

Table: PTMScan® Results, Ubiquitin Remnant Motif (K-epsilon-GG), SILAC

Study design: colorectal carcinoma (HCT 116) cell line; Trypsin digest; Antibody: Ubiquitin Remnant Motif (K-epsilon-GG) XP™, PTMScan® Kit #1990, #5562

Treatments: Untreated (Light), Velcade treated (Heavy)

Index	Fold-Change (Velcade/Untreated)	Protein Name	Ubiquitination Site	Description	Peptide	Accession	kD	Count in Study
1 Adaptor/scaffold								
2	0.2	AKAP12	182	A kinase (PRKA) anchor protein 12 isoform 1	FVGFK*FTVK	Q02952	191	1
3	3.4 to 4.8	AP3S1	149	adaptor-related protein complex 3, sigma 1 subunit	LEK*SEAGLAGAPAR	Q92572	22	1
4	6.6	AP3S1	166	adaptor-related protein complex 3, sigma 1 subunit	AVSAVK*NMNLPPIPR	Q92572	22	1
5	5.4 to 8.3	AP3S1	18	adaptor-related protein complex 3, sigma 1 subunit	LSK*FYQPYSEDTRQQIIR	Q92572	22	4
6	6.2 to 9.1	ENTH	625	epsin 4	QDAFANFANFSK*	Q14677	68	1
7	8.5 to 9.8	RACK1	225	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	DGQAM#LWDLNEGK*HLYTLDDGGDIINALCFSPNR	P63244	35	1
8	15.2 to 30.6	RACK1	271	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1	IIVDELK*QEVISTSSK	P63244	35	7
9	-1.5 to -1.2	14-3-3 beta	51	tyr 3-monooxygenase/trp 5-monooxygenase activ prot, beta polypep	NLLSVAYK*NVVGAR	P31946	28	3
10	3.1 to 4.5	14-3-3 epsilon	50	tyr 3-monooxygenase/trp 5-monooxygenase activ prot, epsilon polypep	NLLSVAYK*NVIGAR	P62258	29	6
11 Adhesion or extracellular matrix protein								
12	4.4	AMOTL2	100	angiomin like 2	LCPOPSK*GEEPLYTEEAK	Q9Y2J4	86	1
13	-1.2	CD44	739	CD44 antigen isoform 1 precursor	NLQNVDMK*IGV	P16070	82	1
14	8.6 to 15.5	CTNNB1	508	catenin (cadherin-associated protein), beta 1, 88kDa	LLHPPSHWPLIK*ATVGLIR	P35222	85	4
15	8.8 to 9.4	HMGCR	142	3-hydroxy-3-methylglutaryl-Coenzyme A reductase isoform 1	ASTLAK*FALSNSQDEVR	P04035	97	2
16	24.1 to 24.5	HMGCR	299	3-hydroxy-3-methylglutaryl-Coenzyme A reductase isoform 1	VSLGLDENVSK*R	P04035	97	4
17	5	HMGCR	381	3-hydroxy-3-methylglutaryl-Coenzyme A reductase isoform 1	NNQK*CDSVEEETGINR	P04035	97	2
18 Calcium-binding protein								
19	4.9	ANXA1	71	annexin I	GVDEATIIDILTK*R	P04083	39	1
20 Cell cycle regulation								
21	11.6 to 39.9	ASNS	272	asparagine synthetase	IGCLLSGGLDSSLVAATLLK*QLK	P08243	64	5
22	3.5	ASNS	478	asparagine synthetase	EAFSDGITSVK*NSWFK	P08243	64	1
23	1.1 to 1.2	CUL1	\$720	cullin 1	IMK*MR	Q13616	90	1
24	1.1	FANCI	\$523	Fanconi anemia, complementation group I isoform 1	K*AMFANQLDAR	Q9NV11	149	2
25	12.1 to 12.5	GADD45A	12	growth arrest and DNA-damage-inducible, alpha	TLEFSAGEQK*TER	P24522	18	4
26	3.5 to 5	GADD45A	18, 29	growth arrest and DNA-damage-inducible, alpha	M#DK*VGDALVELVSK*ALSQR	P24522	18	1
27	12.7 to 12.9	MAD2L1	122	MAD2-like 1	SQK*AIQDEIR	Q13257	24	2
28	8.1	CNAP1	298	non-SMC condensin I complex, subunit D2	DPSGTK*GFAAFLTELAER	Q15021	157	1
29	1.5 to 1.5	PCNA	\$164	proliferating cell nuclear antigen	DLSHIGDAVVISCAK*DGVK	P12004	29	20
30	1.7	PCNA	168	proliferating cell nuclear antigen	DLSHIGDAVVISCAKDGVK*	P12004	29	1
31	3.9	PCNA	254	proliferating cell nuclear antigen	YYLAPK*IEDEEGS	P12004	29	1
32	4.9 to 5.2	PSMB1	146	proteasome beta 1 subunit	NIIGGLDEEGK*GAVYFDPVGSYQR	P20618	26	2
33	7 to 11.8	PSMB1	164	proteasome beta 1 subunit	DSFK*AGGSASAM#LQPLLDNQVGFK	P20618	26	3
34	4.8	PSMB2	185	proteasome beta 2 subunit	IIDK*NGIHLDNISFPK	P49721	23	1
35	7.5 to 8.5	PSMB3	41	proteasome beta 3 subunit	FGIQAGM#VTDFQK*IFPM#GDR	P49720	23	3
36 Chaperone								
37	6.9	CCT2	441	chaperonin containing TCP1, subunit 2	EAVAMESYAK*ALR	P78371	57	1
38	5.3	CCT5	368	chaperonin containing TCP1, subunit 5 (epsilon)	LGFAGLVQEIFSGTK*DK	P48643	60	1
39	10.5	CCT-zeta	127	chaperonin containing TCP1, subunit 6A isoform b	IITEGFEAAK*EK	P40227	58	2
40	8.7	CCT7	463	chaperonin containing TCP1, subunit 7 isoform b	QLCDNAGFDATNLLK*LR	Q99832	59	1
41	8.2 to 10.5	HSP90A	314	heat shock 90kDa protein 1, alpha isoform 1	NPDDITNEEYGFYK*SLTNWEDHLAVK	P07900	85	3
42	-1.9 to -1.6	HSP90A	407	heat shock 90kDa protein 1, alpha isoform 1	EMLQSK*ILK	P07900	85	1
43	3.2	HSP90A	69	heat shock 90kDa protein 1, alpha isoform 1	YESLTPSK*LDSGK	P07900	85	1
44	8.2	HSP70	108	heat shock 70kDa protein 1A	VQVSYK*GETK	P08107	70	1
45	8 to 15	HSP70	159	heat shock 70kDa protein 1A	QATK*DAGVIAGLNVLK	P08107	70	3
46	5.5 to 5.5	HSP70	319	heat shock 70kDa protein 1A	STLEPVEK*ALR	P08107	70	2
47	8.1 to 9.8	HSP70	348	heat shock 70kDa protein 1A	VQK*LLQDFNFR	P08107	70	3
48	7.6 to 8.3	HSP70	\$451	heat shock 70kDa protein 1A	AMTK*DNLLGR	P08107	70	3
49	8.8 to 9.1	HSP70	\$507	heat shock 70kDa protein 1A	ITITNDK*GR	P08107	70	5
50	11.8 to 12.6	HSP70	\$524	heat shock 70kDa protein 1A	MVQAEK*YKADEVQR	P08107	70	3
51	10.8	HSP70	\$526	heat shock 70kDa protein 1A	MVQAEKYK*AEDEVQR	P08107	70	1
52	7 to 11.5	HSP70	56	heat shock 70kDa protein 1A	LIGDAK*NQVALNPQNTVFDK	P08107	70	3

