

Supporting Information

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Fig. S1. ETD MS/MS spectra of the O-GlcNAcylated peptides identified in this study. Peptide sequence and site assignment of the HexNAc mass modification are assigned based on Protein Prospector results. Charged reduced species and common neutral losses (1) are not labeled.

http://msf.ucsf.edu/personal_pages/myers/Myers_2011_Figure_S1.pdf

1. Fällth M, et al. (2008) Analytical utility of small neutral losses from reduced species in electron capture dissociation studied using SwedECD database. *Anal Chem* 80:8089–8094.

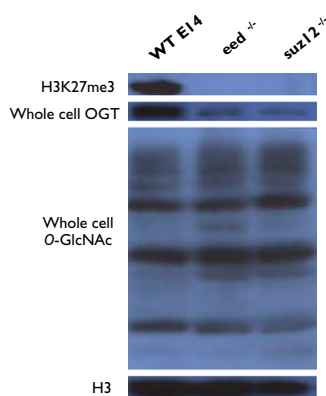


Fig. S2. Whole-cell lysate analysis of H3K27me3, OGT, O-GlcNAc, and H3 in ESC mutants for *eed* or *suz12*.

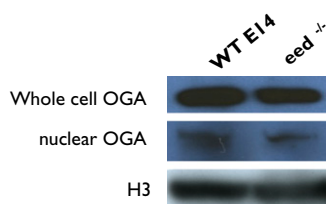


Fig. S3. Analysis of whole-cell and nuclear lysates for the O-GlcNAc hydrolase OGA/NCOAT/MGEA5 (OGA) in WT and *eed*^{-/-} mutant ESCs.

