

Data Set 1

A summary of all phosphopeptides identified in this study

Legends

ET : For comparison: Trypsin samples subjected to LC-MS/MS [ETD]
 EL : For comparison: Lys-C samples subjected to LC-MS/MS [ETD]
 EG : For comparison: Glu-C samples subjected to LC-MS/MS [ETD]
 CT : For comparison: Trypsin samples subjected to LC-MS/MS [CID]
 CL : For comparison: Lys-C samples subjected to LC-MS/MS [CID]
 CG : For comparison: Glu-C samples subjected to LC-MS/MS [CID]
 AG : For comparison: Glu-C samples subjected to alternating LC-MS/MS [CID/ETD]
 AT : For comparison: Trypsin samples subjected to alternating LC-MS/MS [CID/ETD]
 AL : For comparison: Lys-C samples subjected to alternating LC-MS/MS [CID/ETD]
 ELX : Remainder of Lys-C samples subjected to LC-MS/MS [ETD]
 "/" : C-terminal type fragment
 "\" : N-terminal type fragment
 "|" : Both C-terminal type AND N-terminal type fragment
 CS : Charge state
 Mode : Type of fragmentation
 n,k,nk : novel, known, notknown
 Predic. : Predicted protein

#	Exp.	Number of phosphorylation sites			▼ Sequence with fragments	Literature lookup	RefSeq#	Gene
		CS	Mode	Score				Symbol
1	AG	3	CID	17.45	1 (E)G/G P E/A P/I P/P/P/P Q P R E K V s S I\D\L E(I)	S18 =n	NP_001010972.1	ZYX
2	CT	2	CID	12.79	1 (R)s/P G A P/G P L T L K(E)	S1 =k	NP_001010972.1	ZYX
3	AT	2	CID	17.62	1 (R)V S S G Y V P/P/P V/A\t/P F S S K(S)	T12 =n	NP_001010972.1	ZYX
4	EL	4	ETD	16.72	2 (K)R/R N R N A s A\s F Q E L E D K\K(E)	S7 =n,S9 =n	NP_055192.1	ZRF1
5	ELX	4	ETD	11.35	1 (-)m N E/y P K/K R\K(R)	Y4 =n	NP_057415.1	ZNF639
6	ET	4	ETD	8.6	3 (K)T K\s/S S K L\s s C I/A/A/I\A/A L/S/A K(K)	S3 =n,S8 =n,S9 =n	NP_060651.2	ZNF532
7	ET	4	ETD	11.44	1 (K)I/S/L S K S P\t\K t D P K/N E\E E\E\K(R)	T10 =n	NP_861446.2	ZNF326

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
8	ELX	4	ETD	24.27	3 (K)R/R/t R s\R\s P E S Q V I G E\N\T\K(Q)	T3 =n,S5 =n,S7 =n	NP_005446.2	ZNF265
9	ELX	3	ETD	11.27	1 (K)Y K L/D E D E D E\D D\A/D\L s\K(Y)	S15 =n	NP_005446.2	ZNF265
10	ELX	3	ETD	21.41	1 (K)Y/N L D A s E E E\D S N\K\K(K)	S6 =k	NP_005446.2	ZNF265
11	CL	5	CID	16.85	1 (K)R R R D\s D G V D G\F/E/A E/G/K K(D)	S5 =n	NP_057191.2	ZFR
12	EL	4	ETD	14.14	1 (K)R/R R D s/D G V D\G F E A E\G\K\K(D)	S5 =n	NP_057191.2	ZFR
13	ELX	4	ETD	6.67	1 (K)G K s/G E G E N\T D K(L)	S3 =n	NP_078997.2	ZFHX4
14	ELX	4	ETD	19.98	2 (K)T/R R L s S\A\s T G K P\P\L S/V E\D\D F E\K(L)	S5 =n,S8 =n	NP_055642.2	ZC3H11A
15	ELX	4	ETD	14.49	3 (K)T/R R L s/s/A\s\T G\K P P\L S V E D D\F/E\K(L)	S5 =n,S6 =n,S8 =n	NP_055642.2	ZC3H11A
16	ELX	4	ETD	7.8	2 (K)T/R\R L s S A S\T G K P\P L S V\E\D\D F E\K(L)	S5 =n,T9 =n	NP_055642.2	ZC3H11A
17	ELX	3	ETD	14.37	1 (K)s Y/L/S G/G\A G A/A/G G G A D P G N\K(K)	S1 =n	NP_003394.1	YY1
18	ELX	3	ETD	24.89	1 (K)A A D P P\A E N S s A\P E A E Q/G\G\A\E(-)	S10 =n	NP_004450.2	YBX1
19	CL	3	CID	15.07	1 (K)K/T/P/S/K P P A\Q/L s/P S V P\K(R)	S11 =n	NP_006288.1	XRCC1
20	EL	4	ETD	21.44	1 (K)T/K P T\Q A A G P S s P Q K/P P T P E E T\K(A)	S11 =n	NP_006288.1	XRCC1
21	EL	4	ETD	16.23	2 (K)T/K/P T Q A A G P\S s/P Q K/P P t P E E T\K(A)	S11 =n,T17 =n	NP_006288.1	XRCC1
22	AL	3	CID	12.11	2 (K)T K/P/T Q A A\G P S s/P/Q\K P P t/P E E\T K(A)	S11 =n,T17 =n	NP_006288.1	XRCC1
23	ELX	4	ETD	15.68	1 (K)S/K P\E L P P G/L\S P\E/A T A P\V t\P S R P E G G E P\G L\S\K(T)	T18 =n	NP_115721.1	WIBG
24	ET	3	ETD	8.34	2 (R)V/Q/E\H/E D s/G D s E V\E N E/A K(G)	S7 =k,S10 =k	AAH25276.1	WDR50
25	EL	3	ETD	9.59	1 (K)R K s E L/E/F\E T L\K(T)	S3 =n	NP_061918.3	WDR44
26	ELX	4	ETD	17.06	2 (K)R K s\E/L E\F/E T L K\t P\D I D V P\K(E)	S3 =n,T12 =n	NP_061918.3	WDR44
27	CL	2	CID	14.07	1 (K)V/G/N E s/P/V/Q/E/L K(Q)	S5 =n	NP_061918.3	WDR44
28	EL	5	ETD	11.9	3 (K)Y K G y V N S/S S Q I\K\A/S F S\H D F t y L/V/S\G S/E D K(Y)	Y4 =n,T20 =n,Y21 =n	NP_061918.3	WDR44
29	ET	4	ETD	24.4	1 (R)D/G P P/L R G s N m/D/F\R E P T E E E\R(A)	S8 =n	NP_071496.1	WBSCR1
30	ET	4	ETD	9.25	1 (R)F R D G P P L R/G s N m D F R\E P T E E\E\R(A)	S10 =n	NP_071496.1	WBSCR1
31	EG	4	ETD	7.67	1 (E)T/R D/G Q V I\N\E t/S/Q/H H\D D\L\E(-) (K)L/L/E G E E/S R I/S L P L P/N/F S S\L N\L R E T\N\L/D/s\L P\L V	T10 =n	NP_003371.2	VIM
32	EL	5	ETD	12.38	1 D\T/H S\K(R)	S28 =n	NP_003371.2	VIM
33	AL	4	ETD	24.04	1 (K)T/V/E T R\D\G Q/V I N E T s Q H H D\D\L\E(-)	S14 =n	NP_003371.2	VIM
34	ET	3	ETD	19.74	1 (R)D/G/Q V I N E T s Q H H D\D\L\E(-)	S9 =n	NP_003371.2	VIM
35	AT	3	CID	17.87	1 (R)D/G/Q V I N E T/s\Q\H H D D\L\E(-)	S9 =n	NP_003371.2	VIM
36	CT	3	CID	17.05	1 (R)D/G/Q V I N E/t S\Q\H H D D\L\E(-)	T8 =n	NP_003371.2	VIM
37	ET	3	ETD	22.89	1 (R)E/T N L\D s L P L V\D T H S\K(R)	S6 =n	NP_003371.2	VIM
38	AT	3	CID	15.23	1 (R)E T/N/L/D s/L/P/L/V/D/T H S K(R)	S6 =n	NP_003371.2	VIM
39	AT	3	ETD	17.74	1 (R)m/F\G G P\G T A S R P s S\S\R(S)	S12 =k,S13 =nf	NP_003371.2	VIM
40	CT	3	CID	12.96	1 (R)m/F G/G/P G/T A S R\P\S S s R(S)	S14 =n,S12 =nf,S13 =nf	NP_003371.2	VIM
41	AT	3	CID	12.74	2 (R)m F G/G/P G T A S R P S s s R(S)	S13 =k,S14 =n,S12 =nf	NP_003371.2	VIM
42	ET	3	ETD	11.69	2 (R)m/F/G G P G T A s R P S s s R(S)	S9 =n,S13 =k,S12 =nf	NP_003371.2	VIM

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
43	AT	3	ETD	8.67	2 (R)m/F/G G P G t\A S R P s S S\R(S)	T7 =n,S12 =k,S13 =nf	NP_003371.2	VIM
44	ET	3	ETD	4.33	2 (R)m F\G G P G T A s R P s S S\R(S)	S9 =n,S12 =k,S13 =nf	NP_003371.2	VIM
45	AT	2	CID	17.13	1 (R)S L/Y A S/s/P/G/G/V/Y/A T R(S)	S6 =k,S1 =nf	NP_003371.2	VIM
46	CT	2	CID	16.58	1 (R)S L/Y A s/s/P/G/G/V/Y A/T R(S)	S5 =n,S1 =nf,S6 =nf	NP_003371.2	VIM
47	AT	2	CID	15.29	1 (R)S L/Y A S S P/G G V/Y A T R(S)	Y11 =n,S1 =nf,S6 =nf	NP_003371.2	VIM
48	ET	2	ETD	5.85	1 (R)S/L/Y/A/s/S P/G/G/V/Y A\T\R(S)	S5 =n,S1 =nf,S6 =nf	NP_003371.2	VIM
49	AT	3	CID	16.22	1 (R)T Y s/L/G/S A/L/R/P S\T S R(S)	S3 =k,S6 =nf,S11 =nf	NP_003371.2	VIM
50	ET	3	ETD	13.92	1 (R)T/Y s L G S/A/L R\P S T S\R(S)	S3 =k,S6 =nf,S11 =nf	NP_003371.2	VIM
51	ET	3	ETD	11.05	2 (R)T/Y s/L\G/S A L R P\s T S\R(S)	S3 =k,S11 =k,S6 =nf	NP_003371.2	VIM
52	EL	4	ETD	30.14	1 (K)L/R K/V s K Q E E A\S G G P T A P\K(A)	S5 =k	NP_003361.1	VASP
53	AT	3	CID	23.15	1 (R)K R s/E L\S\Q/D A E P A G S\Q E T\K(D)	S3 =n	NP_006640.2	UTP14A
54	ET	3	ETD	6.18	1 (R)K R s\E L S Q/D\A E P A G S\Q E\T\K(D)	S3 =n	NP_006640.2	UTP14A
55	EL	5	ETD	16.48	2 (K)R/E R D/R E R E P\E A A s S/R G s P V R\V\K(R)	S13 =n,S17 =n	NP_006581.2	USP39
56	EL	4	ETD	26.11	1 (K)R/E R E V D E D s E P E R E V R\A\K(N)	S9 =n	NP_006581.2	USP39
57	EL	4	ETD	10.92	2 (K)G/R/P A L A S Q E S\s/L/S S t S P/S\ S P\L P V\K(V)	S11 =n,T15 =n	NP_065769.2	USP31
58	CL	4	CID	16.41	1 (K)N H S V N E E\E Q E Q G E G s E/D E W E/Q V/G P R N K(T)	S16 =k	NP_005144.1	USP10
59	CT	3	CID	17.66	2 (K)K A/P A G Q E E P/G t P/P s S P L/S A E Q L\D R(I)	T11 =k,S14 =n	NP_003353.1	UNG
60	ELX	5	ETD	10.97	2 (K)T A A V A\N S m\N\y L T/K/K G M/s\ S K(E)	Y10 =n,S17 =n	NP_001020948.1	UGCG11
61	EL	4	ETD	11.92	1 (K)K V E E D E A/G G R\F/V\A\F S G E G\Q s\L/R\K(K)	S20 =n	NP_001030324.1	UFD1L
62	EG	4	ETD	14.04	1 (E)R G K L P\E s P K R\A\E\E(I)	S7 =k	NP_055048.1	UBTF
63	EL	3	ETD	17.3	1 (K)R/K A s Q L V G I E\K(K)	S4 =n	NP_054895.1	UBE2T
64	ELX	5	ETD	11.92	1 (K)N/Q R/Q D Y L N/G A V/s G S V Q/A\T/D\R\L m\K(E)	S12 =n	NP_060052.3	UBE2Q1
65	EL	3	ETD	20.98	1 (K)N/P S D S A V H s P F T\K(R)	S9 =k	NP_055662.2	UBAP2L
66	CT	2	CID	16.15	1 (K)N/P/S D/S A/V H s P F\T K(R)	S9 =k	NP_055662.2	UBAP2L
67	CL	3	CID	15.4	1 (K)N/P S/D/S A/V/H/S\P\F\T K(R)	T12 =n,S9 =nf	NP_055662.2	UBAP2L
68	EL	3	ETD	8.31	1 (N)P S/D S A V H s\P\F\T\K(R)	S8 =k	NP_055662.2	UBAP2L
69	EL	4	ETD	16.69	1 (K)E/E/H G/G L I R s P R H\E\K(K)	S9 =n	NP_001012496.1	U2AF2
70	AT	4	ETD	10.5	1 (R)G/A/K E E/H\G\G L I R\s\P\R(H)	S12 =n	NP_001012496.1	U2AF2
71	CT	4	CID	16.94	1 (K)S s P G Q P E A G P\E G A/Q E/R P S Q A\A\ P A V\E A\E G P G S\ S Q\A P R(K)	S2 =n	NP_787048.1	TXLNA
72	CT	3	CID	20.47	1 (R)R/P\E G P G\A Q A P\S s/P R(V)	S12 =n	NP_787048.1	TXLNA
73	ET	3	ETD	17.28	1 (R)R P E G P G A Q A P S s P\R(V)	S12 =n	NP_787048.1	TXLNA
74	CT	4	CID	14.59	2 (R)E T/s R/L A W T\N V/A/s/E V Q V T K L K(V)	S3 =n,S12 =n	NP_003310.2	TTN
75	ELX	3	ETD	8.28	1 (K)s K\T S E N S S A K(R)	S1 =n	NP_443165.1	TSGA13
76	CG	4	CID	13.97	1 (E)G Y/G F/G/S/G/D/D P Y/S S/A E/P H V s G V K/R S R S G E G E(V)	S19 =n,S26 =nf	NP_005753.1	TRIM28
77	CG	3	CID	19.98	1 (E)T K/P V L m A L/A E G P G A\E/G P R/L\A/s/P S G\ S T S S G\L\E(V)	S21 =n	NP_005753.1	TRIM28

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
78	EL	4	ETD	26.62	1 (K)R/S R/s/G E G E V S G L m\R(K)(V)	S4 =k	NP_005753.1	TRIM28
79	EL	4	ETD	26	1 (K)R/S R s G E G E V S G L M\R(K)(V)	S4 =k	NP_005753.1	TRIM28
80	AL	4	CID	14.18	1 (K)R S R s/G E G E V S G L/m R K(V)	S4 =k	NP_005753.1	TRIM28
81	AL	4	CID	12.25	1 (K)R S R\s/G E G E V S G L M\R(K)(V)	S4 =k	NP_005753.1	TRIM28
82	CT	3	CID	24.06	1 (R)G A A A A/A/T/G Q P/G T A P A G t/P G A P P L/A/G m A I V\K(E)	T17 =n	NP_005753.1	TRIM28
83	CT	3	CID	22.25	1 (R)G A A A A A/T/G Q P/G T A P A G t/P G\A P/P L A G\M A I V\K(E)	T17 =n	NP_005753.1	TRIM28
84	AT	2	CID	15.54	1 (R)L D/L D/L/T/A D s Q P P V F K(V)	S9 =n	NP_005753.1	TRIM28
85	AT	2	CID	15.43	1 (R)s G\E G E V S G L/m\R(K)	S1 =k	NP_005753.1	TRIM28
86	ET	3	ETD	20.69	1 (R)S/R s G E G E V S G L m\R(K)	S3 =k	NP_005753.1	TRIM28
87	CT	3	CID	16.51	1 (R)s R S G E G E V S G L/m\R(K)	S1 =n,S3 =nf	NP_005753.1	TRIM28
88	CT	3	CID	16.32	1 (R)S R s G E\G E V S G L M R(K)	S3 =k	NP_005753.1	TRIM28
89	CT	3	CID	10.48	1 (R)s R/S G E/G E V S G/L M R(K)	S1 =n,S3 =nf	NP_005753.1	TRIM28
90	AT	3	CID	9.72	1 (R)S R s G E/G E V S G L m R(K)	S3 =k	NP_005753.1	TRIM28
91	ET	3	ETD	9.05	1 (R)S/R/s\G E G E V S G L M\R(K)	S3 =k	NP_005753.1	TRIM28
92	ELX	3	ETD	6.64	1 (K)L/E/L K S\A/Q/K D/L Q/s A\D\K(E)	S12 =n	NP_005870.2	TRAIP
93	CT	2	CID	15.79	1 (R)L D/S Q/P Q E T/s/P E L P R(R)	S9 =k	NP_006691.1	TRAFD1
94	ELX	4	ETD	23.21	2 (K)T P\A Q P Q/R R s L R\L s A Q\K(D)	S9 =k,S13 =k	NP_036244.2	TPX2
95	CG	2	CID	24.77	1 (E)G N I/D D/s L/I G G N A S A E G P E G E(G)	S6 =k	NP_003286.1	TPT1
96	AL	2	CID	15.12	1 (K)E G/V/Q/G/P L/N V/s/L/S/E E\G K(S)	S10 =n	AAB48030.1	TPR
97	EL	2	ETD	14.09	1 (K)E/G/V/Q/G P/L/N V\s\L\S\E\E\G\K(S)	S10 =n	AAB48030.1	TPR
98	CL	3	CID	13.87	1 (K)R P s T S Q T V\S/T/P/A P V P V/I E\S T E A I\E A K(A)	S3 =n	AAB48030.1	TPR
99	AT	3	CID	19.52	1 (R)T D/G F/A/E A/I/H s/P\Q V A G V P R(F)	S10 =n	AAB48030.1	TPR
100	ET	3	ETD	16.76	1 (R)T/D/G/F A E A I H/s P Q V A G V P\R(F)	S10 =n	AAB48030.1	TPR
101	ELX	5	ETD	15.04	2 (K)Q E G Q L R A Y\G\A G L L s S I G E L K H A L s D K A C V\K(A)	S14 =n,S24 =n	NP_775489.2	TPH2
102	AL	3	ETD	17.45	1 (K)L/G/D M R N s A T F\K(S)	S7 =n	NP_003279.2	TPD52L2
103	AL	3	CID	10.92	1 (K)L/G D M/R N s A/T F K(S)	S7 =n	NP_003279.2	TPD52L2
104	EL	3	ETD	17.56	1 (K)s/F E D R V G T I\K(S)	S1 =n	NP_003279.2	TPD52L2
105	EL	3	ETD	15.02	1 (K)S/F/E D R V G t I\K(S)	T8 =n	NP_003279.2	TPD52L2
106	ET	4	ETD	19.69	2 (R)K/L G D m R N s\A T F K\s\F E D\R(V)	S8 =n,S13 =n	NP_003279.2	TPD52L2
107	ET	3	ETD	13.58	1 (R)N/S/A T F K/s F E D\R(V)	S7 =n	NP_003279.2	TPD52L2
108	AG	3	ETD	17.23	1 (E)D/V/K N s P T F K S F E\K(E)	S5 =n	NP_001020423.1	TPD52
109	AG	3	ETD	13.9	1 (E)D/V/K/N S P/t\F\K S\F E E/K\VE(N)	T7 =n	NP_001020423.1	TPD52
110	AT	3	ETD	18.9	1 (K)K/L E D V K N s P T F\K(S)	S8 =n	NP_001020423.1	TPD52
111	AT	3	CID	14.55	1 (K)K/L E\D\V\K N S\p\T\F\K(S)	T10 =n	NP_001020423.1	TPD52
112	ET	4	ETD	19.66	2 (K)K/L E D V K N s P\T F K s F\E\K(V)	S8 =n,S13 =n	NP_001020423.1	TPD52

#	Exp.	CS	Mode	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
				Score	▼				
113	ET	3	ETD	14.33	1	(K)L/E D V K N s P T F\K(S)	S7 =n	NP_001020423.1	TPD52
114	EL	4	ETD	20.05	2	(K)A/S S/L/H R\T s\S G T s\L S A m H S\S G S S\G\K(G)	S8 =n,S12 =n	NP_005648.1	TP53BP1
115	EL	4	ETD	14.55	1	(K)A/S/S/L H R T S\S\G T S L S A/m/H\S S G S\S G K(G)	S9 =n	NP_005648.1	TP53BP1
116	AL	3	ETD	17.12	1	(K)L/I/T S E E E R s P A\K(R)	S9 =n	NP_005648.1	TP53BP1
117	EL	4	ETD	16.55	2	(K)R R s N V S S\A t P\T A S S S\S S\T T P T R\K(I)	S3 =n,T10 =k,S6 =nf,S7 =nf	NP_005648.1	TP53BP1
118	EL	4	ETD	9.53	3	(K)R/R s\N/V/s/S P A T P/T A S\S\S S s t\T P T R\K(I)	S3 =n,S6 =k,T19 =n,S7 =nf,T10 =nf	NP_005648.1	TP53BP1
119	EL	4	ETD	10.08	1	(K)T/S G/T E P A D/F\A L P S S R G\G P\G\K\L s P R\K(G)	S22 =n	NP_005648.1	TP53BP1
120	ET	4	ETD	20.17	1	(R)K/L I T S E E E R s P A K(R)	S10 =n	NP_005648.1	TP53BP1
121	ELX	3	ETD	15.82	1	(K)R/A L/P N N T/S S s P Q P K(K)	S10 =k	NP_000537.2	TP53
122	CL	3	CID	12.95	1	(K)E A/Q Q/K/V P D E E\N E E/s\D N\E K(E)	S15 =k	NP_001058.2	TOP2A
123	CL	3	CID	18.76	2	(K)E L K/P/Q K s V V/s D/L/E/A\D D V K(G)	S7 =n,S10 =k	NP_001058.2	TOP2A
124	EL	3	ETD	12.46	2	(K)E/L/K/P Q K s V\V s D L E A D D V\K(G)	S7 =n,S10 =k	NP_001058.2	TOP2A
125	CL	3	CID	14.75	1	(K)I K N E/N T E G/s P Q/E/D G V/E/L E/G\L\K(Q)	S9 =k	NP_001058.2	TOP2A
126	CL	2	CID	17.07	2	(K)s V/V s/D/L/E A/D D V K(G)	S1 =n,S4 =k	NP_001058.2	TOP2A
127	ELX	4	ETD	10.92	1	(K)K m S\s K G/L S/G K K(R)	S4 =n	NP_055309.1	TNRC6A
128	EL	3	ETD	13.57	2	(K)N t S\T t S/T G/N K(N)	T2 =n,T5 =n	NP_009046.2	TNFAIP6
129	EL	3	ETD	5.52	2	(K)A t K K t D K/P R Q E D\K(D)	T2 =n,T5 =n	NP_001027454.1	TMPO
130	CT	3	CID	16.65	2	(K)G P P D/F\s s/D/E/E/R E\P T P V L G/S/G A A A A G R(S) (K)G P P D/F S S S D E\E R E P T P/V L G s G A A A/A G/R	S6 =k,S7 =k	NP_001027454.1	TMPO
131	EL	5	ETD	9.24	2	s\R\A A V G R\K(A)	S19 =n,S27 =n,S6 =nf,S7 =nf	NP_001027454.1	TMPO
132	EL	3	ETD	13.89	1	(K)L/A/s/E/R N\L F I S\C\K(S)	S3 =n	NP_003267.1	TMPO
133	CL	3	CID	14.17	1	(K)S S S S S S S Q P E H S A M L V S T/A A s/P S L\I\K(E)	S20 =n	NP_003267.1	TMPO
134	ELX	3	ETD	9.33	1	(K)Y/G V N P G P I/V G t\T R\K(L)	T11 =n	NP_001027454.1	TMPO
135	CT	2	CID	17.21	1	(R)S s T P L P/T I/S S/S/A/E/N T R(Q)	S2 =n,S11 =nf	NP_001027454.1	TMPO
136	ET	2	ETD	5.69	1	(R)S/S/t P/L P/T/I S/S/S A E/N T\R(Q)	T3 =n,S11 =nf	NP_001027454.1	TMPO
137	CT	3	CID	16.79	1	(R)V/L L F L S Q F\C/I L s G G E\S T E\I\P\Y V m\K(C)	S12 =n	NP_079417.1	TM2D3
138	EL	5	ETD	14.4	1	(K)N H H E L/D\H R E R E S\S A\N\N S V s P/S/E\S L R A\S E K(H)	S19 =k	NP_005069.1	TLE3
139	EL	5	ETD	13.87	2	(K)N H H\E\L\D\H R E R E S S A\N\N s/V S P S E\s\L R A\S\E\K(H)	S17 =n,S23 =n,S19 =nf	NP_005069.1	TLE3
140	AT	5	CID	14.87	1	(K)T H K P\D P/G t P Q H/T S/S R\A\A P E P Q K(A)	T8 =n	NP_004808.2	TJP2
141	CL	3	CID	20.13	1	(K)s R E D/L S\A Q P/V Q T K(F)	S1 =n	NP_003248.2	TJP1
142	CL	3	CID	16.41	2	(K)D Q/Q P/s G s/E G/E/D/D/D/A E/A\A\L\K(K)	S5 =n,S7 =n	NP_060206.2	THUMPDI
143	CL	3	CID	12.21	2	(K)D/Q Q P/s G s/E G E D\D\A E A A L K K(E)	S5 =n,S7 =n	NP_060206.2	THUMPDI
144	AT	4	CID	18.01	2	(K)F T/D/K D\Q\Q P/s/G s/E/G E D\D D A E A A L K K(E)	S9 =n,S11 =n	NP_060206.2	THUMPDI
145	ET	4	ETD	11.5	1	(-)m s/K/T/N K/S K S\G S R(S)	S2 =n	NP_005110.1	THRAP3
146	ELX	5	ETD	18.39	1	(K)E/D R/G K R\s E/G/G\H R G F/V/P E\K(N)	S7 =n	NP_005110.1	THRAP3
147	ELX	3	ETD	15.42	1	(K)G R K E s E\F D D E P\K(F)	S5 =n	NP_005110.1	THRAP3

#	Exp.	Number of phosphorylation sites			Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
		CS	Mode	Score				
148	ELX	4	ETD	27.39	1 (K)H/G/L A H D E m K\s P/R E P\G Y\K(A)	S10 =n	NP_005110.1	THRAP3
149	ELX	4	ETD	15.11	1 (K)H/G/L A H D E M K\s P R E P G Y\K(A)	S10 =n	NP_005110.1	THRAP3
150	ELX	3	ETD	8.31	2 (K)K/s P V G K s P P S T G S T Y/G/S S Q\K(E)	S2 =n,S7 =k	NP_005110.1	THRAP3
151	ELX	4	ETD	20.26	2 (K)s P E I/H R R\I\D I s P\S T F R\K(H)	S1 =n,S11 =k	NP_005110.1	THRAP3
152	ELX	4	ETD	10.48	2 (K)W/A/H D/K F/S G E E G E I E D D/E/s G t\N\R E E\K(D)	S18 =k,T20 =n	NP_005110.1	THRAP3
153	AG	5	ETD	9.19	1 (E)Q t K/A L V\T Q\L T/L/F/N\Q I L/V E(L)	T2 =n	NP_009043.1	THBS3
154	EL	3	ETD	14.91	2 (K)D s/S N K/s G/A/E/A K(T)	S2 =n,S6 =n	NP_006455.2	TGOLN2
155	ET	5	ETD	11.32	1 (K)V A/s G E Q K/E\D/Q/S/E/D/K K(R)	S3 =n	NP_057011.2	TGFB111
156	AT	2	CID	14.61	1 (R)F I Q E L S G/S s/P K(R)	S9 =k	NP_003214.1	TFAP4
157	CT	2	CID	17.39	1 (K)Y L L/G/D A P V s/P S/S Q K(L)	S9 =n	NP_061848.2	TERF2IP
158	CG	4	CID	16.75	1 (E)A/K P Q\Q A A/G/m\L/s/P K T G\G K E(A)	S11 =n	NP_000347.2	TCOF1
159	ELX	5	ETD	10.67	1 (K)A G/K/T G N S m P\H P A t/G\K\T/V/A N/L L S G\K S P R\K(S)	T13 =n	NP_000347.2	TCOF1
160	EL	5	ETD	8.7	1 (K)A N\p A\A A R\A\p s A/K G T\I/S A/P G K(V)	S10 =n	NP_000347.2	TCOF1
161	ELX	4	ETD	28.98	1 (K)A/P Q V R A A S A P A K E s P R\K(G)	S14 =n	NP_000347.2	TCOF1
162	ET	4	ETD	18.59	1 (K)D/D P D G K Q\E A K P Q Q A/A G m L\s P\K(T)	S19 =n	NP_000347.2	TCOF1
163	EL	4	ETD	7.43	2 (K)E s P R/K G A A\p/A P P G K t G/P A\A K(A)	S2 =n,T15 =n	NP_000347.2	TCOF1
164	EL	4	ETD	6.08	1 (K)G t\I/S A/P G K/V/V/T/A A A Q/A K(Q)	T2 =n	NP_000347.2	TCOF1
165	ELX	5	ETD	8.93	1 (K)K K K K\L\G A G\E/G\G\E/A s V/S P E K(T)	S14 =k	NP_000347.2	TCOF1
166	ELX	3	ETD	22.75	1 (K)K/L\G A G E\G G E\A S V s P E\K(T)	S13 =k,S11 =nf	NP_000347.2	TCOF1
167	CT	3	CID	14.34	1 (K)K L G A G E\G G\E A S V s/P E K(T)	S13 =k,S11 =nf	NP_000347.2	TCOF1
168	ET	4	ETD	22.55	1 (K)K/L G A/G E G G E A S V/s P\E K\T S\T\T\S\K(G)	S13 =k,S11 =nf	NP_000347.2	TCOF1
169	CT	4	CID	14.61	1 (K)K L G A G\E G\G\E A S V s/P E K T S/T T S\K(G)	S13 =k,S11 =nf	NP_000347.2	TCOF1
170	CT	2	CID	14.03	1 (K)L G A/G E/G/G E A S\V s/P E K(T)	S12 =k,S10 =nf	NP_000347.2	TCOF1
171	ET	3	ETD	14.54	1 (K)L/G A G/E G G E/A/S V s P E K T S T T\T\S\K(G)	S12 =k,S10 =nf	NP_000347.2	TCOF1
172	ELX	5	ETD	7.87	2 (K)Q E\D/S E\s\S\E E\E S D S E E A/A\A S/P/A Q/V K/T/s V K(K)	S6 =n,S26 =n	NP_000347.2	TCOF1
173	ELX	4	ETD	26.48	2 (K)R/K L s G/D Q P A A R t P R\S\K(K)	S4 =n,T12 =n	NP_000347.2	TCOF1
174	EL	4	ETD	21.58	1 (K)R/K L s G\D Q P A A R T P R S\K(K)	S4 =n	NP_000347.2	TCOF1
175	ELX	4	ETD	21.1	2 (K)R/K L s G/D Q P A A R T P R s\K(K)	S4 =n,S15 =n	NP_000347.2	TCOF1
176	EL	4	ETD	18.41	2 (K)R/K L s G/D Q P/A A R t P R\S\K(K)	S4 =n,T12 =n	NP_000347.2	TCOF1
177	ELX	3	ETD	18.68	1 (K)S/L G/N I L Q A K P T S s P A\K(G)	S13 =n	NP_000347.2	TCOF1
178	EL	4	ETD	9.25	1 (K)T/H Q I R A\A L\A\p A K\E s P R\K(G)	S14 =n	NP_000347.2	TCOF1
179	ET	3	ETD	17.13	1 (K)T/S/Q V/G A A S A P A K E s P\R(K)	S14 =n	NP_000347.2	TCOF1
180	AT	3	CID	14.02	1 (K)T/S/Q/V G A\A\A S/A/P A K E s/P R(K)	S14 =n	NP_000347.2	TCOF1
181	ELX	3	ETD	18.4	1 (K)T/S/Q/V/G/A A S A P\A\K E s P R\K(G)	S14 =n	NP_000347.2	TCOF1
182	CL	3	CID	14.83	1 (K)T S/Q/V G A\A S/A/P/A K\E s P R K(G)	S14 =n	NP_000347.2	TCOF1

