSAVKTVGSVVSSVALTGVLSGNGGTNVNMPV	(Hahne et al. 2012)
YTH domain family protein 1	31377750	NP_060268.2	559	S196	QPGFHSDTLSKAPGMNSLEQGMVGLKIGDVSSSAVKTVGSVVSSVALTGVLSGNGGTNVNM	(Wang et al. 2010)
YTH domain family protein 3	91208387	Q8BYK6.2	585	T205	NDTLSKVPGISSIEQGMTGLKIGGDLTAAVTKTVGTALSSSGMTSIATNNVPPVSSAAPKP	(Alfaro et al. 2012)(Trinidad et al., 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
YTH domain family protein 3	74738853	Q7Z739.1	585	T205	NDTLSKVPGISSIEQGMTGLKIGGDLTAAVTKTVGTALSSSGMTSIATNSVPPVSSAAPKP	(Hahne et al. 2012)(Hahne et al. 2012)
YTH domain family protein 3	116235460	NP_689971.4	585	T205	NDTLSKVPGISSIEQGMTGLKIGGDLTAAVTKTVGTALSSSGMTSIATNSVPPVSSAAPKP	(Wang et al. 2010)
Zinc finger and BTB domain-containing protein 20	81914558	Q8K0L9.1	741	S268	HSVDRIYSALYACSMQNGSGERSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQM	(Trinidad et al., 2012)
Zinc finger and BTB domain-containing protein 20	81914558	Q8K0L9.1	741	T480	NSSDKGVLQQPSVNTSIGQPLPSTQLYLRQTETLTSNLRMPLTLTSNTQVIGTAGNTYLPA	(Trinidad et al., 2012)
Zinc finger and BTB domain-containing protein 20	81914558	Q8K0L9.1	741	S465	RSNESEMDNTVITVSNSSDKGVLQQPSVNTSIGQPLPSTQLYLRQTETLTSNLRMPLTLTS	(Trinidad et al., 2012)
Zinc finger E-box-binding homeobox 2	342187350	Q9R0G7.2	1215	T723	EQRKVYQYSNSRSPSLERTSKPLAPNSNPTTKDSLLPRSPVKPMDSITSPSIAELHNSVTS	(Trinidad et al., 2012)
zinc finger protein 281	6912752	NP_036614.1	895	S891	VRTSVSDFSGYTNMMSDVSEPCSTRVKTPTSQSYRBBBBBBBBBBBBBBBBBBBBBBBBBBB	(Wang et al. 2010)
Zinc finger protein 318	166215019	Q99PP2.2	2064	S1186	SKDRDDGKAEVGKAKPIKIKLSGKTVIAHTSPWTPVVTTSTQTKIRPNLPIPSTVLRKSGS	(Myers et al. 2011)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Zinc finger protein 318	166215019	Q99PP2.2	2064	T1185	TSKDRDDGKAEVGKAKPIKIKLSGKTVIAHTSPWTPVVTTSTQTKIRPNLPIPSTVLRKSG	(Myers et al. 2011)
zinc finger protein 40	116805342	NP_002105.2	2718	T2325	SRSPCHQMSVDYPESEEILRSSMAGKAVAITQSPSSVRLPPAAAEHSPQTAAGMPSVASPH	(Wang et al. 2010)
Zinc finger protein 532	81911166	Q6NXK2.1	1036	S455	TAMVTSAVSSAELTPKQVTIKPVATAFLPVSAVKTAGSQVINLKLANNTTVKATVISAASV	(Alfaro et al. 2012)(Trinidad et al., 2012)
Zinc finger protein 532	81911166	Q6NXK2.1	1036	S481	FLPVSAVKTAGSQVINLKLANNTTVKATVISAASVQSASSAIIKAANAIQQQTVVVPASSL	(Trinidad et al., 2012)
Zinc finger protein 608	81882411	Q56A10.1	1511	S155	GIPEISSTGKRQEVQGRPGEATGMNSALGQSVSGGGSSNPNSNGTSTGTSAATAGAGSCGK	(Trinidad et al., 2012)
Zinc finger protein 608	81882411	Q56A10.1	1511	S157	PEISSTGKRQEVQGRPGEATGMNSALGQSVSGGGSSNPNSNGTSTGTSAATAGAGSCGKSK	(Trinidad et al., 2012)
Zinc finger protein 608	81882411	Q56A10.1	1511	S182	LGQSVSGGGSSNPNSNGTSTGTSAATAGAGSCGKSKEEKPGKSHSSRGAKRDKDAARSRKE	(Trinidad et al., 2012)
Zinc finger protein 704	81917386	Q9ERQ3.1	566	T468	TKLVTPLSRSAPTTLYLVHTDHAYQATPPVTIPGSAKFTPNGSSFSISWQSPPVTFTGVPV	(Alfaro et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Zinc finger RNA-binding protein	162416199	O88532.2	1074	S195	TATAAAVAAAAQPQPSVAETYYQTAPKAGYSQGATQYTQAQQARQVTAIKPATPSPATTTF	(Alfaro et al. 2012)(Myers et al. 2011)(Trinidad et al., 2012)
Zinc finger RNA-binding protein	162416199	O88532.2	1074	T135	AYGGYPTAHTATDYGYTQRQQEAPPPPPPATTQNYQDSYSYVRSTAPAVAYDSKQYYQQPT	(Alfaro et al. 2012)(Trinidad et al., 2012)