LEGEND: * = modified residue; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

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Treatments: Untreated (Light), Velcade treated (Heavy)

Index	Fold-Change (Velcade/Untreated)	Protein Name	Ubiquitination Site	Description	Peptide	Accession	kD	Count in Study
53	4.1 to 5.1	HSP70	71	heat shock 70kDa protein 1A	NQVALNPQNTVFDK*R	P08107	70	4
54	6.5 to 7.6	HSPA2	109	heat shock 70kDa protein 2	VQVEYK*GETK	P54652	70	1
55	1.4 to 1.5	HSP70RY	388	heat shock 70kDa protein 4	GCALQCAILSPAFK*VR	P34932	94	4
56	9	GRP78	113	heat shock 70kDa protein 5	TWNDPSVQQDIK*FLPFK	P11021	72	1
57	4.1 to 6.7	GRP78	81	heat shock 70kDa protein 5	LIGDAAK*NQLTSPNPENTVFDK	P11021	72	3
58	3 to 3.6	GRP78	96	heat shock 70kDa protein 5	NQLTSPNPENTVFDK*R	P11021	72	2
59	4.1 to 5.3	HSC70	159	heat shock 70kDa protein 8 isoform 1	QATK*DAGTIAGLNVL	P11142	71	3
60	15 to 18	HSP27	112	heat shock protein beta-1	VSLDVIHFAPDELTVK*TK	P04792	23	4
61	18.7 to 28.8	HSP27	114	heat shock protein beta-1	TK*DGVEITGK	P04792	23	3
62	5.7	HSP27	123	heat shock protein beta-1	DGVVEITGK*HEER	P04792	23	1
63	30.2 to 34.2	HSP27	198	heat shock protein beta-1	AQLGGPEAAK*SDETAAK	P04792	23	7
64	2.7	HSP27	198, 205	heat shock protein beta-1	AQLGGPEAAK*SDETAAK*	P04792	23	1
65	161.5	HSP27	205	heat shock protein beta-1	AQLGGPEAAK*SDETAAK*	P04792	23	2
66	5.5	CCT-alpha	109	T-complex protein 1 isoform b	NADELVK*QA	P17987	60	1
67	29.6 to 34.6	CCT-alpha	466	T-complex protein 1 isoform b	SLLVIPNTLAVNAQDSTDLVAK*LR	P17987	60	3
68 Chromatin, DNA-binding, DNA repair or DNA replication protein								
69	-12.7 to -11.7	H2AFJ	\$119	H2A histone family, member J	VTIAQGGVLPNIQAVLLPK*K	Q9BTM1	14	26
70	-12.7 to -9.7	H2AFJ	\$120	H2A histone family, member J	VTIAQGGVLPNIQAVLLPKK*	Q9BTM1	14	10
71	-12.3 to -8.4	H2AX	\$119	H2A histone family, member X	LLGGVTIAQGGVLPNIQAVLLPK*K	P16104	15	11
72	-5.8 to -4.9	H2BFS	117		HAVSEGTK*AVTK	P57053	14	2
73	-11 to -10.7	H2BFS	121		AVTK*YTSK	P57053	14	4
74	-12.8 to -11.5	H2B1A	\$122	histone cluster 1, H2ba	AVTK*YTSK	Q96A08	14	3
75	0.2	H2B1D	6	histone cluster 1, H2bd	PEPTK*SAPAK	P58876	14	1
76	1.1 to 1.3	H4	\$32	histone cluster 1, H4a	DNIQGITK*PAIR	P62805	11	7
77	11.9 to 14.1	MCM7	308	minichromosome maintenance complex component 7 isoform 1	MNK*SEDDSEGAGELTR	P33993	81	3
78	1.9 to 7.6	MCM7	387	minichromosome maintenance complex component 7 isoform 1	GNINICLM#GDPGVAK*SQLLSYIDR	P33993	81	3
79	4.2 to 5	MCM7	596	minichromosome maintenance complex component 7 isoform 1	EAWASK*DATYSAR	P33993	81	1
80	10.5 to 20	MCM7	648	minichromosome maintenance complex component 7 isoform 1	DSLLGDK*GQIAR	P33993	81	2
81	13.9 to 15.5	MCM7	89	minichromosome maintenance complex component 7 isoform 1	LFADAVQELLPQYK*ER	P33993	81	2
82	7.9 to 10.6	POLD1	885	DNA-directed DNA polymerase delta 1	IDISQLVITK*ELTR	P28340	124	3
83	29.8	TYMS	169	thymidylate synthetase	VIDTIK*TMPDTRR	P04818	36	3
84	4	TYMS	99	thymidylate synthetase	GSTNAK*ELSSK	P04818	36	1
85	0.1 to 0.1	UBE2N	82	ubiquitin-conjugating enzyme E2N	IYHPNVK*LGR	P61088	17	5
86	1.6 to 1.9	VCP	109	valosin-containing protein	LGDVISIQPCPDVK*YGK	P55072	89	2
87	1.6 to 1.9	VCP	112	valosin-containing protein	LGDVISIQPCPDVKYK*	P55072	89	2
88 Cytoskeletal protein								
89	7 to 7.4	ACTA1	193	actin, alpha 1, skeletal muscle	DLTDYLMK*ILTR	P68133	42	11
90	9.2 to 10.1	ACTA1	317	actin, alpha 1, skeletal muscle	MQK*EITALAPSTMK	P68133	42	5
91	5.2	ACTA1	330	actin, alpha 1, skeletal muscle	IK*IAPPER	P68133	42	1
92	7.6 to 8.8	ACTA1	63	actin, alpha 1, skeletal muscle	DSYVGDEAQS*KR	P68133	42	5
93	2.2 to 3.9	ACTB	291	beta actin	K*DLYANTVLSGGTTM#YPGIADR	P60709	42	1
94	3.9	CAPZA1	230	F-actin capping protein alpha-1 subunit	DVQDSLTVSNEAQTAKFEIK*	P52907	33	1
95	-1.6	cofilin 1	112	cofilin 1 (non-muscle)	KEDLVFIFWAPESAPLK*SK	P23528	19	1
96	3.6 to 3.7	cofilin 1	121	cofilin 1 (non-muscle)	MIYASSK*DAIK	P23528	19	1
97	6.6 to 7.1	Destrin	92	destrin isoform b	YALYDASFETK*ESR	P60981	19	1
98	12.3 to 18.9	K1	197	keratin 1	FASFDK*VR	P04264	66	4
99	9.1 to 23.7	K10	163	keratin 10	LASYLDK*VR	P13645	60	5
100	5.8 to 7.4	K18	131	keratin 18	DWSHYFK*IIEDLR	P05783	48	1
101	9	K18	207	keratin 18	LQLETEIEALK*EELLFM#K	P05783	48	1
102	10.6 to 14.6	K18	247	keratin 18	SQDLAK*IMADIR	P05783	48	4
103	20.3 to 22.6	K18	317	keratin 18	NLK*ASLENSLR	P05783	48	4
104	6.1 to 6.2	K18	417	keratin 18	IVDGK*VWSETNDTK	P05783	48	3