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene	
			Mode	Score				▼	Symbol
183	ET	3	ETD	16.31	2	(R)K/L s G D Q P A A R t P\R(S)	S3 =n,T11 =n	NP_000347.2	TCOF1
184	EL	5	ETD	24.17	1	(K)H/R K L s E L E R P\H\K(V) (K)N E G N L E N/E/G K P E\D/E V E P/D D\E G\K/s D/E E E\K P D V/E	S5 =n	NP_003189.1	TCEB3
185	ELX	5	ETD	10.21	1	G\K(T)	S23 =n	NP_001006934.1	TCEAL3
186	ELX	3	ETD	12.67	1	(K)T/D/E/E R P P/V E H s P E\K(Q)	S11 =n	NP_001006640.1	TCEAL1
187	AL	4	CID	10.94	1	(K)D E/T N/A R D T y V/S/S/F/P R A P S T S/D/S V R L K(C)	Y9 =n	NP_006747.1	TCEA1
188	EL	4	ETD	14.4	1	(K)E P A I T S Q N s P\E A/R E E/S T S S G N V/S N\R\K(D)	S9 =k	NP_006747.1	TCEA1
189	AL	4	ETD	12.43	1	(K)E/P\A I T S Q N s/P E\A R\E E s t/S S G N V S N\R\K(D)	T17 =n,S9 =nf	NP_006747.1	TCEA1
190	AL	4	ETD	11.74	1	(K)E/P A I T S Q N S P E A R\E E S T\ S s G N V S N\R\K(D)	S19 =n,S9 =nf	NP_006747.1	TCEA1
191	ET	3	ETD	16.35	1	(K)K/K/E P A I T S Q N\s/P E A\R(E)	S11 =k	NP_006747.1	TCEA1
192	AL	5	ETD	25.79	1	(K)K/K E/P A I T S Q N s P E/A R E E S T S S G N V S\N R\K(D)	S11 =k	NP_006747.1	TCEA1
193	ET	3	ETD	14.17	1	(K)L/L/D G P s T E K D L D E\K(K)	S6 =n	NP_006747.1	TCEA1
194	AL	4	CID	12.81	3	(K)N/A s T/R I G M s V N\A\I\R/K Q S/T\ D E E V T S L A/K s L I K(S)	S3 =n,S9 =n,S28 =n	NP_958845.1	TCEA1
195	EL	5	ETD	18.96	1	(K)S/Q P/R/R\R H A s A P S H V\Q P\S D S E\K(N)	S9 =n	NP_055647.1	TBC1D4
196	CL	3	CID	19.83	1	(K)E L Q/Q E\L Q\E\Y\E V V T E/S E K(R)	Y9 =n	NP_116185.2	SYAP1
197	EL	3	ETD	11.11	1	(K)E L/Q Q\E L Q E y E V V T E S\E\K(R)	Y9 =n	NP_116185.2	SYAP1
198	CL	4	CID	17.62	1	(K)S N G R E Q D/L P L A E/A/V/R\P/K t/P P V V I K(S)	T18 =k	NP_116185.2	SYAP1
199	CG	2	CID	10.58	1	(E)D/G/D G T D D/F\ t/D K E\D\E(K)	T10 =n	NP_059973.2	SURF2
200	EL	4	ETD	21.27	1	(K)K M/s D D E D D/D E\E E Y G K E E H\E\K(E)	S3 =n	NP_003161.2	SUPT6H
201	CL	4	CID	19.04	1	(K)K M\s D\D\E D D D E E E/Y G K E/E H E K(E)	S3 =n	NP_003161.2	SUPT6H
202	CL	2	CID	13.6	1	(K)L/E G Q G D V P t P K(Q)	T9 =n	AAQ76039.1	SUGT1
203	ELX	5	ETD	24.39	2	(K)R P A S P s/S P E H L P A/t P A E/S P\A Q R F E A\R I\E D G\K(L)	S6 =n,T14 =n	NP_071936.2	SUDS3
204	ELX	4	ETD	17.38	2	(K)T/G/E T S R/A L s/S/s K Q\S S S/R D D N m/F/Q I G\K(M)	S9 =n,S11 =n	NP_006704.2	SUB1
205	ELX	4	ETD	14.89	2	(K)T/G/E T/S\R A L s S/S K Q S S S/S/R D\ N m F Q I G K(M)	S9 =n,S17 =n	NP_006704.2	SUB1
206	ELX	4	ETD	12.01	1	(K)T/G/E T S/R A L S\ S K Q\S s S S R\ D N m F/Q I\G K(M)	S15 =n	NP_006704.2	SUB1
207	EL	3	ETD	18	1	(K)E/G/G/A R L/G A\G G G s P E\K(S)	S12 =k	NP_005852.2	STUB1
208	AT	3	CID	19.34	1	(R)L/G/A/G/G/G s/P E K S P S A Q E L K(E)	S7 =k,S11 =nf	NP_005852.2	STUB1
209	AT	3	ETD	18.19	1	(R)L/G/A G/G G s P E K S P S A Q E L\K(E)	S7 =k,S11 =nf	NP_005852.2	STUB1
210	CT	2	CID	10.68	1	(K)E S K/D P A/D/E\ t E\A\ D(-)	T9 =n	NP_005554.1	STMN1
211	CT	2	CID	14.8	1	(K)E S/V/P/E/F P L/s/P P K(K)	S9 =k	NP_005554.1	STMN1
212	ELX	3	ETD	11.14	1	(K)E/S/V P E F P L s P P K\K(K)	S9 =k	NP_005554.1	STMN1
213	EL	3	ETD	19.22	2	(K)R/A s G Q A F E L I L\s P R\ S\K(E)	S3 =k,S12 =k	NP_005554.1	STMN1
214	ELX	3	ETD	17.94	2	(K)R A s\G Q A\F E/L/I\ L\ S P R s\K(E)	S3 =k,S15 =n,S12 =nf	NP_005554.1	STMN1
215	ELX	3	ETD	15.35	1	(K)R A\ S\G\Q A\F E L I L s P R\ S\K(E)	S12 =k,S3 =nf	NP_005554.1	STMN1
216	CL	4	CID	11.41	2	(K)R A\s G\Q A F/E/L/I L/S P R s K(E)	S3 =k,S15 =n,S12 =nf	NP_005554.1	STMN1
217	EL	2	ETD	7.26	1	(K)s/H/E/A/E\V\L\K(Q)	S1 =k	NP_005554.1	STMN1

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
218	CT	2	CID	17.71	1 (R)A S G Q/A/F/E L I L s/P R(S)	S11 =k,S2 =nf	NP_005554.1	STMN1
219	CT	2	CID	15.17	2 (R)A s/G Q/A/F/E L/I/L s/P R(S)	S2 =k,S11 =k	NP_005554.1	STMN1
220	ET	3	ETD	29.01	1 (R)R K/s H E/A E V/L K(Q)	S3 =k	NP_005554.1	STMN1
221	EL	3	ETD	11.5	1 (K)G T/A/L/H S s\Q\K P A E P V\K(R)	S7 =n	NP_006365.2	STK25
222	CL	3	CID	11.24	1 (K)G/T/A/L H\S\ s Q K P A E P V\K(R)	S7 =n	NP_006365.2	STK25
223	CL	2	CID	13.11	1 (K)L A D/F/G V A G Q/L T D\t Q I K(R)	T13 =n	NP_006365.2	STK25
224	CG	3	CID	17.16	1 (E)I/A/t P/P/P P/P/P/P K/K E(T)	T3 =n	NP_006810.1	STIP1
225	CG	2	CID	17.81	1 (E)D/L/K/A\D E P S S E E s D\L\E(I)	S12 =n	NP_003923.2	ST13
226	CG	2	CID	12.92	2 (E)D/L K/A D E P/S\ s E E s D\L\E(I)	S9 =n,S12 =n	NP_003923.2	ST13
227	CG	3	CID	17.14	2 (E)D/L/K/A/D E P S\ s\E E s D L E I D\K\E(G)	S9 =n,S12 =n	NP_003923.2	ST13
228	CL	2	CID	20.68	1 (K)A/D E/P/S/S E/E s/D/L/E I D K(E)	S9 =n	NP_003923.2	ST13
229	AL	2	CID	14.77	2 (K)A D/E P/s S E\E/s/D/L/E I\D K(E)	S5 =n,S9 =n	NP_003923.2	ST13
230	EL	2	ETD	11.85	2 (K)A/D/E/P/S/s/E E/s/D/L\E\I\D\K(E)	S6 =n,S9 =n	NP_003923.2	ST13
231	CL	2	CID	11.84	3 (K)A D E P/s s E E s/D/L/E I D K(E)	S5 =n,S6 =n,S9 =n	NP_003923.2	ST13
232	AL	2	CID	11.63	2 (K)A D/E/P/S/s E\E/s D/L/E I D K(E)	S6 =n,S9 =n	NP_003923.2	ST13
233	AL	3	CID	20.17	3 (K)K V/E E D L\K\A D E P/s s/E E/s D/L/E/I D K(E)	S12 =n,S13 =n,S16 =n	NP_003923.2	ST13
234	ELX	3	ETD	15.45	1 (K)S/S/S/R Q L\ s E S\F\K(S)	S7 =k	NP_003137.1	SSRP1
235	AL	4	ETD	22.29	1 (K)F A s D D E H D E H D E N G A T G P V\K(R)	S3 =k	NP_003133.1	SSB
236	CL	3	CID	16.27	1 (K)F A/s/D/D/E H/D/E H/D E N G A T G P V\K(R)	S3 =k	NP_003133.1	SSB
237	CT	3	CID	20.67	1 (K)F A/s/D D/E\H/D/E/H D/E N G A T/G P V\K R(A)	S3 =k	NP_003133.1	SSB
238	ET	4	ETD	17.76	1 (K)F A s D D E\H D E H D E N G A T G P V\K R(A)	S3 =k	NP_003133.1	SSB
239	AL	4	ETD	20.95	1 (K)T/K F A\ s D D E H\D\E H\D\E N\G\A T G P V\K(R)	S5 =k,T1 =nf	NP_003133.1	SSB
240	AL	3	CID	14.26	1 (K)T K/F A s/D D/E H/D E/H/D E\N G A T G P V\K(R)	S5 =k,T1 =nf	NP_003133.1	SSB
241	ET	4	ETD	12.49	1 (K)T/K F A s\D\D/E/H D/E H D E N\G A T G P V\K R(A)	S5 =k,T1 =nf	NP_003133.1	SSB
242	CG	2	CID	15.45	1 (E)F S/A/S/P/m L K S/G m\ s\ P E(Q)	S12 =k,S4 =nf	NP_057417.2	SRRM2
243	CG	3	CID	14.67	1 (E)G D A/P/F/S/E P/G T T S T Q R P S\ s/P E(T)	S18 =k	NP_057417.2	SRRM2
244	CT	3	CID	17.44	2 (K)A G m/S/S N Q/S I S s/P/V L/D/A V/P/R/t/P S R(E)	S11 =k,T20 =n,S4 =nf	NP_057417.2	SRRM2
245	CT	3	CID	13.39	3 (K)A G m s s N Q\ S I/s S/P/V/L/D/A V/P/R/t/P S R(E)	S5 =n,S10 =n,T20 =n,S4 =nf,S11 =nf	NP_057417.2	SRRM2
246	CT	3	CID	9.56	2 (K)A G m/s S N Q\ S I S/S/P/V L D A V/P R T P\ s R(E)	S4 =k,S22 =n,S11 =nf	NP_057417.2	SRRM2
247	CT	3	CID	8.54	3 (K)A G m s s N Q\ S I/S s/P/V L/D/A V/P/R t/P S R(E)	S5 =n,S11 =k,T20 =n,S4 =nf	NP_057417.2	SRRM2
248	CT	4	CID	8.99	2 (K)A G m s S N Q\ S I/S P V L D/A V P R\ t P/s R E R(S)	T20 =n,S22 =n,S4 =nf,S11 =nf	NP_057417.2	SRRM2
249	ELX	4	ETD	9.52	4 (K)A/L P Q t P R P/R s R s P\ S\ s P\E L N N\K(C)	T5 =n,S10 =n,S12 =k,S15 =k,S14 =nf	NP_057417.2	SRRM2
250	ELX	4	ETD	8.44	4 (K)A/L P Q t P/R P R S R/s P s\ s P\E L N N\K(C)	T5 =n,S12 =k,S14 =k,S15 =k	NP_057417.2	SRRM2
251	ELX	4	ETD	20.21	4 (K)A P/A P R A L P R R s R s\G\ s s S\K(G)	S11 =n,S13 =n,S15 =n,S16 =n	NP_057417.2	SRRM2
252	CT	3	CID	15.7	2 (K)A Q/t P/P/G P S/L/s G S K\ S/P C/P Q E\K(S)	T3 =k,S10 =n	NP_057417.2	SRRM2

#	Exp.	CS	Number of phosphorylation sites			Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score	▼				
253	ELX	4	ETD	10.66	4	(K)D/K P R A A P R A Q s G s D\s s P E P\K(A)	S11 =k,S13 =k,S15 =n,S16 =k	NP_057417.2	SRRM2
254	ELX	4	ETD	24.1	2	(K)D/T/L R/t P P R E R\S\G A G S s P E T\K(E)	T5 =n,S16 =k,S11 =nf	NP_057417.2	SRRM2
255	ELX	4	ETD	19.47	1	(K)D/T/L R T\p P R E R S G A/G S s P\E T\K(E)	S16 =k,S11 =nf	NP_057417.2	SRRM2
256	EL	4	ETD	18.34	2	(K)D/T L/R t P P R E R\S\G A G/s S P\E T\K(E)	T5 =n,S15 =n,S11 =nf,S16 =nf	NP_057417.2	SRRM2
257	ELX	4	ETD	16.2	3	(K)D T L R\t P P R E R\S G\A G s s P\E T\K(E)	T5 =n,S15 =n,S16 =k,S11 =nf	NP_057417.2	SRRM2
258	AL	4	ETD	13.35	2	(K)D t L R/T P P R E R\S G A G/S\s/P/E T\K(E)	T2 =n,S16 =k,S11 =nf	NP_057417.2	SRRM2
259	CT	3	CID	14.7	2	(K)E L/S N s/P/L/R/E N/S/F/G/S/P L/E/F R(N)	S5 =k,S14 =k,S11 =nf	NP_057417.2	SRRM2
260	ET	3	ETD	11.92	3	(K)G/G/R s R s\S S P/V t E L/A\S\R(S)	S4 =n,S6 =n,T11 =n,S8 =nf S4 =n,S6 =n,S15 =n,S17 =n,S8 =nf,S29 =nf	NP_057417.2	SRRM2
261	ELX	5	ETD	10.22	4	(K)G G R s R\s/S S P V\T E L A/s R s/P I R/Q D R\G\E F S\A S P m L\K(S)	=nf	NP_057417.2	SRRM2
262	ELX	5	ETD	26.85	1	(K)G Q S Q/t S P D H\R\S D T S\S\P\E V R Q/S H S E/S P S\L Q\S\K(S)	=nf	NP_057417.2	SRRM2
263	ELX	5	ETD	21.25	1	(K)G Q S Q/T S\P/D H R/s D/T\S S S P E V R\Q S H S E\S P S\L Q\S\K(S)	S11 =k,S15 =nf,S21 =nf,S25 =nf	NP_057417.2	SRRM2
264	ELX	5	ETD	19.98	1	(K)G Q/S Q\T\S P/D H R/S D T\S/s P\E V R Q/S H/S\E S P\S\L Q\S\K(S)	S15 =k,S11 =nf,S21 =nf,S25 =nf	NP_057417.2	SRRM2
265	ELX	5	ETD	16.12	1	(K)G/Q/S/Q T\S P/D H/R S D\t\S S S P E/V R\Q S H/S\E S P S\L Q\S\K(S)	=nf	NP_057417.2	SRRM2
266	ELX	5	ETD	12.23	1	(K)G Q/S Q/T\S P D H\R S D\T S S P E/V R\Q S H S E\S P\S\L Q\S\K(S)	=nf	NP_057417.2	SRRM2
267	EL	4	ETD	10.2	2	(K)G R G P/S P E/G S\S S T/E s s P E H P P K(S)	S14 =n,S15 =n	NP_057417.2	SRRM2
268	ELX	4	ETD	7.14	3	(K)S/P/E K\L/P Q s S S s\E S S P/P S P Q/P/t K(V)	S8 =n,S11 =n,T21 =n,S17 =nf	NP_057417.2	SRRM2
269	ELX	4	ETD	19.24	4	(K)S/R I S S R\R\s R s L/s s P R\S\K(A)	S8 =n,S10 =n,S12 =n,S13 =n	NP_057417.2	SRRM2
270	ELX	4	ETD	18.17	3	(K)S/R I S S/R R s R s L S s P R S\K(A)	S8 =n,S10 =n,S13 =n	NP_057417.2	SRRM2
271	ELX	4	ETD	13.93	4	(K)S/R I s S R R\s R s L S s P R\S\K(A)	S4 =n,S8 =n,S10 =n,S13 =n	NP_057417.2	SRRM2
272	ELX	4	ETD	16.66	4	(K)S/R/L/s L R R\s L s\G S s P\C P\K(Q)	S4 =n,S8 =k,S10 =k,S13 =k,S12 =nf	NP_057417.2	SRRM2
273	ELX	4	ETD	19.48	3	(K)S/R L s/P R R s R S G\S s P E\V\K(D)	S4 =n,S8 =n,S13 =k,S10 =nf,S12 =nf	NP_057417.2	SRRM2
274	ELX	4	ETD	15.11	4	(K)S/R L s P R R s\R\S\G s s P E\V\K(D)	S4 =n,S8 =n,S12 =k,S13 =k,S10 =nf	NP_057417.2	SRRM2
275	ELX	4	ETD	14.36	2	(K)S/R L s/P\R R S\R S G S s P\E\V\K(D)	S4 =n,S13 =k,S10 =nf,S12 =nf	NP_057417.2	SRRM2
276	ELX	4	ETD	12.74	4	(K)S R L s P R R\s\R s G S s P\E V\K(D)	S4 =n,S8 =n,S10 =k,S13 =k,S12 =nf	NP_057417.2	SRRM2
277	ELX	5	ETD	22.09	4	(K)s R/t/P/P R R/R s S R/S s P\E L T R\K(A)	S1 =n,T3 =n,S9 =n,S13 =n	NP_057417.2	SRRM2
278	ELX	5	ETD	19.3	4	(K)s R/t P P R R R s S R S s P\E L T R\K(A)	S1 =n,T3 =n,S10 =n,S13 =n	NP_057417.2	SRRM2
279	EL	5	ETD	14.9	3	(K)S R/t P P R R R\s R S s P\E L T R\K(A)	T3 =n,S9 =n,S13 =n	NP_057417.2	SRRM2
280	EL	5	ETD	14.39	3	(K)S/R\t P P R R R s S S s P E\L T R\K(A)	T3 =n,S10 =n,S13 =n	NP_057417.2	SRRM2
281	ELX	4	ETD	11.93	4	(K)S R t/P P R R R s/s R/S/s P\E L T R\K(A)	T3 =n,S9 =n,S10 =n,S13 =n	NP_057417.2	SRRM2
282	ELX	4	ETD	10.98	4	(K)S R t P P R R R s/S R s/s P\E L T R\K(A)	T3 =n,S9 =n,S12 =n,S13 =n	NP_057417.2	SRRM2
283	ELX	4	ETD	9.08	4	(K)s R t\p/P R R/R S/s R s s P\E L T R\K(A)	S1 =n,T3 =n,S10 =n,S12 =n	NP_057417.2	SRRM2
284	EL	5	ETD	7.48	3	(K)S R\t P P R R/R\S/S R\s s P E\ T\R\K(A)	T3 =n,S12 =n,S13 =n	NP_057417.2	SRRM2
285	ET	4	ETD	16.24	3	(K)S/R\t P/S R H\s\C S G S s P P\R(V)	T3 =n,S8 =n,S13 =n	NP_057417.2	SRRM2
286	ELX	4	ETD	20.52	3	(K)S/R t P S R H\s\C S\G S s P P R V\K(S)	T3 =n,S8 =n,S13 =n	NP_057417.2	SRRM2
287	ELX	4	ETD	17.45	2	(K)S/R T P s R H/S\C S\G S s P P\R\ V\K(S)	S5 =n,S13 =n	NP_057417.2	SRRM2

#	Exp.	CS	Number of phosphorylation sites			Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score	▼				
288	ELX	4	ETD	14.52	2	(K)S/R t P/S R/H\S\C S\G S s P P\R\V\K(S)	T3 =n,S13 =n	NP_057417.2	SRRM2
289	ELX	4	ETD	12.2	2	(K)S/R t P/S R H S\C S\G s S P P R V\K(S)	T3 =n,S12 =n	NP_057417.2	SRRM2
290	ELX	4	ETD	10.28	3	(K)s R/T P/S R H\s C S\G S s P P R\V\K(S)	S1 =n,S8 =n,S13 =n	NP_057417.2	SRRM2
291	ET	3	ETD	21.73	2	(K)T/H T T A L A\G R\s P\s P A S G\R(R)	S10 =k,S12 =k	NP_057417.2	SRRM2
292	ELX	4	ETD	14.75	4	(K)T R t P L R\Q\R\S R s G s s P E V D S\K(S)	T3 =n,S11 =k,S13 =k,S14 =k	NP_057417.2	SRRM2
293	ELX	4	ETD	28.85	2	(K)V/K P E t P\P R Q S H S G S I s P Y P\K(V)	T5 =n,S16 =k,S10 =nf	NP_057417.2	SRRM2
294	ELX	4	ETD	15.1	2	(K)V/K P/E t P\P R\Q\S H S G S I s P y P\K(V)	T5 =n,Y18 =n,S10 =nf,S16 =nf	NP_057417.2	SRRM2
295	AL	3	CID	8.91	2	(K)V/K P E T P P R Q S H S G S I\s P y P K(V)	S16 =k,Y18 =n,S10 =nf	NP_057417.2	SRRM2
296	ET	4	ETD	7.46	3	(K)V/K P E/t/P P R Q s H\S G S I\s P\Y P\K(V)	T5 =n,S10 =k,S16 =k	NP_057417.2	SRRM2
297	AT	3	ETD	7.33	2	(R)A R s R t P S A P S Q S R(M)	T5 =k, S3 =n	NP_057417	SRRM2
298	CT	2	CID	9.68	1	(R)G E/F S A s/P m L K(S)	S6 =k	NP_057417.2	SRRM2
299	CT	3	CID	15.18	1	(R)G E G D/A/P/F/S E P G T T S T Q R/P S s/P E T A T K(Q)	S20 =k	NP_057417.2	SRRM2
300	ET	4	ETD	16.48	3	(R)G K R s L t R s P P A I\R(R)	S4 =k,T6 =k,S8 =k	NP_057417.2	SRRM2
301	ET	4	ETD	13.81	2	(R)H/A s/S S P E/s\P K P\A P A\P G S\H\R(E)	S3 =n,S8 =n	NP_057417.2	SRRM2
302	CT	3	CID	23.44	2	(R)H G G/s P Q P L A/T/T/P L S Q E P V N P/P/s E A S P T\R(D)	=nf,T27 =nf	NP_057417.2	SRRM2
303	CT	3	CID	16.53	2	(R)H G G s P Q/P L\A T T P L S Q E/P V N P/P/S E A s P T\R(D)	=nf	NP_057417.2	SRRM2
304	CT	4	CID	12.62	3	(R)H G G S P Q P L A T/t P L S Q E\P\N N P P/S/E A s P T R(D)	T11 =k,S14 =k,S25 =k,S4 =nf,T27 =nf	NP_057417.2	SRRM2
305	CT	4	CID	11.52	2	(R)H G G S P Q P/L A t T/P/L S Q/E P V/N/P/P/S/E A S P t R(D)	=nf,S25 =nf	NP_057417.2	SRRM2
306	ET	4	ETD	20.12	3	(R)K/R s R s R s P L A I\R(R)	S3 =n,S5 =k,S7 =n	NP_057417.2	SRRM2
307	CT	4	CID	16.28	1	(R)R G E G D\A P F S E P/G/T T/S/T Q R P S s P E T A T K(Q)	S21 =k	NP_057417.2	SRRM2
308	ET	4	ETD	14.62	3	(R)R/R s R s R t P\L L P\R(K)	S3 =n,S5 =k,T7 =n	NP_057417.2	SRRM2
309	ET	4	ETD	16.49	3	(R)R/R s R s R t P\P A I\R(R)	S3 =n,S5 =n,T7 =n	NP_057417.2	SRRM2
310	ET	3	ETD	12.2	3	(R)R/s\R/s V s P\C S N V E S\R(L)	S2 =n,S4 =k,S6 =k	NP_057417.2	SRRM2
311	AT	5	CID	14.1	2	(R)s D t S S P E V R\Q\S/H/S/E S\P/S/L Q S K S Q/T S P K(G)	S1 =k,T3 =n,S5 =nf,S11 =nf,S15 =nf	NP_057417.2	SRRM2
312	AT	3	ETD	11.07	3	(R)s R s R t P L I S\R(R)	S1 =n,S3 =n,T5 =k	NP_057417.2	SRRM2
313	ET	3	ETD	10.7	3	(R)s/R s R t P L L P\R(K)	S1 =n,S3 =k,T5 =k	NP_057417.2	SRRM2
314	ET	3	ETD	8.66	3	(R)s/R s R t P P A I\R(R)	S1 =n,S3 =n,T5 =n	NP_057417.2	SRRM2
315	ET	3	ETD	4.35	3	(R)s/R\s R\ t P\P V T\R(R)	S1 =n,S3 =n,T5 =k	NP_057417.2	SRRM2
316	CT	3	CID*	14.67	3	(R)s R/s S s P V T E L A/S R(S)	S1 =n,S3 =n,S5 =k	NP_057417.2	SRRM2
317	ET	3	ETD*	12.99	3	(R)s/R s s s P V T E L A\S\R(S)	S1 =n,S3 =n,S5 =k	NP_057417.2	SRRM2
318	CT	2	CID	20.04	1	(R)T P A A A A/A/m/N\ A s/P R(T)	S12 =k	NP_057417.2	SRRM2
319	ELX	4	ETD	6.48	3	(K)A A S P\s P Q S V R R V S/S/s/R S V S G/s P/E/P/A/A K(K)	S5 =n,S15 =n,S21 =n	NP_005830.2	SRRM1
320	EL	3	ETD	13.8	1	(K)E/K t\P E L P E P S\V\K(V)	T3 =n	NP_005830.2	SRRM1
321	ELX	3	ETD	14.75	1	(K)E T\E s\E\A\E\D N L\D\D\ E\K(H)	S4 =n	NP_005830.2	SRRM1
322	AL	4	ETD	19.5	2	(K)G/S/s P S\R S T R E A R s\P Q P\N\K(R)	S3 =k,S13 =n,S7 =nf	NP_005830.2	SRRM1

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene	
			Mode	Score				▼	Symbol
323	ET	4	ETD	10.73	1	(K)H L R/E K\A L R\s\M\R K(A)	S9 =n	NP_005830.2	SRRM1
324	EL	3	ETD	15.52	1	(K)K/E K\t P E\L P E P S V\K(V)	T4 =n	NP_005830.2	SRRM1
325	CL	3	CID	12.43	1	(K)K/E K t P/E/L P/E P S\V\K(V)	T4 =n	NP_005830.2	SRRM1
326	EL	3	ETD	17.09	1	(K)K/E T E s\E\A E\D N L D D L E\K(H)	S5 =n	NP_005830.2	SRRM1
327	CT	3	CID	15.7	2	(K)K E/t E\s/E/A\E D N/L D/D\L E\K(H)	T3 =n,S5 =n	NP_005830.2	SRRM1
328	ET	3	ETD	14.76	2	(K)K E t E\s E A\E D N L D D\L E\K(H)	T3 =n,S5 =n	NP_005830.2	SRRM1
329	CL	3	CID	11.93	1	(K)K E T E\s E\A\E D N/L D/D L E\K(H)	S5 =n	NP_005830.2	SRRM1
330	CL	3	CID	17.89	2	(K)K P P A P/P s P V\Q\S Q s/P S T N/W/S/P A\V P\V K(K)	S7 =n,S13 =n	NP_005830.2	SRRM1
331	EL	4	ETD	14.18	2	(K)K/P P A P P\S/P V Q s Q s P S T\N W S P\A V P V\K(K)	S11 =n,S13 =n	NP_005830.2	SRRM1
332	EL	4	ETD	26.87	2	(K)P/R K V/E L s E s E E D K G\G\K(M)	S7 =n,S9 =n	NP_005830.2	SRRM1
333	AL	3	CID	16.39	2	(K)R R t\A s P P P P K(R)	T3 =n,S5 =n	NP_005830.2	SRRM1
334	ELX	3	ETD	7.52	2	(K)R/R t A s P P P P\K(R)	T3 =n,S5 =n	NP_005830.2	SRRM1
335	ELX	3	ETD	18.06	2	(K)S/R V s V s/P G R T S G\K(V)	S4 =n,S6 =n	NP_005830.2	SRRM1
336	EL	4	ETD	8.46	3	(K)T/R R L s P s A s P/P\R\R(R(H)	S5 =n,S7 =n,S9 =n	NP_005830.2	SRRM1
337	AL	3	CID	20.5	1	(K)V/P K P/E P I P/E P K E P s/P E K(N)	S14 =n	NP_005830.2	SRRM1
338	EL	4	ETD	19.13	1	(K)V P/K P E P I\P E P K E P s P E\K(N)	S14 =n	NP_005830.2	SRRM1
339	CL	4	CID	16.44	1	(K)V P K P E P I P/E P/K/E P/s P E K N S K(K)	S14 =n	NP_005830.2	SRRM1
340	EL	4	ETD	12.65	1	(K)V P\K P E P I P E P\K\E P s P E K N S K\K(E)	S14 =n	NP_005830.2	SRRM1
341	AT	2	CID	12.57	1	(R)A/P Q/T/S s S P P\P V\R(R)	S6 =n	NP_005830.2	SRRM1
342	ET	3	ETD	7.35	2	(R)H/R P/s P\A\A\t P P P\K(T)	S4 =k,T8 =k	NP_005830.2	SRRM1
343	AT	3	ETD	16.24	2	(R)K/V E L s E s E E D K G\G\K(M)	S5 =n,S7 =n	NP_005830.2	SRRM1
344	ELX	3	ETD	9.94	1	(K)A G/D Q E E E\S C E F S S A L E y L\K(L)	Y17 =n	NP_004590.2	SREBF2
345	AT	3	CID	20.4	1	(K)A P R s/P P V G S G P A\S/G V E P/T/S/F/P/V E S E A R(L)	S4 =n	NP_001030312.1	SRA1
346	CG	3	CID	16.66	1	(E)s E G P S S L D P S Q E G/P T\G L K\E(A)	S1 =n	NP_003891.1	SQSTM1
347	CG	2	CID	16.53	1	(E)S E/G P/s S/L/D P S/Q E G P T G L\K E(A)	S5 =n	NP_003891.1	SQSTM1
348	EG	3	ETD	9.98	1	(E)S/E/G P S/s L D P\S\Q E G P T G L K\E(A)	S6 =n	NP_003891.1	SQSTM1
349	EL	3	ETD	13.05	1	(K)R S R L t P V S P E S S S T E E\K(S)	T5 =k,S8 =nf	NP_003891.1	SQSTM1
350	ET	4	ETD	18.52	2	(K)H R s s V/G P S/K P V S Q P R(R)	S3 =n,S4 =n	NP_006708.1	SPIN
351	ET	4	ETD	21.51	1	(K)E V/E\K Q E D/T E\N/H/P/K t P E S A P E N\K(D)	T14 =n	NP_055816.2	SPEN
352	ET	4	ETD	17.17	2	(R)E/S G\V/V/A V s P E K/S E/s P\Q K E D G L\S S Q L\K(S)	S8 =n,S14 =n	NP_055816.2	SPEN
353	ELX	4	ETD	11.63	2	(K)F Q\E L S Q/P R s H T\s L\K(D)	S9 =n,S12 =n	NP_003962.3	SPAG9
354	ELX	3	ETD	11.67	2	(K)K/R S s\t L\S Q\L P\G D\K(S)	S4 =n,T5 =n	NP_003962.3	SPAG9
355	ELX	5	ETD	17.12	1	(K)E D D V I V/N K P/H\V\s\D E E E/E/E P P F/Y/H H/P F\K(L)	S13 =n	NP_003094.4	SON
356	ET	4	ETD	9.44	1	(R)L Q/S\G K\E I/N t V K(L)	T9 =n	NP_055947.1	SNX13
357	ELX	4	ETD	16.89	2	(K)K/I P R G P P s P P A P/V m H S\P s R\K(M)	S8 =k,S18 =n,S16 =nf	NP_036377.1	SNW1