Zinc finger RNA-binding protein	162416199	O88532.2	1074	T136	YGGYPTAHTATDYGYTQRQQEAPPPPPPATTQNYQDSYSYVRSTAPAVAYDSKQYYQQPTA	(Alfaro et al. 2012)(Trinidad et al., 2012)
Zinc finger RNA-binding protein	162416199	O88532.2	1074	T202	AAAAQPQPSVAETYYQTAPKAGYSQGATQYTQAQQARQVTAIKPATPSPATTTFSIYPVSS	(Alfaro et al. 2012)(Trinidad et al., 2012)
Zinc finger RNA-binding protein	162416199	O88532.2	1074	T300	AAVYSAASSYYQQQQQQQKQAAAAAAAAAATAAWTGTTFTKKTPFQNKQLKPKQPPKPPQI	(Alfaro et al. 2012)(Trinidad et al., 2012)
Zinc finger RNA-binding protein	162416228	Q96KR1.2	1074	T207	PQPSVAETYYQTAPKAGYSQGATQYTQAQQTRQVTAIKPATPSPATTTFSIYPVSSTVQPV	(Hahne et al. 2012)

Protein associated with mapped O-GlcNAc residue				Detected peptides expanded to include 61 amino acids centered on mapped amino acid		Publication references
Protein/Gene Name as per NCBI (July, 2012)	G.I. No.	Accession No.	Total AA's in Protein	Residue No. Modified	61 Amino Acid Sequence Centered on O-GlcNAc Mapped Site	
Zinc finger RNA-binding protein	162416292	Q562A2.2	1073	S195	TATAAAVAAAAQPQPSVAETYYQTAPKAGYSQGATQYTQAQQARQVTAIKPATPSPATTTF	(Khidekel et al. 2007)
Zinc finger RNA-binding protein	162416199	O88532.2	1074	S148	YGYTQRQQEAPPPPPPATTQNYQDSYSYVRSTAPAVAYDSKQYYQQPTATAAAVAAAAQPQ	(Trinidad et al., 2012)
zinc finger RNA-binding protein	34101286	NP_057191.2	1074	S195	TATAAAVAAAAQPQPSVAETYYQTAPKAGYSQGATQYTQAQQTRQVTAIKPATPSPATTTF	(Wang et al. 2010)
zinc finger RNA-binding protein	34101286	NP_057191.2	1074	T202	AAAAQPQPSVAETYYQTAPKAGYSQGATQYTQAQQTRQVTAIKPATPSPATTTFSIYPVSS	(Wang et al. 2010)
zinc fingers and homeoboxes protein 1	63079680	NP_009153.3	873	S450	VPSQNNIQKSQVPAAQPTAETKPATAAVPTSQSVKHETALVNPDSFGIRAKKTKEQLAELK	(Wang et al. 2010)
Zinc transporter 6	81873983	Q8BJM5.1	460	T374	GPVAPNVLNFSDHHVIPMPLLKNVDERTPVTSTPAKPSSPPPEFSFNTPGKNVSPVILLNT	(Alfaro et al. 2012)
Zinc transporter 6	81873983	Q8BJM5.1	460	S375	PVAPNVLNFSDHHVIPMPLLKNVDERTPVTSTPAKPSSPPPEFSFNTPGKNVSPVILLNTQ	(Trinidad et al., 2012)
Zyxin	342187306	Q62523.2	564	S237	SQPPPQPQAKPQVQLHVQPQAKPHVQPQPVSSANTQPRGPLSQAPTPAPKFAPVAPKFTPV	(Alfaro et al. 2012)

Linked references used in appendix table of *O*-GlcNAc mapped sites: (Roquemore, Dell et al. 1992, Dong, Xu et al. 1993, Greis, Gibson et al. 1994, Chou, Dang et al. 1995, Dong, Xu et al. 1996, Cole and Hart 1999, Cheng and Hart 2001, Wells, Vosseller et al. 2002, Chalkley and Burlingame 2003, Vosseller, Trinidad et al. 2006, Khidekel, Ficarro et al. 2007, Wang, Pandey et al. 2007, Ramirez-Correa, Jin et al. 2008, Chalkley, Thalhammer et al. 2009, Dias, Cheung et al. 2009, Hu, Suarez et al. 2009, Wang, Park et al. 2009, Park, Kim et al. 2010, Sakabe, Wang et al. 2010, Wang, Udeshi et al. 2010, Fujiki, Hashiba et al. 2011, Graham, Thaysen-Andersen et al. 2011, Myers, Panning et al. 2011, Yuzwa, Yadav et al. 2011, Zhao, Viner et al. 2011, Alfaro, Gong et al. 2012, Fong, Nguyen et al. 2012, Hahne, Moghaddas Gholami et al. 2012, Ji, Park et al. 2012, Pathak, Borodkin et al. 2012, Rexach, Clark et al. 2012, Tarrant, Rho et al. 2012, Trinidad, Barkan et al. 2012, Yuzwa, Shan et al. 2012)