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105	2.8 to 6.8	K18	426	keratin 18	VVSETNDTK*VLR	P05783	48	3
106	3.4 to 6.4	K19	208	keratin 19	TDLEM#QIEGLK*EELAYLK	P08727	44	2
107	6.4	K19	216	keratin 19	TDLEM#QIEGLK*EELAYLK*	P08727	44	1
108	17 to 17.1	K2	194	keratin 2	TLNNK*FASFDK	P35908	66	6
109	4.8 to 5.2	K8	117	keratin 8	FLEQQNK*MLETK	P05787	54	1
110	7.1 to 8.1	K8	130	keratin 8	WSLLQQQK*TAR	P05787	54	4
111	13.6 to 14.4	K8	264	keratin 8	SLDM#DSIAEVK*AQYEDIANR	P05787	54	3
112	10.8 to 12.4	K8	304	keratin 8	TK*TEISEMNR	P05787	54	2
113	7.2 to 8.2	K8	325	keratin 8	LQAEIEGLK*GQR	P05787	54	10
114	11.5	K8	96	keratin 8	TOEKEQIK*TLNNK	P05787	54	2
115	-5.7 to -4.7	profilin 1	§54	profilin 1	TFVNIPTAEVGLVVGK*DR	P07737	15	6
116	-2.4 to 0.2	profilin 1	70	profilin 1	SSFYVNGLTGGQK*CSVIR	P07737	15	3
117	1.2 to 1.3	TPT1	171	tumor protein, translationally-controlled 1	DGLEMEK*C	P13693	20	1
118	-1.3 to -1.2	TUBA1A	370	tubulin, alpha 1a	VGINYOPPTVPPGGDLAK*VQR	Q71U36	50	4
119	-1.9 to -1.8	ZFYVE28	§87	zinc finger, FYVE domain containing 28	DFCVK*FPEIR	Q9HC9	97	8
120 Endoplasmic reticulum or golgi								
121	1.8 to 2.2	AUP1	316	ancient ubiquitous protein 1	VQQLVAK*ELGQTGTR	Q9Y679	53	4
122	4.1 to 4.5	GANAB	191	alpha glucosidase II alpha subunit isoform 2	VSQGSK*DPAEGDGAQPEETPR	Q14697	107	1
123 Enzyme, misc.								
124	4.1	AASDHPPT	263	aminoacidipate-semialdehyde dehydrogenase-phosphopantetheinyl transf	HQDVPSQDDSK*PTQR	Q9NRN7	36	1
125	7.5 to 8.5	AGPAT5	183	1-acylglycerol-3-phosphate O-acyltransferase 5	YNPEQTK*VLSASQFAAQR	Q9NUQ2	42	1
126	-1.3 to -1.2	ALDH1A3	360	aldehyde dehydrogenase 1A3	TEQGPQIDQK*QFDK	P47895	56	2
127	5.7	ASPH	104	aspartate beta-hydroxylase isoform a	LGIYDADGGDGFVDDAK*VLLGLK	Q12797	86	1
128	1.9 to 6.9	COX7A2	46	cytochrome c oxidase subunit VIIa polypeptide 2 (liver) precursor	LFQEDDEIPLYK*GGVADALLYR	P14406	9	2
129	11 to 11.5	CYP51A1	121	cytochrome P450, family 51, subfamily A, polypeptide 1 isoform 1	TFTYLLGSDAAALLFNSK*NEDLNAEDVYSR	Q16850	57	1
130	5.5 to 6	CYP51A1	358	cytochrome P450, family 51, subfamily A, polypeptide 1 isoform 1	TVKGCENPLTYDQLK*DLNLLDR	Q16850	57	1
131	10.7 to 11.8	CYP51A1	412	cytochrome P450, family 51, subfamily A, polypeptide 1 isoform 1	LK*DSWVER	Q16850	57	1
132	8.8 to 9.9	DDX3	554	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	NINITK*DLDLLLVEAK	Q00571	73	4
133	5	DHCR7	88	7-dehydrocholesterol reductase	LSDIWAK*TPPI1R	Q9UBM7	54	1
134	5.6 to 6.5	DHFR	156	dihydrofolate reductase	IM#QDFESDTFFPEIDLEK*YK	P00374	21	1
135	5.5	DHFR	158	dihydrofolate reductase	IM#QDFESDTFFPEIDLEK*YK	P00374	21	1
136	4.2	DPM1	80	dolichyl-phosphate mannosyltransferase polypeptide 1	DVAEQLEK*IYGS DR	Q60762	30	1
137	7.6 to 12.8	FASN	1072	fatty acid synthase	LYTLQDK*AQVADV VVSR	P49327	273	3
138	1.8 to 2	FASN iso2	1179	fatty acid synthase	AALQELQLCK*GLVQALQTK	Q4LE83	277	10
139	5 to 8.2	FASN	1239	fatty acid synthase	ACLDTAVENMPSLK*MK	P49327	273	2
140	10.1	FASN	1241	fatty acid synthase	ACLDTAVENMPSLK*MK	P49327	273	1
141	5 to 6	FASN	1429	fatty acid synthase	WVESLK*GILADEDSSRFVWLK	P49327	273	2
142	6.7	FASN	1582	fatty acid synthase	DIM#LATGK*LSPDAIPGK	P49327	273	1
143	5.6 to 11	FASN	1704	fatty acid synthase	VFTTVGSAEK*R	P49327	273	5
144	5.6	FASN	1927	fatty acid synthase	TGYQAK*QVR	P49327	273	1
145	6.2 to 6.5	FASN	213	fatty acid synthase	LGM#LSPGCTCK*AFDTAGNGYCR	P49327	273	3
146	6.4	FASN	235	fatty acid synthase	SEGVAVLLTK*K	P49327	273	1
147	20.8 to 20.8	FASN	2391	fatty acid synthase	VLEALLPK*GLEER	P49327	273	2
148	5.4 to 6.5	FASN	528	fatty acid synthase	SDEAVK*PFG LK	P49327	273	2
149	4.9	FTL	68	ferritin, light polypeptide	LLK*MQNQR	P02792	20	1
150	2.4	GALE	338	UDP-galactose-4-epimerase	WQK*ONPSGFGTQA	Q14376	38	1
151	5 to 7.1	GOT1	97	aspartate aminotransferase 1	LALGDDSPALK*EK	P17174	46	2
152	3.3	GSTP1	82	glutathione transferase	TLGLYK*DOQEALVDM#VNDGVEDLR	P09211	23	1
153	3.8	ISYNA1	393	inositol-3-phosphate synthase 1	YYPYVGDGSK*R	Q9NPH2	61	1
154	10.7	ME1	492	cytosolic malic enzyme 1	QITDNIFLTAEVIAQVSDK*HLEEGR	P48163	64	1
155	13.5 to 30.3	NQO1	209	NAD(P)H menadiene oxidoreductase 1, dioxin-inducible isoform a	IQILEGWK*K	P15559	31	4
156	5.9 to 10.1	NQO1	271	NAD(P)H menadiene oxidoreductase 1, dioxin-inducible isoform a	SIPTDNQIK*AR	P15559	31	2

