

Table S1A. Summary of human α -tubulin PTM sites identified in this study

	modification site	Peptide sequence	Mass error (ppm)	score
phosphorylation site	T361	SIQFVDWCPTGFKVGINYQPP p TVVPGGDLAK	0.0	7.7
	Y319	HGKYMACCLL p YRGDVVPK	9.7	6.9
	T80, T82, T94	p TG p TYRQLFHPEQL p TGKEDAANNYAR	9.1	7.8
	T145, T150, S151	LADQCTGLQGFLVFHFSFGGG p TGSGF p T p SLLMER	0.8	7.2
	T382, Y399	AVCMLSNT p TAVAEAWARLDHKFDLM p YAK	-0.7	7.2
	T73	AVFVDLEP p TVIDEVR	4.3	6.8
	T271, S277	IHFPLA p TYAPV p SAEK	7.6	6.4
	T253, T257	LISQIVSSITASLRFDGALNVDL p TEFQ p TNLVPYPR	-8.9	7.0
	T257, Y262	FDGALNVDLTEFQ p TNLV p P p YPRHFPLATYAPVISAEK	0.0	7.9
	T349	RSIQFVDWC p TGFKVGINYQPPTVVPGGDLAK	-9.1	7.1
	T94	QLFHPEQL p TGK	-5.1	7.3
	S340	p SIQFVDWCPTGFKVGINYQPPTVVPGGDLAKVQR	6.2	6.9
	T334	DVNAAIA p TIKTKR	-9.4	6.9
	Y357, T361	VGIN p YQPP p TVVPGGDLAK	-9.5	7.6
	S170, S187,	LEF p SIYPAPQVSTAVVEPYN p SILTTHTTLEHSDCAFMVD NEAIYDICRR	-5.3	7.6
acetylation site	K40	GNACWELYCLEHGIQPDGQMPSD(ac) K	8.7	7.4
	K60	TIGGGDDSFNTFFSETGAG(ac) K	1.2	7.2
	K96	QLFHPEQLITG(ac)KEDAANNYAR	-0.3	7.8
	K112	EDAANNYARGHYTIG(ac) K	-9.7	6.7
	K163	LADQCTGLQGFLVFHFSFGGGTSGSFTSLLMERLSVDYG(ac) KK	-4.2	7.1
	K311, K326	HG(ac)K _Y MACCLLYRGDVVP(ac) K	6.6	7.1
	K336	GDVVPKDVNAAIATI(ac) K	1.3	6.7
	K394	AVCMLSNTTAIAEAWARLDH(ac) K	0.2	7.3
	K394, K401	VQRAVCMLSNTTAIAEAWARLDH(ac)KFDLMYA(ac) K	2.3	7.7
O-GlcNAc site	S6	ECI(og)SIHVGQAGVQIGNACWELYCLEHGIQPDGQMPS DK	-8.0	7.2
	T41	(og)TIGGGDDSFNTFFSETGAGKHVPR	-3.3	7.1
	T56	TIGGGDDSFNTFFSE(og)TGAGKHVPR	2.3	7.3

T80, T94	(og)TGTYRQLFHPEQLI(og)TGKEDAANNYAR	-9.2	6.9
T80	(og)TGTYRQLFHPEQLITGK	-3.5	6.7
T109	EDAANNYARGHY(og)TIGK	8.2	6.7
T145, S147	LADQCTGLQGFLVHFSFGGG(og)TG(og)SGFTSLLMERL SVD	8.5	6.9
T225	NLDIERPTY(og)TNLNR	-2.9	7.3
T257, T271, S277	FDGALNVDL(og)T EFQTNLVPYPRIHFPLA(og)T YAPVI(og)SAEK	-7.4	7.0
T334	GDVVPKDVNAAIA(og)TIK	-3.9	6.4
T340	R(og)TIQFVDWCPTGFK	3.9	7.1
T381, T382	AVCMLSN(og)T(og)TAIAEAWARLDHK	-8.8	7.7
S419	FDLMYAKRAVHWYVGEEMEEGEF(og)SEAR	9.0	6.7

ubiquitylation site	K60	TIGGGDDSFNTFFSETGAG(Ub)KHVPR	2.1	7.4
	K96	QLFHPEQLITG(Ub)KEDAANNYAR	-2.3	7.5
	K124	(Ub)KLADQCTGLQGFLVHFSFGGGTSGFTSLLMER	-8.3	7.7
	K163	LADQCTGLQGFLVHFSFGGGTSGFTSLLMERLSVDYG(Ub)K	3.2	7.4
	k311	IHFPLATYAPVISA EKAYHEQLSVAEITNACFEPANQMVK CDPRHG(Ub)KYMACL LLYR	8.8	6.9
	K326	GDVVPKDVNAAIATI(Ub)K	5.9	7.0
	K336	DVNAAIATI(Ub)KTK	1.6	7.9
	K336, K338	DVNAAIATI(Ub)KT(Ub)KR	-7.3	6.6
	K352	RSIQFVDWCPTGF(Ub)K	0.1	7.1
	K370	SIQFVDWCPTGFKVGINYQPPTVVPGGDLA(Ub)K	4.3	7.4
	K401	LDHKFDLMYA(Ub)K	-6.8	7.0