Table S1. All O-GlcNAc modified peptides identified in this study

Gene name	Accession no.	O-GlcNAc peptides	Modified residue
Agf1	Q8K2K6	SSSADFGTF TS(HexNAc) QSHQTASTVSK	T301 or S302
Atf7ip	Q7TT18	NSSTTAAPL GT(HexNAc) TLAVQAVPTAHISIVQATR	T902 or T903
Bnc2	Q2TBA4	ATS (HexNAc) GAATPVIASK	S437
Bptf	A2A654	QTV VS(HexNAc) S (HexNAc) TENC*AR	S1742 and S1743
Bptf	A2A654	S(HexNAc) TVTTTTTTVTK	S1750
Bptf	A2A654	ST(HexNAc) VTTTTTTVTK	T1751
Bptf	A2A654	STV T(HexNAc) TT (HexNAc) TTTTVTK	T1754 and T1756
Bptf	A2A654	STV TT(HexNAc) T (HexNAc) TTTTVTK	T1755 and T1756
Bptf	A2A654	STV TT(HexNAc) TTTTV T(HexNAc) K(heavy)	T1755 and T1760
Bptf	A2A654	T(HexNAc) VI TE VTTMTSTVATESK	T1710 or T1713
Bptf (frag)	A2A653	IVAVNVPAT (HexNAc) QGGMVQVQQK	T225
C1orf88	Q9D9W1	VP TST(HexNAc) KGYAIGAR	T82 or S83 or T84
Cdk12	Q14AX6	TS(HexNAc) TLLSQTNSQPVVQVSMK	T588-T590
Cdk13	Q69ZA1	TENQHVP TTS(HexNAc) SSLTDPHAGVK	T1286 or S1287
Cnot2	Q8C5L3	SLSQGTQLPSHV PT(HexNAc) TGVPTMSLHTPPSPSR	T113
Cnot2	Q8C5L3	SLSQGTQLPSHV PT(HexNAc) MSLHTPPSPSR	T118
Dido1	Q8C9B9	ILSSLKPG ST(HexNAc) STVTAP T(HexNAc) TAAITTTASPVTAATSK	T1280 and T1287 or T1288 mix
Ebp	P70245	Ac- T(HexNAc) TNTVPLHPYWPR	T2
Egr1	P08046	AMVETS (HexNAc) YPSQTR	S117
Elf2	Q9JHC9	SPT T(HexNAc) T (HexNAc) APVSAAAAAPR	T375 and T376
Emsy	Q8BMB0	I IS(HexNAc) SNIVSGTTTK	S520
Emsy	Q8BMB0	IT FT(HexNAc) KPSTQTNTTTQK	T228
Emsy	Q8BMB0	IT FTKPS(HexNAc) TQTTNTTTQK	S231
Emsy	Q8BMB0	IT FTKPSQ(HexNAc) TNTTTQK	T234 or T235
Emsy	Q8BMB0	L VT(HexNAc) TPTGTQATYTRPTVSPSLGR	T465
Emsy	Q8BMB0	TITVP VS(HexNAc) GSPK	S200
Emsy	Q8BMB0	TT(HexNAc) SGSITTVPK	T499 and S500 mix
Emsy	Q8BMB0	VII V(HexNAc) T (HexNAc) SPSSTFVNILSK	T246 and T247
Ep400	Q8CHI8	LASPVAP GLT(HexNAc) TSGGSAPAQVVHTQQR	T2594 or T2595
Ep400	Q8CHI8	LASPVAP GLT(HexNAc) APAQVVHTQQR	S2599
Gata2b	Q5JP02	S(HexNAc) ISQSISSGQK	S585
Hcf1	B1AUX1	AP V(HexNAc) VTSLPASVR	T515
Hcf1	B1AUX1	IPP SS(HexNAc) APTIVLSPVAGTTIVK T(HexNAc) VAVTPGTTTLPATVK	S563 and T579
Hcf1	B1AUX1	IT (HexNAc) VAPGALER	T1148
Hcf1	B1AUX1	L VTVP(HexNAc) VSAVKPA V(HexNAc) TLVVK	T861 and T870
