TiO_2-Based Phosphoproteomic Analysis of Schistosomes: Characterization of Phosphorylated Proteins in the Different Stages and Sex of *Schistosoma japonicum*

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Supplementary Table 1 List of the phosphoproteins identified in schistosomula (14 d) of *Schistosoma japonicum*

#	Protein ID	Description[1]	MW	Protein Score	Sequence Coverage	Miss cleavage	Ion score	Expect	Peptides[2]	MD score/ Phospho site probability (%)[3]	MS/MS Spectra
1	CAX69413.1	sjchgc08095 protein	36511	114	11%	0	93	4.60E-05	R.QISVsPTYYHDTSPR.N	23.8/99.47	P1
2	CAX70460.1	fragile x mental retardation 1 isoform 16	87407	110	1%	0	110	5.20E-07	R.QTNQLNHQPDSVsPTR.I	12.6/93.31	P2
3	CAX73031.1	epidermal growth factor receptor pathway substrate 8	57535	303	8%	0	159	1.40E-11	R.AGALDNDSHYHDINDsMLISR.A	69.9/100	P3
						1	92	5.90E-05	R.YVNLGDSTFGMNRsPK.I	41/99.99	P4
4	CAX73091.1	hypotheticial protein	25814	77	4%	1	77	1.00E-03	R.KESsSDLLSR.Y	12/92.31	P5
5	CAX74150.1	zinc c2h2-type domain-containing protein	106115	226	5%	0	68	8.20E-03	R.HTPHHPPPPPTsPSFFVGR.G	9.1/85.3	P6
6	CAX74794.1	proliferation-associated protein 2G4	42827	82	5%	1	83	6.20E-04	M.sDQEsDAEQDVLDDTVVNKYK.M	N/100	P7
7	CAX83069.1	tetratricopeptide repeat domain 14	103388	352	8%	1	63	3.40E-02	R.IKtPPLAPLVTSFR.R	N/100	P8
						1	90	1.00E-04	R.ESSLATGDDAVPSEsPKGDR.G	20.55/99.11	P9
						1	93	6.40E-05	R.RDHtPLsPTAPRPSAGYATHMER.S	28.7/99.87	P10
8	AAP05964.1	cysteine string protein	24000	150	7%	1	114	2.80E-07	R.KLsTSGESLFHVLR.V	9.3/88.52	P11
9	AAP06040.1	nuclear distribution gene c homolog	37878	160	7%	1	89	9.60E-05	K.VGAsLDDPDEEEEDKGK.L	N/100	P12
10	AAP06130.1	rab guanine nucleotide exchange factor 1	17450	105	7%	1	105	2.30E-06	R.ITSDFDDKLsPER.S	72/100	P13
11	AAW24704.1	sjchgc02374 protein	24307	111	7%	0	111	3.60E-07	R.AMsHFETNSIENSLPR.V	17/97.31	P14
12	AAW25147.1	troponin t	38926	126	8%	2	128	2.30E-08	M.sDDEQsPQPSPAFIPKDEEHDDGKSEAK.I	45.5/100	P15
13	AAW25812.1	eukaryotic translation initiation factor	27962	96	7%	1	97	2.00E-05	R.IESRPLHLssDEEDIKR.I	41.6/99.99	P16