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157	16.9	NQ01	31	NAD(P)H menadione oxidoreductase 1, dioxin-inducible isoform a	EAAAAALK*K	P15559	31	1
158	5.2	NQ01	59	NAD(P)H menadione oxidoreductase 1, dioxin-inducible isoform a	DITGK*LKDPANFQYPAESVLYAK	P15559	31	1
159	4.7 to 5.4	NQ01	90	NAD(P)H menadione oxidoreductase 1, dioxin-inducible isoform a	EGHLSPDIVAEQK*K	P15559	31	5
160	12.9	NQ01	91	NAD(P)H menadione oxidoreductase 1, dioxin-inducible isoform a	EGHLSPDIVAEQK*K*	P15559	31	1
161	4.7	NQ02	90	NAD(P)H dehydrogenase, quinone 2	SLASDITDEQK*K	P16083	26	1
162	9.9	WBSCR20A	262	NOL1/NOP2/Sun domain family, member 5 isoform 2	IFAFDLDAK*R	Q96P11-2	50	1
163	6.3	P4HA2	134	prolyl 4-hydroxylase, alpha II subunit isoform 2 precursor	QFFPTDEDEIGAAK*ALMR	O15460	61	1
164	6.6 to 8	PELO	270	pelota homolog	LSDTK*AAGEVK	Q9BRX2	43	1
165	5.5 to 6	PSAT1	94	phosphoserine aminotransferase isoform 2	VIFLOGGGCGQFSAVPLNLIQK*AGR	Q9Y617	40	4
166	5.8	PYGL	514	liver glycogen phosphorylase	IGEDYVK*DLSQLTK	P06737	97	1
167	1 to 1.2	RPN1	538	ribophorin I precursor	LK*TEGSDLCDR	P04843	69	2
168	4.5	RUVBL2	223	RuvB-like 2	DYDAMGSGTK*FVQCPDGELQK	Q9Y230	51	1
169	3.7 to 4	RUVBL2	234	RuvB-like 2	FVQCPDGELQK*R	Q9Y230	51	3
170	4.2 to 4.9	SETD8	236	SET domain-containing 8	SK*AELQSEER	Q9NOR1	43	1
171	-1.3 to -1.3	TKT	281	transketolase isoform 1	NM#AEQIQEIQSIQSK*K	P29401	68	4
172	-1.3	TKT	282	transketolase isoform 1	NM#AEQIQEIQSIQSK*K*	P29401	68	1
173	7.9 to 10	TXNL1	102	thioredoxin-like 1	IDQYQGADAVGLEEK*K	O43396	32	2
174	7.8	TXNL1	104	thioredoxin-like 1	IDQYQGADAVGLEEK*K*	O43396	32	1
175	1.3 to 2.5	WRNIP1	§310	Werner helicase interacting protein isoform 1	DVIK*QAONEK	Q96S55	72	1
176	G protein or regulator							
177	11.2	GNAH1	46	guanine nucleotide binding prot (G prot), a-inhibiting activity polypep 1	LLLLGAGESGK*STIVK	P63096	40	1
178	6.2 to 6.9	Net1	194	neuroepithelial cell transforming gene 1 isoform 1	GEQDLIEDLK*LAR	Q7Z628	68	2
179	-5.1	Rab7	126	RAB7, member RAS oncogene family	DPENFFVVLGNK*IDLENR	P51149	23	1
180	Kinase (non-protein)							
181	2.3 to 2.5	PIP5K1A	§103	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha isoform 3	GAQLGITHTVGSLSLK*PER	Q99755	63	17
182	7	PKLR	348	pyruvate kinase, liver and RBC isoform 1	GDLGIEIPAEM*VFLAQK	P30613	62	1
183	Mitochondrial protein							
184	6.5 to 9.2	ALDOA	28	fructose-bisphosphate aldolase A	IVAPGK*GILAADESTGSIK	P04075	39	2
185	6.6 to 7.1	GAPDH	194	glyceraldehyde-3-phosphate dehydrogenase	TVDGPSGK*LWR	P04406	36	4
186	3.8 to 5.2	GAPDH	215	glyceraldehyde-3-phosphate dehydrogenase	GALQNIIPASTGAAK*AVGK	P04406	36	1
187	6.4	GAPDH	219	glyceraldehyde-3-phosphate dehydrogenase	AVGK*VPELNGK	P04406	36	1
188	4.7 to 11.1	GAPDH	263	glyceraldehyde-3-phosphate dehydrogenase	VVK*QASEGPLK	P04406	36	3
189	6.3 to 7.7	GART	107	phosphoribosylaminoimidazole synthetase isoform 1	SAGVQCFGPTAEAAQLSSK*R	P22102	108	2
190	7.2 to 9	PKM2	475	pyruvate kinase, muscle isoform M2	GIFVVLCK*DPVQEAWADVLR	P14618	58	3
191	Motor or contractile protein							
192	7 to 8.2	MYL6	26	myosin, light chain 6, alkali, smooth muscle and non-muscle isoform 1	TGDGK*ILYSQCGDVMR	P60660	17	3
193	6.2	MYL6	50	myosin, light chain 6, alkali, smooth muscle and non-muscle isoform 1	ALGQNPTNAEVLK*VLGNPK	P60660	17	3
194	6.8 to 9.3	MYL6	81	myosin, light chain 6, alkali, smooth muscle and non-muscle isoform 1	NK*DQGTIEDYVEGLR	P60660	17	3
195	Phosphatase							
196	24.7 to 26.9	MKP-1	280	dual specificity phosphatase 1	VK*LDEAFEFVK	P28562	39	2
197	44.6 to 50.9	MKP-1	289	dual specificity phosphatase 1	LDEAFEFVK*QR	P28562	39	9
198	8	MKP-2	16	dual specificity phosphatase 4 isoform 1	EMDCSVLK*R	O13115	43	1
199	3.4 to 3.6	MKP-2	160	dual specificity phosphatase 4 isoform 1	FSSEYPEFCCK*TK	Q13115	43	2
200	2.2	DUSP5	144	dual specificity phosphatase 5	GGYETFYSEYPECCVDVK*PISQEK	Q16690	42	1
201	8.8 to 9	MKP-3	254	dual specificity phosphatase 6 isoform a	YILNVTPLNPLFNENAGEFK*YK	Q16828	42	2
202	5.8	MKP-3	324	dual specificity phosphatase 6 isoform a	LNLMSMDAYDIVK*M#K	Q16828	42	1
203	8.2	PDP1	202	pyruvate dehydrogenase phosphatase precursor	HPNDYFSK*EASK	Q9P0J1	61	1
204	6.5	PPP1CB	40	protein phosphatase 1, catalytic subunit, beta isoform 1	GLCIK*SR	P62140	37	1
205	1.2 to 1.2	PPP2CA	21	protein phosphatase 2, catalytic subunit, alpha isoform	ELDQWIEQLNECK*QLSESQVK	P67775	36	3
206	4.5	PPP2CA	29	protein phosphatase 2, catalytic subunit, alpha isoform	QLSESQVK*SLCEK	P67775	36	1
207	5.5 to 6.2	PPP2CA	41	protein phosphatase 2, catalytic subunit, alpha isoform	EILTK*ESNVQEVK	P67775	36	2

LEGEND: * = modified residue; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Ubiquitin Remnant Motif (K-epsilon-GG), SILAC

Study design: colorectal carcinoma (HCT 116) cell line; Trypsin digest; Antibody: Ubiquitin Remnant Motif (K-epsilon-GG) XP™, PTMScan® Kit #1990, #5562

Treatments: Untreated (Light), Velcade treated (Heavy)