Hcf1	B1AUX1	L VTPV(HexNAc) VSAVKPA V(HexNAc) TLVVK	T861
Hcf1	B1AUX1	QPETY HT(HexNAc) YTTNTPTTTR	T1238
Hcf1	B1AUX1	QPETY HTYTTNTPTT(HexNAc) TR	T1246
Hcf1	B1AUX1	RT T(HexNAc) NTPTVVR	T1139
Hcf1	B1AUX1	SGT VTVAAQQAQVV(HexNAc)T(HexNAc) VVGGVTK	T651 and T652
Hcf1	B1AUX1	SPI ITTT(HexNAc) KVMTSGTGAPAK	T801
Hcf1	B1AUX1	T(HexNAc) QGVPAVLK	T480
Hcf1	B1AUX1	T(HexNAc) VAVTPGTTTLPATVK	T579
Hcf1	B1AUX1	TAAAQ VGTS(HexNAc) V S(HexNAc) S (HexNAc) AANTSTRPIITVHK	S620 and S622 and S623
Hcf1	B1AUX1	TAAAQ VGTS(HexNAc) V SS(HexNAc) AANTSTRPIITVHK	S620 and S623
Hcf1	B1AUX1	TIPMSA IT(HexNAc) QAGATGVTSPPGK	T779
Hcf1	Q61191	VMT SGT(HexNAc) GAPAK	T808
Hcf1	B1AUX1	VTGP QAT(HexNAc) TGTPLVTRMPASQAGK	T495
Hprt1	A8MSU4	VIGGDDLSTL TGKS(HexNAc) R	S129
Jmjd1c	Q69ZK6	HSVPQSLPQSN YFTLS(HexNAc) NSVVNEPR	S911
Jmjd1c	Q69ZK6	NSPSPWL HQPTPVTS(HexNAc) ADGIGLLSHIPVRPSSAEPHRPHK	T728 or T731 or S732
Jmjd1c	Q69ZK6	SV VS(HexNAc) QAVAQAK	S1250
Kdm3b	Q6ZPY7	VEHSPFSS FVSQASGS(HexNAc) SSATSVTSK	S460 or S461
Kiaa1310	A2RSY1	SSSS EGGG T(HexNAc) ASTTPSVASSATPNAIHTLQSR	Between S699 and T707
Kiaa1310	A2RSY1	V P(HexNAc) TITLTLR	T858
Kiaa1551	Q5DTW7	IST T(HexNAc) VVGSANPTNEVHVK(heavy)	T491
Kiaa1551	Q5DTW7	NNQL PYT(HexNAc) QSLQSK	T40
Kiaa1551	Q5DTW7	QYSY LPAT(HexNAc) T (HexNAc) SLQVK	T232 and T233
Kiaa1551	Q5DTW7	QYSY LPAT(HexNAc) T SLQVK	T232 and T233 mix
Kiaa1551	Q5DTW7	YENQH VQNAQVS(HexNAc) K	S291
Lman1	Q9D0F3	RGAG T(HexNAc) PGQPQGVSQQLD TVVK	T385
Mafk	Q60675	VA TT(HexNAc) SVITIVK	T133 or T143
Med15	Q924H2	C* MTS(HexNAc) RLQLPDK	T761 or S762
Myb	P06876	TPAI KRS(HexNAc) ILESSPR	S454
NCoR1	Q60974	RTP VS(HexNAc) YQNTISR	S1496
NCoR1	Q60974	SVQC* VC*T(HexNAc) S (HexNAc) SALPSGK	T1899 and S1900
NCoR2	Q9WU42	GSPV TT(HexNAc) REPTPR	T1531 or T1532
Nfrkb	Q6P1J4	IQTV PASHLQGT(HexNAc) ASGSSK	T1270
Nfrkb	Q6P1J4	QVPV NTVVTS(HexNAc) QSGKLPTR	S1172
Nup53	Q8R4R6	S(HexNAc) ISGSPVGMEMR	S53
Nup53	Q8R4R6	AS TS(HexNAc) DYQVISDR	S297
Nup98	Q68G59	LP IS(HexNAc) ASHSSK	S426
Nup153	Q80WR0	FG IPS(HexNAc) SSSGLS QTLTSTGNFK	S898 or S899