Table S1B. Summary of human β -tubulin PTM sites identified in this study

	modification site	Peptide sequence	Mass error (ppm)	score
phosphorylation site	S371, T372	TAVCDIPPRGLKMAVTFIGN pSp TAIQELFK	-0.8	7.4
	T55	ISVYYNEA p TGGKYVPR	8.2	7.3
	T166, S172	IREEYPDRIMN p TFSVVP p SPK	-9.9	6.5
	S382	MAVTFIGNSTAIQELFKR p SEQFTAMFR	-2.0	7.1
	T274, S275	LHFFMPGFAPL p TpSR	0.7	7.2
	S48, S75	Ip SVYYNEATGGKYVPRAILVDLEPGTMD p SVR	-8.5	6.8
	T312	YL p TVAAVFRGR	-8.2	6.8
	T214, S234	p TLKLTTPTYGDLNHLVSATM p SGVTTCLR	2.6	7.8
	S126,	KEAE p SCDCLQGFLTHSLGGGTGSGMGTLLISK	-9.4	7.5
	T386	RISEQF p TAM	0.6	7.4
	T285, T290	AL p TVPEL p TQQVFDAK	2.0	6.9
	S322	GRM p SMKEVDEQMLNVQNK	-6.6	7.3
	T312, S322	YL p TVAAVFRGRM p SMK	-5.8	7.1
	T366, T372	GLKMAV p TFIGN p TAIQE	8.6	7.6
	S172	IMNTFSVVP p SPK	9.1	7.4
	T166, S168, S172	EEYPDRIMN p T p SVVP p SPK	-5.3	7.3
	S168	IMNTF p SVVPSPK	-1.6	7.4
	S78, S95	p SGPFGQIFRPDNFVFGQ p SGAGNNWAK	-0.6	7.1
	T218,	L p TTPTYGDLNHLVSATMSGVTTCLRFPGQLNA	1.2	7.2
	S78	p SGPFGQIFRPDNFVFGQSGAGNNWAK	5.3	6.7
S115	GHYTEGAELVD p SVLDVVRK	0.1	7.7	
acetylation site	K58	FWEVISDEHGIDPTGTYHGSDLQLDRISVYYNEATG G(ac)K	3.7	7.3
	K103	SGPFGQIFRPDNFVFGQSGAGNNWA(ac)K	9.0	7.0
	K216	TL(ac)KLTTPPTYGDLNHLVSATMSGVTTCLR	-4.7	7.7
	K297	GSQQYRALTVPELTQQVFDA(ac)KNMMAACDPR	-10.0	7.6
	K 324	HGRYLTVAAVFRGRMSM(ac)K	-5.9	6.8
	K350	NSSYFVEWIPNNV(ac)KTAVCDIPPR	4.4	7.0
	K 362, k379	GL(ac)KMAVTFIGNSTAIQELF(ac)KRISEQFTA	-8.6	7.2
	K 392	ISEQFTAMFRR(ac)K	4.3	7.6

O-GlcNAc site	S168	EEYPDRIMNTF(og)SVVPSPK	-3.9	6.1
	S172	IMNTFSVVP(og)SPK	-6.6	7.2
	T285	AL(og)TVPELTQQVFDAKNMMAACDPR	1.1	6.0
	T290	ALTVPEL(og)TQQVFDAKNMMAACDPRHGR	-1.1	7.2
	T366	AV(og)TFIGNSTAIQELFK	-0.9	7.6
	S382	RI(og)SEQFTAM	-8.7	7.3
	ubiquitylation site	K19	MREIVHIQAGQCGNQIGA(Ub)K	-0.7
K58		ISVYYNEATGG(Ub)KYVPR	2.3	7.8
K103		MDSVRSGPFGQIFRPDNFVFGQSGAGNNWA(Ub)K	8.7	7.9
K174		IMNTFSVVPSP(Ub)K	-7.0	6.6
K324		MSM(Ub)KEVDEQMLNVQNK	1.4	8.1
K336		EVDEQMLNVQN(Ub)KNSSYFVEWIPNNVK	7.2	7.4
K336, K350		EVDEQMLNVQN(Ub)KNSSYFVEWIPNNV(Ub)K	9.6	7.1
K362		GL(Ub)KMAVTFIGNSTAIQELFKRISEQFTA	9.3	6.3
K392		RISEQFTAMFRR(Ub)K	8.4	7.1