		subunit C									
14	AAW26418.1	microtubule-associated protein futsch	105262	107	2%	1	77	2.50E-03	K.DNQEVHsDIDEMEKEFVIPYQR.N	N/100	P17
15	AAW26505.1	sjchgc02563 protein	35545	97	6%	1	76	1.90E-03	R.VRsVSNFELENNR.E	26.5/99.78	P18
16	AAW26588.1	sjchgc01243 protein	38311	134	8%	0	62	5.30E-02	K.NHNITDsPVMSNKPK.L	12/87.34	P19
						0	72	4.10E-03	R.HFsPVAIASSTPK.L	32/99.18	P20
17	AAW26700.1	SJCHGC01107 protein	21285	101	14%	1	101	3.80E-06	K.NTDDENANSERDsPEPLPLIPATIWTR.K	7.1/72.04	P21
18	AAW26770.1	sjchgc06242 protein	21453	82	8%	0	82	6.00E-04	R.NNPFTTMsPLLNELER.D	16/95.43	P22
19	AAW26771.1	nascent polypeptide-associated complex subunit alpha	24461	241	15%	0	112	3.40E-07	K.TVIAEEsEDDEEPDASGLSEK.D	25.7/99.73	P23
20	AAW27129.1	pyruvate kinase	61146	173	7%	0	105	2.90E-06	.MLGSGLSFGGQSFHGVSsVSR.F	11.7/90.25	P24
21	AAW27091.1	cAMP-dependent protein kinase type ii regulatory subunit	19623	91	13%	2	91	1.00E-04	R.RQsVAAESFDPEKDSDDNNEEER.Q	16/93.17	P25
22	AAW27136.1	prothymosin alpha-b	14949	273	27%	0	113	4.20E-07	R.HAEAEsEEDGTDDDASQDTK.G	26.4/99.97	P26
						2	94	3.20E-05	R.KEAGDNASDDKAHsPDSR.H	16.4/96.36	P27
23	AAW27151.1	sjchgc09494 protein	13854	80	20%	0	80	1.30E-03	K.RPIPVGsDDsDAETESNVLCNNELK.T	19.7/98.93	P28
24	AAW27231.1	B-cell receptor-associated protein-associated bap	28074	146	12%	1	67	2.40E-02	K.VNDSDtEDVYPDTVEALKDELLK.L	1.5/53.51	P29
25	P91800.1	translationally-controlled tumor protein homolog	19364	111	12%	0	112	6.00E-07	K.LIAANPSGEEGQEEVsDSTER.V	20/98.99	P30
26	AAX24429.2	sjchgc08077 protein	25746	90	20%	0	90	7.50E-05	R.SLsQGSLLAVASLAGLR.H	0/49.97	P31
27	AAX27349.2	sjchgc06768 protein	52587	348	22%	0	106	2.40E-06	K.SMDDLsDTLVDLNNLTR.H	22.4/99.42	P32
						0	70	8.70E-03	R.HRPAsVSGYLDECGLNR.S	13.9/96.1	P33
						1	133	8.70E-09	R.DIKNEHTLDDDQNIDLsPTIGNDEQIHHQSDHLIQHR.S	21.4/99.27	P34
28	AAX27846.2	tensin 3	50789	138	4%	0	138	1.70E-09	R.GGGASsMIEGLSHIDDHQHPR.A	13.6/95.75	P35

29	CPRT0000000132	cold shock domain protein A	23801	149	7%	0	81	1.80E-06	R.DNYHNEDGsPDMR.D	N/100	P36
30	CPRT0000000218	phosphatase 2A inhibitor i2pp2a	29186	70	6%	0	71	2.20E-05	K.EFHLGDsGEPSSTYTK.I	19.7/98.86	P37
31	CPRT0000000284	Transducin-like enhancer protein 4	130640	94	2%	0	88	4.10E-07	R.DAVsPQSYVIGSNK.S	28.8/99.87	P38
32	CPRT0000000366	hydrocephalus inducing protein homolog	111656	149	1%	1	149	3.60E-13	R.KVsFSDLPIVSGVEER.N	38.4/99.99	P39
33	CPRT0000000669	arginine serine-rich splicing factor	31746	291	23%	1	60	1.70E-04	R.sRsPLGAPVGR.L	N/100	P40
						1	104	1.50E-08	R.NSsYDGHRYPDHDQFSSFR.S	9.5/89.64	P41
34	CPRT0000000835	Protein DEK	45498	124	5%	1	64	1.30E-04	K.KEFDsDEDVPLSNLTSTK.V	36.3/99.98	P42
35	CPRT0000000881	troponin I	103135	49	1%	0	50	2.30E-03	K.KPVLPSKPLsPTSYPTK.I	4.7/69.82	P43
36	CPRT0000001216	centromeric protein	91005	61	3%	0	61	1.70E-04	R.EAsFEEHQIMR.D	N/100	P44
37	CPRT0000001254	peptidyl-prolyl isomerase G	117498	259	8%	0	54	1.00E-03	K.LISLPTTTHEQsPK.L	39.3/99.98	P45
38	CPRT0000001365	scaffold attachment factor B	83496	206	10%	1	94	2.10E-07	R.sRsPPIFQSVQHRPEILEYGHR.S	32/99.89	P46
39	CPRT0000001534	coatomer protein subunit beta 2	74897	124	1%	0	126	6.70E-11	R.SNsPSVDQELQFR.N	27.8/99.82	P47
40	CPRT0000001619	beta chain spectrin	77788	141	7%	0	86	8.60E-07	R.AAtLPSGVAPESQVTSSSSASGK.K	15.5/97.28	P48
41	CPRT0000001632	eukaryotic translation initiation factor 5A	17852	84	13%	1	85	1.20E-06	M.StFEDEEFATGESGASKTEPK.Q	0/50	P49
42	CPRT0000001788	regulatory factor x domain containing 2	87924	75	3%	0	70	2.10E-05	R.NLsDHAIIQSR.R	N/100	P50
43	CPRT0000001895	sjchgc06333 protein	59613	73	2%	1	74	1.20E-05	R.SKsEIINQYMNQADK.S	10.6/92.06	P51
44	CPRT0000002080	protein cGMP- type ii	108795	69	1%	1	69	3.60E-05	K.ILDLVSPTKsQDELQIK.S	15.2/97.06	P52
45	CPRT0000002121	nuclear receptor coactivator 2	50993	87	4%	0	87	8.50E-07	M.TAsPEQVDNSFQSIPESETHFR.S	0/49.98	P53
46	CPRT0000002152	CDC37 cell division cycle 37 homolog	45458	114	16%	1	65	2.10E-04	M.SCLNYSKWDHIEVsDDEDDTHPNIDTPSLFR.W	9.2/86.34	P54
47	CPRT0000002181	heterogeneous nuclear ribonucleoprotein H	53750	83	6%	0	84	2.20E-06	R.sPAYNTGGSQGSQYNNYPLHDDMHYADDIR.Y	5/64.32	P55