Table S1. Cont.

Gene name	Accession no.	O-GlcNAc peptides	Modified residue
Nup153	Q80WR0	QQEPV TS (HexNAc)TSLVFGK	S1102
Nup153	Q80WR0	S (HexNAc)VSVTPFTYK	S1046
Nup153	Q80WR0	SGFNFGTLDT(HexNAc)K	T1044
Nup153	Q80WR0	VDSPALQPTT(HexNAc) T (HexNAc)SSIVYTRPAISTFSSSGIEYGESLK	T627 and T628
Nup188	Q6ZQH8	AQRPS(HexNAc)TTTTTTTTALATPAGC*SSK	S1522
Nup214	Q80U93	AAPGS(HexNAc)GTSTFSFAPPSK	S513
Nup214	Q80U93	FTAVAS(HexNAc)SAPVHSSTSTPSVLPFSSSPKPTASGPLSHPTPLPASSSSMPLK	S589 or S590
Nup214	Q80U93	GGGFFSGLGGKPS(HexNAc)QDAANKNPFSSAGGGFGSTAAPNTSNLFGNSGAK	S1889 or 1899
Nup214	Q80U93	HGAPGPSHT(HexNAc)VAAPQAAAAAALRR	T1091
Nup214	Q80U93	SSASVTGEPPLYPTGS(HexNAc)DSSR	S504
Nup214	Q80U93	VGQAEDSTKPV S (HexNAc)K	S1362
Phc3	Q8CHP6	SAGQT(HexNAc)QSLTIC*HNK	T238
Phf21a	Q6ZPK0	FTPTTLPT S (HexNAc)QNSIHPVR	S286
Pogz	Q8BZH4	RPGVT(HexNAc)GENSNEVAK	T310
Pogz	Q8BZH4	VT(HexNAc)SSIPVFDLQDGGRR	T358
Prdx6	O08709	LKLSILYPAT(HexNAc)TGR	T152
Qser1	A2BIE1	PTDYYVYPT S (HexNAc)PSLESC*DEGFQHQEK	T1077 or S1078 or S1080
Qser1	A2BIE1	TS (HexNAc)QGTVPATALAFER	S105
RanBP2	Q9ERU9	ALGTN TS (HexNAc)TAPNHTLR	T1306 and S1307 mix
RanBP2	Q9ERU9	SVFTT(HexNAc)AASELANK	T1138
Rbbp7	Q5JP02	Ac-DDHT(HexNAc)VC*LWDINAGPK	T4
Rbm14	Q8C2Q3	AQPSVS(HexNAc)LGAAAYR	S244
Rbm14	Q8C2Q3	AQPSVS(HexNAc)LGAPYR	S280
Rprd2	Q3UY82	EKPVEKPAV S (HexNAc) T (HexNAc)GVPTK	S103 and T104
Rprd2	Q6NXI6	EKPVEKPAV S (HexNAc)TGVPTK	S103
Rprd2	Q6NXI6	SIFSSQSTLAAPAGHPPT S (HexNAc)GVEK(heavy)	S1110
Sal4	Q8BX22	LPHAS(HexNAc)VPSAASPLSSGLTSFTLKPQDTR	S299 or S302
Sap130	Q8BIH0	AQSPVIT T (HexNAc) T (HexNAc)AAHAADSTLSRPTLSIQHPPSAAISQRPQQR	T284 and T285
Sap130	Q8BIH0	IT(HexNAc)LPSHPALGTPK	T320
Sap30bp	Q02614	KGTT(HexNAc)NATATSTSTASTAVADAQK	T232 or T233
Sin3a	Q60520	VS(HexNAc)KPSQLQAHTPASQQTPLPPYASPR	S251
Snbo1	Q689Z5	FIQT(HexNAc)TANTRPSVSAPAVR	T124
Sox2	P48432	S (HexNAc)EASSPPVVTSSSHSR	S248
Sox2	P48432	SEASSPPVVT(HexNAc)SSSHSR	T258
Sp2	Q9D2H6	S (HexNAc)STTTTTPVQSGANVVK	S186
Spen	Q62504	TDRPSLEKPEPIHLSV T (HexNAc)PVTQGGTVK	T2896
Spen	Q62504	TDRPSLEKPEPIHLSV T (HexNAc)QGGTVK	T2899
Taf4a	A2AC70	QVS(HexNAc)QAQTTVQPTTLQQR	S123
Taf6	Q62311	TT(HexNAc)LTITQPRPTLTLQAPQPGPR	T49
Tcf20	Q9EPQ8	T (HexNAc)EPSKSPGSLR	T725
Tet1	D0VLQ4	VSIT(HexNAc)GSADVK	T535
Tle4	Q04727	T (HexNAc)DAPTPGNSSTPGLRPVPGKPPGVDPPLASSLR	T340
Trim33	Q99PP7	QHSNPGHAGFPV S (HexNAc)AHNPINPTSPITATMANANR	S350
Trnc6a	Q3UHK8	LWSPGSVT TS (HexNAc)LAHELWK	T1646 or S1647
Vim	Q3TWW0	TYSLGSLRP S (HexNAc)R	S49
Yeats2	Q3TUF7	QEPGEAPHV ST (HexNAc)TGAASQSAFFQYVTVK	S600 and T601 mix
Yeats2	Q3TUF7	QEPGEAPHV ST (HexNAc)GAASQSAFFQYVTVK	T602
Ylpm1	Q9R0I7	QALLPTPV S (HexNAc)FGSTPPSPYHPPQSEQVNSKPLNK	S636
Zfx3	Q15911	NKNFQHPLV S (HexNAc)TANLIGPGHSFYGK	S353
Zfp281	Q3U063	VKT(Phospho)PT(HexNAc)SQSYR	T888
Zfp281	Q3U063	VKTPT S (HexNAc)QSYR	S889
Zfp281	Q3U063	STNAGFTLGHGFQFV S (HexNAc)LSSPLHNHTLFPEK	S691
Zfr	Q88532	AGYS(HexNAc)QGATQYTAQQAR	S195
Znf318	Q99PP2	TVIAHT(HexNAc)SPWTPVTTSTQTK	T1185 and S1186 mix

The gene name and accession number are given. Black denotes the unambiguous assignment of the O-GlcNAc moiety (mass addition of a HexNAc). Red denotes that the exact site is not assigned but can be localized to one of the red-colored residues. Green and blue indicate a mixture of positional isomers, wherein the corresponding colors in the annotated mass spectrum (Fig. S1) identify both positional isomers as O-GlcNAcylated. Ac, acetylation; *, Carbamido-methylation.