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
358	ELX	4	ETD	10.63	2 (K)K/I P R G P P / s P \ P A P / V M / H S P s R \ K (M)	S8 =k, S18 =n, S16 =nf	NP_036377.1	SNW1
359	AT	3	CID*	11.9	2 (R)G/P/P/s/P/P/A/P V m H/s P S R(K)	S4 =k, S14 =k	NP_036377.1	SNW1
360	AT	3	ETD*	8.23	2 (R)G P P s P P I A P V m H s P S I R (K)	S4 =k, S14 =k	NP_036377.1	SNW1
361	EL	4	ETD	12.57	1 (K)E/T/A R R R A m L D S\G/I\Y P P G\s P\G\K(-)	S18 =n	NP_036569.1	SNAPAP
362	EL	5	ETD	15.26	2 (K)N/E E P\V\R s P/E\R/R D R K A s\A N A R\K(R)	S7 =n, S16 =n	NP_003065.2	SMARCC1
363	EL	5	ETD	17.95	3 (K)R K H s\p s P P P P t P T E S\R K\K(S)	S4 =k, S6 =k, T11 =k	NP_003065.2	SMARCC1
364	EL	4	ETD	8.41	3 (K)R/K H/s\p\s P P P P T P t E\S/R K\K(S)	S4 =k, S6 =k, T13 =n, T11 =nf	NP_003065.2	SMARCC1
365	EL	4	ETD	24.84	1 (K)R/R s Q K E E\D E Q\E D\L T\K(D)	S3 =n	NP_003065.2	SMARCC1
366	CL	2	CID	15.37	1 (K)D/G Q/D A I A Q s/P E K(E)	S9 =n	NP_001013865.1	SLTM
367	AL	4	CID	14.04	2 (K)E N D N D S/G T\G\S t A\D T/S S/I/D/L N L/S I/S S/F L\s K(T)	T11 =n, S28 =n	NP_055535.2	SLK
368	AT	2	CID	14.89	1 (K)I/A A S S/s/F R(S)	S6 =n	NP_003016.1	SH3GL1
369	ET	3	ETD	12.77	2 (R)G/s P H Y F/s P F R\p\Y(-)	S2 =n, S7 =n	NP_003760.1	SFRS9
370	ET	3	ETD	12.07	1 (R)G s P H Y F\S/P\F R P\Y(-)	S2 =n	NP_003760.1	SFRS9
371	EG	4	ETD	15.3	1 (E)K/N R/V K L D\D D s D D D E\E S K\E(G)	S10 =n	NP_004583.2	SFRS8
372	ET	3	ETD	15.24	2 (K)A R/s V/s P P P K R(A)	S3 =k, S5 =k	NP_006266.2	SFRS6
373	CT	2	CID	14.4	1 (R)S N s P/L P V P/P S K(A)	S3 =n, S1 =nf	NP_006266.2	SFRS6
374	CT	2	CID	15.76	1 (R)L I V\E N L S/s R(V)	S8 =n	NP_005617.2	SFRS4
375	ET	2	ETD	4.9	1 (R)L/I/V/E/N/L S s\R(V)	S8 =n	NP_005617.2	SFRS4
376	EL	3	ETD	16.94	2 (K)R/G s V/S R G R s Q E\K(S)	S3 =n, S9 =n	NP_005617.2	SFRS4
377	ELX	5	ETD	12.77	2 (K)S E\S/S Q R E/G/R/G E\S E N\A G\T N\Q E t R S R S\R S N/s\K(S)	T21 =n, S29 =n	NP_005617.2	SFRS4
378	EL	3	ETD	17.38	1 (K)S/K P N L P S E S R\S R s\K(S)	S13 =n	NP_005617.2	SFRS4
379	EL	3	ETD	16.2	2 (K)S/K P N L P S E S R s R s\K(S)	S11 =n, S13 =n	NP_005617.2	SFRS4
380	ELX	5	ETD	6.95	1 (K)s R\S R/S\H S A/G/K S/R S K(S)	S1 =n	NP_005617.2	SFRS4
381	ELX	4	ETD	18.52	3 (K)s R/s R s Q/E R R V E E\E\K(R)	S1 =n, S3 =n, S5 =n	NP_005617.2	SFRS4
382	ELX	5	ETD	12.79	1 (K)S R S R s R S G/S R/S R S K S R S R S Q S R S R S\K(K)	S5 =n	NP_005617.2	SFRS4
383	EL	4	ETD	21.2	2 (K)K/R P Q s\p s/p R R E T\G\K(E)	S5 =n, S7 =n	NP_004710.1	SFRS2IP
384	ELX	5	ETD	19.91	3 (K)R/D T T\R/E S/R/R/s\E s L s/P R\R\E\T\S/R\E\N\K(R)	S10 =n, S12 =n, S14 =n	NP_004710.1	SFRS2IP
385	ET	4	ETD	17.93	2 (K)R P H t P T P\G I Y m\G R P T Y G s\S\R(R)	T4 =n, S18 =n	NP_004584.1	SFRS10
386	AT	4	ETD	14.61	2 (K)R/P\H t P\T P/G I\Y\m\G R P T Y G\S s\R(R)	T4 =n, S19 =n	NP_004584.1	SFRS10
387	AT	4	CID	13.95	2 (K)R P H t/P/T P/G I/y/m G R P\T Y G S S R(R)	T4 =n, Y10 =n	NP_004584.1	SFRS10
388	ET	3	ETD	12.39	2 (R)R R\s P s P Y Y S\R(Y)	S3 =k, S5 =k	NP_004584.1	SFRS10
389	ET	3	ETD	20.01	2 (K)V D/G P R/s P/s/Y/G R(S)	S6 =n, S8 =n	NP_008855.1	SFRS1
390	ET	3	ETD	17.69	2 (R)V/K/V D G P R/s P s Y G\R(S)	S8 =n, S10 =n	NP_008855.1	SFRS1
391	ET	4	ETD	11.79	3 (R)V K V D G P R s P s Y G R\S\R(S)	S8 =n, S10 =n, S14 =n	NP_008855.1	SFRS1
392	AT	2	CID	14.75	1 (R)G m/G/P/G t/P/A/G Y/G R(G)	T6 =n	NP_005057.1	SFPQ

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			Mode	Score				
393	CG	2	CID	17.47	1 (E)A m D G S E t/P Q\L F T V L\p E(K)	T7 =n	NP_006833.2	SF3B2
394	EG	4	ETD	11.42	1 (E)S/S/G/D/R E K\D S T R S/R G s/D S P A A D\V\E(I)	S15 =n	NP_006833.2	SF3B2
395	ELX	4	ETD	22.96	3 (K)G/F/E E E H K D s D D s s\D D E Q E\K(K)	S9 =n,S13 =n,S14 =n	NP_006833.2	SF3B2
396	ET	5	ETD	20.8	3 (K)G F/E/E E H K\D s D D\D\s s D\D E Q\E K\K P E A P K(L)	S9 =n,S13 =n,S14 =n	NP_006833.2	SF3B2
397	CT	3	CID	15.72	1 (K)I E/E A m/D G\s E T/P Q/L F/T\V L P E K(R)	S8 =n	NP_006833.2	SF3B2
398	ET	3	ETD	12.42	1 (K)I E/E A m D G S E t P Q L F T V L P\E K(R)	T10 =n	NP_006833.2	SF3B2
399	AT	3	CID	17.25	1 (K)I E/E/A m/D/G S/E t/P Q L F/T V/L/P E/K R(T)	T10 =n	NP_006833.2	SF3B2
400	ET	5	ETD	17.44	3 (K)K K G F/E/E E H K D s/D D D\s s D D E Q E K K P E A P\K(L)	S11 =n,S15 =n,S16 =n	NP_006833.2	SF3B2
401	EL	5	ETD	27.1	1 (K)K/K P/Q R V\R G/V s S E S S G D R E\K(D)	S10 =n	NP_006833.2	SF3B2
402	ELX	4	ETD	6.06	1 (K)K P Q\R V R G/V s S/E/S S G/D/R E\K(D)	S9 =n	NP_006833.2	SF3B2
403	CL	3	CID	24.39	1 (K)A E E/P/P S/Q L D\Q D T Q V Q\D M/D E/G\s/D/D E E E G Q K(V)	S21 =k	NP_001005409.1	SF3A1
404	EL	4	ETD	16.29	1 (K)F/G/E S E E V E\m E V E/s D/E/E D D K Q E\K(A)	S13 =n	NP_001005409.1	SF3A1
405	CL	4	CID	15.14	1 (K)F G E S/E\E V E m/E V/E/s D/E E D D/K Q E K(A)	S13 =n	NP_001005409.1	SF3A1
406	CL	4	CID	18.64	2 (K)L R/T G D\L G\I P/P N P/E D/R s/P/s P E P I Y N S E G K(R)	S16 =k,S18 =k	NP_004621.2	SF1
407	CL	4	CID	16.77	2 (K)L R T G D\L G\I P/P N P/E D/R s/P/S P E P I Y N S E G K(R)	S16 =k,Y23 =n,S18 =nf	NP_004621.2	SF1
408	ELX	4	ETD	15.18	2 (K)L/R T/G/D/L G I P P/N P E\D R/s P s P\E P\I Y N S E\G\K(R)	S16 =k,S18 =k	NP_004621.2	SF1
409	EL	4	ETD	16.05	1 (K)R/K R s R\W/N Q D T M E Q\K(T)	S4 =k	NP_004621.2	SF1
410	CT	2	CID	12.43	2 (R)s P/s P E P I Y/N/S E G K(R)	S1 =k,S3 =k	NP_004621.2	SF1
411	CT	3	CID	19	2 (R)T G D L/G I P/P N/P E D R s/P/s/P E/P I Y N S E G K(R)	S14 =k,S16 =k	NP_004621.2	SF1
412	ET	4	ETD	11.77	2 (R)T/G/D/L G I P P N P E D R s/P s P\E P\I Y N S E\G\K(R)	S14 =k,S16 =k	NP_004621.2	SF1
413	EL	5	ETD	8.58	2 (K)S t/N\m\A\S\V D K G E s/A P/V\R K(N)	T2 =n,S12 =n	NP_036564.2	SETDB1
414	CT	3	CID	11.26	1 (K)E L/N/S/N H D G A/D E/t S E K(E)	T12 =n,S13 =nf	NP_003002.1	SET
415	CT	3	CID	16.98	1 (K)S/T/L s S/m G M S/D\A F S Q S K A\D F S\G m s S\A R(N)	S4 =n	NP_005015.1	SERPINB10
416	ELX	5	ETD	7.03	1 (K)D R K N P\L P P s/V G/V V/D K(K)	S9 =n	AAH26916.1	SERBP1
417	ELX	5	ETD	8.46	1 (K)E/A G G/G G/V/G G/P G\A K S/A A/Q A A A/Q t N S N A A G K Q L\R K(E)	T22 =n	AAH26916.1	SERBP1
418	ELX	4	ETD	28.59	1 (K)R/E F D R H s\G\S D R S G\L\K(H)	S7 =n	NP_001018078.1	SERBP1
419	ELX	5	ETD	30.27	1 (K)R/E F D R H S G S D R S s\F/S H Y S G\L\K(H)	S13 =n	AAH26916.1	SERBP1
420	ELX	4	ETD	20.5	2 (K)R/E F D R H s\G S D R S s/F S/H/Y S G L\K(H)	S7 =n,S13 =n	AAH26916.1	SERBP1
421	ELX	3	ETD	19.17	1 (K)R/G G S G s H\N W G T V\K(D)	S6 =n	AAH26916.1	SERBP1
422	ELX	4	ETD	24.84	1 (K)R/G G S\G S\H N W\G T V K D E L T\E s P K(Y)	S19 =n	AAH26916.1	SERBP1
423	ELX	5	ETD	28.43	1 (K)S/K s E E A H A E D\S V m D H H F R\K(P)	S3 =n	AAH26916.1	SERBP1
424	ELX	5	ETD	26.18	1 (K)S K s E E A H A E D\S V M D H H F R\K(P)	S3 =n	AAH26916.1	SERBP1
425	ELX	4	ETD	13.13	1 (K)s K S E/E\A H A E D\S V m D H H\F\R\K(P)	S1 =n	AAH26916.1	SERBP1
426	ET	3	ETD	10.52	1 (R)E/K y R K L L E R L\K(E)	Y3 =n	NP_067640.2	SENP2
427	ELX	3	ETD	7.12	2 (K)A/V/A A R A A G s t V/R Q R\K(N)	S9 =n,T10 =n	NP_006799.1	SEC61B

#	Exp.	Number of phosphorylation sites			Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
		CS	Mode	Score				
428	ELX	3	ETD	20.48	1 (M)P/G P T P S G/T N V G S S G R S P s\K(A)	S18 =n,S16 =nf	NP_006799.1	SEC61B
429	ELX	3	ETD	20.07	2 (M)P/G P/T/P S G T N V G S S G R s P s\K(A)	S16 =k,S18 =n	NP_006799.1	SEC61B
430	ELX	3	ETD	20.05	1 (M)P/G P/T P S G T N V G S S G R/s P\s\K(A)	S16 =k	NP_006799.1	SEC61B
431	EL	5	ETD	15.51	4 (E)R/S/M/N P N\ V\s/m V s s A/s S P S\S/S R/T P(Q)	S8 =n,S11 =n,S12 =n,S14 =n	NP_056080.1	SATB2
432	EL	4	ETD	8.87	1 (K)V A/R L E/Q N/G\s P/m G/A R\G R P N G A\ V\A\K(A)	S9 =n	NP_056080.1	SATB2
433	CT	2	CID	15.27	1 (K)V/T/P/D I E E/s/L/L/E P E/N E K(I)	S8 =k	NP_055464.1	SAFB2
434	EL	3	ETD	11.16	2 (K)s G s R/G T E R T V M D\K(S)	S1 =n,S3 =n	NP_002958.2	SAFB
435	ELX	5	ETD	8.23	1 (K)Q G\ V\ L\ T\ H\ G R V R\ L\ L\ S K(G)	S14 =n	NP_001001.2	RPS6
436	ELX	4	ETD	20.05	3 (K)R/R R L s\s L R A s T S\K(S)	S5 =k,S6 =k,S10 =k,S12 =nf	NP_001001.2	RPS6
437	EL	4	ETD	15.83	2 (K)R/R R L s s L R A S T S\K(S)	S5 =k,S6 =k,S10 =nf,S12 =nf	NP_001001.2	RPS6
438	AT	3	ETD	14.56	2 (R)L/s S L R A s T S\K(S)	S2 =k,S7 =k,S3 =nf,S9 =nf	NP_001001.2	RPS6
439	AT	3	ETD	19.67	3 (R)R/L s s L R A s T S\K(S)	S3 =k,S4 =k,S8 =k,S10 =nf	NP_001001.2	RPS6
440	AT	3	ETD	14.21	2 (R)R/L S s L R A s T S\K(S)	S4 =k,S8 =k,S3 =nf,S10 =nf	NP_001001.2	RPS6
441	ET	4	ETD	29.3	4 (R)R/L/s s L R A/s T S K s E S S Q\K(-)	=nf,S15 =nf	NP_001001.2	RPS6
442	ET	4	ETD	28.57	3 (R)R L s s L R A s T S K S E S S Q\K(-)	=nf,S15 =nf	NP_001001.2	RPS6
443	ET	3	ETD	6.17	3 (R)R/R L s s L R/A s\T/S\K(S)	S4 =k,S5 =k,S9 =k,S11 =nf	NP_001001.2	RPS6
444	CT	2	CID	17.39	1 (K)D/E I L P T t P I/S E Q K(G)	T7 =k	NP_000996.2	RPS3
445	AT	3	CID	15.49	1 (K)D/T/G K t P V/E P/E/V/A/I/H\R(I)	T5 =n	NP_001014.1	RPS20
446	CL	3	CID	16.82	1 (K)T H/t R V S V/Q R T Q A P A\ V\A\T\T(-)	T3 =n	NP_002943.2	RPS2
447	ELX	4	ETD	20.34	1 (K)I/G/R I E D V\T P I/P/S D\S t R R\K(G)	T15 =n	NP_001020241.1	RPS14
448	CL	3	CID	15.22	1 (K)K/P/R P s E G\ D E D C L P A S K(K)	S5 =n	NP_006404.1	RPP30
449	EL	3	ETD	13.41	1 (K)K P R P s E G D E D\C L P\A\S\K(K)	S5 =n	NP_006404.1	RPP30
450	EL	4	ETD	19.83	1 (K)K P R P s/E G D E D\C L P A\S K\K(A)	S5 =n	NP_006404.1	RPP30
451	CL	4	CID	16.22	1 (K)K P R/P s E/G D E D C L P A S K K(A)	S5 =n	NP_006404.1	RPP30
452	ELX	4	ETD	7.64	1 (K)D/A L/D P/R Q P G\Y Q P\ N\ P H P G P\S/s P P\A A P/A S\K(R)	S21 =n	NP_060263.1	RPP25
453	AT	2	CID	16.82	2 (K)K E E s E/E s D D m G F\G\L F\D(-)	S4 =k,S7 =k	NP_000994.1	RPLP1
454	AT	2	CID	14.82	1 (K)K E E S E\ E s\D D m G F\G L\F\D(-)	S7 =k,S4 =nf	NP_000994.1	RPLP1
455	EL	2	ETD	13.11	1 (K)K/E/E s\ E E S\D\D\D m\G\F\G\L F\D(-)	S4 =k,S7 =nf	NP_000994.1	RPLP1
456	EL	2	ETD	12.43	2 (K)K/E E s E E s\ D D D\M\G\F\G\L\F\D(-)	S4 =k,S7 =k	NP_000994.1	RPLP2
457	EL	2	ETD	11.52	2 (K)K/E E s E E s\ D D D\M\G\F\G\L\F\D(-)	S4 =k,S7 =k	NP_000994.1	RPLP1
458	EL	2	ETD	11.29	1 (K)K/E E S E\ E s\D\D\D\M\G\F\G\L F\D(-)	S7 =k,S4 =nf	NP_000994.1	RPLP2
459	ET	2	ETD	11.19	2 (K)K/E E s E E s\ D D D\M\G\F\G\L\F\D(-)	S4 =k,S7 =k	NP_000994.1	RPLP1
460	EL	4	ETD	12.45	2 (K)K/V E A K K E E s E E s\ D D D\M G\F\G L\F\D(-)	S9 =k,S12 =k	NP_000994.1	RPLP1
461	EL	3	ETD	14.82	1 (K)K A s F\ L R A Q E R\ A\ A\E\S(-)	S3 =n	NP_000960.2	RPL5
462	ELX	3	ETD	9.65	1 (K)A M/s A R A E A\ I\K(I)	S3 =n	NP_000983.1	RPL29

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
463	ELX	3	ETD	18.26	1 (K)A/Q/A A A P A s V/P A Q A P\K(G)	S8 =n	NP_000983.1	RPL29
464	ELX	3	ETD	9.09	2 (K)F/Q R A I t G/A/s L/A D I\m A\K(R)	T6 =n,S9 =n	NP_000977.1	RPL24
465	EL	3	ETD	10.4	2 (K)R/R s/P/s/P K/P\T\K(V)	S3 =k,S5 =k	NP_006702.1	RNPS1
466	CL	3	CID	17.86	2 (K)A A y G D L S s E E E\E E N/E P E/S L G\V V Y\K(S)	Y3 =n,S8 =n	NP_008909.1	RNF113A
467	ELX	4	ETD	10.4	2 (K)A N\R\I\K/E C L/s\K G t/F/S D\V\T F K(L)	S9 =n,T12 =n	NP_055651.1	RHOBTB1
468	CT	3	CID	13.11	2 (K)s/K S G/R/S\L/N E E\L G D/E D s E\K(K)	S1 =n,S16 =n	NP_002917.1	RGS12
469	AL	4	ETD	26.94	1 (K)R P P s D I/H D S D G S S S/S\H Q S\L\K(S)	S4 =n	NP_001005339.1	RGS10
470	CL	4	CID	13.19	1 (K)R P\p s\D I/H/D/S D G S S S/S S H Q S L K(S)	S4 =n	NP_001005339.1	RGS10
471	CT	3	CID	23.02	1 (R)E R E E s E D E L E E A N\G N/N/P I D I E V D Q N K(E)	S5 =k	NP_055971.1	RCOR1
472	EL	4	ETD	12.76	1 (K)A/A/A A\A W/E E P/S S/G/N/G t A R A G P R\K(R)	T15 =n	NP_061185.1	RCC2
473	ELX	3	ETD	13.23	1 (K)R/R s P\p A D A I P\K(S)	S3 =k	NP_001260.1	RCC1
474	ELX	4	ETD	11.36	1 (K)A/D/R E V Q A\E Q P S S/S\ S P R R\K(T)	S14 =k	NP_057108.1	RBMX2
475	ET	3	ETD	19.03	2 (R)D/S Y S\S s R s D L Y S S/G\R(D)	S6 =n,S8 =n	NP_002130.2	RBMX
476	AT	3	CID	15.87	1 (R)K R s V\Q/E G E N P/D D G V R(G)	S3 =n	NP_055829.1	RBM34
477	AT	3	ETD	11.51	1 (R)K/R s V\Q E/G/E N P/D D G V\R(G)	S3 =n	NP_055829.1	RBM34
478	CT	2	CID	15.93	1 (R)s/V/Q/E/G/E N P D/D/G\V\R(G)	S1 =n	NP_055829.1	RBM34
479	ELX	2	ETD	7.18	1 (K)L/G/A/S/N s P\G Q P N\S\V\K(R)	S6 =k	NP_067062.1	RBM25
480	EL	4	ETD	22.09	1 (K)E/L P R D/F P/Y E E D/S R P R S Q\s\S\K(A)	S18 =n	NP_116294.1	RBM17
481	ET	3	ETD	16.4	1 (R)R P D P D/s D E D E D Y E R(E)	S6 =n	NP_116294.1	RBM17
482	EL	5	ETD	16.75	4 (K)R R s L s/s D/R/G R T T H s P Y E E R S/R T\K(G)	S3 =n,S5 =n,S6 =n,S14 =n	NP_037418.3	RBM15B
483	CL	4	CID	13	1 (K)H R\T T A P/T\E G\K\s/P L/K(K)	S11 =n	NP_073605.4	RBM15
484	EL	4	ETD	24.16	1 (K)H/R T T A P T E G K s P\L K\K(E)	S11 =n	NP_073605.4	RBM15
485	ET	4	ETD	21.27	1 (R)H L D R s/P E S D/R P R(K)	S5 =n	NP_073605.4	RBM15
486	ET	4	ETD	22.48	1 (R)T T/A P/T E G K\s/P L K K E D\R(S)	S9 =n	NP_073605.4	RBM15
487	EL	4	ETD	22.33	2 (K)R/S R/s R s P H E A G F C V Y\L\K(G)	S4 =n,S6 =n	NP_006038.2	RBM12
488	EL	5	ETD	18.95	4 (K)S P s G Q K R s/R s R s P\H E A G F C V Y\L\K(G)	S3 =n,S8 =n,S10 =n,S12 =n	NP_006038.2	RBM12
489	AT	3	ETD	8.27	1 (K)L/A/S/D D R/P s P P R(G)	S8 =n	NP_690595	RBM10
490	CG	2	CID	17.28	1 (E)N/I Y/N D E E S D V t T\S\E(L)	T11 =n	NP_002884.1	RBBP7
491	CG	2	CID	12.61	1 (E)N/I Y N/D E E\s D V T\T\S\E(L)	S8 =n	NP_002884.1	RBBP7
492	ELX	5	ETD	24.21	1 (K)D/T/H E D/H D T s\T/E N T D E S\N\H D P Q F E P I V S L P E Q E I K(T)	S9 =n	NP_002873.1	RANBP1
493	AT	5	CID	19.99	2 (K)D T H E D H D\T s\T/E N T D E s\N H D\p Q F E P I V S L P E Q E\I K(T)	T8 =n,S16 =n	NP_002873.1	RANBP1
494	AT	5	CID	18.78	1 (K)D T H E D H D\T s\T/E N T D E s\N H D\p Q F E P I V S L P E Q E\I K(T)	T2 =n	NP_002873.1	RANBP1
495	CL	4	CID	14.25	2 (K)D T H E D H D T S T/E N t D E s\N\H D P Q\F E P I/V S L P E Q E\I\K(T)	T13 =n,S16 =n	NP_002873.1	RANBP1

#	Exp.	CS	Mode	Score	Number of phosphorylation sites ▼ Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
496	ELX	5	ETD	13.06	1 (K)D/T/H E D H D T S t/E N T\D/E S/N H D P Q\F E\p I V/S L P E Q E I\K(T)	T10 =n	NP_002873.1	RANBP1
497	ELX	5	ETD	7.54	2 (K)D/T/H E D H D T S t/E N T\D/E S/N H D P Q\F E\p I V/S L P E Q E I\K(T)	S9 =n,T13 =n	NP_002873.1	RANBP1
498	ET	4	ETD	16.29	1 (K)Q E K P A E K P A E t P V/A T S P T A T D S T S G D/S S\R(S)	T11 =n	NP_002865.1	RAD23B
499	CT	3	CID	21.3	1 (R)E D/K s/P S/E/E S/A P T/T/S/P E/S\V/S/G S V P S S G S S G R(E)	S4 =n	NP_005044.1	RAD23A
500	AT	3	CID	15.76	1 (R)E D/K S P S E E s A P T T S P E/S\V/S/G/S/V/P S S G S S G R(E)	S9 =n	NP_005044.1	RAD23A
501	EL	4	ETD	22.89	2 (K)R/R s T s R Q\F V D G P\p G P V\K(K)	S3 =n,S5 =n	NP_037409.2	RACGAP1
502	CT	3	CID	17.4	1 (K)T P L/S Q S\m s\V/L P T/S K/P E K(V)	S8 =n	NP_001002814.1	RAB11FIP1
503	AL	2	CID	14.16	1 (K)A A s/T/D L/G A/G/E/T V/V\G K(V)	S3 =n	NP_056176.2	R3HDM1
504	CT	3	CID	18.86	1 (K)E K/L Q/E E/G G G s D E E E T/G/S/P/S/E/D G m Q S A R(T)	S10 =k,S17 =nf	NP_008993.1	PWP1
505	CT	3	CID	23.3	1 (K)L Q E E/G G G s D E E E T G/S P/S/E/D/G m/Q S A R(T)	S8 =k,S15 =nf	NP_008993.1	PWP1
506	CT	3	CID	19.46	2 (K)L Q E E/G G G s D E E E T G S P/S/E/D/G m/Q/S A R(T)	S8 =k,S17 =n,S15 =nf	NP_008993.1	PWP1
507	EG	3	ETD	15.2	1 (E)N/V/G/L\m Q Q Q K s F\R(-)	S10 =n	NP_002825.3	PTPN11
508	CT	3	CID	24.94	1 (R)V/y\E/N V G L m/Q/Q\K(S)	Y2 =k	NP_002825.3	PTPN11
509	ET	3	ETD	13.76	1 (R)V/y\E N V G L m Q Q Q\K(S)	Y2 =k	NP_002825.3	PTPN11
510	CG	3	CID	19.47	1 (E)V/D G A D D D\ S Q/D s D D E K m P D\L\E(-)	S11 =n	NP_006592.3	PTGES3
511	CG	3	CID	16.38	2 (E)V/D/G A/D D D\s/Q D s D D E K/m P D\L\E(-)	S8 =n,S11 =n	NP_006592.3	PTGES3
512	CT	4	CID	24.24	1 (R)F/S/E m m N N m G G D E D V D L P/E/V/D G A/D D/D s Q D S D D E/K m P D\L\E(-)	S26 =n	NP_006592.3	PTGES3
513	CT	4	CID	21.02	2 (R)F S E m m N N m\G G D E D\V D L P/E V D G A D D D s Q D S D D E/K/m/P D L E(-)	S26 =n,S29 =n	NP_006592.3	PTGES3
514	CT	4	CID	20.12	1 (R)F S/E m m N N m\G G D E D V D L P/E V D/G A D D D S Q D S D D E/K/m/P D L E(-)	S29 =n	NP_006592.3	PTGES3
515	ELX	3	ETD	8.45	1 (K)I/N E/T\R A F/s\G(-)	S8 =n	NP_077748.2	PSTPIP2
516	EL	3	ETD	20.69	1 (K)E/S L K E E D E/s D D D N\M(-)	S9 =k,S2 =nf	NP_002779.1	PSMA3
517	CL	2	CID	15.21	1 (K)E S L K/E E D E s D D\N\M(-)	S9 =k,S2 =nf	NP_002779.1	PSMA3
518	AL	2	CID	13.85	1 (K)E S/L K/E E D E s D/D D\N m(-)	S9 =k,S2 =nf	NP_002779.1	PSMA3
519	AL	3	ETD	11.76	1 (K)E/S L/K E/E D\E/s D D D N\M(-)	S9 =k,S2 =nf	NP_002779.1	PSMA3
520	ET	4	ETD	25.26	1 (K)E/T S V/S K\E D\T/D H\E E K\A s\N\E D\V\T\K(A)	S16 =n	NP_066967.2	PSIP1
521	ELX	4	ETD	25.16	2 (K)E/T/S V S\K E D t D\H\E\E K A s N E D V\T\K(A)	T9 =n,S16 =n	NP_066967.2	PSIP1
522	CL	2	CID	10.21	1 (K)Q S N A/S/s/D V/E/V/E/E K(E)	S6 =k	NP_066967.2	PSIP1
523	ELX	3	ETD	15.35	2 (K)T/G/V T/S T s D s/E\E E G D\D Q E\G E\K(K)	S7 =n,S9 =k	NP_066967.2	PSIP1
524	EL	4	ETD	17.4	1 (K)W/D E Q/T/S N T K G D D D E E s D E\E A V\K\K(T)	S16 =n	NP_004689.1	PRPF3
525	ET	3	ETD	18.28	1 (R)A E A P P L E R E\D s G T F S L G\K(M)	S11 =n	NP_003681.1	PRKRA
526	CT	4	CID	14.31	2 (R)A P/A/S V/L P A A t P R\Q/s/L\G H P P P/E P G P D R(V)	T10 =n,S14 =n,S4 =nf	NP_004148.1	PRKAR2A
527	CT	3	CID	13.53	2 (R)V A D A K G/D s E s E E D E\D/L E V P\V P S R(F)	S8 =k,S10 =k	NP_004148.1	PRKAR2A
528	EL	4	ETD	23.03	1 (K)A/G/T R T D S R E D E I s P P P P N P\V\K(G)	S13 =k	NP_002725.1	PRKAR1A

#	Exp.	CS	Mode	Score	Number of phosphorylation sites ▼ Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
529	AG	5	ETD	11.15	2 (E)L Q Q A/I S K L E A Q L\N V\L E K/s/S P G/H/R\A\T A P Q T Q H V\s P m R/Q V E(S)	S18 =n,S33 =n	XP_949815.1	Predic.
530	ELX	3	ETD	16.12	1 (K)D/E/L/H\I V E\A E A m N Y K G s P\I\K(V)	S16 =n	XP_945199.1	Predic.
531	AL	4	ETD	12.81	1 (K)E/S C E\S T S L K/K/t P N R\K(Q)	T11 =n	XP_059482.5	Predic.
532	ELX	4	ETD	12.32	2 (K)K s/S F E\N T/V\V\R K V/S/V/t L K(E)	S2 =n,T15 =n	XP_945327.1	Predic.
533	EL	4	ETD	10.09	1 (K)L/Q T/D\E E R\E/K\N G s E E/D\D\D E K P G\K(R)	S12 =n	XP_379933.2	Predic.
534	ET	4	ETD	10.55	2 (K)Q L I V G V N K m\D S T E P P y s H K(R)	Y16 =n,S17 =n	XP_950453.1	Predic.
535	ELX	3	ETD	14.46	1 (K)S/E/s P K E P K Q L R\K(L)	S3 =n	XP_379885.2	Predic.
536	ELX	3	ETD	15.54	2 (K)S P/Q L S/L s P R P A s P\K(A)	S7 =n,S12 =n	XP_950070.1	Predic.
537	AT	4	ETD	11.98	2 (R)C V/Q A/S t A\A P G\G R/L s K(D)	T6 =n,S13 =n	XP_951336.1	Predic.
538	CT	2	CID	15.84	1 (R)Y F Q\I S Q D E D\E S E s E\D(-)	S13 =n	XP_947405.1	Predic.
539	ET	4	ETD	24.51	1 (K)H G/E V\C P A\G W K\A/P G S D t I K P\A V Q\K(S)	T15 =n	NP_002565.1	PRDX1
540	AL	4	CID	17.94	1 (K)H G E V C P A G W K P G S D t I K P D V Q K(S)	T15 =n	NP_002565.1	PRDX1
541	AL	4	ETD	28.91	2 (K)I/A A P E L H K\G D s D s E E D E P T\K(K)	S11 =n,S13 =n	NP_005964.3	PRCC
542	EL	3	ETD	24.63	1 (K)N/H S D S S T S E S E V S S V s P L\K(N)	S16 =n	NP_777567.1	PPP4R2
543	CL	3	CID	16.65	1 (K)N H S D S/S T/S/E S E V S/S V s P L\K(N)	S16 =n	NP_777567.1	PPP4R2
544	ELX	4	ETD	25.44	1 (K)N/K T/s T T S S M V A S A E Q P/R/G N\V\D E E L\S\K(K)	S4 =n	NP_006232.1	PPP1R2
545	ELX	4	ETD	16.86	1 (K)N/K T/s T T S S m V A S A E Q P R/G N\V\D E E L\S\K(K)	S4 =n	NP_006232.1	PPP1R2
546	ELX	4	ETD	18.38	2 (K)Y/R I Q E Q\E s s G E E D S D/L S P/E E\R E\K(K)	S8 =k,S9 =k	NP_006232.1	PPP1R2
547	ET	4	ETD	12.91	2 (R)S S G/S D P R\S W E y R/s G E A S E E K E E\K(A)	Y11 =n,S13 =n	NP_055145.2	PPP1R15A
548	EL	4	ETD	10.59	1 (K)S m H/L G/R L P\s R P\A P/L/P G\S G\G S\Q S G A\K(M)	S9 =n	NP_057231.1	PPME1
549	EL	4	ETD	7.73	1 (K)R/K L E E/V L s\T\E G A E E\N G N\S D\K(K)	S8 =n	NP_002698.1	PPM1G
550	EL	4	ETD	12.98	1 (K)R K L\E E V\L s T\E\G A E\N G N S\D\K\K(K)	S8 =n	NP_002698.1	PPM1G
551	EL	3	ETD	11.99	2 (K)I/T/D/H R N V/s\E s P N R\K(N)	S8 =n,S10 =n	NP_004783.2	PPIG
552	EL	4	ETD	12.64	2 (K)D/S P H S R s G/S S V\S S R\S Y s P\E R\S\K(S)	S7 =n,S17 =n	NP_057572.5	PPHLN1
553	EL	4	ETD	20.84	3 (K)E/R/P V Q\S L K\T/s R/D T S/P S s G S A V S S\S\K(V)	T9 =n,S10 =n,S17 =n	NP_057572.5	PPHLN1
554	EL	4	ETD	20.79	2 (K)E/R P V Q/S L K T S R D t s P\S S G S A V S S\S\K(V)	T13 =n,S14 =n	NP_057572.5	PPHLN1
555	AL	4	ETD	19.17	2 (K)E/R P V Q S L\K T s R D T s P\S/S G S A V S S\S K(V)	S10 =n,S14 =n	NP_057572.5	PPHLN1
556	EL	4	ETD	18.93	2 (K)E/R P V Q/S L K t s R\D t s P\S S G S A V S S\S\K(V)	T9 =n,T13 =n	NP_057572.5	PPHLN1
557	ELX	4	ETD	18.58	2 (K)E/R P V Q\S L K t s R\D T S\P/s S G S A V\S/S S\K(V)	T9 =n,S16 =n	NP_057572.5	PPHLN1
558	EL	4	ETD	18.29	2 (K)E/R/P V Q S L K T s R/D/T s P\S S G S A V S S\S\K(V)	S10 =n,S14 =n	NP_057572.5	PPHLN1
559	EL	4	ETD	16.63	3 (K)E/R P V/Q S L K T\s R\D T s P\S/s G\S A V/S\S S\K(V)	S10 =n,S14 =n,S17 =n	NP_057572.5	PPHLN1
560	EL	4	ETD	16.39	2 (K)s/F Y/S/S/H Y A R E R s P\Y\K(R)	S1 =n,S12 =n	NP_057572.5	PPHLN1
561	EL	3	ETD	12.26	1 (K)R/I N P P S S G G T S S s P I\K(A)	S13 =k	NP_002688.2	POU2F1
562	ET	5	ETD	24.99	1 (K)R G D G E K s D E E\N E E K E G\S\K/E\K(S)	S7 =n	NP_006458.1	POLR3G
563	ELX	3	ETD	7.46	2 (K)G/A/V/G/A/s V T S s\T H E\K\K(S)	S6 =n,S10 =n	NP_060552.3	POLR3B