Index	Fold-Change (Velcade/Untreated)	Protein Name	Ubiquitination Site	Description	Peptide	Accession	kD	Count in Study
208 Protease								
209	5 to 6.2	APEH	180	N-acylaminoacyl-peptide hydrolase	AESFFQTK*ALDVSASDDEIAR	P13798	81	1
210	4.5	PSMA2	165	proteasome subunit alpha type 2	ATAMGK*NYVNGK	P25787	26	1
211	3.9 to 4	PSMA2	171	proteasome subunit alpha type 2	NYVNGK*TFLEK	P25787	26	2
212	7.4 to 7.5	PSMA4	199	proteasome alpha 4 subunit isoform 1	VLNK*TMDSVK	P25789	29	1
213	5.3 to 7.9	PSMA5	192	proteasome alpha 5 subunit	SMTLK*EAIK	P28066	26	2
214	6.9	PSMA5	239	proteasome alpha 5 subunit	EELVEVK*DI	P28066	26	1
215	4.1 to 5.1	PSMB6	67	proteasome beta 6 subunit	VTDK*LTIPIHDR	P28072	25	2
216	5.3 to 7.7	PSMB7	249	proteasome beta 7 subunit proprotein	CEK*GTTAVLTEK	Q99436	30	1
217	4.7	PSMB7	72	proteasome beta 7 subunit proprotein	ATEGMVVADK*NCSK	Q99436	30	1
218	9.8 to 15.9	PSMC2	248	proteasome 26S ATPase subunit 2	VIGSELVQK*YVGEGAR	P35998	49	2
219	-1.7 to -1.3	PSMC6	197	proteasome 26S ATPase subunit 6	AVASQLDCLNFK*VSSSIVDK	P62333	44	7
220	-1.3 to 1.3	PSMD1	310	proteasome 26S non-ATPase subunit 1	TSSAFVGK*TPESASPEPK	Q99460	106	3
221	2.1	PSMD1	840	proteasome 26S non-ATPase subunit 1	VSTAVLSITAKAK*	Q99460	106	1
222	6.6 to 7.7	PSMD12	52	proteasome 26S non-ATPase subunit 12 isoform 1	LOEVITLLSLEK*QTR	Q00232	53	4
223	6.5 to 8.7	PSMD14	152	26S proteasome-associated pad1 homolog	AVAVVVDPIQSVK*GK	Q00487	35	5
224	8.2 to 8.7	PSMD14	253	26S proteasome-associated pad1 homolog	EMLELAK*NYNK	Q00487	35	2
225	3.7 to 6.3	PSMD14	257	26S proteasome-associated pad1 homolog	NYNK*AVEEEDKMTPEQLAIK	Q00487	35	3
226	5.2	PSMD2	860	proteasome 26S non-ATPase subunit 2	VGQAVDVVGGQAGPK*	Q13200	100	1
227	4.6 to 5.7	PSMD3	440	proteasome 26S non-ATPase subunit 3	LQLDSPEDAEIFVAK*AIR	Q43242	61	1
228	5.7	PSMD4	40	proteasome 26S non-ATPase subunit 4	LOAQQDAVNIVCHSK*TR	P55036	41	1
229	5 to 6.3	SEC11A	114	SEC11-like 1	FLTK*GDMNAVDDR	P67812	21	2
230	3.8	USP48	170	ubiquitin specific protease 48 isoform b	YIDPSGFVK*ALGLDGTGQQDAQEFSK	Q86UV5	119	1
231 Protein kinase, Ser/Thr (non-receptor)								
232	15.5 to 17.2	CDK1	20	cell division cycle 2 isoform 3	IGEGTYGWYK*GR	P06493	34	4
233	10.8	CDK1	238	cell division cycle 2 isoform 3	ALGTPNNEVWPEVESLDQYK*NTFFPK	P06493	34	1
234	14.2	CDK1	274	cell division cycle 2 isoform 3	MLIYDPAK*R	P06493	34	1
235	4.9	CDK1	34	cell division cycle 2 isoform 3	TTGQVAMKK*	P06493	34	1
236	12.7	CDK1	56	cell division cycle 2 isoform 3	EISLLK*ELR	P06493	34	2
237	4.6 to 5.7	CDK9	35	cyclin-dependent kinase 9	IGQGTGFGEVFK*AR	P50750	43	2
238	3.7 to 5.1	MELK	650	maternal embryonic leucine zipper kinase	LVEDILSSCK*V	Q14680	75	1
239	6.4	Pim1	285	non-specific serine/threonine protein kinase	LIDFGSGALLK*DTVYTFDFGTR	P11309	45	1
240	5.7	DNA-PK	225	protein kinase, DNA-activated, catalytic polypeptide isoform 2	LPVLAGCLK*GLSSLCLNFTK	P78527	469	1
241 Protein kinase, atypical								
242	0.3	TIF1-beta	261	tripartite motif-containing 28 protein	LLASLVK*R	Q13263	89	1
243 RNA processing								
244	6.2 to 6.3	eIF4A1	193	eukaryotic translation initiation factor 4A isoform 1	GFK*DQIYDIFQK	P60842	46	3
245	26.7 to 32.4	eIF4A1	309	eukaryotic translation initiation factor 4A isoform 1	DFTVSAMHGDMQK*ER	P60842	46	8
246	6.8 to 14.7	eIF4A1	369	eukaryotic translation initiation factor 4A isoform 1	K*GVAINMVTDEEKR	P60842	46	3
247	14	eIF4A1	381	eukaryotic translation initiation factor 4A isoform 1	KGVAINMVTDEEK*R	P60842	46	1
248	0.1 to 0.1	hnRNP A/B	82	heterogeneous nuclear ribonucleoprotein A/B isoform b	MFVGGLSWDTSK*K	Q99729	36	1
249	0.1	hnRNP A/B	83	heterogeneous nuclear ribonucleoprotein A/B isoform b	MFVGGLSWDTSKK*	Q99729	36	1
250	5.4	hnRNP H1	35	heterogeneous nuclear ribonucleoprotein H1	FFSDCK*IQNGAQGIR	P31943	49	1
251	2.6	hnRNP E1	351	poly(rC) binding protein 1	LSSEK*GMGCS	Q15365	37	1
252	10 to 10.5	RNaseH2A	64	ribonuclease H2, large subunit	LADLEALK*VADSK	Q75792	33	1
253	6.2 to 8	SF3B1	1102	splicing factor 3b, subunit 1 isoform 2	AIGPHDVLATLLNLLK*VQER	Q75533	146	3
254	3.7	TARDBP	181	TAR DNA binding protein	LPNSK*QSQDEPLR	Q13148	45	1
255 Receptor, channel, transporter or cell surface protein								
256	9.7 to 10.8	ABCE1	158	ATP-binding cassette, sub-family E, member 1	GSELQNYFTK*ILEDLTK	P61221	67	4
257	5.7	BSG	173	basigin isoform 1 precursor	WLK*GGVWLK	P35613	42	1
258	17.6 to 25.5	CPNE1	157	copine I isoform b	DFLGK*SDPFLFFRR	Q99829	59	1
259	11	DNAJC1	216	DnaJ (Hsp40) homolog, subfamily C, member 1	K*PQWHDLPLCK	Q96KC8	64	1

LEGEND: * = modified residue; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Ubiquitin Remnant Motif (K-epsilon-GG), SILAC

Study design: colorectal carcinoma (HCT 116) cell line; Trypsin digest; Antibody: Ubiquitin Remnant Motif (K-epsilon-GG) XP™, PTMScan® Kit #1990, #5562

Treatments: Untreated (Light), Velcade treated (Heavy)