Table S2. All O-GlcNAc–modified peptides identified in the SILAC analyses, along with PRC2/WT ratios, as described in the main text

Gene name	O-GlcNAc–modified peptides identified from SILAC analyses	eed ^{-/-} /WT SILAC ratios	SD, n = 3
Agfg1	SSSADFGTFST(SHexNAc)QSHQTASTVSK	0.67	
Atrx	IC(Carbamidomethyl)GS(HexNAc)GLNS(Phospho)DM(Oxidation)MENNKEEGASTSEK	0.29	
Bnc2	ATS(HexNAc)GAATPVIASK	0.27	
Bptf	QTVVS(HexNAc)S(HexNAc)TENC(Carbamidomethyl)AR	1.0	0.1
Bptf	S(HexNAc)TVTTTTTVTK	0.52	0.03
Bptf	STVTTT(HexNAc)TTT(VT(HexNAc)K	0.12	
Bptf	T(HexNAc)VITEVTTMTSTVATESK	1.00	
Bptf	TVIT(HexNAc)EVT(HexNAc)TMTSTVATESK	0.27	0.02
Bptf (fragment)	IVAVNVPAT(HexNAc)QGGMVQVQK	0.91	
C1orf88 homolog	VPTST(HexNAc)KGYAIGAR	0.92	0.08
Cdk12	TS(HexNAc)TLSSQNTSQQPVQVSMK	2.42	
Cnot2	SLSQGTQLPSHVPTT(HexNAc)GVPTMSLHTPPSPSR	1.12	
Dido1	ILSSLKPGST(HexNAc)STVTAPTT(HexNAc)AAITTTASPVAATSK	1.12	
Egr1	AMVETS(HexNAc)YPSQTR	2.03	
Emsy	IIS(HexNAc)SNIVSGTTK	0.06	
Emsy	ITFT(HexNAc)KPSTQTTNTTQK	1.37	0.09
Emsy	TITVPVS(HexNAc)GSPK	0.45	
Emsy	TTS(HexNAc)GSIITVVPK	1.1	0.3
Ep400	LASPVAPGTLTSSGG(SHexNAc)APAQVVHTQQR	0.59	
HcfC1	APVT(HexNAc)VTSLPASVR	1.72	
HcfC1	IPPSSAPT(VLSPAGT(HexNAc)TIVKTAVT(HexNAc)PGTTTLPATVK	0.47	
HcfC1	IT(HexNAc)VAPGALER	0.97	0.06
HcfC1	LVTVPVT(HexNAc)VS(VKPAVTTLVVK	6.93	
HcfC1	QPETYHT(HexNAc)YTTNTPTTTR	1.2	0.3
HcfC1	QPETYHTYTTNTPTT(HexNAc)R	6.67	
HcfC1	SGTVTVAQQAQVVT(HexNAc)T(HexNAc)VVGVTK	0.78	
HcfC1	SPITIT(HexNAc)KVMSTSGTGAPAK	1.0	0.1
HcfC1	T(HexNAc)VAVTPGTTTLPATVK	1.44	0.08
HcfC1	TAAAQVGT(SHexNAc)VS(HexNAc)S(HexNAc)AANTSTRPIITVHK	0.33	
HcfC1	TAAAQVGT(SHexNAc)VSS(HexNAc)AANTSTRPIITVHK	0.76	0.09
HcfC1	TAAAQVGT(SHexNAc)VSS(HexNAc)AANTSTRPIITVHK	1.77	
HcfC1	TIPMSAIT(HexNAc)QAGATGVTSPPGIK	0.9	0.3
HcfC1	VMTSGT(HexNAc)GAPAK	0.77	
HcfC1	VTGPQAT(HexNAc)TGTPLVMTMRPASQAGK	0.70	
Jmjd1	NSPSPWLHQTPVT(HexNAc)SADGIGLLSHIPVRPSSAEPHRPHK	0.47	
Kiaa1310	VPT(HexNAc)TITLTLR	13.87	
Kiaa1551	ISTT(HexNAc)VVGANPTNEVHVK	0.41	
Kiaa1551	NNQLPTYT(HexNAc)QSLQSK	0.59	
Kiaa1551	YENQHVQNAQPVS(HexNAc)K	0.4	0.3
Lman1	RGAGT(HexNAc)PGQPGQVSSQQLDVTVK	4.9	0.2
MafK	VATT(HexNAc)SVITIVK	1.13	
Myb	TPAIKRS(HexNAc)ILESSPR	6.45	
NCoR2	GSPVTT(HexNAc)REPTPR	0.85	0.03
Nfrkb	IQTVPASHLQQGT(HexNAc)ASGSSK	0.38	
Nfrkb	QVPVNTTVVSTS(HexNAc)QSGKLPTR	0.46	
Nup53	ASTS(HexNAc)DYQVISDR	0.45	
Nup53	S(HexNAc)ISGSPVGVMEMR	0.50	
Nup153	FGIPSSSSGLS(HexNAc)QTLTSTGNFK	0.28	
Nup153	QQEPVTS(HexNAc)TSLVFGK	0.41	
Nup153	S(HexNAc)VSVTPFTYK	0.40	
Nup214	AAPGS(HexNAc)GTSTFSFAPPSK	0.45	
Nup214	HGAPGPSHT(HexNAc)VAAPQAAAAAALRR	0.28	
Nup214	SSASVTGEPPLYPTGS(HexNAc)DSSR	0.72	
Nup214	VGQAEDSTKPV(SHexNAc)K	0.67	
Phc3	SAGQT(HexNAc)QSLTIC(Carbamidomethyl)HNK	5.10	
Phf21a	FTPTTLPTS(HexNAc)QNSIHPVR	1.31	
Pogz	RPGVT(HexNAc)GENSNEVAK	0.34	
Qser1	DSTQVS(HexNAc)NGVLPQK	0.96	
Qser1	TS(HexNAc)QGTVPALAFER	0.65	
RanBP2	SVFTT(HexNAc)AASELANK	0.8	0.6
Rbm14	AQPSVS(HexNAc)LGAPYR	0.29	0.03
Rprd2	EKPVEKPAVS(HexNAc)T(HexNAc)GVPTK	0.6	0.1