48	CPRT0000002239	phosphofurin acidic cluster sorting protein 1	125562	101	1%	0	102	1.60E-08	R.NIsPESTSHGTISAPR.S	42.7/99.87	P56
49	CPRT0000002347	14-3-3 family protein	25816	144	11%	2	145	1.50E-12	R.DNLNLWNPCNDGEKDTAAsPKGEEK.-	20.9/99.2	P57
50	CPRT0000002522	tubulin-specific chaperone C	79727	45	1%	0	45	5.00E-03	K.HStPPILSSK.R	10.4/91.59	P58
51	CPRT0000002551	Importin alpha-2 subunit	17579	56	6%	1	47	3.40E-03	R.RTDQsIELR.K	18.9/98.73	P59
52	CPRT0000002705	hypotherical protein	27929	85	8%	1	85	1.50E-06	K.DKPDAESDLFAsDsEDDKEAER.I	16.9/97.71	P60
53	CPRT0000002762	arginine serine-rich splicing factor	24795	46	10%	1	36	4.00E-02	R.RHsPPGYER.N	N/100	P61
54	CPRT0000002896	ubiquitin specific peptidase 7	97653	47	5%	1	42	1.10E-02	K.QGKLsPNTPK.M	9.6/95.15	P62
55	CPRT0000002916	phosphate cytidylyltransferase ethanolamine	47612	48	2%	1	48	2.70E-03	R.RTQsLDSVLK.N	5.6/62.34	P63
56	CPRT0000003012	eukaryotic translation initiation factor 3 subunit 10	75064	44	2%	1	45	9.10E-03	R.DRNPHTVsFDNTPSYR.N	9.9/89.9	P64
57	CPRT0000003210	hypothetical protein	39314	178	19%	2	127	9.30E-11	K.RLsIDTTGEDEPDKENNANLSLPNVR.S	12/93.88	P65
58	CPRT0000003479	RAS-gap sh3 binding protein related	40758	89	4%	0	90	3.10E-07	M.VSVVENNPsPDSAFTVVR.M	19.7/98.9	P66
59	CPRT0000003518	disulfide-isomerase precursor	26123	66	7%	2	92	7.40E-05	R.SLPDKWQHDMFQDARsPK.G	80.2/100	P67
60	CPRT0000003603	sjchgc09241 protein	39546	445	21%	1	34	6.20E-02	K.AADTsVVKR.D	9.5/89.91	P68
						0	150	3.70E-13	K.EFtPPPDGVAVGILESNPKPR.A	135.1/100	P69
						1	114	1.10E-09	K.KSsFIDESITVAPEATR.S	9.9/90.69	P70
61	CPRT0000003639	myelin expression factor 2	60032	93	2%	1	94	1.10E-07	R.SIKYEDSEsPDIPSR.G	11.4/93.07	P71
62	CPRT0000003713	glycyl-tRNA synthetase	117527	102	4%	1	105	1.90E-08	K.ATSESHLsADEVNVEVLHDKAESSTLS NNPK.H	2.1/42.6	P72
63	CPRT0000003765	RNA-binding protein	74909	48	1%	1	49	2.80E-03	R.sVDKYDHHGSR.Q	37.4/99.97	P73
64	CPRT0000003898	sjchgc07201 protein	53500	78	2%	0	79	2.10E-06	R.GSHsPISLTER.F	26.2/99.76	P74
65	CPRT0000003916	GPI-anchored membrane protein 1	56776	110	7%	0	92	2.00E-07	R.SSsPLSSGNINQTISLK.S	3.3/52.12	P75
66	CPRT0000004133	vacuolar protein sorting-associated protein	383946	116	2%	1	117	4.20E-10	R.KTsLTTVADELR.S	15/96.92	P76