Index	Fold-Change (Velcade/Untreated)	Protein Name	Ubiquitination Site	Description	Peptide	Accession	kD	Count in Study
260	5.1	FDF1	358	farnesyl-diphosphate farnesyltransferase 1	IPDSDPSSSK*TR	P37268	48	1
261	4.8 to 5.1	GNAL	60	guanine nucleotide binding prot (G prot), a-activating activity polypep	STIVK*QMR	P38405	44	1
262	6.5 to 11.4	G-alpha-s	274	GNAS complex locus GNASL	LQEALNLFK*SIWNNR	P63092	46	4
263	11.1	G-alpha-s	307	GNAS complex locus GNASL	SK*IEDYFPEFAR	P63092	46	2
264	10.3 to 10.9	HAAA	200	major histocompatibility complex, class I, A precursor	YLENGK*ETLQR	P01892	41	4
265	1.4	myoferlin	102	myoferlin isoform a	SLPYK*LISLLNEK	Q9NZM1	235	2
266	4.5	NUP107	690	nucleoporin 107kDa	AEALK*QGNAIMR	P57740	106	1
267	4.7 to 6.3	NUP155	740	nucleoporin 155kDa isoform 2	NSQFAGGPLGNPNTAK*VQQR	Q75694	155	3
268	3.4	NUP188	109	nucleoporin 188kDa	DSVK*TVLQDER	Q5SRE5	196	1
269	7.4 to 7.6	NUP205	321	nucleoporin 205kDa	LQDSQLWK*LPLGLQATVR	Q92621	228	1
270	8.4 to 11.9	NUP205	69	nucleoporin 205kDa	VQK*ASTEGVAIQGQGGTR	Q92621	228	2
271	3.2 to 3.9	NUP88	150	nucleoporin 88kDa	NSEFEGGK*STVNCSTTPVAER	Q99567	84	1
272	8.5	NUP93	243	nucleoporin 93kDa	QMTDVLTPATDALK*NR	Q8N1F7	93	2
273	9.1 to 17.1	SCD	162	stearoyl-CoA desaturase 1	AHKK*FSETHADPHNSR	Q00767	42	4
274	7.4 to 8.8	SCD	196	stearoyl-CoA desaturase 1	EK*GSTLDLSDLEAEK	Q00767	42	2
275	12.7 to 17.3	SCD	341	stearoyl-CoA desaturase 1	VSK*AAILAR	Q00767	42	2
276	8 to 8.9	SCD	60	stearoyl-CoA desaturase 1	DDIYDPTYK*DK	Q00767	42	1
277	13	SCD	62	stearoyl-CoA desaturase 1	DDIYDPTYKDK*	Q00767	42	1
278	1.4	SLC1A5	537	solute carrier family 1 member 5 isoform 2	GPAGDATVASEK*ESVM	Q15758	57	1
279	7.5 to 7.9	SLC3A2	368	solute carrier family 3 member 2 isoform a	DASSFLAEWQNTK*GFSEDR	P08195	68	2
280	6.4	VDAC-2	31	voltage-dependent anion channel 2	DIFNK*GFGFLVK	P45880	32	1
281	Transcriptional regulator							
282	5.9 to 7.9	calreticulin	159	calreticulin precursor	NVLINK*DIR	P27797	48	1
283	3.7 to 3.9	calreticulin	62	calreticulin precursor	FYGDEEK*DKGLQTSQDAR	P27797	48	1
284	7.8 to 9.6	CCND1	33	cyclin D1	AMLK*AEETCAPSVSYFK	P24385	34	2
285	5.1 to 6.8	NF-GMB	124	cold shock domain protein A isoform b	EDVFNHQAIAIK*K	P16989	40	3
286	5.2	NF-GMB	125	cold shock domain protein A isoform b	EDVFNHQAIAIK*	P16989	40	1
287	11.3 to 16.4	ENO1	221	enolase 1	DATNVGDEGGFAPNILENK*EGLELLK	P06733	47	1
288	1.7 to 4.9	ENO1	285	enolase 1	SFIK*DYPVWSIEDPFDQDDWGAWQK	P06733	47	2
289	11.8	Id1	20	inhibitor of DNA binding 1 isoform a	VASGSATAAAGPSCALK*AGK	P41134	16	2
290	6.7 to 6.9	Id1	23	inhibitor of DNA binding 1 isoform a	AGK*TASGAGEVVR	P41134	16	1
291	140.5	ILF2	141	interleukin enhancer binding factor 2	ILPTLEAVALGNK**VVESLR	Q12905	43	1
292	3	CRSP6	169	mediator complex subunit 17	LTK*SVTENQENK	Q9NVC6	73	1
293	4.6 to 4.8	CRSP6	178	mediator complex subunit 17	SVTENQENK*LQR	Q9NVC6	73	1
294	4.4 to 5.5	CRSP6	415	mediator complex subunit 17	LSGPQAFDK*NEINLSQSEGLLEK	Q9NVC6	73	1
295	9.2 to 9.4	Myc	389	myc proto-oncogene protein	DQIPELENNEK*APK	P01106	49	2
296	3	NONO	279	non-POU domain containing, octamer-binding isoform 1	ALIMEK*QQDQVDR	Q15233	54	1
297	4 to 4.7	POLR2A	1350	DNA-directed RNA polymerase II A	VLSEK*DVPVVR	P24928	217	2
298	4.8 to 6.7	POLR2B	264	DNA directed RNA polymerase II polypeptide B	IVATLPYIK*QEVPIIVFR	P30876	134	3
299	3 to 3.8	POLR2B	869	DNA directed RNA polymerase II polypeptide B	VSGDDVIIGK*TVTLPENEDELESTNR	P30876	134	2
300	6.6 to 7	POLR2B	993	DNA directed RNA polymerase II polypeptide B	VSANK*GEIGDTPFNDAVNVQK	P30876	134	2
301	7.4	TBP7	238	proteasome 26S ATPase subunit 4 isoform 1	VVGSEFVQK*YLGEGR	P43686	47	1
302	17.6	TBP7	273	proteasome 26S ATPase subunit 4 isoform 1	ENAPAFIDEIDAIATK*R	P43686	47	1
303	4.9 to 7.7	PSMC5	287	proteasome 26S ATPase subunit 5	TMLELLNLQDGFQATK*NIK	P62195	46	3
304	7.4	PSMC5	290	proteasome 26S ATPase subunit 5	TMLELLNLQDGFQATKNIK*	P62195	46	2
305	-2	PTMA	103	prothymosin, alpha isoform 1	AAEDDEDVDTK*K	P06454	12	2
306	-2	PTMA	104	prothymosin, alpha isoform 1	AAEDDEDVDTKK*	P06454	12	1
307	4.5 to 6.6	SQSTM1	91	sequestosome 1 isoform 2	SYVK*DDIFR	Q13501	48	1
308	4.4 to 5	TRXR1	430	thioredoxin reductase 1 isoform 3	IICNTK*DNER	Q16881	54	1
309	6.4	TRXR1	457	thioredoxin reductase 1 isoform 3	VVGFHVLGPNAGEVTQGFAAALK*CGLTK	Q16881	54	2

Table: PTMScan® Results, Ubiquitin Remnant Motif (K-epsilon-GG), SILAC

Study design: colorectal carcinoma (HCT 116) cell line; Trypsin digest; Antibody: Ubiquitin Remnant Motif (K-epsilon-GG) XP™, PTMScan® Kit #1990, #5562

Treatments: Untreated (Light), Velcade treated (Heavy)