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
564	AL	4	ETD	17.65	1 (K)s Y R G D\R E A F E E\T H\L T S L\D P V\K(Q)	S1 =n	NP_060599.1	PNPO
565	EL	3	ETD	10.73	1 (K)H/R R s V D R\K(R)	S4 =n	AAB48304.1	PNN
566	EL	4	ETD	13.82	3 (K)N/S R S D\R K\R s I s E S\s R S G\K(R)	S9 =k,S11 =n,S14 =n	AAB48304.1	PNN
567	ET	3	ETD	11.48	1 (K)S/L/s P G K\E N\V/S A L D m\E\K(E)	S3 =k	AAB48304.1	PNN
568	ET	4	ETD	17.98	1 (K)S L/s P G K E N/V S A L D m E K E S E K E E\K(E)	S3 =k	NP_002678.2	PNN
569	ET	5	ETD	11.12	3 (K)s\S K\G G/s\s/R D/T/K\G S K(D)	S1 =n,S6 =n,S7 =n	AAB48304.1	PNN
570	ET	4	ETD	8.53	1 (R)E S/R Q E S/D P\E/D D D V\K K P A L Q s S\V V A T\S\K(E)	S20 =n	AAB48304.1	PNN
571	ET	4	ETD	14.35	1 (R)Q/E s D P E/D D/D V/K/K P A L Q/S S\V\V A\T\S\K(E)	S3 =n	AAB48304.1	PNN
572	ET	5	ETD	22.16	2 (R)R/E\s R Q E s D P E/D D/D V\K\K\P\A\L Q\S S V\V A T\S\K(E)	S3 =n,S7 =n	NP_002678.2	PNN
573	ET	4	ETD	6.53	2 (R)R/E\S R Q E s D P E D D D V K K P A L Q s S V\V A\T\S\K(E)	S7 =n,S21 =n	NP_002678.2	PNN
574	ET	5	ETD	8.09	4 (R)s H\K/S s K\G G s\s R D T/K\G/S K(D)	S1 =n,S5 =n,S9 =n,S10 =n	NP_002678.2	PNN
575	ET	5	ETD	16.34	2 (R)T/R R E s\R Q E s\D\P E D D\D V K\K P\A L Q\S S\V\V A T\S\K(E)	S5 =n,S9 =n	NP_002678.2	PNN
576	EL	4	ETD	22.84	2 (K)E/A R L A R S s P E Q P R P s T S\K(A)	S8 =n,S15 =n	NP_002666.1	PML
577	AL	5	CID	11.12	1 (K)A N V T P\Q S s\S\E\L R P T T/T A A L A S/G V E A K(K)	S8 =n	NP_000924.2	PLCB4
578	CT	4	CID	10.45	2 (R)L D I\D s P P I/T/A/R N/t G I I/C T I G P\A S R(S)	S5 =n,T13 =n	NP_002645.3	PKM2
579	CT	3	CID	15.53	3 (R)M/m s/Q\L F L\D t P V/s\K T E K(T)	S3 =n,T9 =n,S12 =n	NP_000288.1	PKD2
580	CT	2	CID	11.3	1 (R)V/D/R/m/E H\s I\G S I V S K(I)	S7 =n	NP_000288.1	PKD2
581	CG	2	CID	14.53	2 (E)P/Y/t/D F D/G T R V Y s\P\P\E(W)	T3 =n,S12 =n	NP_006866.2	PIM2
582	CG	2	CID	13.92	1 (E)P/Y/T/D F D/G\T R V Y s\P\P\E(W)	S12 =n	NP_006866.2	PIM2
583	CL	4	CID	19.06	2 (K)T A H N S E A\A D L E E s F N E H E L E P s s P K(S)	S13 =n,S22 =n	NP_115711.2	PHF6
584	CL	4	CID	10.68	2 (K)T A H N/s E\A A D L E E S F N E H E L E P s s P K(S)	S5 =n,S23 =n	NP_115711.2	PHF6
585	ELX	4	ETD	29.43	2 (K)T A/H N/s E A D L E E S F N E H E L E P s P\K(S)	S5 =n,S22 =n	NP_001015877.1	PHF6
586	ELX	4	ETD	26.15	2 (K)T A/H\N/S\E/A\D L E\E s F N E H\E L E P s S P\K(S)	S12 =n,S21 =n	NP_001015877.1	PHF6
587	ET	4	ETD	12.82	2 (R)D R s P H R S s P/S D T R P K(C)	S3 =n,S8 =n	NP_001015877.1	PHF6
588	ET	3	ETD	15.78	2 (R)R A s K A/s L/P P L T K(D)	S3 =n,S6 =n	NP_004418.2	PHC2
589	AL	2	CID	16.51	1 (K)E G E/E P/T/V Y s/D/E E E\P K(D)	S9 =k	NP_006658.1	PGRMC1
590	EL	4	ETD	25.55	1 (K)E/G/E E P T V Y s D E E E P K\D E S\A R\K(N)	S9 =k	NP_006658.1	PGRMC1
591	CL	3	CID	10.68	1 (K)E/G/E E/P/T V/Y/s D/E E E/P K D/E S A R K(N)	S9 =k	NP_006658.1	PGRMC1
592	EL	4	ETD	16.99	1 (K)E/G/E E/P T V Y s D E E E P K D\E\S\A R K N\D(-)	S9 =k	NP_006658.1	PGRMC1
593	AL	4	CID	20.26	1 (K)I V R G D\Q P A A S/G/D/s/D/D/D E/P/P/P L P R L K(R)	S13 =k	NP_006658.1	PGRMC1
594	EL	4	ETD	18.84	1 (K)I/V/R\G D Q P A A\S\G D s/D D D E\P P P L P/R L\K(R)	S13 =k	NP_006658.1	PGRMC1
595	ELX	5	ETD	10.12	1 (K)G K\D A s G\N/K V K A E P/A K(I)	S5 =n	NP_000282.1	PGK1
596	ELX	3	ETD	5.25	1 (-)M t H E E H H\A/A K(T)	T2 =n	NP_000280.1	PFKM
597	EL	3	ETD	20.8	1 (K)A/K P s P A P P S T T T A P D A S G P\Q\K(R)	S4 =n	NP_002848.1	PEX19
598	CL	3	CID	15.24	1 (K)A K/P s P\A P P S T T/T A P D A/S G P Q\K(R)	S4 =n	NP_002848.1	PEX19

#	Exp.	CS	Mode	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
				Score	▼				
599	CL	4	CID	16.27	1	(K)A K P S P A P P S T/T/T/A P/D A/S G P Q K R s P G D T A K(D)	S23 =n	NP_002848.1	PEX19
600	CL	4	CID	13.12	1	(K)A M E G L G M D E G D G E G N/I/L P/I m Q s\I m Q N L L S K(D)	S22 =n	NP_002848.1	PEX19
601	EL	3	ETD	22.06	1	(K)N/A T/D/L Q/N S s m S E E L\T\K(A)	S9 =n	NP_002848.1	PEX19
602	CL	3	CID	20.5	1	(K)N A/T/D/L Q N S s m/S/E/E/E\T\K(A)	S9 =n	NP_002848.1	PEX19
603	CL	3	CID	19	1	(K)N A/T D/L Q N s S M/S E/E E\T\K(A)	S8 =n	NP_002848.1	PEX19
604	EL	3	ETD	13.33	1	(K)N/A\T D/L Q/N/S s M S E E L T\K(A)	S9 =n	NP_002848.1	PEX19
605	EL	2	ETD	10.21	1	(K)N/A T/D/L Q/N/S/S/m s s E E E\T\K(A)	S11 =n	NP_002848.1	PEX19
606	EG	5	ETD	23.03	2	(E)L/D/T K L/T R I P s/A K K/Y K D I I R Q\p\S\E\E(E)	S10 =k,Y14 =n,S22 =nf	NP_003759.1	PEA15
607	EG	5	ETD	11.05	2	(E)Y G t L L/Q/D L T/N N I T L E D L E Q L K s\A C K\E(D)	T3 =n,S22 =n	NP_003759.1	PEA15
608	ET	3	ETD	20.42	1	(K)D/I/I/R Q P s E E I\I\K(L)	S7 =k	NP_003759.1	PEA15
609	EL	3	ETD	16.73	2	(K)A P/R P F G s V S s P\K(V)	S7 =n,S10 =n	NP_006448.2	PDLIM5
610	AL	3	CID	11.9	2	(K)A/P/R P F G s V s S/P K(V)	S7 =n,S9 =n	NP_006448.2	PDLIM5
611	EL	5	ETD	11.08	1	(K)H I V E/R\Y T E/F y H V P/T/H\S\D A S\K(K)	Y10 =n	NP_001011513.1	PDLIM5
612	EG	4	ETD	15.2	1	(E)K H A R E R V T P/P E G\y\E(V)	Y13 =k	NP_066272.1	PDLIM1
613	ELX	3	ETD	12.71	1	(K)G D/P N/K P S/G F R/s\V\K(A)	S11 =n	NP_066272.1	PDLIM1
614	ELX	4	ETD	27.6	2	(K)T/A A S G V E A/N\S R P\L D H A Q P P s L\V I\D\K(E)	S20 =n,S21 =n	NP_066272.1	PDLIM1
615	ELX	4	ETD	24.96	1	(K)T/A/A/S G V E A N S R/P L D/H/A Q/P P S s L\V I\D\K(E)	S21 =n	NP_066272.1	PDLIM1
616	ET	5	ETD	16.42	1	(K)T A A/S G V/E/A N S R P L D H/A Q P/P s\S L V I D K E/S\E\V Y\K(M)	S20 =n	NP_066272.1	PDLIM1
617	ELX	3	ETD	15.69	1	(K)R/F\V\s E G D G G R L K P\E\S\Y(-)	S4 =k	NP_055271.2	PDCD4
618	ELX	3	ETD	13.13	1	(K)R/m Q S L s L N\K(-)	S6 =n	NP_055706.1	PDAP1
619	ELX	3	ETD	12.13	1	(K)S L/D S D E\s E D\E E D D Y Q Q\K(R)	S7 =k,S4 =nf	NP_055706.1	PDAP1
620	ELX	3	ETD	10.79	1	(K)S L/D/S D E/S E D\E E D D Y Q Q K(R)	Y14 =n,S4 =nf,S7 =nf	NP_055706.1	PDAP1
621	ELX	3	ETD	8.63	1	(K)S/L D s D/E\S E D\E E D D Y Q Q\K(R)	S4 =k,S7 =nf	NP_055706.1	PDAP1
622	ELX	3	ETD	6.99	2	(K)S/L/D s D E s/E D E E D D Y Q Q K(R)	S4 =k,S7 =k	NP_055706.1	PDAP1
623	ET	3	ETD	14.07	2	(R)Y K/s t T S/V\S E E D V\S S\R(Y)	S3 =n,T4 =n	NP_002574.2	PAWR
624	CT	3	CID	11.05	2	(R)y K S T T\ s V S E E D V S S R(Y)	Y1 =n,S6 =n	NP_002574.2	PAWR
625	EL	3	ETD	17.66	1	(K)A/S/R T\A/R/I/A\s D E E I Q G\T\K(D)	S9 =n	NP_057165.2	PALLD
626	AT	2	CID	20.25	2	(R)T L s N/A/E D Y L D D E\D s\D(-)	S3 =n,S14 =n	NP_036515.3	OSTF1
627	EL	4	ETD	15.61	1	(K)V/E E E G s P G D\p D H E A/S T Q G R\T\C G P E H S\K(G)	S6 =n	NP_031372.2	OGFR
628	EG	3	ETD	21.77	1	(E)T Q/s P/S L F/G\S T K L Q Q\E(S)	S3 =n	NP_009103.2	NUP50
629	CG	2	CID	16.62	1	(E)t/Q S/P S/L/F/G S/T K L Q\Q\E(S)	T1 =n	NP_009103.2	NUP50
630	ELX	3	ETD	8.5	1	(K)E R S s L\L A V S N\K(Y)	S4 =n	NP_005076.3	NUP214
631	ET	5	ETD	14.52	1	(K)D A/E N H E A/Q L K N/G S L D/s P G\K\Q D T E/E D E E E D/E K D\K(G)	S16 =n	NP_006591.1	NUDC
632	EL	3	ETD	14.49	1	(K)L/S/D/L D S E T\R\s m V E\K(M)	S10 =n	NP_006591.1	NUDC
633	CL	3	CID	18.91	1	(K)N G S L/D/s/P\G K Q D/T/E E D/E E/E D\E K(D)	S6 =n	NP_006591.1	NUDC

#	Exp.	CS	Number of phosphorylation sites			Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score	▼				
634	AL	3	CID	17.01	1	(K)N G S/L/D/S/P/G K Q D t/E E D E/E E\D\E K(D)	T12 =n	NP_006591.1	NUDC
635	CL	3	CID	15.04	2	(K)N G S/L/D/s/P/G K Q D t E/E D E/E/E D\E K(D)	S6 =n,T12 =n	NP_006591.1	NUDC
636	ET	4	ETD	10.11	1	(K)N/G/S/L D S P/G K Q D t E E E D E E D\E K/D K\G\K(L)	T12 =n	NP_006591.1	NUDC
637	CL	3	CID	15.58	1	(K)T/P/S P/K E\E\D E\E P\E s/P P E K(K)	S13 =k,S3 =nf	NP_073568.2	NUCKS1
638	ELX	3	ETD	7.4	1	(K)T P/S P K E E D E\E P E\s P P E\K(K)	S13 =k,S3 =nf	NP_073568.2	NUCKS1
639	AL	4	ETD	15.58	1	(K)S/A/E/T/R E S T Q L S P A D L/t E G K P T D P S K(L)	T16 =n,S11 =nf	NP_060225.4	NSUN2
640	ET	3	ETD	22.39	1	(R)K/K s P N E L V D D L F K(G)	S3 =n	NP_057227.2	NSFL1C
641	CT	2	CID	20.46	1	(R)L G/A/A P E/E/E S/A/y V/A/G E K(R)	Y11 =n	NP_057227.2	NSFL1C
642	CT	3	CID	15.73	1	(R)L/G/A A P/E E E s A Y/V A/G E/K R(Q)	S9 =n	NP_057227.2	NSFL1C
643	ET	3	ETD	14.54	1	(R)L/G/A/A P E E E S/A y V\A G E\K\R(Q)	Y11 =n	NP_057227.2	NSFL1C
644	CL	3	CID	14.03	1	(K)T P\t P E P A E V/E/T R K(V)	T3 =k	NP_037524.1	NRBP
645	EL	3	ETD	8.48	1	(K)t P T P/E/P/A\E V E T R\K(V)	T1 =n,T3 =nf	NP_037524.1	NRBP
646	EL	5	ETD	15	1	(K)D A A A H L Q T S\H K P S\A E D A/E G Q S/P L S\Q K Y/s P\S\T E\K(C)	S28 =n	NP_110386.1	NRBF2
647	EG	3	ETD	16.42	1	(E)K T/P K t P K G P\S\S\V\E(D)	T5 =k,T2 =nf	NP_002511.1	NPM1
648	EG	3	ETD	11.09	2	(E)K/t P\K t P K\G P S\S V\E(D)	T2 =k,T5 =k	NP_002511.1	NPM1
649	AG	5	ETD	27.56	1	(E)K/T/P/K t P K G/P S S V E D I K A K m Q A S\I\E(K)	T5 =k,T2 =nf,S22 =nf	NP_002511.1	NPM1
650	EG	4	ETD	13.64	2	(E)K/t P/K t P K G P S S V E D I\K A\K m Q\A S I\E(K)	T2 =k,T5 =k,S22 =nf	NP_002511.1	NPM1
651	CT	4	CID	18.71	1	(K)C G S G/P/V H I S G/Q H L V A V\E E D\A\E\s E\D E E E E\D\V\K(L)	S22 =k	NP_002511.1	NPM1
652	CT	3	CID	17.47	1	(K)D/E/L H I V E\A\E\A m N/Y E G s P I\K(V)	S16 =k	NP_002511.1	NPM1
653	ELX	3	ETD	13	1	(K)D/E/L/H I V E A\E\A m N Y E G s P I\K(V)	S16 =k	NP_002511.1	NPM1
654	ET	3	ETD	12.72	1	(K)G/G/s L P/K V E A\K(F)	S3 =n	NP_002511.1	NPM1
655	CT	3	CID	11.42	1	(K)G G s L/P K/V/E A K(F)	S3 =n	NP_002511.1	NPM1
656	ELX	4	ETD	22.72	2	(K)K/Q E K t P\K t P/K G P/S\S\V E D\I\K(A)	T5 =k,T8 =n	NP_954654.1	NPM1
657	CL	2	CID	10.19	1	(K)L/L s I/S/G/K(R)	S3 =n	NP_002511.1	NPM1
658	EL	2	ETD	7.25	1	(K)L/L/s I/S\G\K(R)	S3 =n	NP_002511.1	NPM1
659	ET	4	ETD	24.17	1	(K)m Q A S I E K\G\G s L/P K V E\A\K(F)	S10 =n,S4 =nf	NP_002511.1	NPM1
660	EL	3	ETD	16.76	1	(K)S I R\D t\P A K N A\Q\K(S)	T5 =k	NP_002511.1	NPM1
661	ELX	3	ETD	14.23	2	(K)t/P K\t P K G P S S V E D\I\K(A)	T1 =k,T4 =k	NP_002511.1	NPM1
662	ET	3	ETD	10.91	1	(K)T P/K t P K G P\S S V E D\I\K(A)	T4 =k,T1 =nf	NP_002511.1	NPM1
663	ET	4	ETD	26.5	1	(K)T/P/K t P K G P/S S V E D I K\A\K(M)	T4 =k,T1 =nf	NP_002511.1	NPM1
664	CT	4	CID	13.78	1	(R)T V S L G/A G A K D\E\L\H I V E A E\A m N Y E G s P I/K V/T L A T L K(M)	S25 =k	NP_002511.1	NPM1
665	EL	5	ETD	15.55	3	(K)R/K L L N K\L t/K s\t/E K L\E\K(E)	T8 =n,S10 =n,T11 =n	NP_443178.1	NOSTRIN
666	EG	3	ETD	12.85	1	(E)L/Q/R A A s/Q D H V R G\F\L\E(K)	S6 =n	NP_057037.1	NOSIP
667	ELX	4	ETD	29.28	1	(K)E L Q R A A s Q D H V R G F L E\K(E)	S7 =n	NP_057037.1	NOSIP

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			Mode	Score				
668	CG	2	CID	21.63	1 (E)G I G A I/G/G t P P/A/F/N R\A A P G A\E(F)	T8 =n	NP_031389.3	NONO
669	AG	3	ETD	15.16	1 (E)G/I G/A I G G t P/P A F N R\A A P G\A\E(F)	T8 =n	NP_031389.3	NONO
670	EL	3	ETD	11.87	1 (K)G/K/G s P R P Q A\P\K(A)	S4 =n	AAH01883.1	NOLC1
671	AL	2	CID	19.98	1 (K)G T D/T\Q T P A/V L s P S K(T)	S11 =k	NP_001028886.1	NOL1
672	EL	2	ETD	10.09	1 (K)G T/D/T/Q/T P/A/V\L s P\S\K(T)	S11 =k	NP_001028886.1	NOL1
673	CL	3	CID	17.57	1 (K)R/R L\G s V E A P K(T)	S5 =n	NP_001028886.1	NOL1
674	EL	3	ETD	13.59	1 (K)R R L/G s V E A P\K(T)	S5 =n	NP_001028886.1	NOL1
675	CL	3	CID	11.7	2 (K)R s D\L/y\A\V\E\m K(K)	S2 =n,Y5 =n	NP_064587.1	NIT2
676	EL	3	ETD	5.38	1 (K)H Q T L\E\V S L\S R\D s\P\L\K(T)	S12 =n	NP_116204.3	NFATC2IP
677	CG	4	CID	18.74	3 (E)L P M V E R Q/D t/D S C L/V Y G/G/Q/Q\M I L t/G Q N F\T\s E(S)	T9 =n,T23 =n,S29 =n	NP_036472.2	NFATC2
678	ET	4	ETD	16.77	1 (R)Q/Q y H N D m K E I R\K(K)	Y3 =n	NP_954983.1	NEK5
679	CL	3	CID	20.43	1 (K)A E/E/A/K/D\E P P/s E/G/E A E E E\E\K(D)	S10 =n	NP_006149.1	NEFL
680	EL	3	ETD	14.13	1 (K)A/E E A K\D E P P s E G E A E E E E\K(D)	S10 =n	NP_006149.1	NEFL
681	EG	3	ETD	13.32	1 (E)K/A K S\P V/P/K s/P\V\E\K(K)	S9 =k,S4 =nf	NP_005373.1	NEF3
682	EG	3	ETD	13.08	1 (E)K G K S P V P K s P\V\E\K(K)	S9 =n	NP_005373.1	NEF3
683	CG	3	CID	12.76	1 (E)K/G K S P V P/K s/P V E E(K)	S9 =n	NP_005373.1	NEF3
684	CG	3	CID	10.1	2 (E)K/G K s P V P\K s\P\V\E\K(K)	S4 =n,S9 =n	NP_005373.1	NEF3
685	EG	5	ETD	19.64	2 (E)L/V/A D A K V\E K P E K A/K s P/V P K s P V\E\K(K)	S15 =k,S20 =k	NP_005373.1	NEF3
686	CL	3	CID	19.84	2 (K)A K s/P/V P K s P V E A\K(S)	S3 =n,S8 =n	NP_005373.1	NEF3
687	EL	3	ETD	11.4	2 (K)A/K\s P\V P K/s P V E E\A\K(S)	S3 =n,S8 =n	NP_005373.1	NEF3
688	AL	3	CID	14.27	2 (K)A/K\s/P/V P K s P V E E K(G)	S3 =k,S8 =k	NP_005373.1	NEF3
689	ET	3	ETD	12.86	2 (K)A/K s P V P K\s P V E E\K(G)	S3 =k,S8 =k	NP_005373.1	NEF3
690	ET	4	ETD	10.12	1 (K)E/A/A E E K E E E P E A E E E E V A A K\K\s P V\K(A)	S22 =k	NP_005373.1	NEF3
691	ET	4	ETD	7.89	2 (K)E K E K\A G/G\E G G s\E/E/E G/s/D/K/G/A K(G)	S11 =n,S16 =n	NP_005373.1	NEF3
692	AL	3	CID	17.48	2 (K)G K\s/P V P K\s/P V E E K(G)	S3 =n,S8 =n	NP_005373.1	NEF3
693	CT	3	CID	17.32	2 (K)G K s/P V P K\s/P V E E K(G)	S3 =n,S8 =n	NP_005373.1	NEF3
694	ET	3	ETD	15.19	1 (K)G K S P V P K/s P\V E E\K(G)	S8 =n	NP_005373.1	NEF3
695	AL	3	ETD	12.52	2 (K)G/K/s P V P K s/P V E E\K(G)	S3 =n,S8 =n	NP_005373.1	NEF3
696	CL	3	CID	10.49	1 (K)K A E s/P V K E E A V A E V V T I T\K(S)	S4 =k	NP_005373.1	NEF3
697	EL	3	ETD	9.37	1 (K)K/A E s P V K E E A\V A E V V T I T\K(S)	S4 =k	NP_005373.1	NEF3
698	CL	3	CID	17.48	1 (K)S P V P K s/P/V/E E A K(S)	S6 =n	NP_005373.1	NEF3
699	AL	3	CID	19.72	1 (K)S/P V P K s P\V/E E K(G)	S6 =k,S1 =nf	NP_005373.1	NEF3
700	CL	2	CID	17.2	1 (K)S P/V P K s/P V E E\K(G)	S6 =k,S1 =nf	NP_005373.1	NEF3
701	AL	3	ETD	13.44	1 (K)S P/V/P K s/P V E E\K(G)	S6 =k,S1 =nf	NP_005373.1	NEF3
702	ET	3	ETD	13.31	1 (K)S P V P K s P V E E\K(G)	S6 =k,S1 =nf	NP_005373.1	NEF3

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
703	EL	4	ETD	21.87	1 (K)N/R D/G/G/E R R P s S T S V P L\G\D\K(G)	S10 =n	NP_060138.1	NDE1
704	EL	4	ETD	13.38	2 (K)N R D/G G E R\R P s\s T S V P L G\D\K(G)	S10 =n,S11 =n	NP_060138.1	NDE1
705	ELX	5	ETD	13.58	2 (K)E R L M/R/s S T\D/S L P G P I s R Q P L\G\A\T S G A S L\K(T)	S6 =n,S16 =n	NP_066018.1	NCOA5
706	CG	2	CID	18.31	1 (E)I E/P/A A/m/K\A\A A A P A\s E(D)	S15 =n	NP_005372.2	NCL
707	CG	2	CID	22.74	1 (E)I/E/P/A/A m K A A A A P/A\s E D\E(D)	S15 =n	NP_005372.2	NCL
708	CG	2	CID	19.39	1 (E)I E/P/A A m K A A A A P A s E D E D D\E(D)	S15 =n	NP_005372.2	NCL
709	AG	2	CID	14.85	1 (E)P/A A m K A\A A A A P A s E D\E(D)	S13 =n	NP_005372.2	NCL
710	CG	2	CID	12.63	1 (E)P/A A m K A A\A\A A P A\s E D E D D\E(D)	S13 =n	NP_005372.2	NCL
711	EG	5	ETD	24.1	1 (E)T/t P A K G K K A A K V V P V K A K N V A E D\E(D)	T2 =n	NP_005372.2	NCL
712	CT	2	CID	12.01	1 (K)K/V/V V s/P\T\K(K)	S5 =k	NP_005372.2	NCL
713	AL	5	ETD	25.17	1 (K)R/E I E/G R A I R L/E L/Q G P R G s P N A\R S Q\P S\K(T)	S18 =n	NP_005372.2	NCL
714	ET	4	ETD	13.41	1 (R)A/I/R L E/L Q G P\R G s P N\A\R(S)	S12 =n	NP_005372.2	NCL
715	CT	3	CID	17.95	2 (K)R/K/P/s V P D\S A S/P/A D\D s/F\V D P G E R(L)	S4 =k,S15 =n	NP_006144.1	NCK1
716	CT	2	CID	19.08	1 (R)L y D L N m P\A/Y\V\K(F)	Y2 =n	NP_006144.1	NCK1
717	CT	3	CID	19.11	1 (K)D G A V/N/G/P S V/V G D Q/t/P I E P Q/T S I E R(L)	T14 =k	NP_002473.2	NASP
718	CL	3	CID	22.08	1 (K)D G A/V/N/G/P/S/V/V/G\D Q t/P I/E/P Q T S I\E R L T E T K(D)	T14 =k	NP_002473.2	NASP
719	CL	4	CID	14.52	2 (K)E G E E T/E G s E/E D D/K E/N\D K\T E E M P N/D s V\L E N K(S)	S8 =n,S25 =n	NP_002473.2	NASP
720	AL	4	CID	10.88	2 (K)E G E E t E G s E E\D/D K E N\D\K/T E/E M/P N/D/S/V/L E N K(S)	T5 =n,S8 =n	NP_002473.2	NASP
721	CL	4	CID	10.09	1 (K)G G A A P E G P/N E\A E/V t/S/G K/P/E Q E\V P/D\A E E E K(S)	T14 =n	NP_002473.2	NASP
722	AL	4	ETD	21.2	1 (K)R/K P\E E E s P R K\D D\A\K(K)	S7 =n	NP_002473.2	NASP
723	CL	4	CID	18.81	1 (K)R R E F I T\G D V/E\P/T D A\E\S\E\W\H s E N E E E E\K(L)	S20 =k	NP_005960.1	NAP1L4
724	EL	5	ETD	15.2	1 (K)R/R E F I T\G D V E\P T\D A A E S E\W\H s E/N\E E E E K(L)	S20 =k	NP_005960.1	NAP1L4
725	CL	5	CID	13.1	1 (K)R R E F I T\G D V E\P T D\A\E\S\E W\H\S E N E\E E E K L A G D M K s K(V)	S34 =n,S20 =nf	NP_005960.1	NAP1L4
726	CG	2	CID	12.42	1 (E)Q s E L D/Q D L D D V\E\K(V)	S2 =n	NP_004528.1	NAP1L1
727	AG	2	CID	12.9	1 (E)R L D G L V E t/P T\G\Y I\E(S)	T8 =k	NP_004528.1	NAP1L1
728	CT	4	CID	16.48	1 (K)V Q G E A V\S N I Q/E N T Q T P T V/Q E E s E E E/E V/D/E T G\V/E\K(D)	S22 =k	NP_005585.1	NACA
729	ELX	3	ETD	8.32	1 (-)M L A S G s L G Q\K(F)	S6 =n		N/A
730	AL	4	CID	17.03	1 (-)m s H P I Q\N I N K/E/I\E I V E K N/Q I/E/I L E L K(S)	S2 =n		N/A
731	AG	3	CID	16.86	2 (E)A t/M t N I S G Q R m R\m G I/K N R N E\A\E(L)	T2 =n,T4 =n		N/A
732	AT	4	CID	15.01	1 (K)A Q/A A\D/Q/L A/S/Q\Q\s/G A R(L)	S12 =n		N/A
733	ELX	5	ETD	13.78	1 (K)D/A/V S/T G/L/T/G A\V K L/A K G\T V Q/T G m D T t\K(T)	T25 =n		N/A
734	EL	5	ETD	12.55	1 (K)E/S E/D K P E/I\E D V G s D E E E E E K K D G D\K(K)	S13 =n		N/A
735	CL	3	CID	18.73	1 (K)E S K/D K/P/E I/E/D/V G/s/D/E/E E E\K(K)	S13 =n		N/A
736	ELX	3	ETD	13.59	1 (K)E/S/K/D/K P E I E D V G s D E E E E\K(K)	S13 =n		N/A

#	Exp.	CS	Mode	Score	▼	Number of phosphorylation sites Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
737	ELX	4	ETD	27.61	1	(K)E/S/K D K P E I E D V G s D E E E E K K(D)	S13 =n		N/A
738	AL	3	CID	16.73	1	(K)E S K D/K/P E I/E/D V/G s/D/E/E E E K K(D)	S13 =n		N/A
739	CT	4	CID	12.01	1	(K)E T F/P/R/D G L t/S P/T/P Q m G C W Q I(-)	T9 =n		N/A
740	ELX	3	ETD	8.28	1	(K)S Q P L Q D y G/E E K K(R)	Y7 =n		N/A
741	AT	4	CID	17.11	1	(R)s C L Y G G G G Q/Y F A K P Q N/Q/G G Y/G/G/S/S/S/S/S/Y/G S G R(R)	S1 =n		N/A
742	ET	4	ETD	17.67	1	(R)V E E E E A S S K Q N m t K(R)	T13 =n		N/A
743	EL	3	ETD	10.65	3	(K)L/D E E G s K C s I L s K(H)	S6 =n,S9 =n,S12 =n	NP_056275.2	MYRIP
744	CL	3	CID	16.09	1	(K)G A G D/G s/D/E E/V/D G K/A D G A/E/A K P A E(-)	S6 =k	NP_002464.1	MYH9
745	EL	3	ETD	11.04	1	(K)G/A G D G s D E E V D G K A D G A E A K P A E(-)	S6 =k	NP_002464.1	MYH9
746	EG	5	ETD	12.44	1	(E)G/s L E Q E K K V/R m/D/L E(R)	S2 =n	NP_000248.1	MYH6
747	EL	5	ETD	14	1	(K)A E V P G A/T/G G D s P H L Q P/A E P P G E P R R E P/H P A E A E K(Q)	S11 =n	NP_057216.2	MYEF2
748	EL	4	ETD	21.48	1	(K)R/R N s R D G D P L P S S L S C K(V)	S4 =n	NP_002452.1	MVD
749	CL	4	CID	17.36	2	(K)Q G R/V H T S t t m T V/A I L P Q P t E I/N L V I N P K(D)	T8 =n,T18 =n	NP_061914.2	MTRF1L
750	ELX	3	ETD	12.94	1	(K)S/Q/E/P I P D D Q K V/s D D D K(E)	S12 =n	NP_848927.1	MTDH
751	ELX	3	ETD	8.86	1	(K)N/I/P/E/G s H Q Y E L L K(H)	S6 =n	NP_060691.1	MOBK11A
752	CT	2	CID	14.18	1	(R)L A/I Q G P E/D s P S R(Q)	S9 =k	NP_005430.1	MLF2
753	ET	4	ETD	11.4	1	(R)T V/R D s D/S G L E Q m/S I G H H I R(D)	S5 =n	NP_005430.1	MLF2
754	CL	2	CID	20.97	1	(K)s/Q V A E/L/N/D D/D/K/D D/E/I V F K(Q)	S1 =n	NP_115766.2	MKI67IP
755	EL	3	ETD	11.14	1	(K)s Q V A E L N D D D K D D E I V F K(Q)	S1 =n	NP_115766.2	MKI67IP
756	EL	4	ETD	15.86	2	(K)T/V D S Q G P t P V C T P t F L/E R R K(S)	T8 =k,T14 =n,T12 =nf	NP_115766.2	MKI67IP
757	ELX	3	ETD	13.84	2	(K)A/m/H t P K P s V G E E K(D)	T4 =n,S8 =n	NP_002408.2	MKI67
758	ELX	4	ETD	15.59	1	(K)D/L Y T/T/G R R E s V N L G K(S)	S10 =k	NP_002408.2	MKI67
759	CT	3	CID	10.32	2	(K)I/A/C/K s P P P/E/S V D t/P T S T K(Q)	S5 =k,T13 =k	NP_002408.2	MKI67
760	ELX	4	ETD	8.23	2	(K)I/A C R s P Q P D P V G t P/T I/F K P Q S K(R)	S5 =k,T13 =k	NP_002408.2	MKI67
761	ELX	4	ETD	23.04	2	(K)I/R E Q E P/A R R V s/R/S/s F S S D P D E K(A)	S11 =n,S14 =n	NP_002408.2	MKI67
762	ET	3	ETD	13.78	1	(K)T P V Q Y S Q Q Q N s P Q K(H)	S11 =k	NP_002408.2	MKI67
763	CT	3	CID	10.23	2	(K)V/A C/K/S s Q/P D/L D K N/P A S s K(R)	S6 =n,S17 =n	NP_002408.2	MKI67
764	CT	2	CID	12.58	1	(R)s G A S E/A N L I V A K(S)	S1 =k	NP_002408.2	MKI67
765	CL	3	CID	21.96	1	(K)T P/E/P/V/V P/T/A/P/E P/H/P T t S T D Q P V T P K(L)	T16 =n	NP_055456.1	MDC1
766	AT	4	ETD	19.46	1	(R)K/R s L A T m D S P P H Q K(Q)	S3 =n	NP_055456.1	MDC1
767	AT	4	CID	15.42	1	(R)K/R s L/A T m D S P P H Q K(Q)	S3 =n	NP_055456.1	MDC1
768	CT	3	CID	17.15	2	(K)D/G D/S/Y/D P/Y D/F/s D t E/E/E/m P Q V H T P K(T)	S11 =n,T13 =k,T22 =nf	NP_002379.2	MCM3
769	ET	3	ETD	22.27	1	(R)G P/s L N P V L D Y D H/G S R(S)	S3 =n	NP_061322.2	MATR3
770	AT	4	CID	20.62	1	(R)R D s/F/D D/R G P S L N P V L/D/Y/D/H G S R(S)	S3 =n	NP_061322.2	MATR3