67	CPRT0000004202	heat shock protein 90	82188	323	3%	2	164	1.70E-14	K.EVsDDEAEKEETKNESEEAEDKPK.V	100.6/100	P77
68	CPRT0000004242	protein phosphatase	76968	50	5%	0	53	1.40E-03	R.VTsLVNLNSPSDTLLR.G	3.5/69.07	P78
69	CPRT0000004561	fragile x mental retardation 1	69914	95	3%	1	96	1.10E-07	R.RGsEDsDIVEPNNIPDGTPGDR.A	37.4/99.98	P79
70	CPRT0000004658	guanine monphosphate synthetase	58090	103	3%	0	104	1.20E-08	R.QSNLsGGGMHPHIESR.N	34.6/99.97	P80
71	CPRT0000004688	ankyrin 23 unc44	264545	45	0%	0	47	5.30E-03	R.SLNGISSTsPNLNISR.E	9.6/89.64	P81
72	CPRT0000004690	mucoidy inhibitor A	69128	133	3%	0	70	2.30E-05	R.GGsIENTYATGLR.A	40/100	P82
73	CPRT0000004960	sh3 domain-binding glutamic acid-rich-like protein	38619	80	3%	1	82	1.20E-06	R.KTsDQPVESIR.K	10.4/91.54	P83
74	CPRT0000004986	sjchgc02101 protein	30544	113	4%	1	114	9.70E-10	R.RSsNTNSEESPVTR.R	19.2/98.74	P84
75	CPRT0000005000	alpha fucosyltransferase	218756	60	1%	1	57	3.80E-04	R.IAISRLsPTAGR.S	3.1/62.13	P85
76	CPRT0000005165	myosin heavy chain	204958	349	6%	0	67	4.40E-05	R.GVsVAPGAAPGHGNR.A	N/100	P86
						1	55	6.80E-04	R.ARKPTAsLAPEEE.-	9.2/92.37	P87
77	CPRT0000005313	thymidylate kinase	25311	211	7%	1	84	1.00E-06	R.DSsGGNKFETMDFQK.R	13.7/95.87	P88
78	CPRT0000005334	Conserved hypothetical protein	53707	86	8%	0	86	7.00E-07	K.MQTGKPASSVHFsPTR.V	0/49.98	P89
79	CPRT0000005336	protein cAMP dependent type isoform cra_a	53108	37	5%	0	37	3.90E-02	R.GLMAAsPSGVNLTR.R	20.6/99.1	P90
80	CPRT0000005420	pleckstrin homology domain family c member 1 isoform 2	77049	88	2%	0	83	1.10E-06	R.DIsPIGGYLHTGR.Y	71/100	P91
81	CPRT0000005690	sjchgc00797 protein	18016	131	20%	0	99	4.20E-08	K.QVPVYNALsPSPGPLNFER.Y	19/98.75	P92
82	CPRT0000005681	coatomer subunit beta	120852	74	1%	0	75	6.80E-06	R.SHsPVNTLLNSH.-	24/97.34	P93
83	CPRT0000005797	calnexin	65986	145	9%	0	66	9.20E-05	R.DNsEEEAPNEFEGNENVPAAK.Q	N/100	P94
84	CPRT0000006118	p38 MAPK	29378	291	9%	2	147	7.50E-13	K.SKsPGPPPTEEVASSISAPLKKPR.L	13.6/95.80	P95
85	CPRT0000006130	Phosphofructokinase	86159	75	1%	1	77	4.30E-06	R.RGtELLPGMEGK.Y	N/100	P96
86	CPRT0000006131	uncoordinated family member (unc-44)	233254	109	1%	2	111	3.50E-09	R.KRsDPVNLGLSEPFSTSLVATTTLMSG MNDFISK.S	53/100	P97