Index	Fold-Change (Velcade/Untreated)	Protein Name	Ubiquitination Site	Description	Peptide	Accession	kD	Count in Study
310 Translation								
311	1.2 to 1.2	eEF-2	239	eukaryotic translation elongation factor 2	FAAK*GEGQLGPAER	P13639	95	9
312	1.5	eEF-2	275	eukaryotic translation elongation factor 2	YFDPANGKFSK*	P13639	95	2
313	6.3	CDA02	305	eukaryotic translation initiation factor 2A	ATIFNLK*CDPVDFGTGPR	Q9BY44	65	2
314	6.9 to 7.8	eIF3E	120	eukaryotic translation initiation factor 3, subunit 6 48kDa	MLFDYLADK*HGFR	P60228	52	2
315	-1.1 to -1.1	eIF3E	193	eukaryotic translation initiation factor 3, subunit 6 48kDa	LK*ETIDNNSVSSPLQSLQQR	P60228	52	3
316	7 to 10.6	eIF3E	265	eukaryotic translation initiation factor 3, subunit 6 48kDa	YLTTAVITNK*DVR	P60228	52	2
317	5	eIF3E	29	eukaryotic translation initiation factor 3, subunit 6 48kDa	HLVFPLLLEFLSVK*EYNEK	P60228	52	1
318	5.9	eIF3E	35	eukaryotic translation initiation factor 3, subunit 6 48kDa	EYNEK*ELLOGK	P60228	52	1
319	9.3 to 16.8	eIF3E	383	eukaryotic translation initiation factor 3, subunit 6 48kDa	LDAK*IDSK	P60228	52	1
320	11.7 to 19	eIF3E	82	eukaryotic translation initiation factor 3, subunit 6 48kDa	TTVVAQLK*QLQAETEPIVK	P60228	52	5
321	6.5	eIF3E	93	eukaryotic translation initiation factor 3, subunit 6 48kDa	QLQAETEPIVK*MFEDPETTR	P60228	52	4
322	5.7 to 5.9	eIF3-beta	141	eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa	DPSQIDNNPEYMK*IPCNDSK	Q13347	37	1
323	11.6 to 12.2	eIF3-beta	30	eukaryotic translation initiation factor 3, subunit 2 beta, 36kDa	EGDLLFTVAK*DPVNWVWYSVNGER	Q13347	37	3
324	5	RPL10	101	ribosomal protein L10	INK*MLSCAGADR	P27635	25	1
325	8.5 to 10	RPL10	§188	ribosomal protein L10	FNADEFEDMVAEK*R	P27635	25	3
326	19 to 20.8	RPL15	140	ribosomal protein L15	FFEVILIDPFHK*AIR	P61313	24	10
327	5.1	RPL18a	136	ribosomal protein L18a	VEEIAASK*CR	Q02543	21	1
328	9.2 to 10.2	RPL19	46	ribosomal protein L19	LIK*DGLIIR	P84098	23	1
329	2.5	RPL23A	152	ribosomal protein L23a	LAPDYDALDVANK*IGII	P62750	18	1
330	5	RPL34	19	ribosomal protein L34	LSYNTASNK*TR	P49207	13	1
331	4 to 5.5	RPL35A	45	ribosomal protein L35a	DETEFLGK*R	P18077	13	1
332	3.8 to 6.7	RPL35A	63	ribosomal protein L35a	NNTVTPGGK*PNK	P18077	13	1
333	16.8 to 18.3	RPL38	67	ribosomal protein L38	QSLPPGLAVK*ELK	P63173	8	2
334	2.1 to 2.7	RPL6	207	ribosomal protein L6	IDISNVK*IPK	Q02878	33	1
335	-1.6 to -1.5	RPL9	21	ribosomal protein L9	TILSNQTVDPENVDITLK*GR	P32969	22	4
336	0.2	RPS10	107	ribosomal protein S10	PK*GLEGERPAR	P46783	19	1
337	3.3 to 6.3	RPS11	45	ribosomal protein S11	NIGLGFK*TPK	P62280	18	1
338	5	RPS14	106	ribosomal protein S14	TK*TPGGAQSALR	P62263	16	1
339	9.9	RPS16	50	ribosomal protein S16	TLQYK*LLEPVLLLGK	P62249	16	1
340	0.2	RPS17	107	ribosomal protein S17	EM#LK*LLDFGSLSNLQVTQPTVGM#NFK	P08708	16	1
341	-5.5 to -4.9	RPS20	§8	ribosomal protein S20 isoform 2	DTGK*TPVEPEVAIHR	P60866	13	6
342	5.6	RPS27	16	ribosomal protein S27	DLLHPSPEEEK*R	P42677	9	1
343	-3.5 to -3.3	RPS27A	37	ubiquitin and ribosomal protein S27a precursor	YYKVDENK*ISR	P62979	9	18
344	2.7	RPS3	62	ribosomal protein S3	TQNVLGEK*GR	P23396	27	1
345	8.2 to 11.8	RPS5	182	ribosomal protein S5	TIAECLADELINAAK*GSSNSYAIAK	P46782	23	4
346	4.5 to 6.6	TARS	243	threonyl-tRNA synthetase	ILNEK*VNTPTTIVY	P26639	83	1
347 Tumor suppressor								
348	1.9 to 2.2	NM23	§100	non-metastatic cells 1, protein (NM23A) expressed in isoform b	VMLGETNPADSK*PGTIR	P15531	17	2
349	1.2	NM23	12	non-metastatic cells 1, protein (NM23A) expressed in isoform b	TFIAIK*PDGVQR	P15531	17	1
350	0.1	SASH1	211	SAM and SH3 domain containing 1	M#ITIEALARLK*	Q94885	137	1
351 Ubiquitin conjugating system								
352	-5.2 to 0.1	BIRC6	2242	baculoviral IAP repeat-containing 6	GSSYK*LLVEQAK	Q9NR09	528	2
353	-1.6 to -1.3	CUL5	724	Vasopressin-activated calcium-mobilizing receptor-1	TOEAIQIMK*MR	Q93034	91	26
354	6.4	ETE1	146	UBX domain containing 8	VTDPVGDIVSFMHSFEK*YGR	Q96CS3	53	1
355	3.5 to 4	HUWE1	3452	HECT, UBA and WWE domain containing 1	SLLTEK*LLR	Q72627	482	2
356	5.1	RNF167	156	ring finger protein 167	ALFVYEK*GAR	Q9H6Y7	38	1
357	7.7 to 11.9	TRIAD3	362	ring finger protein 216 isoform a	IDFFDYSK*LTPLDQR	Q9NWF9	99	1
358	8.2	TRIM47	257	tripartite motif-containing 47	TVALIK*SAVAER	Q96LD4	69	2

LEGEND: * = modified residue; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Ubiquitin Remnant Motif (K-epsilon-GG), SILAC

Study design: colorectal carcinoma (HCT 116) cell line; Trypsin digest; Antibody: Ubiquitin Remnant Motif (K-epsilon-GG) XP™, PTMScan® Kit #1990, #5562

Treatments: Untreated (Light), Velcade treated (Heavy)