#	Exp.	CS	Mode	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
				Score	▼				
771	ET	4	ETD	16.64	1	(R)R/D s F/D D R G P S L N P V L D Y\D H\G\S\R(S)	S3 =n	NP_061322.2	MATR3
772	ELX	3	ETD	27.18	1	(K)A P/R G D V T A E\E A A G A s P\A\K(A)	S15 =k	NP_075385.1	MARCKSL1
773	ELX	4	ETD	15.61	1	(K)A P/R G D V/T/A/E/E\A/A G A s P/A/K A N G Q\E N G H\V\K(S)	S15 =k	NP_075385.1	MARCKSL1
774	ELX	4	ETD	19.98	1	(K)E G G G/D S S A S S P t E E E Q/E Q G E I G A C\S D E G T A Q E G K(A)	T12 =n,S10 =nf,S25 =nf	NP_075385.1	MARCKSL1
775	ELX	4	ETD	9.63	2	(K)E G G G/D s/S A S S P t E\E E Q/E Q G E I G A C S D E G T A Q E G K(A)	S6 =n,T12 =n,S10 =nf,S25 =nf	NP_075385.1	MARCKSL1
776	ELX	4	ETD	7.77	1	(K)E G G G/D S S/A S S P T E E\E\Q E Q G E/I G A C s\D E\G/T A Q E G K(A)	S25 =k,S10 =nf	NP_075385.1	MARCKSL1
777	ELX	4	ETD	15.62	1	(K)G A E A S A/A/S E E/E A G P Q A T E P S t P S G P E S\G P T P A/S A E Q N\E(-)	T21 =k,S5 =nf,S8 =nf,S23 =nf	NP_075385.1	MARCKSL1
778	ELX	4	ETD	14	1	(K)G A E A S A/A S E E/E A G P Q\A t E P\S T P S G P E/S\G P T P A S A E Q N\E(-)	T17 =n,S5 =nf,S8 =nf,T21 =nf,S23 =nf	NP_075385.1	MARCKSL1
779	ELX	3	ETD	9.5	1	(K)G E/V P P K E t P\K(K)	T8 =n	NP_075385.1	MARCKSL1
780	ELX	3	ETD	10.49	1	(K)G E/V P/P K/E t P K\K(K)	T8 =n	NP_075385.1	MARCKSL1
781	ELX	3	ETD	17.87	2	(K)K P F K L s G L s F\K(R)	S6 =n,S9 =k	NP_075385.1	MARCKSL1
782	ELX	3	ETD	14.78	2	(K)P/F K L s G L s F\K(R)	S5 =n,S8 =k	NP_075385.1	MARCKSL1
783	ELX	3	ETD	23.2	1	(K)A/E/D/G A T P S\P/S N E t P\K\K(K)	T13 =k	NP_002347.4	MARCKS
784	ELX	3	ETD	17.85	2	(K)A/E/D/G A T P s P\S N E t P K\K(K)	S8 =n,T13 =k	NP_002347.4	MARCKS
785	ELX	3	ETD	7.38	1	(K)A/E/D/G A T P s P S N E\T P K\K(K)	S8 =n,T13 =nf	NP_002347.4	MARCKS
786	ELX	3	ETD	23.04	1	(K)G/E/A/A/A/E R P G E A A V A S S P s\K(A)	S18 =n,S16 =nf	NP_002347.4	MARCKS
787	ELX	4	ETD	11.33	1	(K)G E A A A E R P G E\A\A\A S s/P S K A N\G Q\E N G H V\K(V)	S16 =k	NP_002347.4	MARCKS
788	ELX	3	ETD	17.74	2	(K)s F K L s G F S F\K(K)	S1 =k,S5 =k,S8 =nf	NP_002347.4	MARCKS
789	ELX	3	ETD	15.02	2	(K)S/F K\L s G F s F\K(K)	S5 =k,S8 =k,S1 =nf	NP_002347.4	MARCKS
790	ELX	3	ETD	16.67	3	(K)s/F K L s G\F s F K\K(N)	S1 =k,S5 =k,S8 =k	NP_002347.4	MARCKS
791	ELX	3	ETD	13.73	2	(K)s/F/K/L/s\G F S F K\K(N)	S1 =k,S5 =k,S8 =nf	NP_002347.4	MARCKS
792	ELX	3	ETD	9.38	1	(K)T/A/A/K\G/E A A A/E R P G E A\A V A s/S P S\K(A)	S19 =n,S20 =nf	NP_002347.4	MARCKS
793	ELX	4	ETD	8.35	1	(K)T/A A K G/E A A A E R P G E\A\A V A S\ S P s K(A)	S22 =n,S20 =nf	NP_002347.4	MARCKS
794	ELX	4	ETD	6.72	2	(K)s/K\D G\t G\S\D/D K/K/A K\G/A D G/K/T K(I)	S1 =n,T5 =n	NP_058525.1	MAPT
795	ELX	3	ETD	17.28	2	(K)V/A/V V R t P P K s P S S\A\K(S)	T6 =k,S10 =k,S12 =nf,S13 =nf	NP_005901.2	MAPT
796	ET	4	ETD	22.54	2	(K)S/S P\A A K P/G S T P/s R P S s A K\R(A)	S12 =n,S16 =n	NP_055083.1	MAPRE2
797	EL	4	ETD	25.64	1	(K)K P L T/s/S\A A P Q R\ P I S T Q R T A A A P\K(A)	S5 =n	NP_036457.1	MAPRE1
798	EL	4	ETD	24.58	2	(K)K P L T s S S A A P Q R\ P I S t Q R T A A A P\K(A)	S5 =n,T16 =n	NP_036457.1	MAPRE1
799	AL	4	ETD	9.47	1	(K)S G L\Q I K K/N/A/I/I/D D y K(V)	Y14 =n	NP_004750.1	MAPKAPK2
800	AG	2	CID	14.18	2	(E)A L N s/P H\S E\ S F\V S P\E(A)	S4 =n,S9 =n	NP_002366.2	MAP4
801	AG	2	CID	13.07	1	(E)A L/N S P H\S E s F V S P\E(A)	S9 =n	NP_002366.2	MAP4
802	AG	2	CID	20.14	1	(E)m/A/L G/K/D\V t P/P/P\E\T\E(V)	T8 =k	NP_002366.2	MAP4

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
803	EG	3	ETD	17.59	1 (E)V/A/L A K D m E s P T K\L\D(V)	S9 =k	NP_002366.2	MAP4
804	EG	4	ETD	22.95	1 (E)V/A/L A K D m E S\p t K L D V\T L A\K D\m\Q P S m\E(S)	T11 =n,S9 =nf	NP_002366.2	MAP4
805	AG	3	CID	16.29	1 (E)V/A L A K D m E\s P/T K L D\V\T/L A K D\m\Q P S m E(S)	S9 =k	NP_002366.2	MAP4
806	AG	2	CID	15.38	1 (E)V/G L L K D m s/P L S E(T)	S8 =k	NP_002366.2	MAP4
807	CG	2	CID	16.41	1 (E)V G L L/K D m s P L\S\E\T\E(M)	S8 =k	NP_002366.2	MAP4
808	AL	3	ETD	8.23	1 (K)A/T P/M P S R/P\s T T P F/I D\K(K)	S9 =n	NP_002366.2	MAP4
809	ET	3	ETD	24.07	1 (K)D/m E s P T K L D V T L\A\K(D)	S4 =k	NP_002366.2	MAP4
810	EL	3	ETD	21.39	1 (K)D/M E s P\T K L D V T L\A\K(D)	S4 =k	NP_002366.2	MAP4
811	AT	3	CID	16.99	1 (K)D/m E/s P/T/K L/D V/T L A K(D)	S4 =k	NP_002366.2	MAP4
812	CT	3	CID	14.32	1 (K)D M E/s P/T K L D V/T L A K(D)	S4 =k	NP_002366.2	MAP4
813	CT	3	CID	13.48	1 (K)D m E/S P/t/K L/D/V/T L A K(D)	T6 =n,S4 =nf	NP_002366.2	MAP4
814	ET	3	ETD	15.33	1 (K)E/T/E/R\A s\p I K m D L A P\S\K(D)	S6 =n	NP_002366.2	MAP4
815	AT	3	CID	13.8	1 (K)E T/E/R A\s/P I/K/m D L/A/P S\K(D)	S6 =n	NP_002366.2	MAP4
816	CT	3	CID	13.12	1 (K)E T/E/R A\s/P I/K/m/D L/A/P S\K(D)	S6 =n	NP_002366.2	MAP4
817	ET	4	ETD	9.1	1 (K)E T/E R/A/s\p I K\M D L A P S\K(D)	S6 =n	NP_002366.2	MAP4
818	CL	4	CID	14.41	1 (K)G I S E D S H L\E s L Q/D V G/Q S A A/P T F M I/S/P E T V\T G T G K K(C)	S10 =n	NP_002366.2	MAP4
819	CL	3	CID	10.8	1 (K)K C s/L P A E E D S V/L E\K(L)	S3 =n	NP_002366.2	MAP4
820	CT	3	CID	12.49	1 (K)K P m/S L\A s G L V P/A A P P K(R)	S7 =n	NP_002366.2	MAP4
821	AT	5	CID	13.35	3 (K)K P m S L A\S\G L V P A A\p/P K R/P A/V A s/A R P s/I/L P s K(D)	S22 =n,S26 =n,S30 =n	NP_002366.2	MAP4
822	ELX	3	ETD	18.64	1 (K)K/V s Y S H I Q S\K(C)	S3 =n	NP_002366.2	MAP4
823	ELX	3	ETD	11.88	1 (K)K V s Y S H I Q S\K(C)	S3 =n	NP_002366.2	MAP4
824	ET	3	ETD	7.63	3 (K)T/E V A L/A/K D M E s/P t K/L D V t L/A K(D)	S11 =k,T13 =n,T18 =n	NP_002366.2	MAP4
825	AL	3	CID	18.78	1 (K)T T/T/A/A/V/A S T G/P/S S R S P S t L L\p K(K)	T19 =n,S16 =nf	NP_002366.2	MAP4
826	CT	3	CID	14.11	1 (K)T T/T/A/A/V/A S T G/P/S S R S P/s T L L\p K(K)	S18 =n,S16 =nf	NP_002366.2	MAP4
827	AT	2	CID	11.53	1 (R)L A/t/N/T/S/A P D L K(N)	T3 =n,S6 =nf	NP_002366.2	MAP4
828	EG	5	ETD	12.44	1 (S)N A\V T\K T\A/G\p I\A S A/Q K Q P A G\K\V Q I/V/S/K K V s y S(H)	Y30 =n	NP_002366.2	MAP4
829	EL	3	ETD	7.45	2 (K)E/L/E/A E R\s L\m S s P E D L\T\K(D)	S7 =n,S11 =n	NP_005900.1	MAP1B
830	CL	2	CID	13.4	1 (K)G E A E Q/s/E/E/E A D E E D K(A)	S6 =n	NP_005900.1	MAP1B
831	AL	4	CID	13.15	2 (K)Q V s S\L\s/S\G V I Q\E A L A/T N m K(L)	S3 =n,S6 =n	NP_036222.3	MACF1
832	EL	3	ETD	11.1	2 (K)A I/G/A/L/A\S s R R/S\s S E G\L S\K(G)	S8 =n,S12 =n	NP_361013.2	LUZP1
833	ET	3	ETD	13.17	1 (R)A/m/L/D/Q\L m G t\s R\D G D T T\R(Q)	T9 =n	NP_057103.1	LUC7L2
834	ET	5	ETD	16.14	2 (R)F/R D Q\D/L A S\C D R D R\S\s R D R\s P\R(D)	S15 =n,S19 =n	NP_057103.1	LUC7L2
835	CL	2	CID	15.87	1 (K)S Q/D\V A V s/P/Q/Q/Q Q/C S K(S)	S7 =n	NP_079359.2	LSM16
836	EG	3	ETD	13	1 (E)L/N A L K S T/G D/G\T L G R\A S\E(V)	T11 =n	NP_004726.1	LRRFIP1
837	AL	5	CID	15.54	1 (K)T D y T\H\A\N/L/V/D/K A L/Q/L L K(E)	Y3 =n	NP_060879.2	LRP2BP

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
838	ET	4	ETD	10.22	1 (R)N/L/t/P/G G K D S\A A/R\S L\N\K(L)	T3 =n	NP_056051.1	LPHN3
839	AL	3	CID	8.65	2 (K)S R Q P s/y V P/A P/L\R K\K(K)	S5 =n,Y6 =n	NP_005349.3	LMO7
840	AT	2	CID	14.26	1 (R)A/G/G/P/T/T P\L s/P T R(L)	S9 =k,T6 =nf	NP_005564.1	LMNB1
841	CT	2	CID	16.11	1 (R)S G A Q/A S S T P/L/s/P T R(I)	S11 =k,T8 =nf	CAA27173.1	LMNA
842	ET	4	ETD	22.2	1 (R)m G P S G E G m/E\P/E/R R D\s Q D\G\S/S\Y\R(R)	S16 =k	AAH07560.1	LASP1
843	AG	3	CID	13.04	2 (E)Q m/D/G/R\K/N\t F t/A W S\D\E(E)	T8 =n,T10 =n	NP_056130.2	LARP1
844	AG	4	CID	10.01	2 (E)S R F s H L T S L/P Q\Q L P S Q/Q L M s K/D\Q D E Q E(E)	S4 =n,S20 =n	NP_056130.2	LARP1
845	AG	3	CID	17.44	3 (E)T E/s/A/P/G\s P/R A V/t P V/P T K T E\E(V)	S3 =n,S7 =n,T12 =n	NP_056130.2	LARP1
846	AL	3	CID	15.08	3 (K)E T E/s/A/P G s/P/R A/V t/P V/P\T K(T)	S4 =n,S8 =n,T13 =n	NP_056130.2	LARP1
847	EL	3	ETD	7.84	3 (K)E/T/E/s A P G s P R A/V t P V P\T\K(T)	S4 =n,S8 =n,T13 =n	NP_056130.2	LARP1
848	ET	3	ETD	8.77	2 (R)T/P R t P R t P Q L\K(D)	T4 =n,T7 =n	NP_056130.2	LARP1
849	CT	4	CID	14.48	2 (R)Q L R\E y Q\E L M s V\K(L)	Y5 =n,S10 =n	NP_005547.3	KRT7
850	CT	2	CID	20.3	1 (K)M I G F P/S/S A G S V/s/P R(S)	S12 =n	NP_705694.1	KRT13
851	CT	4	CID	16.41	2 (R)m S G E C A P N V/s/V\S V S/t\S H T/T/I S G G G S\R(G)	S10 =n,T15 =n	NP_006112.2	KRT1
852	ELX	3	ETD	18.79	1 (K)T/N L S/G R Q s P S F\K(L)	S8 =n	AAH72409.1	KIAA2010
853	ET	4	ETD	10.72	1 (K)V/Q/T L S N Q P L L K\s\p A\p P/L\H V A\A L G\Q\K(Q)	S12 =n	NP_066997.3	KIAA1967
854	ELX	4	ETD	22.61	1 (K)K/K P/N\E/D E V\N Q D s/V K\K(N)	S12 =n	NP_065747.1	KIAA1143
855	ELX	5	ETD	26.64	1 (K)R I/Q P/Q/P P D E\D G D/H\s D K/E\D E\Q P Q V V L\K(K)	S14 =n	NP_065747.1	KIAA1143
856	ELX	4	ETD	17.86	2 (K)D/R K\T s A V s S P L/L D Q Q R/N\S\K(T)	S5 =n,S8 =n,S9 =nf	NP_055885.2	KIAA0853
857	AL	3	ETD	15.96	1 (K)V/V T Q R s E I G E\K(Q)	S6 =n	NP_055627.1	KIAA0470
858	ET	5	ETD	24.48	1 (R)K P L T/T S G F\H H/S\E E\G\T\S S S G\s\K\R(W)	S20 =n	NP_055627.1	KIAA0470
859	ET	4	ETD	11.33	2 (R)K P/L T/T s G/F H H S E E\G T/S S S G s K\R(W)	S6 =n,S20 =n	NP_055627.1	KIAA0470
860	ET	3	ETD	15.98	2 (R)L G/s/L S/A R s D S E A T I S\R(S)	S3 =k,S8 =n	NP_055627.1	KIAA0470
861	EL	5	ETD	11.99	2 (K)K/K C H K Q A L V G s D/s A E D E K R K R\K(C)	S11 =n,S13 =n	NP_056139.1	KIAA0409
862	CT	3	CID	13.35	1 (K)I G G D A A T/T V N/N S t/P D F/G F G\G Q K(R)	T13 =n	NP_003676.1	KHSRP
863	CT	2	CID	16.76	1 (R)S/G/s/M/D P S G/A/H P S V R(Q)	S3 =k	NP_006550.1	KHDRBS1
864	ET	3	ETD	14.9	1 (R)S/G/s/M D P S\G A/H P S\V\R(Q)	S3 =k	NP_006550.1	KHDRBS1
865	ET	3	ETD	24.87	1 (R)S P/S/G G A\A G P L L T P S Q s L D G S\R(R)	S16 =n,S3 =nf	NP_612453.1	KCTD12
866	ET	3	ETD	23.21	1 (R)s P/S G G A\A G P L L T P S Q s L D G S\R(R)	S1 =n,S3 =nf	NP_612453.1	KCTD12
867	AT	3	CID	22.89	3 (R)S P s G G A G/P L L t/P/s Q/S/L/D/G S R(R)	S3 =k,T12 =n,S14 =n	NP_612453.1	KCTD12
868	AT	3	CID	22.64	2 (R)S P S G G A G P L L t/P/s Q/S L/D/G S R(R)	T12 =n,S14 =n,S3 =nf	NP_612453.1	KCTD12
869	CT	3	CID	22.49	1 (R)S P S G G A A G P L L T P/S Q\s L/D/G S R(R)	S16 =n,S3 =nf	NP_612453.1	KCTD12
870	AT	3	CID	22.25	2 (R)s/P S G G A/A G/P L L T P/s Q/S/L/D/G S\R(R)	S1 =n,S14 =n,S3 =nf	NP_612453.1	KCTD12
871	CT	3	CID	21.29	2 (R)S P S G G A G P L L t/P/s Q/s/L/D G S R(R)	T12 =n,S16 =n,S3 =nf	NP_612453.1	KCTD12
872	ET	3	ETD	20.88	2 (R)S P/S G G A A\G P L L t/P S Q/s L D G S\R(R)	T12 =n,S16 =n,S3 =nf	NP_612453.1	KCTD12

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			Mode	Score				▼	Symbol
873	AT	3	ETD	17.66	2	(R)S P S G G A A\G/P L\L T/P s Q s L D G S\R(R)	S14 =n,S16 =n,S3 =nf	NP_612453.1	KCTD12
874	CT	2	CID	17.09	1	(R)S P S G G/A A/G/P L L t/P S Q S L D/G S R(R)	T12 =n,S3 =nf	NP_612453.1	KCTD12
875	CT	2	CID	16.2	2	(R)S P S G G A A/G/P/L/L t/P S Q s\L D/G S R(R)	T12 =n,S16 =n,S3 =nf	NP_612453.1	KCTD12
876	AT	3	ETD	15.96	1	(R)S P/S/G/G\A A G P L L T P S Q s\L/D G S\R(R)	S16 =n,S3 =nf	NP_612453.1	KCTD12
877	AT	2	CID	15.31	2	(R)s P/S G G A/A/G/P/L/L/T/P/S Q s L D G S\R(R)	S1 =n,S16 =n,S3 =nf	NP_612453.1	KCTD12
878	AT	3	ETD	10.63	3	(R)S P/s G G A A G P L L T P s\Q s\L D G S\R(R)	S3 =k,S14 =n,S16 =n	NP_612453.1	KCTD12
879	AT	3	CID	15.34	2	(R)S P/S/G/G/A/A/G/P/L L\T/P/S Q S L D\G s R R(S)	T12 =n,S20 =n,S3 =nf	NP_612453.1	KCTD12
880	CT	3	CID	14.59	3	(R)s P S/G/G/A/A/G/P/L/L/t/P/S Q s L D G S R R(S)	S1 =n,T12 =n,S16 =n,S3 =nf	NP_612453.1	KCTD12
881	ET	3	ETD	6.05	2	(R)S P/S/G/G/A A G P L L t\p s Q S L D\G\S R\R(S)	T12 =n,S14 =n,S3 =nf	NP_612453.1	KCTD12
882	ET	5	ETD	11.75	2	(R)L A\R I\R\V A\K\T/G S S N/A/y/L H S K(R)	T9 =n,Y15 =n	NP_004971.2	KCND3
883	ET	4	ETD	10.15	1	(R)G S Q/E D\L\E\A R/N G/t S/P/S R(G)	T12 =n	NP_063945.2	INPP5E
884	EL	3	ETD	6.33	1	(K)D K M E G s D F E S\S G G\R\G\L\K(K)	S6 =n	NP_115705.2	ING5
885	ET	3	ETD	21.95	1	(K)R P m E E D G E E/K s P S K(K)	S11 =k	NP_004507.2	ILF3
886	ET	3	ETD	17.6	1	(K)R P m E E D/G E E/K s P S K(K)	S11 =k	NP_004507.2	ILF3
887	EL	3	ETD	16.33	1	(K)R P M E E D G/E E K\s P S\K(K)	S11 =k	NP_004507.2	ILF3
888	CL	3	CID	12.34	1	(K)R P\M E E D G E E K\s/P S\K(K)	S11 =k	NP_004507.2	ILF3
889	AL	3	ETD	11.28	1	(K)R P m E E D G/E E K S P s\K(K)	S13 =n,S11 =nf	NP_004507.2	ILF3
890	ELX	4	ETD	8.02	2	(K)E L/E/E/N/D/s E N\S\E\F\E D D/G\s E/K V L D\E\E\G(S)	S7 =n,S17 =n	NP_055315.2	HTATSF1
891	ELX	4	ETD	26.4	1	(K)E/S/E E/G N P V R G S E E D s P K\K(E)	S15 =n	NP_055315.2	HTATSF1
892	CT	2	CID	12.78	1	(K)L/F E D D D/s N E K(L)	S7 =k	NP_055315.2	HTATSF1
893	EL	3	ETD	14.3	1	(K)L/F/E\E s D D K E D E D A D G\K(E)	S5 =n	NP_055315.2	HTATSF1
894	AL	4	ETD	24.64	1	(K)L/F/E E s D D K E D\E D/A/D G\K E V\E D\A D/E\K(L)	S5 =n	NP_055315.2	HTATSF1
895	CL	2	CID	14.02	1	(K)V/F D D\E/s D E K(E)	S6 =k	NP_055315.2	HTATSF1
896	AL	3	CID	17.33	1	(K)V/F D/D/E/s D/E/K E/D E E/Y A D E K(G)	S6 =k	NP_055315.2	HTATSF1
897	EL	3	ETD	10.92	1	(K)V/F/D/D E s D E K E D E Y A D E\K(G)	S6 =k	NP_055315.2	HTATSF1
898	CT	2	CID	13.33	1	(K)V/L D E\E G/s/E R(E)	S7 =n	NP_055315.2	HTATSF1
899	ELX	4	ETD	14.85	2	(K)V/L D E\E G s E R/E F D E D s\D E/K E E\E\E/D T Y E\K(V)	S7 =n,S15 =k	NP_055315.2	HTATSF1
900	AG	4	ETD	12.51	1	(E)L/N\N T\C E/P/V V/T Q\p K P\K/I\E\s P/R/L\E(R)	S18 =k	NP_006635.2	HSPH1
901	ET	3	ETD	9.87	1	(K)I/E s P K L E\R(T)	S3 =k	NP_006635.2	HSPH1
902	AL	3	CID	14.17	1	(K)I E/s/P K/L/E/R T/P\N G P N\I D\K(K)	S3 =k	NP_006635.2	HSPH1
903	AL	4	ETD	13	1	(K)I/E s P K/L/E R\T/P N/G P N I D\K(K)	S3 =k	NP_006635.2	HSPH1
904	EL	5	ETD	17.03	1	(K)I/E\s P K/L E\R/T P N G P N I D\K\K\E/E\D\L E\D\K(N)	S3 =k	NP_006635.2	HSPH1
905	CL	4	CID	19.37	1	(K)N V Q Q D N S E\A G T Q P Q V/Q T/D A\Q/Q/T S Q S P/P s P E L/T/S E E N\K(I)	S28 =k	NP_006635.2	HSPH1
906	ELX	4	ETD	20.46	1	(K)E/E/E\D K D/D E E\K\P K/I E D V G s D\E E D D S G\K(D)	S18 =k,S24 =nf	NP_031381.2	HSPCB

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				Score	▼				Symbol
907	ELX	5	ETD	22.25	1	(K)E/E E D K D/D E E K P K I E D/V G s D E E D D S G K D K(K)	S18 =k	NP_031381.2	HSPCB
908	AL	2	CID	10.81	1	(K)E I s D/D E/A E/E E K(G)	S3 =n	NP_031381.2	HSPCB
909	ELX	3	ETD	20.36	1	(K)E/I s D D E A E E E K G E K(E)	S3 =n	NP_031381.2	HSPCB
910	ELX	4	ETD	30.76	1	(K)E/I s D D E A E E E K G E K E E E D K(D)	S3 =n	NP_031381.2	HSPCB
911	ELX	5	ETD	21.19	1	(K)E I s D/D E A E E E K G E K E E E D K D D E E K(P)	S3 =n	NP_031381.2	HSPCB
912	ELX	5	ETD	20.52	1	(K)E I s D D E A E/E E K G E K E E E D K D D E E K P K(I)	S3 =n	NP_031381.2	HSPCB
913	CT	4	CID	11.83	1	(K)K S Q I F S T A S D N Q P T V T I K V y E G E R P L T K(D)	Y20 =n	NP_005338.1	HSPA5
914	CL	3	CID	27.79	1	(K)E L E Q V C N P I I I S G L y Q G A G G P G G F G A Q G P K(G)	Y14 =n	NP_005336.2	A1B
915	ELX	4	ETD	13.52	1	(K)D/D E E K P K I E D V G s D E E D D S G K(D)	S13 =k,S19 =nf	NP_001014390.1	HSPCB
916	AL	2	CID	19.28	1	(K)I E D V G s D E E D D S G K(D)	S6 =k,S12 =nf	NP_001014390.1	HSPCB
917	AL	2	ETD	12.39	1	(K)I E D V G s D E E D D S G K(D)	S6 =k,S12 =nf	NP_001014390.1	HSPCB
918	ELX	3	ETD	20.74	1	(K)I E D V G s D E E D D S G K D K(K)	S6 =k,S12 =nf	NP_001014390.1	HSPCB
919	AL	3	CID	9.5	1	(K)I E D V G s D E E D D S G K D K(K)	S6 =k,S12 =nf	NP_001014390.1	HSPCB
920	ELX	3	ETD	19.38	1	(K)P K I E D V G s D E E D D S G K(D)	S8 =k,S14 =nf	NP_001014390.1	HSPCB
921	EL	3	ETD	13	1	(K)P K I E D V G s D E E D D S G K(D)	S8 =k,S14 =nf	NP_001014390.1	HSPCB
922	ELX	4	ETD	25.83	1	(K)P K I E D V G s D E E D D S G K D K(K)	S8 =k,S14 =nf	NP_001014390.1	HSPCB
923	ELX	4	ETD	15.78	1	(K)E E E N K D D E E K P K I E D V G s D E E D D S G K(D)	S18 =n	NP_001014390.1	HSP90AB2P
924	EL	4	ETD	16.45	1	(D)K D D E E K P K I E D V G s D E E D D S G K(D)	S14 =k	NP_031381.2	HSP90AB1
925	EL	5	ETD	21.04	1	(K)G E K E E E D K D D E E K P K I E D V G s D E E D D S G K(D)	S21 =k	NP_031381.2	HSP90AB1
926	EL	5	ETD	19.64	1	(K)G E K E E E D K D D E E K P K I E D V G s D E E D D S G K D K(K)	S21 =k	NP_031381.2	HSP90AB1
927	ET	5	ETD	19.52	1	(D)K E V s D D E A E E K E D K E E E K E E K(E)	S4 =k	NP_001017963.1	HSP90AA1
928	EL	3	ETD	19.12	1	(D)K P E I E D V G s D E E E E K(K)	S9 =k	NP_005339.2	HSP90AA1
929	ELX	3	ETD	14.07	1	(D)K P E I E D V G s D E E E E K(K)	S9 =k	NP_005339.2	HSP90AA1
930	EL	3	ETD	17.5	1	(D)K P E I E D V G s D E E E E K(K)	S9 =k	NP_005339.2	HSP90AA1
931	ELX	4	ETD	12.48	1	(K)E R D K E V s D D E A E E K E D K(E)	S7 =k	NP_001017963.1	HSP90AA1
932	ELX	4	ETD	25.93	1	(K)E R D K E V s D D E A E E K E D K E E E K(E)	S7 =k	NP_001017963.1	HSP90AA1
933	CL	3	CID	17.1	1	(K)E S E D K P E I E D V G s D E E E E K(K)	S13 =k	NP_001017963.1	HSP90AA1
934	ELX	4	ETD	29.13	1	(K)E S E D K P E I E D V G s D E E E E K(K)	S13 =k	NP_001017963.1	HSP90AA1
935	CL	4	CID	16.09	1	(K)E S E D K P E I E D V G s D E E E E K(K)	S13 =k	NP_001017963.1	HSP90AA1
936	ELX	4	ETD	11.28	1	(K)E S E D K P E I E D V G s D E E E E K(K)	S13 =k	NP_001017963.1	HSP90AA1
937	EL	4	ETD	16.78	1	(K)E S E D K P E I E D V G s D E E E E K K D G D K(K)	S13 =k	NP_001017963.1	HSP90AA1
938	ELX	4	ETD	29.68	1	(K)E V s D D E A E E K E D K E E E K(E)	S3 =k	NP_001017963.1	HSP90AA1
939	AL	3	CID	15.41	1	(K)E V s D D E A E E K E D K E E E K(E)	S3 =k	NP_001017963.1	HSP90AA1
940	CL	5	CID	15.12	2	(K)Q D R t L t I V D T G I G m T K A D L I N N L G T I A K S G T K(A)	T4 =n,T6 =n	NP_005339.2	HSP90AA1
941	ET	4	ETD	11.45	1	(R)D K E V s D D E A E E K E D K E E E K(E)	S5 =k	NP_001017963.1	HSP90AA1