87	CPRT0000006221	RNA-binding protein 4	26526	133		1	135	1.50E-11	R.YGPAWDDGYGGPYAPPPRNsPR.G	N/100	P98
88	CPRT0000006463	tat-binding protein 10	48646	39	9%	2	36	5.90E-02	M.AALEVESYPRRsPK.Y	12.7/94.87	P99
89	CPRT0000006620	upstream activation factor subunit uaf30	25101	51	5%	1	52	1.40E-03	R.NKAsDDEDYAR.S	N/100	P100
90	CPRT0000006676	dentin sialophosphoprotein precursor	85411	247	8%	0	55	6.90E-04	K.GIAsPGNYGDAR.R	45.5/100	P101
						0	53	1.10E-03	R.MHsIsPPYNDR.S	29.9/99.89	P102
						1	75	1.20E-05	K.NTHsPANNTESLREPPHTR.S	11.5/93.22	P103
91	CPRT0000006702	sjchgc01166 protein	39554	56		1	59	2.20E-04	R.RQsLQNLLR.L	N/100	P104
92	CPRT0000007051	plasminogen activator inhibitor 1 rna-binding protein	45889	93	5%	1	93	2.20E-07	R.VSRsPNANEPPPVVFEDVQITSAK.E	16.5/97.82	P105
93	CPRT0000007240	programmed cell death-involved	58881	80	7%	0	66	4.80E-05	R.FIsETDSVYR.T	17.8/98.36	P106
94	CPRT0000007300	Expressed protein	50510	107	6%	0	104	9.40E-09	R.SSsPSEDIELIMDR.A	13.5/94.47	P107
95	CPRT0000007395	secretory carrier membrane protein 2	26211	69	15%	1	68	7.50E-05	.MENPFADPVARLtPTQSHDNSQVSR.V	9.1/85.67	P108
96	CPRT0000007659	placenta-specific gene 8 protein	13424	89	11%	1	91	2.20E-07	.MEsPTTKQPYAVR.Q	22/99.05	P109
97	CPRT0000007759	sjchgc05800 protein	66670	275	14%	1	65	6.80E-05	R.RTsELSTDLANLK.L	14.9/96.86	P110
						0	56	6.90E-04	K.HLSDDVHFtPFDR.K	67/100	P111
						0	79	3.60E-06	R.QSVNIsPTSDLHSQGK.F	9.7/86.09	P112
98	CPRT0000007860	glycogen synthase kinase 3	56751	58	2%	0	59	3.60E-04	K.EMVPGTANVSyISSR.Y	9.8/89.44	P113
99	CPRT0000008142	zinc finger protein	31916	142	4%	2	82	2.00E-06	R.ERRDsDDEFDEFGR.K	N/100	P114
100	CPRT0000008289	ubx domain containing 2	48307	55	8%	0	56	6.60E-04	R.LSHMPDNsDDEQAR.W	19/95.60	P115
101	CPRT0000008409	af287985_1synapsin isoform	36298	55	4%	2	56	7.10E-04	R.RFsSGDLQGELADKR.M	9.4/82.80	P116
102	CPRT0000008586	beta thymosin	8688	41	16%	0	41	1.90E-02	K.QLLQEIEtPPSLK.H	21.7/99.33	P117
103	CPRT0000008913	major egg antigen	39370	142	13%	1	109	5.20E-09	K.NSGSESSVPLSESTISGsHRR.L	1/55.81	P118
104	CPRT0000008924	transcription elongation regulator 1	37650	108	9%	1	42	1.10E-02	R.KLDDSPtVR.E	9.6/88.95	P119
105	CPRT0000008950	U2 small nuclear rna auxiliary factor 2	34484	105	7%	1	80	2.00E-06	R.KLSsPQGGVDDR.N	11.8/93.74	P120

106	CPRT0000009359	sjchgc04698 protein	55791	89	4%	0	47	8.00E-03	K.IAEEISPTEVFGEGAsEGETVVK.K	37.1/99.98	P121
107	CPRT0000009445	heterochromatin protein 1	51650	140	3%	1	100	2.90E-08	K.NSREsEEsGGEDEFQVEK.I	25/99.67	P122
108	CPRT0000009921	sjchgc09590 protein	180556	417	7%	1	183	2.30E-16	K.QEALLAEQVDDIPKEHLFVEsDEER.Y	N/100	P123
						1	41	4.80E-02	K.VIKENNMLAEEsDEQsNNELECELK.Q	N/100	P124
109	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	23045	234	20%	0	90	3.20E-07	K.ANEsDEDEDEEPMPMPPQR.V	38/99.98	P125
						1	140	6.30E-12	K.AASENRPNKANEsDEDEDEEPMPMPPQR.V	15.8/97.48	P126
110	CPRT0000012199	importin 7	116719	117	1%	0	118	4.00E-10	K.ALGsDEDEVDEESVR.Y	80/100	P127

1, Protein IDs were obtained from NCBInr or LSBI-Sjr ((http://lifecenter.sgst.cn/schistosoma/).

2, The underlined phosphopeptides were also identified in our previous study by using an IMAC-based phosphoproteomic method. For a phosphopeptide with MD score < 9, the second ranked phosphosite was framed in a phosphopeptide.

3, “N/100” in the column of “MD score/ Phospho site probability (%)” indicated 100% probability of a phosphosite identified in a phosphopeptide.

Supplementary Table 2 List of the phosphoproteins identified in adult female schistosomes (35d) of *Schistosoma japonicum*