Table S2. Cont.

Gene name	O-GlcNAc-modified peptides identified from SILAC analyses	eed ^{-/-} /WT SILAC ratios	SD, n = 3
Sap30bp	KGT(HexNAc)TTNATATSTASTAVADAQK	1.41	0.03
Sap130	AQSPVIT(HexNAc)T(HexNAc)AAHAADSTLSRPTLSIQHPPSAAISQRPAQSR	0.82	
Sap130	IT(HexNAc)LPSPALGTPK	0.21	
Sin3a	VS(HexNAc)KPSQLQAHTPASQQTPLPPYASPR	0.69	
Snbo1	FIQT(HexNAc)TANTRPSVSAPAVR	0.45	
Sp2	S(HexNAc)STTTTPVQSGANVVK	0.37	
Spn	TDRPSLEKPEPIHLSVST(HexNAc)PVTQGGTVK	1.03	0.06
Taf4a	QVS(HexNAc)QAQTTVQPTTLQR	0.33	
Taf6	TT(HexNAc)LTITQPRPTLTLSQLAPQGPGR	2.23	
Tet1	VSIT(HexNAc)GSADVK	0.83	
Tle4	T(HexNAc)DAPTPGSNSTPGLRPVPGKPPGVDPLASSLR	1.2	0.7
Trim33	QHSNPGHAGPFPVVS(HexNAc)AHNPINPTSPTTATMANANR	0.91	
Yeats2	QEPGEAPHVSTT(HexNAc)GAASQSAFPQYVTVK	0.65	0.02
Zfhx3	NKNFQHPLVS(HexNAc)TANLIGPGHSFYGK	2.85	
Zfp281	STNAGFTLGHGFQFVS(HexNAc)LSSPLHNHTLFPEK	0.46	
Zfp281	VKT(Phospho)PT(HexNAc)SQSYR	0.47	0.02
Zfp281	VKTPTS(HexNAc)QSYR	0.6	0.2
Zfr	AGYS(HexNAc)QGATQYTAQQAR	0.38	