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
942	ET	5	ETD	16.65	1 (R)D/K/E/V s D/D\E A\E\E K E\D K E E E K E\K(E)	S5 =k	NP_001017963.1	HSP90AA1
943	ET	5	ETD	19.86	1 (R)D K/E/V s/D\D E\A E E/K E\D K E/E E K\E K E E\K(E)	S5 =k	NP_005339.2	HSP90AA1
944	AT	4	CID	16.31	3 (K)K E P D D S R\D\E D E D E\D\E s\ s E E\D\s E/D E E P P P K(R)	S16 =n,S17 =n,S21 =n	NP_057371.2	HP1BP3
945	ELX	5	ETD	13.24	1 (K)E/S/T L I P P P P P F E\Q T F P\ s\ L Q P G A/S T L Q R P R S Q\K(R)	S17 =n	NP_002136.1	HOXB2
946	EG	4	ETD	27.68	1 (E)L/K K R R L\s D K G L K A\E(L)	S7 =n	NP_004492.2	HNRPU
947	EL	5	ETD	21.83	1 D P\H\K(T)	T4 =n	NP_001524.2	HNRPL
948	CL	5	CID	13.06	1 D P H K(T)	T4 =n	NP_001524.2	HNRPL
949	EL	4	ETD	14.71	1 P\H\K(T)	Y30 =n	NP_001524.2	HNRPL
950	CL	4	CID	11.75	1 H\K(T)	Y30 =n	NP_001524.2	HNRPL
951	CG	2	CID	20.74	1 (E)G/L Q L P s/P T A T S Q L P L\E(S)	S6 =k	NP_002131.2	HNRPK
952	CG	3	CID	16.58	1 (E)G L Q\L P s P T A\T S Q L P L E S D\A\V\E(C)	S6 =k	NP_002131.2	HNRPK
953	CT	2	CID	13.32	1 (R)D/Y D D M s P R(R)	S6 =k	NP_002131.2	HNRPK
954	AT	3	ETD	16.17	1 (K)H T G P N\s P D T A N\D G F\V\R(L)	S6 =k,T2 =nf	NP_001027565.1	HNRPH1
955	CT	3	CID	15.55	1 (K)H T G P N\s P/D t A N D G F\V\R(L)	T9 =n,T2 =nf,S6 =nf	NP_001027565.1	HNRPH1
956	ET	4	ETD	10.75	1 (K)I/D/A/S/K N\E E D E G H S N\s S P R(H)	S15 =k,S16 =nf	NP_002129.2	HNRPD
957	ET	3	ETD	3.89	3 (K)I/D A/S K N\E E D E G H s N s s P R(H)	S13 =n,S15 =k,S16 =k	NP_002129.2	HNRPD
958	ET	4	ETD	8.67	2 (K)I D A S K N\E/E/D/E/G H\S N S\s P R/H\s E A A/T/A Q R(E)	S16 =k,S20 =k,S15 =nf	NP_002129.2	HNRPD
959	ELX	5	ETD	24.62	1 (K)I/D/A S K N\E/E D\E G H S N\s S P R\H S E A A T\A Q R E E W\K(M)	S15 =k,S16 =nf,S20 =nf	NP_002129.2	HNRPD
960	ELX	5	ETD	20.91	1 (K)I/D A/S K N\E/E D E G H S N S S P R\H S E A A T A Q\R E E W\K(M)	S16 =k,S15 =nf,S20 =nf	NP_002129.2	HNRPD
961	ELX	5	ETD	14.81	2 (K)I/D A/S K N\E E/D E G H S N/S S P R H\S E A A T A Q\R E/E W\K(M)	S13 =n,S20 =k,S15 =nf,S16 =nf	NP_002129.2	HNRPD
962	ELX	4	ETD	20.14	1 (K)N/E E D E G H S N/S S P R H S E A A T\A\Q\R E E W\K(M)	S11 =n,S10 =nf	NP_112738.1	HNRPD
963	ELX	5	ETD	30.45	1 (K)N/E E D E G H S N\S S P R H S E A A T A Q\R E E W\K(M)	S11 =k,S10 =nf,S15 =nf	NP_002129.2	HNRPD
964	ELX	5	ETD	27.23	2 (K)N/E E D E G H S N S\s P R\H S E A A T A Q R E E W\K(M)	S8 =n,S11 =k,S10 =nf,S15 =nf	NP_002129.2	HNRPD
965	ELX	5	ETD	12.29	2 (K)N/E E D E G H S N s S P R H\S E/A A t/A\Q R E E W\K(M)	S10 =k,T19 =n,S11 =nf,S15 =nf	NP_002129.2	HNRPD
966	CG	3	CID	25.56	1 (E)s/E G G A D D S A/E E G D L L D D D D n E/D R\G D\D\Q\L\E(L)	S1 =k	P07910	HNRPC
967	CG	3	CID	19.84	1 (E)S E G G A D D S A/E E G D L L D D D D n E/D R\G D\D\Q\L\E(L)	S8 =n,S1 =nf	P07910	HNRPC
968	CT	3	CID	15.27	1 (K)m E s E G G A D D/S/A/E E G D\L/L/D/D D/D/N E\D R(G)	S3 =k,S10 =nf	NP_004491.1	HNRPC
969	ELX	4	ETD	17.13	1 K(D)	S10 =k,S3 =nf	NP_004491.1	HNRPC
970	ELX	4	ETD	14.23	1 I\K(D)	S10 =k,S3 =nf	NP_004491.1	HNRPC
971	ELX	5	ETD	13.02	1 K D D E\K(E)	S10 =k,S3 =nf	NP_004491.1	HNRPC
972	ELX	5	ETD	11.92	1 K D D E K(E)	S10 =k,S3 =nf	NP_004491.1	HNRPC
973	ET	4	ETD	24.45	1 (K)N/D K S E E E Q S S S s V K K D E T N\V\K(M)	S12 =n	NP_004491.1	HNRPC
974	ELX	4	ETD	23.45	3 (K)N/D/K s E E E Q s/S S\s V K K D E T N\V\K(M)	S4 =n,S9 =n,S12 =n	NP_004491.1	HNRPC
975	ET	4	ETD	13.68	2 (K)N D/K S E E E Q s S S\s V\K\K D E T N\V\K(M)	S9 =n,S12 =n	NP_004491.1	HNRPC
976	ELX	4	ETD	7.36	2 (K)N/D/K/S E/E/E Q s S S V K\K D E T N V\K(M)	S9 =n,S10 =n	NP_004491.1	HNRPC

#	Exp.	CS	Mode	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene	
				Score	▼				Symbol	Symbol
977	AT	4	ETD	12.77	1	(K)Q/A V E m K N D\K s\E E E\Q S S/S S V\K(K)	S10 =n	NP_004491.1	HNRPC	
978	ET	3	ETD	12.3	1	(K)Q A V E M K N D K\ s E E E Q S S S V\K(K)	S10 =n	NP_004491.1	HNRPC	
979	ELX	4	ETD	9.14	1	(K)Q/A/V E m K N D/K/s E E E Q S S S V/K K(D)	S10 =n	NP_004491.1	HNRPC	
980	ET	4	ETD	8.77	2	(K)Q A V E M K/N D K S\E E\E Q/s/S s S\ V K K D E T N V K(M)	S15 =n,S17 =n	NP_112604.1	HNRPC	
981	ELX	4	ETD	19.52	2	(K)S/E/E\E Q\ s S S S V K K D E T N V\K(L)	S6 =n,S9 =n	NP_004491.1	HNRPC	
982	ELX	3	ETD	8.18	1	(K)S/E/E/E Q S S s S V\K K D E T N V\K(L)	S8 =n	NP_004491.1	HNRPC	
983	AT	2	CID	10.34	1	(R)m Y s Y/P\A/R(V)	S3 =n	NP_004491.1	HNRPC	
984	ELX	5	ETD	15.39	1	(K)E V y Q Q Q Q Y G S G G R\G N R\N R G N\ R G S G G/G G G G\G\G\Q\G S T N Y G\K(S)	Y3 =n	NP_004490.2	HNRPA3	
985	CL	4	CID	9.49	1	(K)G G S F/G/G R\ s S G S/P/Y/G/G G Y/G S G G G S/G G Y G S R R F(-)	S8 =n	NP_919223.1	HNRPA3	
986	ET	3	ETD	12.17	1	(R)E D/s\ V K P\G A H L T\ V\K(K)	S3 =n	NP_005749.1	HNRPA3	
987	ELX	4	ETD	23.24	1	(K)Y/H t I N G/H N A\E V R\K(A)	T3 =n	NP_002128.1	HNRPA2B1	
988	CT	3	CID	21.48	1	(R)G F G D/G Y N G/Y G/G/G P/G G N F/G G s/P G Y G G G R(G)	S21 =n	NP_002128.1	HNRPA2B1	
989	CT	4	CID	14.62	3	(R)N M G G P Y G\G G/N/Y/G P\G G s G G/s\G G/y G/G R S R Y(-)	S16 =k,S19 =k,Y22 =n	NP_002128.1	HNRPA2B1	
990	CT	4	CID	12.26	1	(R)S G R G G N\F\G F G/D s/R G G G G N/F/G/P/G/P/G/S/N F R(G)	S12 =n	NP_002128.1	HNRPA2B1	
991	EG	4	ETD	12.37	1	(E)D/s Q R P G\A H L T/V K\K I/F\ V\G\G\I\K\E(D)	S2 =n	NP_001011724.1	HNRPA1	
992	ELX	3	ETD	20.77	1	(K)G/G/N/F/G G/R S s G P Y G G G G Y F A\K(P)	S9 =n	NP_002127.1	HNRPA1	
993	ELX	5	ETD	30.03	1	(K)R/A V S R E D/s Q R P G A H L T\ V\K(K)	S8 =n	NP_002127.1	HNRPA1	
994	ELX	4	ETD	19.2	2	(K)R/A V\ s R/E D s Q R P\G\A H L T\ V\K(K)	S4 =n,S8 =n	NP_002127.1	HNRPA1	
995	AT	3	CID	19.46	1	(K)S E s P K E P E Q L R\K(K)	S3 =k	NP_002127.1	HNRPA1	
996	AT	3	ETD	17.83	1	(K)S/E s P K E P E Q L R\K(K)	S3 =k	NP_002127.1	HNRPA1	
997	ELX	4	ETD	27.1	1	(K)S/E s P K E P E Q L R\K(L)	S3 =k	NP_002127.1	HNRPA1	
998	AT	3	CID	14.72	1	(K)S E s P K E P E Q L R K(L)	S3 =k	NP_002127.1	HNRPA1	
999	ET	4	ETD	6.15	1	(K)y H T\ V N G H\N\C\E/V R(K)	Y1 =n	NP_002127.1	HNRPA1	
1000	ET	3	ETD	15.16	1	(R)E/D/s Q R P G A H L T\ V\K(K)	S3 =n	NP_001011724.1	HNRPA1	
1001	ET	2	ETD	9.27	1	(R)S/s/G P/Y/G/G/G/G/Q Y\F\A\K(P)	S2 =n	NP_001011724.1	HNRPA1	
1002	AT	4	ETD	11.4	1	(R)A/V/s R E D S A/R P/G A H A\K(V)	S3 =n	NP_006796.1	HNRPA0	
1003	ELX	3	ETD	12.85	1	(K)K/H P D/S s\ V\N F A E F S\K(K)	S6 =k	NP_002120.1	HMGB2	
1004	ELX	4	ETD	8.86	1	(K)Y E K D I/A\A/y/R A K(G)	Y8 =n	NP_002119.1	HMGB2	
1005	ELX	4	ETD	7.45	1	(K)y\E K D I\A\A/Y/R A\K(G)	Y1 =n	NP_002119.1	HMGB2	
1006	ELX	3	ETD	21.51	1	(K)K H P D A s V N F S E F S\K(K)	S6 =n	NP_002119.1	HMGB1	
1007	EG	5	ETD	31.35	1	(E)K/T P/V K K K A R K s A G A A K R K A/S/G/P P V S\E(L)	S11 =k,T2 =nf	NP_005312.1	HIST1H1E	
1008	AG	5	ETD	23.94	2	(E)K/t P V K K K A R K s\A/G\A\A\K\R K A S G P P V S\E(L)	T2 =k,S11 =k	NP_005312.1	HIST1H1E	
1009	ELX	3	ETD	12.81	1	(K)R/K\A s G P P V/S E L I T\K(A)	S4 =n	NP_005311.1	HIST1H1D	
1010	CT	3	CID	11.53	1	(K)R K/A s G P/P V/S/E L I T K(A)	S4 =n	NP_005311.1	HIST1H1E	
1011	EG	5	ETD	19.34	1	(E)K/t/P V K K K A K K A G\A\T A G K R K A S G P P V S\E(L)	T2 =n	NP_005311.1	HIST1H1D	

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
1012	ET	2	ETD	3.17	1 (K)t P/Q P/K K\A\K(S)	T1 =k	NP_005311.1	HIST1H1D
1013	AT	3	CID	20.24	1 (R)K A s/G P P V S E\L/I\T\K(A)	S3 =n	NP_005310.1	HIST1H1C
1014	AT	3	ETD	17.7	1 (R)K/A s G P P V S E L I T\K(A)	S3 =n	NP_005310.1	HIST1H1D
1015	CT	2	CID	17.09	1 (R)K A/s/G/P/P V S/E L I T K(A)	S3 =n	NP_005310.1	HIST1H1E
1016	AG	5	ETD	25.15	1 (E)K/A P V K K/K A A\K/K A/G G t P R K A S G P\ P V S\E(L)	T15 =n	NP_005310.1	HIST1H1C
1017	ELX	4	ETD	7.2	2 (K)K/A G/G/t P R K A/s G P P/V/S E\L I T\K(A)	T5 =n,S10 =n	NP_005310.1	HIST1H1C
1018	EG	5	ETD	19.15	1 (S)L/V S K\G/T\L V\Q T K\G T G/A S\G s F K L\N K K A A S\G\E(A)	S18 =n	NP_005310.1á	HIST1H1C
1019	CL	3	CID	8.96	1 (K)K P/A A\T\R\K S\S\K(N)	T5 =n	NP_005316.1	HIST1H1A
1020	ELX	4	ETD	9.75	3 (K)E/A A/s s G D D s G\R D R E P P\V Q R\K(S)	S4 =n,S5 =n,S9 =n	NP_003600.2	HIRIP3
1021	ELX	4	ETD	19.19	2 (K)N/G V A A/E/V s P\A K/E E N P R R A s\K(A)	S8 =k,S19 =n	NP_003600.2	HIRIP3
1022	ELX	4	ETD	31.06	2 (K)Q/A/R E E s\E E s E A E P V/Q R T\A\K(K)	S6 =k,S9 =k	NP_003600.2	HIRIP3
1023	ELX	4	ETD	27.85	3 (K)R L/s G s s E D E E D S G K G E P\T\A\K(G)	S3 =n,S5 =n,S6 =n	NP_003600.2	HIRIP3
1024	ELX	3	ETD	10.54	2 (K)S/L/K E s E/Q E/s E E E/I/L\A/Q\K(K)	S5 =k,S9 =k	NP_003600.2	HIRIP3
1025	ELX	4	ETD	27.02	2 (K)S/L/K E s E\Q E\s E E E I\L\A\Q K\K(E)	S5 =k,S9 =k	NP_003600.2	HIRIP3
1026	ELX	3	ETD	5.4	1 (K)K P\s L D D L\K(E)	S3 =n	NP_056416.2	HERC4
1027	EL	5	ETD	12.26	3 (K)G G I V/L I D A H K\D t L/I s/M/K/W\D P T G H\I L M t\C/A K(E)	T12 =n,S15 =n,T27 =n	NP_003913.2	HERC1
1028	ELX	3	ETD	13.02	2 (K)G N/A/E G s s/D/E E G K L V I/D/E P\A\K(E)	S6 =k,S7 =k	NP_004485.1	HDGF
1029	ELX	3	ETD	11.57	2 (K)K G N A E G\s s D E E G K L V\I/D E P\A\K(E)	S7 =k,S8 =k	NP_004485.1	HDGF
1030	ELX	3	ETD	22.52	1 (K)R R A/G D L L E D s P\K(R)	S10 =k	NP_004485.1	HDGF
1031	CL	3	CID	13.24	1 (K)R/R\A G\D L\L\E\D s/P K(R)	S10 =k	NP_004485.1	HDGF
1032	ELX	4	ETD	29.53	1 (K)R/R A G D L L E D s P K R P\K(E)	S10 =k	NP_004485.1	HDGF
1033	CL	4	CID	9.25	1 (K)R R\A G D\L L\E D s P\K R P K(E)	S10 =k	NP_004485.1	HDGF
1034	CL	3	CID	11.47	1 (K)s C V/E/E/P/E/P E/P E/A A E G D G D K K(G)	S1 =n	NP_004485.1	HDGF
1035	ELX	4	ETD	8.05	2 (K)S C V/E/E P E P/E P\E A A E G D/G D K K G N\A E G s s D E E G\K(L)	S26 =k,S27 =k	NP_004485.1	HDGF
1036	CT	2	CID	15.84	1 (R)A G/D L L E D s P K(R)	S8 =k	NP_004485.1	HDGF
1037	ET	3	ETD	18.53	1 (R)A G/D/L/L E D s P K R P K(E)	S8 =k	NP_004485.1	HDGF
1038	ET	3	ETD	28.16	1 (R)R A G D L/L E D/s P K/R P K(E)	S9 =k	NP_004485.1	HDGF
1039	ET	3	ETD	6.33	1 (R)Q/N/P/Q S P P Q D S S/V t S\K R\N I K\K(G)	T13 =n,S5 =nf	NP_006035.2	HDAC6
1040	EL	4	ETD	16.41	2 (K)R/I\A\C D E E F/s D\s E/D E G E G G R R\N\V\A D H\K(K)	S9 =k,S11 =k	NP_001518.1	HDAC2
1041	AL	5	ETD	15.99	2 (K)R/I A C/D E E F s D s E D E G E G G\R R N\V A D H K\K(G)	S9 =k,S11 =k	NP_001518.1	HDAC2
1042	AL	3	ETD	12.59	1 (K)R/I s I R A S D\K(R)	S3 =n	NP_001518.1	HDAC2
1043	AT	4	CID	20.28	1 (R)m L/P H A P/G V\Q\m Q/A I P/E\A\A\H E D s G D/E D/G E/D/P D K R(I)	S22 =k	NP_001518.1	HDAC2
1044	EL	4	ETD	18.71	2 (K)R I A\C E E E F s/D/s E E/E\G E\G G R\K(N)	S9 =k,S11 =k	NP_004955.2	HDAC1
1045	CL	3	CID	13.74	1 (K)D A/Q/R L s P I P E\E V P K(S)	S6 =n	NP_057662.3	HBXAP
1046	CL	3	CID	17.31	1 (K)E D/R S A s S G A E G D V S S E R\E\(-)	S6 =n	NP_543010.3	HARS2

#	Exp.	CS	Number of phosphorylation sites			Sequence with fragments	Literature lookup	RefSeq#	Gene
			Mode	Score	▼				Symbol
1047	AL	3	CID	12.84	2	(K)E D/R\ S A/s S\G A\ E G\ D V/s\ S/E/R\ E\ P(-)	S6 =n,S14 =n	NP_543010.3	HARS2
1048	CL	2	CID	10.05	1	(K)A G G S/A A L s/P S K(K)	S8 =k	NP_006017.1	H1FX
1049	CL	3	CID	14.35	2	(K)N I S S M S/N M N s\ S\R\m\ D/s\ P K(R)	S10 =n,S15 =n	NP_000824.1	GRIN2A
1050	CL	3	CID	20.39	1	(K)S P/P R E/G/S Q G E L\T P A N S Q S/R m\ s T N m(-)	S21 =n	NP_004118.3	GPS1
1051	CL	4	CID	9.69	2	(K)s P P R/E\G\ S Q G E L/T\ P A\ N S Q\ S\ R m s T N M(-)	S1 =n,S21 =n	NP_004118.3	GPS1
1052	CL	2	CID	14.85	2	(K)I S/L/P/G Q/m A/G\ t/P I t/P L K(D)	T10 =n,T13 =k	NP_056345.3	GORASP2
1053	ELX	4	ETD	7.51	1	(K)H R N/D H/L T S T T\ S\ s P G V I\ V P\ E\ S S\ E\ N K(N)	S12 =n	NP_056979.1	GMNN
1054	ELX	3	ETD	5.99	1	(K)L/P C R/D D\ D G\ V/T A\ K D L s\ K(Q)	S15 =n	NP_054749.2	GIT1
1055	ELX	4	ETD	10.91	2	(K)N L/L H\ S L Q s/s G/I G\ S K(A)	S8 =n,S9 =n	NP_006827.1	GCN1L1
1056	CT	3	CID	18.3	1	(R)L Q Q Q A A L s/P T/T/A P A/V S S V S\ K(Q)	S8 =n	NP_065750.1	GATAD2B
1057	EL	4	ETD	17.03	1	(K)E D H s L E H R C V\ E S\ A\ K(I)	S4 =n	NP_009216.1	GABARAPL2
1058	AT	3	CID	20.63	2	(K)S T/t P/P P A E P V s/L/P Q/E/P P K/P R(V)	T3 =k,S11 =n	NP_987100.1	G3BP2
1059	ET	4	ETD	12.52	1	(K)S/T/t P/P P A E P\ V S L P Q E P P/K P\ R(V)	T3 =k	NP_987100.1	G3BP2
1060	ET	4	ETD	17.36	3	(R)R/R s/R s R s F D Y N\ Y\ R(R)	S3 =n,S5 =n,S7 =k	NP_006616.1	FUSIP1
1061	ET	3	ETD	14.02	3	(R)s R s R s F D Y N\ Y\ R(R)	S1 =n,S3 =n,S5 =k	NP_006616.1	FUSIP1
1062	EG	3	ETD	9.26	1	(E)Y/L F D K H\T/L/G D s D/N\ E\ S(-)	S11 =k	NP_001008698.1	FTH1FTHL16
1063	AL	3	CID	18.23	2	(K)E E/A/P/A/s/P L R/P L/Y P/Q/I s\ P\ L K(I)	S6 =n,S16 =n	NP_001032242.1	FOXK1
1064	ET	3	ETD	19.62	1	(R)E/G s P I P H D P E/F/G S K(L)	S3 =n	NP_001032242.1	FOXK1
1065	ELX	3	ETD	7.6	1	(K)G/K\G\G T/Q\ V D/T\ E I/E/E\K/D E/E t K(A)	T18 =n	NP_055738.2	FNDC3A
1066	EL	3	ETD	6.25	1	(K)V/Q/t T P\K/V/E E E Q D\ L\ K(F)	T3 =n	NP_056123.1	FNBP4
1067	AL	4	CID	12.2	2	(K)R t V S D/N s/L S/N/S R G E G K P\ D L\ K(F)	T2 =n,S7 =n,S4 =nf	NP_055848.1	FNBP1
1068	AL	4	ETD	12.01	2	(K)R/T V/s D N/s L S N/S R G\ E\ G K/P D L\ K(F)	S4 =k,S7 =n	NP_055848.1	FNBP1
1069	AG	5	ETD	9.78	3	(E)Y D\H\m N G s\R\ E S/P V D C S\ V/s K C s\ K/L V\ G G G E(S)	S7 =n,S17 =n,S20 =n	NP_002008.2	FLI1
1070	ELX	4	ETD	17.61	2	(K)G P/T T G E G/A/L D/L S D V H s P P K\ s P/E\ G\ K(T)	S16 =k,S20 =k	NP_008976.1	FGFR1OP
1071	AL	4	ETD	16.57	2	(K)D/R D L P\F S R P Q L R V s/P A/t P K(A)	S14 =n,T17 =n	NP_071897.1	FBS1
1072	ELX	5	ETD	15.44	2	(K)S P T M E Q A V Q t A S A H L P A P A/A\ V G R R\ S P V s/T/R P\ L P\ S A S Q\ K(A)	T10 =n,S28 =n	NP_056393.1	FAM61A
1073	ELX	5	ETD	14.62	2	(K)S P T M E Q A V Q T A s/A H L P A P A A V G R R s P/V S T R P\ L P\ S A S Q\ K(A)	S12 =n,S25 =n	NP_056393.1	FAM61A
1074	ELX	5	ETD	10.48	2	(K)S P\ T M E Q A V Q t A S A H L P A P A A V G R\ R\ s/P/V S T R P\ L P\ S A S\ Q\ K(A)	T10 =n,S25 =n	NP_056393.1	FAM61A
1075	ELX	5	ETD	8.11	2	(K)s P T m E Q A V/Q T A S A/H L P A P A A V G R R S P\ V s T\ R\ P\ L P\ S\ A\ S\ Q\ K(A)	S1 =n,S28 =n	NP_056393.1	FAM61A
1076	ELX	4	ETD	28.71	2	(K)T/Q/L/s Q G R S s P Q L D P L R\ K(S)	S4 =n,S9 =n	NP_056393.1	FAM61A
1077	EL	4	ETD	8.16	1	(K)D/T D s D R E\ A G\ T\ E T G G E N N D/K E E E\ K(K)	S4 =n	NP_004447.2	EZH2
1078	ELX	4	ETD	11.84	2	(K)N V s\ E\ S\ P\ S\ K\ H\ E\ N\ s K(D)	S3 =n,S12 =n	NP_055880.1	EXPH5
1079	ET	5	ETD	16.19	1	(R)Q L/P/A K W S\G A\C/V/L G t/I/R/P S F/F L m\ P L K(Q)	T14 =n	NP_001007254.1	ERV3

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
1080	CL	4	CID	20.15	1 (K)E Y I P G Q P P L S Q \ S D s s P \ T R \ N S E P / A / G L E / T P E A K (V)	S15 =n,T28 =nf	NP_004437.2	EPRS
1081	ELX	4	ETD	15.38	1 (K)E Y I P G Q P / P / L S Q S S D S \ s P / T R N S \ E P \ A \ G L E T P E / A K (V)	S16 =n,T28 =nf	NP_004437.2	EPRS
1082	EL	4	ETD	13.2	1 (K)E Y I P G / Q P P \ L / S Q \ S \ S / D S / S P T R N / s E \ P / A G L \ E T P E A \ K (V)	S21 =n,T28 =nf	NP_004437.2	EPRS
1083	EL	4	ETD	13.27	1 (K)G S Q P P P / A / A E S Q S s L R \ R \ Q \ K (R)	S13 =n	NP_001422.1	EPB41L2
1084	EL	2	ETD	7.38	1 (K)s / Y / T / L / V V A \ K (D)	S1 =n	NP_001422.1	EPB41L2
1085	AT	4	CID	16.09	1 (R)V / T / E / G / T / I / R E / E Q / E y E E / E / V / E E / E P R P A \ A K (V)	Y12 =n	NP_001422.1	EPB41L2
1086	ET	5	ETD	17.76	1 (K)R P K s Q / V S E E / G K \ E V E \ S D \ K \ E \ K (G)	S4 =n	AAD42222.1	EPB41
1087	ELX	3	ETD	13.32	1 (K)A / K Y P s L G Q \ K (P)	S5 =n	NP_004427.1	ENSA
1088	ELX	4	ETD	27.2	1 (K)A / K Y P s L G Q K P / G G S D F L m K (R)	S5 =n	NP_004427.1	ENSA
1089	ELX	2	ETD	7.93	1 (K)Y / F / D / S / G D / y / N m A \ K (A)	Y7 =n	NP_004427.1	ENSA
1090	ELX	3	ETD	9.16	1 (K)Y / F D S / G D \ y N / M A \ K A K (M)	Y7 =n	NP_004427.1	ENSA
1091	ELX	3	ETD	15.66	1 (K)Y P \ s L G Q \ K P G G S D F L m \ K (R)	S3 =n	NP_004427.1	ENSA
1092	AT	5	ETD	11.4	1 (R)y m G \ K / G / V \ S / K / A / V \ E H / I N K (T)	Y1 =n	NP_001419.1	ENO1
1093	AG	3	CID	20.09	1 (E)T G P T / L / P R \ Q N s Q L P A Q V Q \ N G P S Q \ E E (L)	S10 =n	NP_001008493.1	ENAH
1094	EL	5	ETD	12.83	1 (K)A / S S / T \ S / T / P E P T R \ K P W E R \ T \ N t \ m \ N \ G \ S K (S)	T19 =n	NP_001008493.1	ENAH
1095	EL	5	ETD	16.11	2 (K)A / S / S T / S T P E P T R K P W E R / T N / t m N G \ S K \ s \ P V I S R P \ K (S)	T19 =n,S25 =n	NP_060682.2	ENAH
1096	AL	4	CID	12.35	1 (K)L R K V S R M E D t \ S \ F \ P S G G N \ A I G V / N \ S A S \ S K (T)	T10 =n	NP_001008493.1	ENAH
1097	AL	4	ETD	12.04	1 (K)L / R K V s R / M / E \ D T S F / P S \ G / G N A I \ G \ V / N S \ A \ S \ S \ K (T)	S5 =n	NP_001008493.1	ENAH
1098	EL	4	ETD	9.96	2 (K)P / W E \ R \ T N t m N G S K / s P V I S / R P \ K (S)	T7 =n,S13 =n	NP_060682.2	ENAH
1099	ET	4	ETD	10.91	1 (R)T N / T \ m N / G \ S K s P V I S R P \ K (S)	S9 =n	NP_060682.2	ENAH
1100	EG	3	ETD	24.59	1 (E)V / V / y S K A A S V P K \ V \ E (T)	Y3 =n	NP_001960.2	EIF5
1101	EL	3	ETD	11.61	1 (K)A / A / s V P K \ V E T \ V \ K (S)	S3 =n	NP_001960.2	EIF5
1102	CL	3	CID	19.39	2 (K)E A E E E s s \ G G E \ E \ E D E / D E N I E V V Y \ S K (A)	S6 =k,S7 =k	NP_001960.2	EIF5
1103	EL	3	ETD	9.8	1 (K)N / P P / E N s D / S G / T / G K K \ E \ K (E)	S6 =n	NP_001960.2	EIF5
1104	ELX	4	ETD	19.01	1 (K)A / A / s L T E D R D R / G / R D A V \ K (R)	S3 =k	NP_004944.2	EIF4G1
1105	ELX	3	ETD	14.64	1 (K)F / L / m E C R N s P V \ T \ K (T)	S8 =k	NP_004086.1	EIF4EBP1
1106	ELX	5	ETD	19.43	2 (K)t P P R / D / L P / T I P G V T S P S / S D E \ P P m \ E \ A S Q S \ H L \ R N \ s P \ E D \ K (R)	T1 =k,S32 =k,S14 =nf	NP_004086.1	EIF4EBP1
1107	ELX	5	ETD	16.27	1 (K)T P / P / R D L P T / I P G \ V T / S P S / S D E / P P m E / A \ s Q / S \ H L R \ N S P E / D \ K (R)	S25 =n,T1 =nf,S14 =nf,S32 =nf	NP_004086.1	EIF4EBP1
1108	ELX	5	ETD	12.22	1 (K)T P P R D / L P / T / I P / G V T S P S / S D / E / P P m E A s / Q / S H \ L R N S P / E D \ K (R)	S25 =n,T1 =nf,S14 =nf,S32 =nf	NP_004086.1	EIF4EBP1
1109	EL	4	ETD	20.92	1 (K)D / R D D R S F G R D R N R D s \ D \ K (T)	S15 =n	NP_001408.2	EIF4B
1110	ELX	4	ETD	24.92	1 (K)E / E D \ C H s P T S K P P K P D Q P \ L \ K (V)	S6 =n	NP_001408.2	EIF4B
1111	EL	4	ETD	19.02	1 (K)E / E D \ C H S P t \ S \ K P P K P D Q P \ L \ K (V)	T8 =n	NP_001408.2	EIF4B
1112	ELX	4	ETD	22.78	1 (K)R / S \ S N P P / A \ R s Q S \ S \ D \ T E Q \ Q S P T S G G G \ K (V)	S9 =n,S12 =nf,S18 =nf	NP_001408.2	EIF4B
1113	ELX	5	ETD	17.58	1 (K)S / L E / N / E / T / L N K E E D \ C H S P t \ S K P P \ K P D Q P \ L \ K (V)	T17 =n	NP_001408.2	EIF4B

#	Exp.	CS	Mode	Score	Number of phosphorylation sites ▼ Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
1114	ET	5	ETD	14.82	1 (K)S/L E N E T L N K E \ E D \ C H s / P T \ S / K P / P K P D Q P \ L \ K (V)	S15 =n	NP_001408.2	EIF4B
1115	AG	3	CID	22.78	1 (E)L V/T/K P V \ G G N Y G \ K \ Q P L L L s E \ D \ E \ E (D)	S18 =n	NP_003743.1	EIF3S8
1116	AG	3	CID	15.29	1 (E)S H I T S Y \ K \ Q \ N P E Q s A D \ E (D)	S13 =k	NP_003743.1	EIF3S8
1117	CL	2	CID	13.23	1 (K)Q/N/P/E Q/s A/D/E D/A E K(N)	S6 =k	NP_003743.1	EIF3S8
1118	CG	2	CID	16.68	1 (E)L L K/G I P/L A T G D t S/P E \ P E(L)	T12 =k,S13 =nf	NP_003746.2	EIF3S4
1119	CG	2	CID	13.79	1 (E)L L K/G I P/L A T G D T s P E \ P E(L)	S13 =k,T12 =nf	NP_003746.2	EIF3S4
1120	CT	2	CID	11.96	1 (R)N/t V S Q S/I/S G D P \ E / I D/K K(I)	T2 =n	NP_114414.2	EIF2A
1121	CT	3	CID	15.19	1 (R)S D K S/P D \ L A P / t / P A P Q \ S T P R(N)	T10 =n	NP_114414.2	EIF2A
1122	ET	3	ETD	7.75	1 (R)S/D/K s P D L \ A P T P A P Q S T P \ R(N)	S4 =n	NP_114414.2	EIF2A
1123	AG	5	CID	15.06	1 (E)A S K m Q Q S G \ H P W s \ G / P / K P R / L \ T S S / V / K \ E / L / G / G / V D / L V I E(A)	S12 =n	NP_001957.2	EHHADH
1124	CT	2	CID	15.47	1 (R)A D L N Q / G / I G / E P Q s / P \ S R(R)	S12 =n	NP_077305.2	EFHD2
1125	AT	4	ETD	8.8	1 (K)M A \ s Q / P / F G R / G / A \ m R(E)	S3 =n	NP_037434.1	EEF2K
1126	ELX	4	ETD	26.5	1 (K)A/G/I/I/A/S A/R A \ G E / T R F \ t \ D \ T R \ K(D)	T15 =k,T12 =nf,T17 =nf	NP_001952.1	EEF2
1127	AG	2	CID	20.16	1 (E)D/D D \ I D L F G s D N E \ E(E)	S9 =n	NP_001951.2	EEF1D
1128	AG	2	CID	21.92	1 (E)D/D D \ I D L F G s D N E \ E \ E(D)	S9 =n	NP_001951.2	EEF1D
1129	CG	2	CID	25.29	1 (E)D/D D \ I D L F G / s / D / N E E E D \ K E(A)	S9 =n	NP_001951.2	EEF1D
1130	CG	3	CID	12.22	1 (E)N I/Q K s \ L A \ G \ S / S / G P G A S / S G T / S / G D \ H G E(L)	S5 =n	NP_001951.2	EEF1D
1131	CL	4	CID	23.61	1 (K)K P A T \ P A E \ D D \ E \ D D D \ I \ D L F G / s / D / N \ E E E \ D K(E)	S19 =n	NP_001951.2	EEF1D
1132	AL	3	CID	23	2 (K)K P A t / P A E \ D D E \ D D D / I D L F G / s / D / N E / E E \ D K(E)	T4 =n,S19 =n	NP_001951.2	EEF1D
1133	EL	4	ETD	22.01	1 (K)K P A T P A E \ D \ D \ E \ D D D I \ D L F / G s D N E E E D \ K(E)	S19 =n	NP_001951.2	EEF1D
1134	EL	4	ETD	14.83	2 (K)K P A / t P A E / D D E \ D \ D D I D \ L \ F \ G / s D N E E E D K(E)	T4 =n,S19 =n	NP_001951.2	EEF1D
1135	CT	4	CID	20.36	2 (K)K P A t P A E D D E D D D / I / D L F G / s / D / N \ E / E E D / K / E / A / A Q L R(E)	T4 =n,S19 =n	NP_001951.2	EEF1D
1136	CT	4	CID	19.55	1 (K)K P A T \ P A E D / D E D D / D I D L F G / s / D / N E E E D K / E / A A Q L R(E)	S19 =n	NP_001951.2	EEF1D
1137	ET	4	ETD	7.25	1 (K)K P A / t / P A E D / D E D D D I D L \ F G S D N E E E D / K E A A Q \ L \ R(E)	T4 =n	NP_001951.2	EEF1D
1138	AT	5	CID	16.07	1 (K)K P A T \ P A E / D D E / D / D D I D L / F G / s D / N E E E D K E A A Q L R E / E R(L)	S19 =n	NP_001951.2	EEF1D
1139	ET	5	ETD	12.82	1 (K)K P A \ T / P A E D D E D \ D D I D / L F G s D / N E / E E D / K E A A \ Q L / R E / E \ R(L)	S19 =n	NP_001951.2	EEF1D
1140	AL	5	ETD	28.54	1 (K)S/S P G H R / A / T A P / Q T Q H V s P M R Q \ V E P P A \ K(K)	S16 =k	NP_001951.2	EEF1D
1141	AL	5	ETD	23.85	1 (K)S/S P G H R / A \ T \ A P \ Q T / Q / H / V s P \ m R Q V E P P A \ K(K)	S16 =k	NP_001951.2	EEF1D
1142	EL	5	ETD	22.72	1 (K)S/S P G H R \ A \ T \ A P Q T Q \ H \ V s P M R Q \ V E P P \ A \ K(K)	S16 =k	NP_001951.2	EEF1D
1143	EL	5	ETD	14.85	2 (K)S/s P G H \ R / A \ T A P Q T Q H \ V s P M \ R / Q \ V \ E P \ P \ A \ K(K)	S2 =n,S16 =k	NP_001951.2	EEF1D
1144	CL	5	CID	11.59	1 (K)S S P G H R A T A / P / Q \ T Q H V s P \ M R Q V / E / P P A K(K)	S16 =k	NP_001951.2	EEF1D
1145	AL	4	CID	11.06	1 (K)S S P G H / R / A T / A / P Q T Q H \ V s / P M \ R / Q \ V E / P P A K(K)	S16 =k	NP_001951.2	EEF1D
1146	EL	4	ETD	7.91	2 (K)S/S P G H R A T A P / Q \ t Q H V s P m R Q V / E P P A \ K(K)	T12 =n,S16 =k	NP_001951.2	EEF1D