#	Protein ID[1]	Description	MW	Protein score	Sequence coverage	Miss cleavage	Ion score	Expect	Peptides[2]	MD score/ Phospho site probability (%)[3]	MS/MS Spectra
1	CAX70460.1	fragile x mental retardation 1 isoform 16	87407	80	1%	0	80	1.90E-04	R.QTNQLNHQPDSVsPTR.I	11/90.31	P1
2	CAX73244.1 /CPRT0000004561	fragile x mental retardation 1	85594	72	2%	1	74	4.70E-03	R.RGsEDsDIVEPNNIPDGTPGDR.A	25.4/90.98	P2
3	AAX25971.2	epidermal growth factor receptor pathway substrate 8	30090	104	6%	1	106	2.20E-06	R.YVNLGDSTFGMNRsPK.I	51.1/100	P3
4	CAX73605.1	cAMP-dependent protein kinase R2	40108	73	6%	1	73	7.70E-04	R.RHsVAAESFNPATVNDLEPVVHPK.S	18.4/96.26	P4
5	CAX74259.1	cell division cycle and apoptosis regulator protein 1	125508	209	5%	1	86	2.50E-04	K.ALQLVTIDKsPQVPEEQVKPVNAESGSK.L	20/94.89	P5
						0	66	2.20E-02	K.IANtPEAEDGFESMGPK.N	40/100	P6
6	CAX83069.1	tetratricopeptide repeat domain 14	103388	215	10%	1	58	1.00E-01	R.IKtPPLAPLVTSFR.R	N/100	P7
7	AAP05964.1	cysteine string protein	24000	126	6%	1	126	1.90E-08	R.KLsTSGESLFHVLR.V	17.5/97.39	P8
8	AAP06040.1	nuclear distribution gene C homolog	37878	103	5%	1	103	1.00E-06	K.VGAsLDDPDEEEEDKGK.L	N/100	P9
9	AAP06130.1	rab guanine nucleotide exchange factor 1	17450	86	7%	1	86	1.80E-04	R.ITSDFDDKLsPER.S	50/100	P10
10	AAP06472.1	pyruvate kinase 3	29794	89	7%	0	91	8.30E-05	.MLGSGLSFGGQSFHGVSsVSR.F	9/88.18	P11
11	AAW24532.1	sorting nexin-6	47576	69	3%	1	69	2.40E-03	K.SIPMPDIKsPTTR.Q	11/89.82	P12
12	AAW27136.1	prothymosin alpha-b	14949	167	12%	1	112	1.20E-06	K.EAGDNASDDKAHsPDSR.H	22.4/99.36	P13
				99	14%	0	99	9.00E-06	R.HAEAEsEEDGtDDDASQDTK.G	49.7/100	P14
13	AAW27231.1	B-cell receptor-associated protein-associated bap	28074	200	9%	1	201	2.00E-15	K.VNDsDTEDVYPDTVEALKDELLK.L	9/87.82	P15
14	AAW27390.1	transcription elongation regulator 1	52564	68	2%	1	68	1.70E-02	R.KLDDSPtVR.E	11.6/94	P16
15	AAX26240.2	splicing factor u2af 65 kda subunit	28128	80	5%	0	82	5.30E-04	R.LVVTSFFsPNSYHR.R	35.3/95.96	P17
16	AAX27349.2	sjchgc06768 protein	52587	149	10%	0	90	2.00E-05	K.SMDDLsDTLVDLNNLTR.H	15/93.24	P18

17	AAX30518.2	major vault protein	12169	81	11%	2	81	6.10E-04	R.KRTsDAIDNIDTK.-	9.6/90.2	P19
18	CPRT0000000132	cold shock domain protein A	23801	82	7%	0	82	1.50E-06	R.DNYHNEDGsPDMR.D	43.9/100	P20
19	CPRT0000000345	alkaline phosphatase	204906	112	0%	0	112	1.70E-09	R.LTTDsGSAATAFLSGAK.G	27/99.63	P21
20	CPRT0000000366	Hydrocephalus-inducing protein homolog	111656	85	2%	1	85	8.00E-07	R.KVsFSDLPIVSGVEER.N	27.8/96.35	P22
21	CPRT0000000669	splicing arginine serine-rich 7	31746	237	26%	1	92	2.60E-07	R.NsSYDGHRYPDHDQFSSFR.S	9.1/89.7	P23
22	CPRT0000000687	ferritin-1 heavy chain	11618	63	19%	1	64	1.40E-04	R.VGTGLGEYTFDKETLHGEsD.-	20.7/99.15	P24
23	CPRT0000000835	Protein DEK	45498	58	4%	0	59	4.10E-04	K.EFDsDEDVPLSNLTSTK.V	52.4/100	P25
24	CPRT0000001007	dynein cytoplasmic 1 intermediate chain 2	68240	108	2%	0	108	5.40E-09	R.ELEsPSHDVNDSILQR.N	27.4/98.99	P26
25	CPRT0000001178	p30 dbc protein	100463	48	1%	0	49	3.30E-03	R.NDsQNGYNDEQDDVK.I	25.7/99.73	P27
26	CPRT0000001254	peptidyl-prolyl isomerase G	117498	295	6%	0	64	1.00E-04	K.LISLPTTTHEQsPK.L	41/99.99	P28
						1	70	2.50E-05	K.YQSKsPILMIsPK.L	21.3/99.18	P29
						0	62	0.00013	K.SQVsPQLHLR.I	16/97.53	P30
27	CPRT0000001534	Coatomer subunit beta	74897	105	1%	0	106	6.00E-09	R.SNsPSVDQELQFR.N	32.9/99.93	P31
28	CPRT0000001619	beta chain spectrin	77788	114	4%	0	61	3.00E-04	R.AAtLPSGVAPESQVTSSSSASGK.K	20/98.82	P32
29	CPRT0000001632	eukaryotic translation initiation factor 5A	17852	75	13%	1	76	9.10E-06	M.StFEDEEFATGESGASKTEPK.Q	0/50	P33
30	CPRT0000001788	regulatory factor x domain containing 2	87924	67	1%	0	68	2.90E-05	R.NLsDHAIIQSR.R	N/100	P34
31	CPRT0000002152	cdc37 cell division cycle 37 homolog	45458	149	0.16	0	151	4.1E-13	K.WDHIEVsDDEDDTHPNIDTPSLFR.W	17/92.34	P35
32	CPRT0000002181	heterogeneous nuclear ribonucleoprotein H	53750	97	6%	0	98	9.80E-08	R.sPAYNTGGSQGSQYNNYPLHDDMHYAD DIR.Y	5.5/70.84	P36
33	CPRT0000002347	14-3-3 family protein	25816	126	11%	2	127	1.00E-10	R.DNLNLWNPCNDGEKDTAAsPKGEEK.-	18.7/95.78	P37
34	CPRT0000002428	glyceraldehyde 3-phosphate dehydrogenase	36566	86	7%	0	86	1.20E-06	K.VINDNFEIVEGLMTTVHSFTAtQK.T	15/97.54	P38
35	CPRT0000002551	importin alpha-related	17579	46	6%	1	46	4.50E-03	R.RTDQsIELR.K	17/96.21	P39
36	CPRT0000002705	hypotherical protein	27929	110	8%	1	110	4.20E-09	K.DKPDAESDLFAsDsEDDKEAER.I	54/100	P40
37	CPRT0000002762	arginine serine-rich splicing factor	24795	101	16%	1	36	3.90E-02	R.RHsPPGYER.N	N/100	P41
38	CPRT0000002916	phosphate cytidylyltransferase	47612	42	2%	1	42	1.00E-02	R.RTQsLDSVLK.N	2/59.99	P42