SDs are reported if the particular glycopeptide was identified between biological replicates.

Table S3. O-GlcNAcylated peptides identified from this study that overlap with those reported by Wang et al. (1) and Chalkley et al. (2)

Gene name	Modification position in human, unless noted (UniProt)	UniProt ID [Wang et al. (1)]	Modified peptide sequence from Wang et al. (1) overlapping with this study	Also reported in Chalkley et al. (2)
HcfC1	T495	P51610	VTGPQAT(HexNAc)TGTPLVTRMPASQAGK	
HcfC1	S563	P51610	IPPS5(HexNAc)APTVLVSPAGTTIVK	
HcfC1	T779	P51610	TIPM-oxSAIIT(HexNAc)QAGATGVTSPPGIK	
HcfC1	T800	P51610	SPITIIIT(HexNAc)K	
HcfC1	T808	P51610	VMTSGT(HexNAc)GAPAK	
HcfC1	T861	P51610	LVTVPV(HexNAc)VSVAVKPAVTTLVVK	
Emsy	S236	Q7Z589	TITVPVS(HexNAc)GSPK	
Emsy	T501	Q7Z589	LVT(HexNAc)TPTGTQATYTRPTVSPSIGR	
Emsy	(T534/T535)	Q7Z589	(TT)(HexNAc)SGSIITVVPK	X
Emsy	S557	Q7Z589	IISS(HexNAc)NIVSGTTTK	
Nup153	S908	P49790	FGVS(HexNAc)SSSSGPSQTLTSTGNFK	
Nup153	S909	P49790	FGVSS(HexNAc)SSSSGPSQTLTSTGNFK	
Bptf	S1749 & T1753	Q12830	S(HexNAc)TVTT(HexNAc)TTTTVTK	
Rbm14	S244	Q96PK6	AQPSVS(HexNAc)LGAAAYR	
Rbm14	S280	Q96PK6	AQPSVS(HexNAc)LGAPYR	
Nfrkb	T1273	Q6P4R8	IQTVPASHLQGGT(HexNAc)ASGSSK	
Zfr	S195	Q96KR1	AGYS(HexNAc)QGATQYTAQQTR	
Qser1	(T104/S105)	Q2KHR3	(TS)(HexNAc)QGTVPALAFER	
Kiaa1310	T860	Q9P2N6	VPTT(HexNAc)ITLTLR	
NCoR1	S1487	O75376	TPVS(HexNAc)YQNTMSR	X
NCoR2	(T1569/T1570)	Q9Y618	GSPV(TT)(HexNAc)REPTPR	
Taf4a	S528	O00268	QVS(HexNAc)QAQTTVQPSATLQR	
Zfp281	S891	Q9Y2X9	TPTS(HexNAc)QSYR	

Red indicates differences in site assignments between studies.

1. Wang Z, et al. (2010) Extensive crosstalk between O-GlcNAcylation and phosphorylation regulates cytokinesis. *Sci Signal*, 10.1126/scisignal.2000526.
2. Chalkley RJ, Thalhammer A, Schoepfer R, Burlingame AL (2009) Identification of protein O-GlcNAcylation sites using electron transfer dissociation mass spectrometry on native peptides. *Proc Natl Acad Sci USA* 106:8894-8899.