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
1147	CT	3	CID	17.49	1 (R)A T A/P/Q T Q H V s/P m R(Q)	S10 =k	NP_001951.2	EEF1D
1148	AT	3	ETD	16.64	1 (R)A T/A P Q T Q H V s/P\m\R(Q)	S10 =k	NP_001951.2	EEF1D
1149	ET	3	ETD	15.97	1 (R)A/T/A P Q T Q H V s P M\R(Q)	S10 =k	NP_001951.2	EEF1D
1150	CT	3	CID	14.85	1 (R)A T A/P/Q T Q/H V s/P\M\R(Q)	S10 =k	NP_001951.2	EEF1D
1151	AT	3	CID	13.84	1 (R)A/T A/P/Q T Q/H V s/P m R(Q)	S10 =k	NP_001951.2	EEF1D
1152	CL	2	CID	18.43	1 (K)D/D D D\I\D\L F G/s D D\E/E/E/S E E A K(R)	S10 =k,S16 =nf	NP_001950.1	EEF1B2
1153	EL	4	ETD	25.57	1 (K)R/L R E E R L A Q Y E s\K(K)	S12 =n	NP_001950.1	EEF1B2
1154	CL	4	CID	14.23	1 (K)R L R E E R L A\Q\y\E S K(K)	Y10 =n	NP_001950.1	EEF1B2
1155	CT	3	CID	16.46	1 (K)S s/I/L/L/D V K/P W D D/E/T D/m A K(L)	S2 =n	NP_001950.1	EEF1B2
1156	EL	3	ETD	13.34	1 (K)S/s I L L D V K\p W D D E T D M\A\K(L)	S2 =n	NP_001950.1	EEF1B2
1157	AL	2	CID	21.11	1 (K)Y G/P/A/D V/E D T/T/G/S\G A/T D\s K(D)	S17 =n	NP_001950.1	EEF1B2
1158	CL	2	CID	12.16	1 (K)Y G/P/A D\V E/D T/T/G S G A t D S K(D)	T15 =n	NP_001950.1	EEF1B2
1159	CT	4	CID	13.13	1 (R)E H A L/L A Y T L G V K Q/L\I\V G/V N\K\m/D S T/E P/P y S Q K(R)	Y28 =n	NP_001393.1	EEF1A1
1160	CT	3	CID	8.43	1 (K)S V s T/P S\E A G S Q D S G D G A V G\S R(T)	S3 =n	NP_001369.1	DYNC112
1161	ELX	2	ETD	6.58	1 (K)S P A\s/K L D\K\S\K(R)	S4 =n	NP_056363.2	DST
1162	ELX	4	ETD	10.12	1 (K)T t/I/K E I\S/m\Q K(E)	T2 =n	NP_004406.2	DSP
1163	EG	5	ETD	17.03	1 (E)C K/T V/A L/K R/R K A s S R L E(N)	S12 =n	NP_001929.1	DR1
1164	CT	3	CID	16.15	2 (K)E/m/G t/P L/A/D/t/P T R P\V\T R(H)	T4 =n,T9 =n	NP_064519.2	DPYSL5
1165	CT	3	CID	15.88	1 (K)E m/G T/P/L/A/D t/P T R/P\V\T R(H)	T9 =n	NP_064519.2	DPYSL5
1166	ET	3	ETD	13.33	1 (K)E/m G T P L A D T P t\R P/V T R(H)	T11 =n	NP_064519.2	DPYSL5
1167	ET	4	ETD	16.45	1 (R)D L H E S S F s L S G/S Q I/D D H V P\K(R)	S8 =n	NP_064519.2	DPYSL5
1168	ELX	5	ETD	26.56	1 (K)R G\A P D P R V D D D s/L G\E F P V T N S R A R\K(R)	S12 =k	NP_006259.1	DPF2
1169	ET	4	ETD	16.27	2 (R)A/H P P E\D P R L s F\p/s I K P D T D\Q T\L\K(K)	S10 =n,S13 =n	NP_006259.1	DPF2
1170	EL	4	ETD	13.75	1 (K)S/D/G E A K/P\E P S P\s/P R\I\T R\K(S)	S12 =n	NP_001370.1	DNMT1
1171	CL	2	CID	17.22	1 (K)E L/G/L/D E/G/V/D/s L K(A)	S10 =n	NP_056005.1	DNAJC9
1172	EL	2	ETD	13.67	1 (K)E/L/G/L/D/E/G/V D s\L\K(A)	S10 =n	NP_056005.1	DNAJC9
1173	ELX	4	ETD	23.92	1 (K)N/F E/E/s R/D G R\V\D/S W R N F Q A N\T K(G)	S5 =n	NP_055095.1	DNAJC8
1174	EL	4	ETD	10.15	2 (K)R/K/R/E s E s\E S D E T P P\A A P Q L\I\K(K)	S5 =n,S7 =k,S9 =nf	NP_001354.1	DKC1
1175	CL	3	CID	14.32	1 (K)K/t H K/N I M/I/N L m D I L\E\V D\T K(K)	T2 =n	NP_055577.1	DHCR24
1176	EG	3	ETD	18.02	1 (E)F/A/K L T V E N/s P K\Q\E(A)	S9 =n	NP_003668.2	DENR
1177	CL	3	CID	17.44	1 (K)L t V E/N/S/P K\Q E A\G I S/E/G Q/G/T A G E/E E E\K(K)	T2 =n	NP_003668.2	DENR
1178	ELX	4	ETD	14.14	1 (K)L/T/V\E\N\s P K Q E A G I/S\E G/Q G\T A G E E E E\K(K)	S6 =n	NP_003668.2	DENR
1179	CL	3	CID	15.45	1 (K)E P E m/P/G P R E E s E E E\E/D/E/D/D/E/E/E E E E K(E)	S11 =n	NP_003463.1	DEK
1180	ELX	4	ETD	25.28	3 (K)N/K E E s s D D E D K\E s E E P P K\K(T)	S5 =n,S6 =n,S13 =n	NP_003463.1	DEK
1181	ELX	4	ETD	20.91	2 (K)N/K/E E s s D D\E D K E S/E E E P P K\K(T)	S5 =n,S6 =n	NP_003463.1	DEK

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
1182	EL	4	ETD	17.95	2 (K)R/G G F N t F R D R E N\Y D R\G\Y\S/s L\L\K(R)	T6 =n,S19 =n	NP_004387.1	DDX5
1183	EL	3	ETD	12.95	1 (K)D/A/Y S/S F G S R S D s R\G\K(S)	S12 =n,Y3 =nf,S8 =nf	NP_001347.2	DDX3X
1184	EL	3	ETD	8.97	2 (K)D/A Y/S/S F G s\R s\D S R\G\K(S)	S8 =k,S10 =n,Y3 =nf	NP_001347.2	DDX3X
1185	EL	3	ETD	11	1 (K)F/E/R/G G N s R\W\C D\K(S)	S7 =n	NP_001347.2	DDX3X
1186	AL	3	CID	16.31	1 (K)K A E P\S E V D M/N s P K(S)	S11 =k	NP_004719.2	DDX21
1187	AL	3	ETD	9.1	1 (K)K/K E E P S Q N D\I s P\K(T)	S11 =k	NP_004719.2	DDX21
1188	EL	4	ETD	8.99	1 (K)K V T\K/N E E\p s/E/E/E I\D A P/K P\K(K)	S9 =k	NP_004719.2	DDX21
1189	EL	3	ETD	17.24	1 (K)N/E E P s E E\E I D A P K\K(K)	S5 =k	NP_004719.2	DDX21
1190	CL	3	CID	16.96	1 (K)N E E P/s E\E E I/D A/P\K P K(K)	S5 =k	NP_004719.2	DDX21
1191	ELX	4	ETD	6.77	2 (K)K G\K\T t I K t G/A S/V/L\N K(W)	T5 =n,T8 =n	NP_004930.1	DDX1
1192	EL	3	ETD	10.51	3 (K)E/R A/M/s T\T s I S s P Q P G\K(L)	S5 =n,S8 =n,S11 =n	NP_001014436.1	DBNL
1193	EL	3	ETD	8.65	1 (K)L/R s P\F L Q\K(Q)	S3 =k	NP_001014436.1	DBNL
1194	ET	3	ETD	12.17	1 (K)Q L t Q P E T H F G\R(E)	T3 =n	NP_001014436.1	DBNL
1195	EL	3	ETD	15.17	1 (K)R V G K D s F W A\K(A)	S6 =n	NP_001014436.1	DBNL
1196	ET	3	ETD	7.19	1 (R)L/S s\p V L\H\R(L)	S3 =k,S2 =nf	NP_004386.2	DBN1
1197	ET	3	ETD	13.89	1 (R)S P/S D S S T A S t P V\A E Q I E\R(A)	T10 =k,S3 =nf,S6 =nf	NP_004386.2	DBN1
1198	ET	5	ETD	13.12	1 (K)K/Q/T\G\S\G P L/G N S/y/V\E/R(Q)	Y12 =n	NP_001341.1	DAXX
1199	ELX	5	ETD	22.93	1 (K)H P s P R T Q H I Q Q P R\K(-)	S3 =n	NP_004385.1	DAP
1200	EL	5	ETD	19.96	2 (K)R M/H/I\E K D\E\T P L s\T\p/T A R\D S\L D\K(L)	T9 =n,S12 =n	NP_542937.1	DACH1
1201	EL	5	ETD	16.09	2 (K)R m H I E K D E\T P/L/s T P t A R D/S L\D\K(L)	S12 =n,T15 =n	NP_542937.1	DACH1
1202	ELX	3	ETD	14.41	1 (K)H C/s Q V\D\S/V R G F G G\K(F)	S3 =n	NP_005222.2	CTTN
1203	ELX	3	ETD	11.04	2 (K)H C\s Q V D/s V\R G F G G\K(F)	S3 =n,S7 =n	NP_005222.2	CTTN
1204	CT	3	CID	19.01	2 (K)T Q t P/P V s P/A P Q/P T E/E R(L)	T3 =k,S7 =k	NP_005222.2	CTTN
1205	AT	2	CID	16.47	2 (K)t Q T P/P V s/P/A/P Q P T E E R(L)	T1 =n,S7 =k,T3 =nf	NP_005222.2	CTTN
1206	ET	3	ETD	11.2	2 (K)t Q T P P/V s P A/P Q P T E E\R(L)	T1 =n,S7 =k,T3 =nf	NP_005222.2	CTTN
1207	CT	3	CID	18.1	2 (R)A K/t Q T P P V s P/A P\Q/P\T E/E R(L)	T3 =n,S9 =k,T5 =nf	NP_005222.2	CTTN
1208	AT	3	ETD	10.52	2 (R)A/K t Q T P P V s P A P Q P T E E\R(L)	T3 =n,S9 =k,T5 =nf	NP_005222.2	CTTN
1209	CT	2	CID	15.56	2 (R)L P/s S/P/V/y E/D A/A/S F K(A)	S3 =n,Y7 =k,S4 =nf	NP_005222.2	CTTN
1210	AL	4	CID	17.32	2 (K)N L G/G L E t E D\D\Y S Y Q G H m/Q s C N F S\A E K A K(V)	T7 =n,S19 =n	NP_003784.2	CTSF
1211	EG	4	ETD	21.71	1 (E)A/T/F S N P K T t/s P N K G/K E K\E(A)	T9 =n	NP_001007554.1	CSDE1
1212	EG	4	ETD	18.92	1 (E)A/T/F S N P K T T s P N K G K E K E A\E(D)	S10 =n	NP_001007554.1	CSDE1
1213	CL	3	CID	13.32	1 (K)L Q R D/F/N s/E/L/L R\L R\Q/H W\K\L R\K(V)	S7 =n	NP_004259.3	CRSP6
1214	CG	3	CID	17.49	2 (E)t/V P/G G/Q A/Q t G A\S\T\E/S G R\Q\E(W)	T1 =n,T9 =n	NP_057274.1	CRNN
1215	AT	4	CID	14.03	3 (K)T S A V/N y M t\Q V/V R C D t K(M)	Y6 =n,T8 =n,T15 =n	NP_113664.1	CRISPLD2
1216	ELX	3	ETD	6.05	1 (K)G/T/s G N R G L Q G E\K(G)	S3 =n	NP_056534.1	COL5A3

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
1217	ELX	5	ETD	8.11	1 (K)N S I/A y m/D Q/A S/G N V K K(A)	Y5 =n	NP_000081.1	COL3A1
1218	AL	3	CID	13.16	1 (K)R A/F Q L E E G E E t E P D/C\K(Y)	T11 =k	NP_004636.1	COIL
1219	CT	3	CID	15.83	1 (K)L T L/Q P/V/D N\ S T I s\L/Q/m\G\T N\K(V)	S12 =n	NP_001830.1	CNN3
1220	CT	3	CID	24.79	1 (K)F E E E S K E P/V A\D\E\E E D s D\D D V E P I T E/F R(F)	S17 =n	NP_001284.1	CLNS1A
1221	ET	4	ETD	11.49	1 (R)G S K G G H/G A A/s/P/S E K(G)	S10 =n	NP_006816.2	CKAP4
1222	CL	3	CID	17.09	1 (K)K/s S P S\V K P/A/V/D P A A A K(L)	S2 =n	NP_064709.1	CIAPIN1
1223	EL	3	ETD	16.89	1 (K)S/S P s V\K P\A V\D P A A\A\K(L)	S4 =n	NP_064709.1	CIAPIN1
1224	CL	3	CID	14.31	1 (K)S S P/s V K P A\V/D P A A A K(L)	S4 =n	NP_064709.1	CIAPIN1
1225	CL	2	CID	12.84	1 (K)V/L L/S/D/s/N L/H D\A(-)	S6 =n	NP_064709.1	CIAPIN1
1226	AL	5	CID	12.49	1 (K)Q L T M V E K R M\L M K F L T/F C m/E/y E K(Y)	Y20 =n	NP_000381.1	CHM
1227	EL	3	ETD	19.34	1 (K)R/M s P K P E L T E E Q\K(Q)	S3 =n	NP_004335.1	CETN2
1228	ET	3	ETD	19.01	1 (K)R m s P K P E L T E E Q K(Q)	S3 =n	NP_004335.1	CETN2
1229	CT	4	CID	16.06	1 (K)R m\s/P K P/E/L/T E E\Q K Q E I R(E)	S3 =n	NP_004335.1	CETN2
1230	ET	4	ETD	20.74	1 (R)K/R m/s P K P E L T E/E Q K(Q)	S4 =n	NP_004335.1	CETN2
1231	ET	4	ETD	9.25	1 (R)K/R m/s P K P\E L T E\E Q\K(Q)	S4 =n	NP_004335.1	CETN2
1232	ET	3	ETD	8.95	1 (R)m/s P K P E\L\T E E Q\K(Q)	S2 =n	NP_004335.1	CETN2
1233	ET	4	ETD	11.98	1 (R)m/s P\K P/E\L/T E E Q K Q E I\ R(E)	S2 =n	NP_004335.1	CETN2
1234	ET	3	ETD	10.39	3 (K)R/D A N s/S F\F D\N\s/S s P\H L L D Q\L K(A)	S5 =n,S11 =n,S13 =n	NP_057427.3	CENPF
1235	ELX	5	ETD	20.4	1 (K)E/R/s N R A A S A A G\A A G/S/A G\G\S\G A A G A/A G G\G A G A G/T R P G\D G G\T A\S A\G A A G\A\A T\K(A)	S3 =n	NP_060018.1	CDV3
1236	ELX	3	ETD	22.45	1 (K)L/Q L\D N Q y A V L E N Q\K(S)	Y7 =k	NP_060018.1	CDV3
1237	ELX	3	ETD	16.23	1 (K)T P Q/G P P\E I y S D T Q F P/S\L/Q/S T/A K(H)	Y9 =k	NP_060018.1	CDV3
1238	ELX	3	ETD	13.72	2 (K)T P Q G\ P P E\I\y S\D T\Q\F P s/L Q S T/A K(H)	Y9 =k,S16 =n	NP_060018.1	CDV3
1239	AL	2	CID	15.99	1 (K)L/T/A E A I Q t/P L K(S)	T8 =n	NP_060571.1	CDC48
1240	AL	4	CID	15.36	1 (K)T P/G L R T P A/A G E R I\Y\N\I S G\N G s/P/L A D\S K(E)	S21 =k	NP_060571.1	CDC48
1241	CL	2	CID	11.68	1 (K)I/G E/G/T/y/G\V/V/Y K(A)	Y6 =k,T5 =nf	NP_001249.1	DK3
1242	EL	2	ETD	10.06	2 (K)I/G/E/G/t/y/G V\V\Y\K(A)	T5 =k,Y6 =k	NP_001249.1	DK3
1243	ET	3	ETD	18.43	1 (K)H S L D s D E E/E D D D D G G S S K(Y)	S5 =n	NP_006101.1	CD2BP2
1244	EL	3	ETD	10.18	1 (K)G/R K\E s A Q P P\A H\L(-)	S5 =n	NP_005116.1	CCS
1245	CT	2	CID	13.95	2 (K)L D/Q P V s A P P/s/P R(D)	S6 =k,S10 =k	NP_005427.2	CCDC6
1246	CT	2	CID	18.51	1 (R)A/E/Q E E/E F/I S N t/L F K(K)	T11 =n	NP_005427.2	CCDC6
1247	CL	3	CID	21.75	1 (K)A A L/L/A Q Y A D V\ t D E E D E A D E K(D)	T11 =n	NP_653210.1	CCDC43
1248	ET	3	ETD	7.02	1 (R)L/y L L R/H F R K Q T E L R R(S)	Y2 =n	NP_056254.1	CCDC28A
1249	EG	5	ETD	18.73	1 (E)S N/K/R K s N F S/N S/A\D D I K\S K\K K R\E(Q)	S6 =n	NP_036249.1	CBX5
1250	ELX	5	ETD	17.26	1 (K)K/R E Q s N/D I A R/G F E/R G\L\E P E K(I)	S5 =n	NP_036249.1	CBX5

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			Mode	Score				
1251	ELX	3	ETD	22.59	1 (K)R/K s N F S N S A D D I\K(S)	S3 =n	NP_036249.1	CBX5
1252	ELX	3	ETD	10.34	4 (K)R t A D s s s s E\D\E E E Y V V E K(V)	T2 =n,S5 =n,S7 =n,S8 =n	NP_036249.1	CBX5
1253	EG	5	ETD	22.98	1 (E)A/F/L N/S/Q/K A G K E/K D G T K R K s L S D\s\E(S)	S19 =k,S21 =nf	NP_009207.2	CBX3
1254	ET	3	ETD	26.06	1 (K)R K s L/S/D S E/S D D S K(S)	S3 =k,S5 =nf	NP_009207.2	CBX3
1255	EL	3	ETD	15.06	2 (K)R/K s L\s D S E S D D S\K(S)	S3 =k,S5 =k	NP_009207.2	CBX3
1256	CT	3	CID	20.92	1 (R)A s L E/N V/H P P I/A P P T/E/I/P E\R(F)	S2 =n	NP_079090.1	CBLL1
1257	ELX	3	ETD	8.77	1 (K)S L/T P A V P V E\s K P D K P S\G\K(S)	S10 =n	NP_001741.3	CAST
1258	CT	3	CID	19.05	3 (R)E R s/P s P/L R/G N/V V P s/P L/P T\R(R)	S3 =n,S5 =n,S14 =n	NP_055131.1	CARHSP1
1259	CT	2	CID	13.59	1 (R)G N\V V P s/P L P T R(R)	S6 =n	NP_055131.1	CARHSP1
1260	EL	3	ETD	17.44	1 (K)N/P S L R/A Q G G Q T Q s P\T\K(S)	S13 =n	NP_006357.1	CAP2
1261	AT	3	ETD	15.67	1 (R)V/F/D\K D G N G Y I S A A E L\R(H)	Y9 =k	NP_001734.1	2CALM3
1262	AT	3	CID	14.17	1 (R)V F D/K D G/N/G\Y I S A A/E/L R(H)	Y9 =k	NP_001734.1	2CALM3
1263	ELX	4	ETD	27.18	1 (K)H T E N T F S R\p G G R A s V D T\K(E)	S14 =n	NP_004333.1	CALD1
1264	ELX	4	ETD	24.19	1 (K)T P D/G N K s P A P K P S D/L/R P\G D\V S\S\K(R)	S7 =k	NP_004333.1	CALD1
1265	ELX	4	ETD	9.36	1 (K)T/P\D G/N\K/S P A P K P s D L/R P\G D V/S S\K(R)	S13 =n,S7 =nf	NP_004333.1	CALD1
1266	ET	4	ETD	15.94	1 (K)I/Y/E D G D D D m K R\t I\N\K(A)	T12 =n	NP_001007215.1	CACYBP
1267	EL	3	ETD	5.72	2 (K)K/s s G/S G/D K(C)	S2 =n,S3 =n	NP_619584.1	CABYR
1268	ET	3	ETD	11.01	1 (K)N/A/E D C/L y E L P E N I R(V)	Y7 =n	NP_057566.1	C9orf78
1269	ET	4	ETD	16.5	1 (R)V/G/D T/E K P E P\E R s P P\N\R(K)	S12 =n	NP_057604.1	C9orf78
1270	CT	3	CID	16.03	2 (K)R I D F I P/V s P A P S P t R(G)	S8 =n,T14 =n	NP_612206.3	C9orf42
1271	CG	2	CID	18.8	1 (E)A D/P/P G Q V A A s/P D P\T\T(-)	S10 =n	NP_006434.1	C6orf108
1272	ET	4	ETD	11.3	2 (K)L/t/E G E Q D\E/A s/N/A/A/M L L\E\K(E)	T2 =n,S10 =n	NP_203528.2	C3orf15
1273	AG	5	ETD	10.35	2 (E)L H\H\E\S/G Q y Q M E/Q N G/S P T/S\S K/s R\K G E(A)	Y8 =n,S21 =n	NP_653230.1	C2orf11
1274	EL	3	ETD	11.34	1 (K)L/S/M E D S K s P P P\K(A)	S8 =n	NP_067038.1	C20orf77
1275	ELX	5	ETD	15.99	3 (K)Q/P/E T/P K s\W E N N\V E s/Q\K\H S L\t/S Q S Q/I\s P\K(S)	S7 =n,S14 =n,T20 =n	NP_001002259.1	C1QDC1
1276	CL	3	CID	13.79	1 (K)A/R L L P E\G/E E T\L E s D\D\E\K(D)	S13 =n	NP_932343.1	C1orf52
1277	ELX	3	ETD	10.62	1 (K)A/R/L\L P E G E\E\T L E\s/D D\E\K(D)	S13 =n	NP_932343.1	C1orf52
1278	ELX	4	ETD	17.22	1 (K)A/R/L L P E G/E/E T L E s/D/D E K D\E H T\S\K(K)	S13 =n	NP_932343.1	C1orf52
1279	ET	4	ETD	26.29	1 (R)L/L P E\G E E T L E s D D E K D E H T\S\K(K)	S11 =n	NP_932343.1	C1orf52
1280	ELX	4	ETD	23.25	2 (K)A R/S C\s A A R\A A s\A\Q E V A\G S T S\A\K(T)	S5 =n,S11 =n	NP_997239.1	C1orf174
1281	ELX	4	ETD	19.64	2 (K)R/P T s N G V\V S s P N\S/T\S R P/T L P\V\K(S)	S4 =n,S10 =n	BAC77399.1	C1orf144
1282	ELX	4	ETD	19.28	1 (K)R/P T S N G V V\S s P N S T S R P/T L P\V\K(S)	S10 =n	BAC77399.1	C1orf144
1283	CL	3	CID	20	1 (K)V/Y E/D S G I P L P/A E/s P K K(G)	S13 =n	NP_777553.1	C17orf49
1284	AL	3	ETD	19.32	1 (K)V/Y/E D/S/G I/P L/P A E s P K\K(G)	S13 =n	NP_777553.1	C17orf49
1285	CT	2	CID	14.34	1 (R)D/L F S L/D/S/E D P/S P A s/P P L R(S)	S14 =k	NP_078792.1	C16orf53

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			Mode	Score				
1286	ELX	3	ETD	22.42	1 (K)A/A/R s I P/A G A E P\G E\K(G)	S4 =n	NP_653171.1	C16orf34
1287	ELX	4	ETD	29.82	1 (K)A A/R S I/P\A G A E P G E K\G s A R\K(A)	S16 =n	NP_653171.1	C16orf34
1288	ELX	3	ETD	13.07	1 (K)D/H V\F\L C E/G/E E P K s/D L\K(A)	S13 =n	NP_653171.1	C16orf34
1289	AL	3	CID	15.16	1 (K)s F G R Y P S L M/E N N N m R\I\Q/D T L D L V M\K(T) (K)S F G R/Y P/S/L M\E N N\N m/R I/Q D T/L D\L V M K t L S\ S H t\ S/C\ P	S1 =n	NP_758953.1	C14orf50
1290	AL	5	ETD	9.31	3 K(-)	Y5 =n,T26 =n,T31 =n	NP_758953.1	C14orf50
1291	EL	3	ETD	17.13	1 (K)R K/A/s P E\ P P D S\A E G A\L\K(L)	S4 =n	NP_078772.1	C14orf4
1292	AL	3	CID	16	1 (K)R K A s/P/E P/P/D S A E/G A L\K(L)	S4 =n	NP_078772.1	C14orf4
1293	AT	3	CID	17.46	2 (K)L/A/P/V/P/s P E/P\Q K P A/P V S\ P E s V K(A)	S6 =k,S19 =n,S16 =nf	NP_115812.1	C13orf8
1294	ELX	3	ETD	8.11	1 (K)S/S/R G/G s P\D L W\K(S)	S6 =k	NP_115812.1	C13orf8
1295	ET	4	ETD	18.45	3 (R)K P/G P P L s P E/I R s P A G s P\E L\R(K)	S7 =n,S12 =n,S16 =k	NP_115812.1	C13orf8
1296	AT	2	CID*	10.9	1 (K)A/A/L/L K A/s P K(K)	S7 =n	NP_003449	BSN
1297	AT	2	ETD*	6.2	1 (K)A/A/L/L K A/s P K(K)	S7 =n	NP_003449	BSN
1298	CL	5	CID	14.83	1 (K)R R K\ P E D V\L\D\D\D\D\A G\S/A P/L K S/s/G Q H Q N D K(G)	S21 =n	NP_001719.2	BSG
1299	CL	5	CID	17.63	2 (K)R R R P R Y R/K\R L/R S/s S/S/S L/S S/S/G/A/P/s P K G K(Q)	S13 =n,S24 =n	NP_694984.2	BRWD3
1300	AL	3	ETD	9.44	1 (K)S/K P P P T Y/E s E E E D K(C)	S9 =n	NP_055114.1	BRD4
1301	EL	4	ETD	13.64	1 (K)R K A\D T/T T P T/T S A I T\A s R S E S P P P L/S D P\K(Q)	S16 =n,S20 =nf	NP_031397.1	BRD3
1302	EL	5	ETD	25.84	1 (K)V/V/A R R E s G/G\R P I K P P\K\K(D)	S7 =n	NP_031397.1	BRD3
1303	CT	2	CID	12.4	1 (R)S E s P/P/P/L S D P K(Q)	S3 =k	NP_031397.1	BRD3
1304	ET	4	ETD	19.51	1 (R)R/E s G R P I K P P R(K)	S3 =n	AAH63840.1	BRD2
1305	EL	4	ETD	24.45	1 (K)G L/A G/G D R\A/S R P/L s\A\R S E P S E\K(G)	S13 =n	NP_060644.4	BPY2IP1
1306	CT	3	CID	14.58	1 (K)K T T E E/Q V Q A S/t/P/C P R(T)	T11 =n	NP_056016.1	BOP1
1307	CG	2	CID	14.57	1 (E)A L D Y F s D/K\E(S)	S6 =k	NP_055554.1	BCLAF1
1308	EG	5	ETD	27.27	1 (E)G/L/K/Y/K S K V S L K\G N\ R E s D\G F\R\E\E(K)	S16 =n	NP_055554.1	BCLAF1
1309	EG	5	ETD	22.5	2 (E)G/L/K Y K S K V\ s L K\G N R E s D\G\F\R\E E(K)	S9 =n,S16 =n	NP_055554.1	BCLAF1
1310	EG	4	ETD	7.05	1 (E)G/L/K Y K S K V/s L K G/N R E S\D G\F R E\E(K)	S9 =n	NP_055554.1	BCLAF1
1311	EG	5	ETD	26.85	1 (E)K/S/T F R E/E s P/L R/I K m I\A S\D\S\H R P\E(V)	S8 =n	NP_055554.1	BCLAF1
1312	AG	5	CID	7.74	2 (E)R G D s K\G\S\R E S\S/G s R K/Q E(K)	S4 =n,S13 =n	NP_055554.1	BCLAF1
1313	AG	5	ETD	6.97	3 (E)R I t V K K\E t Q S/P E Q V K s E(K)	T3 =n,T8 =n,S16 =n,S10 =nf	NP_055554.1	BCLAF1
1314	AG	5	ETD	17.31	2 (E)T/Q s\ P E Q V K S E K L K\D L F D Y\ s\ P P L\H K\N L\D\A R\E(K)	S3 =k,S19 =k	NP_055554.1	BCLAF1
1315	AG	5	ETD	11.97	2 (E)T Q S P E Q V K S E K L K D\L\F\D y S P P L H\K\N L D\A R\E(K)	S9 =n,Y18 =n,S3 =nf,S19 =nf	NP_055554.1	BCLAF1
1316	ELX	3	ETD	16.99	1 (K)D/L F D Y s P/P L H\K(N)	S6 =k	NP_055554.1	BCLAF1
1317	ELX	3	ETD	10.39	1 (K)D/T/F/E H D P/S E s\I\D E F N\K(S)	S10 =n	NP_055554.1	BCLAF1
1318	AT	2	CID	20.42	1 (K)F N D/s/E/G/D D T/E/E/T/E D Y R(Q)	S4 =n	NP_055554.1	BCLAF1
1319	ELX	4	ETD	15.74	1 (K)F/N D s E G/D D T E E T/E D\Y R Q F R\K(S)	S4 =n	NP_055554.1	BCLAF1
1320	EL	4	ETD	15.44	2 (K)F/N D s E G D D T E E/t/E D Y R\Q\F\R\K(S)	S4 =n,T12 =n	NP_055554.1	BCLAF1