		ethanolamine									
39	CPRT0000003234	RNA binding motif protein 39	50448	53	2%	1	53	1.20E-03	R.QKsPELSPEER.D	36.3/99.98	P43
40	CPRT0000003518	disulfide-isomerase precursor	26123	59	7%	2	89	3.90E-04	R.SLPDKWQHDMFQDARsPK.G	76.3/100	P44
41	CPRT0000003916	GPI-anchored membrane protein 1	56776	92	3%	0	94	1.10E-07	R.SSsPLSSGNINQTISLK.S	8/86.13	P45
42	CPRT0000004133	vacuolar protein sorting-associated protein	383946	101	1%	1	99	2.40E-08	R.KTsLTTVADELR.S	14/94.21	P46
43	CPRT0000004202	heat shock protein 90	82188	556	10%	3	176	1.30E-15	R.TKEVsDDEAEKEETKNESEEAEDKPK.V	40/99.97	P47
44	CPRT0000004798	eukaryotic translation initiation factor subunit D	47998	140	6%	1	143	2.90E-12	K.TYSFPEENPFKDDEDEDsDNPNPSHNR.N	62.2/100	P48
45	CPRT0000005165	myosin heavy chain	204958	505	9%	1	38	3.60E-02	R.ARKPTAsLAPEEE.-	9/89.14	P49
						0	46	5.10E-03	R.GVsVAPGAAPGHGNR.A	N/100	P50
46	CPRT0000005313	thymidylate kinase	25311	123	7%	1	85	9.70E-07	R.DSsGGNKFETMDFQK.R	12.3/94.46	P51
47	CPRT0000005420	pleckstrin homology domain family c member 1 isoform 2	77049	71	1%	0	72	1.30E-05	R.DIsPIGGYLHTGR.Y	61/100	P52
48	CPRT0000005681	coatomer protein subunit beta 1	120852	66	2%	0	66	4.90E-05	R.SHsPVNTLLNSH.-	19/92.31	P53
49	CPRT0000005718	solute carrier family 6 member 5	86218	71	1%	1	73	1.70E-05	R.TEFISMIKsNEsLHR.S	38/99.98	P54
50	CPRT0000005797	calnexin	65986	131	7%	0	53	2.10E-03	R.DNsEEEAPNEFEGNENVPAAK.Q	N/100	P55
51	CPRT0000006130	Phosphofructokinase	86159	59	1%	1	61	1.60E-04	R.RGtELLPGMEGK.Y	N/100	P56
52	CPRT0000006218	Myosin-7	88487	51	2%	1	54	1.50E-03	K.RLEEAAIAtPPKPIIPQSDPSDR.N	41.6/99.99	P57
53	CPRT0000006221	RNA-binding protein 4	26526	113	9%	1	115	1.50E-09	R.YGPAWDDGYGGPYAPPPRNsPR.G	N/100	P58
54	CPRT0000006676	dentin sialophosphoprotein precursor	85411	56	1%	0	57	3.70E-04	K.GIAsPGNYGDAR.R	49.5/100	P59
55	CPRT0000006702	sjchgc01166 protein	39554	58	2%	1	59	2.20E-04	R.RQsLQNLLR.L	N/100	P60
56	CPRT0000007051	plasminogen activator inhibitor 1 RNA-binding protein	45889	92	5%	1	92	2.60E-07	R.VSRsPNANEPPPVVFEDVQITSAK.E	19/98.65	P61
57	CPRT0000007069	translationally-controlled tumor protein homolog	23826	88	10%	0	90	4.10E-07	K.LIAANPSGEEGQEEVsDSTER.V	17/95.99	P62