Index	Fold-Change (Velcade/Untreated)	Protein Name	Ubiquitination Site	Description	Peptide	Accession	kD	Count in Study
359		Unknown function						
360	-1.6 to -1.4	ADRM1	§34	adhesion regulating molecule 1 precursor	MSLK*GTTVTPDKR	Q16186	42	19
361	9.3	AP2S1	133	adaptor-related protein complex 2, sigma 1 subunit isoform AP17	VLK*QLLM#LQSLQ	P53680	17	1
362	17.8 to 29.3	ARL6IP	96	ADP-ribosylation factor-like 6 interacting protein	IFGSNK*WTEQQQR	Q15041	23	6
363	5.2 to 7.2	ARMC6	361	armadillo repeat containing 6	AIAGNDVVK*DAIVR	Q6NXE6	54	2
364	10.9 to 12.1	Bap31	234	B-cell receptor-associated protein 31 isoform b	GAAVDGGK*LDVGNAEVK	P51572	35	5
365	5.1 to 6.9	Bap31	310	B-cell receptor-associated protein 31 isoform b	LQAAVDGPMVK*KEE	P51572	35	2
366	11.7	Bap31	311	B-cell receptor-associated protein 31 isoform b	LQAAVDGPMVK*EE	P51572	35	1
367	5.1	Bcl-2L12	227	BCL2-like 12 isoform 3	BCL2-like 12 isoform 3	Q9HB09	37	2
368	2.5 to 5.5	C10orf119	635	chromosome 10 open reading frame 119	LQQQK*CVNGNEL	Q9BTE3	73	1
369	4.3 to 6.1	C7orf127	729	hypothetical protein LOC221927	DK*IASYSSLR	Q6PJG6	88	1
370	4.3	CDC123	35	cell division cycle 123	SVILPLQNVK*DYLLDDGTLVWSGR	Q75794	39	1
371	6.8 to 7	CNOT8	206	CCR4-NOT transcription complex, subunit 8	NLK*GGLEQVADQLDLQR	Q9UFF9	34	2
372	5.5 to 5.7	CNOT8	269	CCR4-NOT transcription complex, subunit 8	LYGLGTGVAQK*QNEVDVSAQEK	Q9UFF9	34	2
373	4.3	COMMD4	59	COMM domain containing 4	LTADAK*FESGDVK	Q9H0A8	22	1
374	13.9 to 15.4	DDIT4	129	RTP801	LLM#PSQLVSVQVK*ELLR	Q9NX09	25	16
375	3.7 to 8.8	GTF2A2	101	general transcription factor IIA, 2, 12kDa	IVACDVK*NTGNSNTE	P52657	12	1
376	7	KPNA2	353	karyopherin alpha 2	TNIQK*EATWTMSNITAGR	P52292	58	1
377	8.8 to 11.1	LAS1L	139	LAS1-like	VPLK*CLAQEVNIPDWIVDLR	Q9Y4W2	83	2
378	10.3	LAS1L	312	LAS1-like	VECVLAEK*GVTCENR	Q9Y4W2	83	1
379	7.5	NOC2L	649	nucleolar complex associated 2 homolog	LEDLNFPEIK*R	Q9Y3T9	85	1
380	3.7	NPL4	587	nuclear protein localization 4	NEELAQTKW*R	Q9P229	74	1
381	13 to 14.7	NUP37	103	nucleoporin 37kDa	FCTSAADMK*IR	Q8NFH4	37	3
382	6.3 to 11.8	OSGIN1	139	oxidative stress induced growth inhibitor 1 isoform 1	K*LTEAPGVSVLQDLDLSEGLEGR	Q9UJX0	61	2
383	9 to 12.8	PHLDA2	25	pleckstrin homology-like domain family A member 2	SDSLFQLWK*K	Q53GA4	17	3
384	11.1	PM20D2	24	aminoacylase 1-like 2	SELELLK*LR	Q8IY51	48	1
385	5.1 to 5.9	PMAIP1	48	phorbol-12-myristate-13-acetate-induced protein 1	LLNLISK*LFCSGT	Q13794	6	5
386	3.8	PPP2R1A	374	alpha isoform of regulatory subunit A, protein phosphatase 2	DNTIEHLPLFLAQLK*DECPEVR	P30153	65	1
387	5.9	PPP2R1A	416	alpha isoform of regulatory subunit A, protein phosphatase 2	QLSQSLPAIVELAEDAK*WR	P30153	65	1
388	5	PPP2R1A	542	alpha isoform of regulatory subunit A, protein phosphatase 2	FNVAK*SLQK	P30153	65	1
389	5.5	PTOV1	176	prostate tumor overexpressed 1	DCDSLK*GLCR	Q86YD1	47	1
390	0.2	RAD23B	76	UV excision repair protein RAD23 homolog B	NFVVMVTK*PK	P54727	43	1
391	6 to 7.9	TMBIM6	§7	resistance to inhibitors of cholinesterase 3 homolog isoform b	K*INFDALLK	P55061	27	3
392	-1.2 to 1	S100A6	47	S100 calcium-binding protein A6	ELTIGSK*LQDAEIAIR	P06703	10	4
393	2 to 2.1	SLC7A5	§30	solute carrier family 7 member 5	MLAAK*SADGSAPAGEGEGVTLQR	Q01650	55	2
394	5.1	SSR3	98	signal sequence receptor gamma subunit	EDAVSK*EVTR	Q9UNL2	21	1
395	2.8 to 5.9	TBCD	788	beta-tubulin cofactor D	CGFSLALGALPGFLK*GR	Q9BTW9	133	3
396	-1.1 to 1.3	UBFD1	529	ubiquitin-binding protein homolog	DTVLGK*WQYF	Q14562	57	2
397	3.8 to 7	Wdr34	361	WD repeat domain 34	LFILGTEGGFPLK*CSLAAGEAALTR	Q96EX3	58	3
398	13.8	ZFAND2A	34	zinc finger, AN1-type domain 2A	QDFCK*DHFPPYAAHK	Q8N6M9	16	2
399		Vesicle protein						
400	2	CLTC	1441	clathrin heavy chain 1	AVNYFSK*VK	Q00610	192	1
401	1.4	CLTC	1443	clathrin heavy chain 1	AVNYFSKVK*	Q00610	192	1
402		Small g protein						
403	5	ARF4	142	ADP-ribosylation factor 4	QDLPNAM#AISEM#TDK*LGLQSLR	P18085	21	2
404	1	RAC1	184	ras-related C3 botulinum toxin substrate 1 isoform Rac1	AVLCPPPVKK*	P63000	21	1
405	1.4 to 1.7	RhoA	135	ras homolog gene family, member A	MK*QEPVKEEGR	P61586	22	4

LEGEND: * = modified residue; # = oxidized methionine, fold changes greater than 5 upon drug treatment are highlighted

Table: PTMScan® Results, Ubiquitin Remnant Motif (K-epsilon-GG), SILAC

Study design: colorectal carcinoma (HCT 116) cell line; Trypsin digest; Antibody: Ubiquitin Remnant Motif (K-epsilon-GG) XP™, PTMScan® Kit #1990, #5562

Treatments: Untreated (Light), Velcade treated (Heavy)

Index	Fold-Change (Velcade/Untreated)	Protein Name	Ubiquitination Site	Description	Peptide	Accession	kD	Count in Study
406		Inhibitor						
407	8 to 8.3	AZIN1	140	ornithine decarboxylase antizyme inhibitor	VGVNILTCDNEIELK*K	Q14977	50	1
408	4.6 to 5.5	RNH1	205	ribonuclease/angiogenin inhibitor	DSPCQLEALK*LESCGVTS DNCR	P13489	50	2
409	11.6 to 14.9	RNH1	226	ribonuclease/angiogenin inhibitor	DLCGIVASK*ASLR	P13489	50	2
410	4.4	TTRAP	23	TRAF and TNF receptor-associated protein	EAAEEEGEPEVK*K	O95551	41	1
411		Translation initiation						
412	2.8 to 3.6	eIF3M	344	eukaryotic translation initiation factor 3, subunit M	TFGK*QQWQQLYDTLNAWK	Q7L2H7	43	7
413		Ubiquitin-like modifier						
414	-1.1 to 1.1	NEDD8	48	neural precursor cell expressed, developmentally down-regulated 8	LIYSGK*QMNDEK	Q15843	9	2
415	3.1 to 3.2	ubiquitin	\$11	ubiquitin and ribosomal protein S27a precursor	TLTGK*TITLEVEPSDTIENVK	P62988	9	19
416	2.7 to 2.8	ubiquitin	\$27	ubiquitin and ribosomal protein S27a precursor	TITLEVEPSDTIENVK*AK	P62988	9	5
417	2.7 to 2.8	ubiquitin	\$29	ubiquitin and ribosomal protein S27a precursor	TITLEVEPSDTIENVKAK*	P62988	9	22
418	6.3 to 6.6	ubiquitin	\$48	ubiquitin and ribosomal protein S27a precursor	LIFAGK*QLEDGR	P62988	9	98
419	4.2 to 4.8	ubiquitin	\$6	ubiquitin and ribosomal protein S27a precursor	MQIFVK*TLTGK	P62988	9	26
420	4.7 to 4.7	ubiquitin	\$63	ubiquitin and ribosomal protein S27a precursor	TLSDYNIQK*ESTLHLVLR	P62988	9	54
421	12.5	SUMO2	42	SMT3 suppressor of mif two 3 homolog 2 isoform b precursor	HTPLSK*LMK	P61956	11	3