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
1321	ELX	4	ETD	12.77	1 (K)F/N D S E G/D D t/E E T E D\Y R\Q F R\K(S)	T9 =n	NP_055554.1	BCLAF1
1322	ELX	4	ETD	10.69	2 (K)F/N D s E G D D T E E T E D\y R\Q\F\R\K(S)	S4 =n,Y15 =n	NP_055554.1	BCLAF1
1323	AT	3	ETD	14.65	1 (K)G/N/R E s D G F R E E\K(N)	S5 =n	NP_055554.1	BCLAF1
1324	AT	3	CID	19.16	1 (K)K A/E\G\Q\Q E E s/P L\K(S)	S10 =k	NP_055554.1	BCLAF1
1325	ELX	3	ETD	17.08	1 (K)K/A E G E P Q/E E\ s P\L\K(S)	S10 =k	NP_055554.1	BCLAF1
1326	ET	4	ETD	24.14	1 (K)K/A E G E/P Q E E s P L K\S\K(S)	S10 =k	NP_055554.1	BCLAF1
1327	AT	3	CID	12.87	1 (K)K/A E/G E P Q E\E s P L\K S\K(S)	S10 =k	NP_055554.1	BCLAF1
1328	ET	3	ETD	13.33	1 (K)L/K D L F D y S P P L H\K(N)	Y7 =n,S8 =nf	NP_055554.1	BCLAF1
1329	ET	4	ETD	24.43	1 (K)N/T P S Q H\S H S I Q H s\P E\R(S)	S13 =n	NP_055554.1	BCLAF1
1330	AT	4	ETD	18.45	2 (K)N/T P S Q H S H s I Q H s P E\R(S)	S9 =n,S13 =n	NP_055554.1	BCLAF1
1331	CL	4	CID	10.69	1 (K)Q K/F N D s E/G D/D/T/E/E/T E D/Y/R Q F R K(S)	S6 =n	NP_055554.1	BCLAF1
1332	ELX	4	ETD	9.1	1 (K)S/K s/Q E E P K/D T F\ E H D P S E S I D/E F N K(S)	S3 =n	NP_055554.1	BCLAF1
1333	ELX	5	ETD	24.66	2 (K)s P E/I/H R\R I D\I s P S T L R\K(H)	S1 =n,S11 =k	NP_055554.1	BCLAF1
1334	CT	3	CID	12.81	1 (K)S/T F/R/E E s/P\L R(I)	S7 =n	NP_055554.1	BCLAF1
1335	AT	3	ETD	11.73	1 (K)S/T F R E E s/P L\R(I)	S7 =n	NP_055554.1	BCLAF1
1336	EL	3	ETD	16.67	1 (K)S/T/F/R/E E/s P\L R\I\K(M)	S7 =n	NP_055554.1	BCLAF1
1337	EL	3	ETD	10.81	2 (K)s/T\F R E E s P L\R I\K(M)	S1 =n,S7 =n	NP_055554.1	BCLAF1
1338	ELX	3	ETD	8.7	2 (K)S t F R E E s P L R I\K(M)	T2 =n,S7 =n	NP_055554.1	BCLAF1
1339	ELX	5	ETD	23.15	1 (K)T I/A P Q N/A P/R D E S R G R S s\F Y/P\D G G\D Q\E T\A\K(T)	S17 =n	NP_055554.1	BCLAF1
1340	CT	3	CID	12.94	2 (R)D E s R/G R s S/F/Y P\D\G/G D Q E T A\K(T)	S3 =n,S7 =n	NP_055554.1	BCLAF1
1341	AT	2	CID	12.49	1 (R)I/D I s P/S T L R(K)	S4 =k	NP_055554.1	BCLAF1
1342	ET	3	ETD	12.23	2 (R)I/D I s P/S t L R\K(H)	S4 =k,T7 =n	NP_055554.1	BCLAF1
1343	ET	3	ETD	15.62	2 (R)R/I D I s P S t L R\K(H)	S5 =k,T8 =n	NP_055554.1	BCLAF1
1344	ET	4	ETD	11.42	2 (R)S G/S G\S V G N G/S S R Y\S/P s\Q N s P I\H H I P\S\R(R)	S16 =n,S19 =k,S14 =nf	NP_055554.1	BCLAF1
1345	CT	3	CID	11.11	2 (R)S G S/G s/V G N G S S R/Y S/P/S Q N S P/I\H H\I P s R(R)	S5 =n,S26 =n,S14 =nf,S19 =nf	NP_055554.1	BCLAF1
1346	ET	4	ETD	20.7	2 (R)Y/s P S Q N s P I H H I P S\R(R)	S2 =k,S7 =k	NP_055554.1	BCLAF1
1347	AT	3	CID	14.08	2 (R)y S P/s\Q N S/P\I H/H/I/P S R(R)	Y1 =n,S4 =n,S2 =nf,S7 =nf	NP_055554.1	BCLAF1
1348	AT	4	CID	13.11	2 (R)Y s P S Q/N/s/P\I/H/H\I P S R(R)	S2 =k,S7 =k	NP_055554.1	BCLAF1
1349	EG	4	ETD	12.18	2 (E)A/m\T Y\R I/G H H S T S/D D S S/A\y\ R s V\D\E(V)	Y18 =n,S20 =k,S10 =nf	NP_000700.1	BCKDHA
1350	CL	4	CID	13.53	1 (K)R R A V E s G V P Q P P D P P V\Q R D E E/E E K(E)	S6 =n	NP_057651.1	BCCIP
1351	ELX	5	ETD	11.29	1 (K)E/R E/S A E Q/S S G P G P S L R P Q N s T\T W R D G G G/R G P D\E L E G P D S\K(L)	S20 =n	NP_004629.2	BAT2
1352	ET	4	ETD	23.62	2 (K)L/K F s D E E D G R D s D E E G A E G H\R(D)	S4 =n,S12 =n	NP_004629.2	BAT2
1353	ELX	5	ETD	17.84	2 (K)L/K F s D E E D/G R D s D E E G\A E G H/R D\S Q S A S\G\ E E R P P\E\A D G\K(K)	S4 =n,S12 =n	NP_004629.2	BAT2
1354	CT	3	CID	21.34	1 (K)S/S D/A/S/T/A/Q P/P E/S/Q P L/P A/s\Q T/P A S N Q P K(R)	S18 =n	NP_004629.2	BAT2

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
1355	AT	3	ETD	16.85	2 (R)E/R S D s\G/G s S S E P F D\R(H)	S5 =n,S8 =n	NP_004629.2	BAT2
1356	AT	3	CID	12.26	2 (R)E R S D\s/G G/s S/S E P/F D R(H)	S5 =n,S8 =n	NP_004629.2	BAT2
1357	AT	3	CID	14.69	1 (R)L K/A E/P A\A P P A A P S t/P/A P P P A V\ P K(E)	T14 =n	NP_004629.2	BAT2
1358	ET	3	ETD	15.82	1 (R)R/K Q s S\S E I S L A\ V\E\R(A)	S4 =n	NP_004629.2	BAT2
1359	AG	3	CID	21.52	1 (E)A A/A/A A P/Q/R S Q s/P L R\G\m P E(T)	S11 =n	NP_004272.2	BAG3
1360	EG	3	ETD	13.16	1 (E)A/A/A/A/A P Q R S Q s P\L R G m P\E(T)	S11 =n	NP_004272.2	BAG3
1361	ELX	4	ETD	11.58	1 (K)T/H Y P A Q Q G E y/Q T H Q P V\Y\H\K(I)	Y10 =k	NP_004272.2	BAG3
1362	ET	3	ETD	8.96	2 (R)S/S/t P L H s P S P\I\R(V)	T3 =n,S7 =n	NP_004272.2	BAG3
1363	EG	4	ETD	17.6	2 (E)K H S A V Q R Q G\s\G\R\E s P\s\L A\S R\E(G)	S10 =n,S14 =n	NP_009176.2	ATXN2L
1364	AT	3	CID	22.26	1 (K)E K E V D G L L T S E P/m/G s/P V/S S K(T)	S15 =k	NP_009176.2	ATXN2L
1365	CT	3	CID	20.97	1 (K)G P P Q/s/P V F E G V Y N/N\S R(M)	S5 =k	NP_009176.2	ATXN2L
1366	ELX	5	ETD	30.44	1 (K)H/S A V Q R Q\G S/G R E s\P/S L/A S\R E\G\K(Y)	S13 =n	NP_009176.2	ATXN2L
1367	ELX	5	ETD	29.93	1 (K)H/S A V Q R Q\G S/G R E S P s L/A\S R E\G\K(Y)	S15 =n	NP_009176.2	ATXN2L
1368	ELX	4	ETD	29.17	2 (K)H/S A V Q R Q G s G R\E S P s\L/A\S R E\G\K(Y)	S9 =n,S15 =n	NP_009176.2	ATXN2L
1369	ELX	4	ETD	21	2 (K)H/S A V Q R Q G\s G R\E s/P S L A S R E\G\K(Y)	S9 =n,S13 =n	NP_009176.2	ATXN2L
1370	ELX	5	ETD	17.05	1 (K)H/S A V Q R\Q\G s/G R E S P/S\L/A\S R E G K(Y)	S9 =n	NP_009176.2	ATXN2L
1371	CT	3	CID	19.72	2 (K)L Q P/S S s P/E/N s L D P/F P P R(I)	S6 =k,S10 =n	NP_009176.2	ATXN2L
1372	CT	3	CID	10.77	2 (K)L Q/P/s s S/P E N\S L D P F P P R(I)	S4 =n,S5 =n,S6 =nf	NP_009176.2	ATXN2L
1373	ELX	3	ETD	12.75	1 (K)E/N/I K P N E\t S P S F\S\K(A)	T8 =n	NP_002964.2	ATXN2
1374	ELX	3	ETD	11.71	1 (K)E/N/I K P N E\t s P S F S\K(A)	S9 =n	NP_002964.2	ATXN2
1375	ELX	5	ETD	8.6	2 (K)s R D L\I K D K/I E/P/s/A K(D)	S1 =n,S12 =n	NP_002964.2	ATXN2
1376	EL	3	ETD	11.34	2 (K)s/K S s/G S S R S K(R)	S1 =n,S4 =n	NP_000480.2	ATRX
1377	AT	5	ETD	10.96	1 (K)m Q\D\G N/V D/A S Q/s/K/A K(Q)	S11 =n	NP_001001331.1	ATP2B2
1378	CL	3	CID	14.71	1 (K)K A s/S E G G T A A/G/A/G L D/S L H\K(N)	S3 =n	NP_005711.1	ARPC1B
1379	ELX	3	ETD	12.47	1 (K)S/S/s P E L V T H L\K(W)	S3 =n	NP_004299.1	ARHGAP1
1380	ELX	4	ETD	26.48	1 (K)A/S/E\L G/H s L N E N V L K P A\Q E\K(V)	S7 =n	NP_060679.1	ARFGAP1
1381	EL	3	ETD	17.45	1 (K)L/S/L E G D/H S T P P S A Y G S V\K(A)	Y14 =k,S8 =nf,S16 =nf	NP_001002857.1	ANXA2
1382	CL	4	CID	19.1	1 (K)E E I/Q D E\E\D\D\D/D/y V E E G/E/E/E E/E E E G G L R G E K(R)	Y12 =n	NP_112182.1	ANP32E
1383	CG	4	CID	15.99	1 (E)N V/F K L L\ P Q\ L/T/Y/L D/G Y D\R D D K\E A P D\s D A\E(G)	S25 =n	NP_006296.1	ANP32A
1384	CL	3	CID	13.69	1 (K)I H G S G H V E\E P/A s P L/A A Y Q K(S) (E)G G R\S D S L R S F/S S/D/R S\H T/L s\H A\S Y L R D S A V/M/D D S V	S12 =n	NP_001140.2	ANK3
1385	AG	5	ETD	7.72	1 V I/P/S H Q V S T/L\A/K/E/A E(R)	S19 =n	NP_001139.3	ANK2
1386	AG	5	ETD	8.36	2 (E)V s E/M K Q/D L I K M/T A I\L T t/D/V S D K\A\G/S I\K V K E(L) (E)V s E m K Q\ D L I K M T A I/L T/t D\V\S\D K A/G\S I/K V K E L V K A	S2 =n,T17 =n	NP_001139.3	ANK2
1387	AG	5	CID	9.19	2 A E(E)	S2 =n,T17 =n	NP_001139.3	ANK2
1388	EL	3	ETD	16.87	1 (K)T D/G P V F H S\N t L E R\K(T)	T10 =n	NP_573572.1	AMOT

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene	
			Mode	Score				▼	Symbol
1389	EG	5	ETD	11.13	2	(E)G/T/L/L K/P/N M V t/P/G/H A C t Q K F S H\E(E)	T10 =n,T16 =n	NP_000025.1	ALDOA
1390	CL	3	CID	15.25	1	(K)Y T/P/S G Q A G A A/A/S E s L/F V S\N H\A\Y(-)	S14 =n	NP_000025.1	ALDOA
1391	CT	3	CID	14.05	1	(K)Y T P/S G Q A\G A\A/A s E S L/F V S N H A\Y(-)	S12 =n	NP_000025.1	ALDOA
1392	EL	3	ETD	5.58	1	(K)Y T P S G Q A G A A A S/E/s L F V S N\H\A\Y(-)	S14 =n	NP_000025.1	ALDOA
1393	AT	4	CID	22.78	2	(R)A A/T/A/A/R/P/P A\P/P/P/A P/Q/P/P s/P T/P/s/P P R P T L A R(E)	S18 =n,S22 =n	NP_115751.1	AKT151
1394	ELX	5	ETD	12.41	1	(K)R E\Q S/H/A E I s P P A/E/S G Q\A\V\E E\C\K\E E G E\E\K(Q)	S9 =n	NP_005091.2	AKAP12
1395	ELX	4	ETD	26.23	2	(K)R/V R\R P s E s D K E D E L D\K(V)	S6 =n,S8 =n	NP_005091.2	AKAP12
1396	EL	4	ETD	21.08	1	(K)R/V R R P s E S D K E D E L D\K(V)	S6 =n	NP_005091.2	AKAP12
1397	ET	2	ETD	8.15	2	(K)S/A/E/s P T/s P V T S\T S\T\G\A\T F\K(K)	S4 =n,S7 =n	NP_005091.2	AKAP12
1398	EL	4	ETD	13.99	1	(K)S P P/s P V E R E m\V\Q\Q V\E R E\K(T)	S4 =n	NP_005091.2	AKAP12
1399	ET	4	ETD	10.55	2	(R)V R R P s E\ s D K E D E L D\K V\K(S)	S5 =n,S7 =n	NP_653080.1	AKAP12
1400	EL	3	ETD	20.47	1	(K)S/R S P G s P V G E G T G S P P\K(W)	S6 =k	NP_001110.2	ADD1
1401	CL	3	CID	19.09	1	(K)S R s\P\G S P V G E G T G\A P P K(W)	S3 =n,S6 =nf	NP_001110.2	ADD1
1402	CL	3	CID	17.83	1	(K)s/R S\P\G S P V G E G T/G\A P P K(W)	S1 =n,S6 =nf	NP_001110.2	ADD1
1403	CL	4	CID	17.98	1	(K)T R W L\N S G/R G\D\E A\S\E\E\G\Q\N G\S s P K(S)	S21 =k,T1 =nf	NP_001110.2	ADD1
1404	EL	4	ETD	11.13	1	(K)T/R\W\L N S G/R G D E\A S E E G Q N G\S\ s P\K(S)	S21 =k,T1 =nf	NP_001110.2	ADD1
1405	EG	3	ETD	13.77	1	(E)A S/s/P P P/H/P Q\L H\S\E\E\E(I)	S3 =n	NP_055792.1	ACIN1
1406	EG	4	ETD	6.62	3	(E)I/K S/S Q\G L K E K s/K s P/s P P\R L\T\E(D)	S11 =k,S13 =k,S15 =k	NP_055792.1	ACIN1
1407	EG	3	ETD	13.08	2	(E)K/S K s P s/P P R\L T\E(D)	S4 =k,S6 =k,S2 =nf	NP_055792.1	ACIN1
1408	EL	5	ETD	26.06	1	(K)E/G/R R A s H T L\L/P\S H R\L\K(Q)	S6 =n	NP_055792.1	ACIN1
1409	ELX	4	ETD	32.6	1	(K)E/R T S T S S S/S V Q A R R L s Q P E S A\E\K(H)	S16 =k	NP_055792.1	ACIN1
1410	ELX	5	ETD	8.22	3	(K)E/s s L P/K S/F K\R K I S/V/V/S/A/t\K(G)	S2 =n,S3 =n,T18 =n	NP_055792.1	ACIN1
1411	EL	5	ETD	20.76	2	(K)G/E/R R s s R\ V R Q A R\A A\K(L)	S5 =n,S6 =n	NP_055792.1	ACIN1
1412	ELX	3	ETD	16.61	1	(K)G/V P/A/G N s D\T E G/G\Q P G R\K(R)	S7 =n	NP_055792.1	ACIN1
1413	ELX	4	ETD	22.95	1	(K)H/V/T Q R\L Q P E R G s P\K(K)	S12 =n	NP_055792.1	ACIN1
1414	ELX	4	ETD	27.15	2	(K)K V T L G D t L/T/R\R s I S Q Q\K(S)	T7 =n,S12 =n	NP_055792.1	ACIN1
1415	ELX	4	ETD	15.02	2	(K)K V/T L G D T L T R\R s I\ s Q\Q\K(S)	S12 =n,S14 =n	NP_055792.1	ACIN1
1416	ELX	4	ETD	7.69	2	(K)K V T/L G/D\T\L t R R\ s I S\Q\Q\K(S)	T9 =n,S12 =n	NP_055792.1	ACIN1
1417	ELX	4	ETD	7.49	2	(K)K V/T\L G D t L\T/R\R\ S I s\Q\Q\K(S)	T7 =n,S14 =n	NP_055792.1	ACIN1
1418	ELX	5	ETD	14.26	1	(K)L/S E/G S/Q P A E/E E E D\Q E t P S R/N L R V R\A\D R N\L\K(T)	T16 =n,S2 =nf,S5 =nf	NP_055792.1	ACIN1
1419	ELX	5	ETD	12.37	1	(K)L/S E G S Q P\A E\E E E D Q E T\ P\ s R/N L R V R\A\D R N\L\K(T)	S18 =n,S2 =nf,S5 =nf	NP_055792.1	ACIN1
1420	ELX	4	ETD	22.08	2	(K)S K/s P s P\ P R L T E D R\K(K)	S3 =k,S5 =k,S1 =nf	NP_055792.1	ACIN1
1421	ELX	4	ETD	11.26	2	(K)S/K s/P\ s P\ P R L/T E D R K\K(A)	S3 =k,S5 =k,S1 =nf	NP_055792.1	ACIN1
1422	AT	4	CID	19.96	1	(K)S/S S/I/S E E K/G D s D/D/E K P R(K)	S11 =n	NP_055792.1	ACIN1
1423	AT	4	ETD	16.55	1	(K)S/S/S/I S/E E K G D s D D/E K P\R(K)	S11 =n	NP_055792.1	ACIN1

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score				
1424	EL	5	ETD	19.04	3 (K)V/R E G/P R s R s R s R D\R\R K\K(E)	S7 =n,S9 =n,S11 =n	NP_055792.1	ACIN1
1425	ET	4	ETD	25.61	2 (R)K/S/S s I S E E K G D s D D E K P\R(K)	S4 =n,S12 =n	NP_055792.1	ACIN1
1426	ET	4	ETD	12.1	2 (R)s/R s R S R D R R R\K E\R(A)	S1 =n,S3 =n	NP_055792.1	ACIN1
1427	ET	4	ETD	8.88	1 (K)N L/L/V\t/m L I D/Q L C G\R(D)	T5 =n	NP_942131.1	ACACA
1428	ET	5	ETD	12.94	2 (R)G G/S W V V/I\ D S/s/I N\ P R/H\m E m/y A\D R\E\S\R(G)	S10 =n,Y19 =n	NP_942131.1	ACACA
1429	EL	3	ETD	15	1 (K)N/Y I A R F\G H G s A\K(L)	S10 =n	NP_005683.2	ABCF2
1430	CL	3	CID	14.95	1 (K)G/G N V/F/A/A/L I Q/D Q s E\E/E E E E\E\K(H)	S13 =n	NP_001020262.1	ABCF1
1431	CL	3	CID	24.42	1 (K)K/A E Q G s E E E G E G E/E E/E E E G\G\E\S\K(A)	S6 =n	NP_001020262.1	ABCF1
1432	ET	3	ETD	18.04	1 (R)E/D s Q R P G A/H/L T V K(K)	S3 =n	NP_001011724.1	HNRPA1
1433	CT	4	CID	14.57	2 (R)M L F y T M/K P S E/T S\F/Q\t\L\E E \V\ P D Y V K K(A)	Y4 =n,T15 =n	NP_001004320.1	392636
1434	AL	4	CID	16.29	2 (K)T D L s I\Q T R N A E E K I m N T W y P\K(V)	S4 =n,Y19 =n	NP_940966.1	375347
1435	ELX	5	ETD	10.56	3 (K)S R\S\H/G R\H\S\D s I\A/R s/P C K s P\K(G)	S10 =n,S14 =n,S18 =n	NP_542781.2	135295
1436	EG	5	ETD	15.85	1 (E)K/G/K P K P R\s P Q P P S R Q A E P P K K\E(A)	S8 =k	NP_653205.2	124245
1437	EG	5	ETD	27.32	1 (E)D/S/K L K\G G K A P R\V A/T s S K\V\T\R A Q I\E(D)	S15 =n	NP_612451.1	115098
1438	ET	3	ETD	11.79	1 (R)A/Q I E D t L R\R(D)	T6 =n	NP_612451.1	115098
1439	EL	4	ETD	10.19	2 (K)K/R P Q/R A t s N V/F\A M/F\ D Q S Q I Q E F\K(E)	T7 =n,S8 =n	NP_291024.1	103910
1440	EL	4	ETD	9.59	2 (K)K/R P Q R A t s N\ V F A m F D Q S\Q I Q E F\K(E)	T7 =n,S8 =n	NP_291024.1	103910
1441	ELX	5	ETD	13.07	3 (K)E/R/R/R E R A D/R G/E A/E R G s G G s\s G\D E/L R\E D D E P V\K(K)	S16 =n,S19 =n,S20 =n	NP_001001520.1	84717
1442	ET	4	ETD	23.43	1 (K)G E/S/A E D K\E H E E G\R D s\E E G\P\R(C)	S15 =n	NP_001001520.1	84717
1443	ELX	4	ETD	11.94	4 (K)G R/G R G P P/s\s\s\D s E P E A E L E R E A\K(K)	S8 =n,S9 =n,S10 =n,S12 =n	NP_001001520.1	84717
1444	ET	4	ETD	12.72	4 (K)K A P/S A s\D s D s K A D s D G A\K P E P\V A m\A\R(S)	S6 =n,S8 =n,S10 =n,S14 =n	NP_001001520.1	84717
1445	EL	5	ETD	21.74	1 (K)V/E R T R\K R s E G F S m D R\K(V)	S8 =n	NP_001001520.1	84717
1446	EL	5	ETD	18.39	2 (K)V/E/R T R\K R s E G F/s m D R\K(V)	S8 =n,S12 =n	NP_001001520.1	84717
1447	ET	4	ETD	19.82	3 (R)A/D/R G E A E R G s G G s\s G D E L R E D D E P V\K(K)	S10 =n,S13 =n,S14 =n	NP_001001520.1	84717
1448	ET	5	ETD	21.98	3 (R)A/D/R G E A E R G s\G\G/s s/G\D\E/L R E D D E P V\K\K(R)	S10 =n,S13 =n,S14 =n	NP_001001520.1	84717
1449	AT	2	CID	15.36	1 (R)A R G D\s E A L D\E\E\S(-)	S5 =n	NP_001001520.1	84717
1450	ET	4	ETD	23.99	3 (R)G E/A E R/G s G/G s s G/D/E L R E D D E P V\K(K)	S7 =n,S10 =n,S11 =n	NP_001001520.1	84717
1451	ET	4	ETD	12.79	3 (R)G E A\E R G s G G/s s G D E L R E D D E P V\K\K(R)	S7 =n,S10 =n,S11 =n	NP_001001520.1	84717
1452	ET	3	ETD	18.17	1 (R)K R/s E/G/F/S M D R(K)	S3 =n	NP_001001520.1	84717
1453	ELX	5	ETD	12.85	2 (K)K R G R Y\R Q Y N S E I L E E A I/s/V V\m/s G K/M S/V S K(A)	S18 =n,S22 =n	NP_115816.1	84458
1454	CT	3	CID	21.99	1 (K)G E/A V/L/R P/G\L\D\A E P E L s P E E Q R(V)	S16 =n	NP_115726.1	84310
1455	ET	3	ETD	11.42	1 (R)D/S S/D s A D/G R A T P\S\E N L V P S S A\R(V)	S5 =n	NP_079087.2	79869
1456	AG	4	ETD	25.84	1 (E)S K/T A N K R S A/s T E K L\E(Q)	S10 =n	AAH40518.1	79649
1457	ELX	4	ETD	30.49	2 (K)E/R/S S s L/N R R\D s N L H\S S T D\K(E)	S5 =n,S11 =n	AAH40518.1	79649
1458	ET	4	ETD	18.62	1 (R)R D s N L H S/S T D K E Q A E\R(K)	S3 =n	AAH40518.1	79649

#	Exp.	CS	Number of phosphorylation sites			Sequence with fragments	Literature lookup	RefSeq#	Gene Symbol
			Mode	Score	▼				
1459	EL	5	ETD	10.12	1	(K)M D I N R R R Y/P\A H/L\A\R\S S S\R\K(Y)	S17 =n	NP_077001.1	79077
1460	CT	3	CID	13.63	3	(R)K S/P S G P V/K\S/P/P/L\S P/V/G t T P\V\K(L)	S9 =n,S13 =n,T17 =n	NP_076998.1	79074
1461	ELX	3	ETD	7.39	1	(K)K Q\K\t E D E/V L T\S K(G)	T4 =n	NP_076943.1	79002
1462	CT	3	CID	15.38	1	(R)A F/V E D s E/D/E\D\G A G/E/G/G/S/S/L/L Q\K(R)	S6 =n	NP_075384.2	65095
1463	ET	3	ETD	10.34	1	(R)A F V E/D/s E D\E D G/A G E\G G S S L L Q\K(R)	S6 =n	NP_075384.2	65095
1464	EL	4	ETD	19.02	1	(K)m/E/A/V P/D V E R K E D K P\E G\Q\s P\V\K(A)	S18 =n	NP_071349.2	63893
1465	AL	3	CID	9.37	2	(K)V/R S/G G\G s G G\S\G/G/Q V s L K(K)	S7 =n,S15 =n	NP_067051.1	58506
1466	ELX	3	ETD	7.01	1	(K)F/G F A I/G s\Q T T K\K(A)	S7 =n	NP_065090.1	57092
1467	ELX	3	ETD	22.42	1	(K)N/I G/R D T/P T s A G P N S F N\K(G)	S9 =n	NP_065090.1	57092
1468	ELX	3	ETD	18.92	2	(K)N/I G R D\t P\T/s A G P N S F N\K(G)	T6 =n,S9 =n	NP_065090.1	57092
1469	ELX	3	ETD	12.13	3	(K)N/I G/R/D t P T\T s A G P N S F N\K(G)	T6 =n,S9 =n,S14 =n	NP_065090.1	57092
1470	ELX	3	ETD	19.53	1	(K)R S A\E E E A A D L P\T K P t\K(I)	T15 =n	NP_065090.1	57092
1471	ELX	4	ETD	12.45	1	(K)R/S/A/E E E A A\D L P T K P/T\K I s\K(F)	S18 =n	NP_065090.1	57092
1472	AL	2	CID	15.72	2	(K)A/A/V L s D s E/D E E K(A)	S5 =k,S7 =k	NP_060439.1	55677
1473	CL	2	CID	13.46	2	(K)T I A s D s E/E/E/A G K(E)	S4 =k,S6 =k	NP_060439.1	55677
1474	ET	3	ETD	14.65	2	(K)T/I A s D s E/E E A G K E L S D\K(K)	S4 =k,S6 =k	NP_060439.1	55677
1475	ET	3	ETD	11.7	2	(R)K A/A/V L s D/s E/D\E E K A S A\K(K)	S6 =k,S8 =k	NP_060439.1	55677
1476	ELX	4	ETD	30.97	1	(K)Q/R K D s\A S E E E A R V G A\G\K(R)	S5 =k	NP_060286.1	55646
1477	EL	4	ETD	24.88	2	(K)Q/R K D\s A s E E E A R V G A G\K(R)	S5 =k,S7 =n	NP_060286.1	55646
1478	EL	3	ETD	11.77	1	(K)R/R H/s E/V E T D\S\K(K)	S4 =n	NP_060286.1	55646
1479	AT	4	CID	15.59	2	(R)t N T t A V G I/S K P A N/I H V K\S P/C S V/V G N S N S Q N K(I)	T1 =n,T4 =n	NP_060639.2	55196
1480	EL	4	ETD	15.32	1	(K)L/I/G V P/A D/A/E A/L S\E R S\G N T/P/N/s P R L A A E\S\K(L)	S21 =n	NP_060255.2	54908
1481	EL	3	ETD	9.88	1	(K)s R/R N L D F/Q D V\L\D\K(L)	S1 =n	NP_055121.1	51493
1482	CT	3	CID	11.76	1	(K)S E V/Q Q P V H P K/P L s/P D S R(A)	S13 =n	NP_057441.1	51474
1483	ET	3	ETD	12.64	1	(R)E/T P H\s P/G V E D\A P\I\A\K(V) (E)R A K K Y G G S V G S Q P P P V A P/E P/G P V P/s\S/P S Q E/P P T K	S5 =k	NP_057441.1	51474
1484	CG	5	CID	26.22	1	R E(Y)	S25 =n	NP_056937.2	51035
1485	AT	4	CID	19.53	1	(K)K Y G G S V G S/Q\P P P V A P/E/P G P\V P s S P S Q E P P T K(R)	S22 =n	NP_056937.2	51035
1486	AT	4	CID	23.7	1	(K)K Y G G S V G S Q P/P/P V A P/E/P G/P/V/P/s S/P S Q E/P P T K R(E)	S22 =n	NP_056937.2	51035
1487	AT	4	CID	12.67	2	(K)K y G G S V G S/Q P/P/P V A P E P/G/P V\p s S/P S Q E P P T K R(E)	Y2 =n,S22 =n	NP_056937.2	51035
1488	CL	3	CID	20.04	1	(K)Y/G G S V/G S Q P/P/P V A P E P G P V P s S/P S Q/E P P T K(R)	S21 =n	NP_056937.2	51035
1489	AT	3	CID	23.73	1	(K)Y G G S V G S Q P/P P V A P E P/G P V P S s P S Q E/P P T K R(E)	S22 =n	NP_056937.2	51035
1490	ET	4	ETD	12.85	1	(K)Y G G S/V/G S Q P P P V A P E P G P V P S S\p S Q\E P P t K\R(E)	T29 =n	NP_056937.2	51035
1491	EL	4	ETD	20.74	1	(K)N/S/E P S A R H/V D S L S\Q R\s P\K(A)	S16 =n	AAF23374.1	SEPT9
1492	EL	5	ETD	15.72	2	(K)N S E P S A R H/V D S/L/s Q R\S P K A\s\L/R/R V\E\L/S G P K(A)	S13 =n,S20 =n	AAF23374.1	SEPT9

#	Exp.	CS	Number of phosphorylation sites		Sequence with fragments	Literature lookup	RefSeq#	Gene	
			Mode	Score				▼	Symbol
1493	ET	4	ETD	12.39	1	(K)R A E V/L G H\K t/P\E P A P\R(R)	T9 =n	AAF23374.1	SEPT9
1494	AL	4	ETD	20.72	1	(K)A/N/W E\A Q Q R I L E Q\Q\N/S S\R\t L/E\K(N)	T18 =n	NP_001011553.1	SEPT7
1495	AL	4	CID	14.23	1	(K)A N W/E/A/Q/Q R/I L E/Q Q N s\S R\T L E K(N)	S15 =n	NP_001011553.1	SEPT7
1496	ET	3	ETD	19.42	1	(R)I/L/E Q Q N S\S R t L E\K(N)	T10 =n	NP_001011553.1	SEPT7
1497	CL	3	CID	22.67	1	(K)T A/A/E/L L\Q S/Q G S Q/A G/G/S/Q t L\K(R)	T18 =n	NP_055944.2	SEPT6
1498	EL	3	ETD	21.36	1	(K)T A A E/L L Q S Q G/S Q A/G G S Q t L\K(R)	T18 =n	NP_055944.2	SEPT6
1499	EL	3	ETD	24.23	1	(K)I/Y/H L P\D A E s D E D E D F\K(E)	S9 =k	NP_001008491.1	SEPT2
1500	CL	2	CID	18.85	1	(K)I Y/H L P D A\E\s D E D E D/F K(E)	S9 =k	NP_001008491.1	SEPT2
1501	ET	4	ETD	27.7	1	(K)I/Y H L P D A/E s D/E D E D F K E Q\T\R(L)	S9 =k	NP_001008491.1	SEPT2
1502	AT	4	CID	19.74	1	(K)I Y/H L P/D A\E\s D/E/D E/D F K/E/Q T R(L)	S9 =k	NP_001008491.1	SEPT2
1503	CT	4	CID	15.56	1	(R)M K R E E\G A\G A T E P E Y/y H Y\I/P P A H C K(V)	Y15 =n	NP_001002909.1	23131
1504	EL	4	ETD	7.47	1	(K)G V P H P E/D\D H S\Q\V\E\G\P E s L R(-)	S17 =n	NP_055842.1	23042
1505	AL	5	ETD	19.32	1	(K)V/S/Y I P D E/Q I A Q G P/E N G R R/G G\F G S R G Q/P R Q G\s P V A\A\G A P\A\K(Q)	S31 =k	NP_006537.3	10642
1506	CG	2	CID	23.29	1	(E)D/A Q/K/S/S s/P\A P A\D I A Q T V\Q\E(D)	S7 =k,S5 =nf,S6 =nf	NP_005745.1	10146
1507	CG	3	CID	12.56	1	(E)D A Q K s\S S P\A P A\D I A Q\T\V\Q\E(D)	S5 =k,S6 =nf,S7 =nf	NP_005745.1	10146
1508	AG	3	CID	21.69	1	(E)E T A/P E/D A Q K\S S\S/P A P A D I A Q T\V Q\E(D)	S12 =k,S10 =nf,S11 =nf	NP_005745.1	10146
1509	AG	3	CID	19.24	1	(E)T A/P E/D A Q K S\S s P A P A\D I A Q\T\V Q\E(D)	S11 =k,S9 =nf,S10 =nf	NP_005745.1	10146
1510	CT	2	CID	20.76	1	(K)S s S/P A P A/D I A Q/T/V/Q/E/D/L\R(T)	S2 =k,S1 =nf,S3 =nf	NP_005745.1	10146
1511	AT	3	CID	18.12	1	(K)S S/s P A P A D I\A/Q T V Q/E D/L\R(T)	S3 =k,S1 =nf,S2 =nf	NP_005745.1	10146
1512	ET	3	ETD	17.86	1	(K)S/s S P/A P A\D I A\Q T V Q E D L\R(T)	S2 =k,S1 =nf,S3 =nf	NP_005745.1	10146
1513	EL	4	ETD	11.81	1	(K)S S s P\A P A D I A/Q/T V\Q E D/L R T\F S\W A S V\T\S\K(N)	S3 =k,S1 =nf,S2 =nf	NP_005745.1	10146
1514	EL	5	ETD	18.54	1	(K)A/R R G R\s P/K\G\E\F\K D E E E\T V T T\K(H)	S6 =n	NP_055481.1	9685
1515	EL	4	ETD	11.25	1	(K)H I H I T Q A T E T/T t T R H\K(R)	T12 =n	NP_055481.1	9685