58	CPRT0000007295	sjchgc05354 protein	25195	44	14%	1	45	4.90E-03	R.RYsFSTQR.N	16/94.12	P63
59	CPRT0000007659	placenta-specific protein 8 protein	13424	46	11%	1	47	4.70E-03	MEsPTTKQPYAVR.Q	17.8/98.23	P64
60	CPRT0000007759	sjchgc05800 protein	66670	243	16%	0	89	3.30E-07	R.QSVNIsPTSDLHSQGK.F	9.7/86.09	P65
						1	77	4.60E-06	R.RTsELSTDLANLK.L	10.7/84.82	P66
61	CPRT0000007860	glycogen synthase kinase 3	56751	67	2%	0	68	4.20E-05	K.EMVPGTANVSyISSR.Y	N/100	P67
62	CPRT0000008142	zinc finger protein	31916	143	4%	2	78	4.10E-06	R.ERRDsDDEFDEFGR.K	N/100	P68
63	CPRT0000008289	ubx domain-containing protein 4	48307	65	3%	0	67	5.50E-05	R.LSHMPDNsDDEQAR.W	22.9/99.49	P69
64	CPRT0000008664	lamin b2	38122	38	3%	0	38	2.70E-02	R.SEAsPTSFSR.S	19.1/97.4	P70
65	CPRT0000009445	heterochromatin protein 1	51650	166	6%	1	103	1.80E-08	K.NSREsEEsGGEDEFQVEK.I	24.7/99.66	P71
66	CPRT0000009893	ATP-binding sub-family c member 2	127765	62	1%	1	62	1.40E-04	K.KLsLETPDSFSR.F	19.4/98.85	P72
67	CPRT0000009921	sjchgc09590 protein	180556	269	2%	1	201	3.50E-18	K.QEALLAEQVDDIPKEHLFVEsDEER.Y	N/100	P73
68	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	23045	197	13%	1	104	2.40E-08	K.AASENRPNKANEsDEDEDEEPMPMPPQR.V	12/92.78	P74
69	CPRT0000012199	importin 7	116719	131	4%	0	127	5.60E-11	K.ALGsDEDEVDEESVR.Y	89.8/100	P75

1, Protein IDs were obtained from NCBInr or LSBI-Sjr ((http://lifecenter.sgst.cn/schistosoma/).

2, The underlined phosphopeptides were also identified in our previous study by using an IMAC-based phosphoproteomic method. For a phosphopeptide with MD score < 9, the second ranked phosphosite was framed in a phosphopeptide.

3, “N/100” in the column of “MD score/ Phospho site probability (%)” indicated 100% probability of a phosphosite identified in a phosphopeptide.

Supplementary Table 3 List of the phosphoproteins identified in adult male schistosomes (35d) of *Schistosoma japonicum*

#	Protein ID[1]	Description	MW	Protein score	Sequence coverage	Miss cleavage	Ion score	Expect	Peptides[2]	MD score/ Phospho site probability (%)[3]	MS/MS Spectra
1	CAX73031.1	epidermal growth factor receptor pathway substrate 8	57535	163	12%	1	90	5.30E-05	R.YVNLGDSTFGMNRsPK.I	18.3/97.09	P1
2	CAX73091.1	hypotheticial protein	25814	78	4%	1	78	8.10E-04	R.KEsSSDLLSR.Y	16/97.54	P2
3	CAX73605.1	cAMP-dependent protein kinase r2	40108	72	6%	1	73	5.20E-03	R.RHsVAAESFNPATVNDLEPVVHPK.S	21.3/99.26	P3
4	CAX74259.1	cell division cycle and apoptosis regulator protein 1	125508	168	5%	0	90	7.90E-05	K.IANtPEAEDGFESMGPK.N	46.3/100	P4
5	CAX75242.1	fragile x mental retardation 1 isoform 16	87421	149	5%	0	94	3.40E-05	R.QTNQLNHQPDSVsPTR.I	14/96.13	P5
6	CAX83069.1	tetratricopeptide repeat domain 14	103388	145	5%	1	64	2.50E-02	R.IKtPPLAPLVTSFR.R	N/100	P6
7	AAP05964.1	cysteine string protein	24000	115	6%	1	115	2.30E-07	R.KLsISGESLFHVLR.V	0/49.19	P7
8	AAP06040.1	nuclear distribution gene C homolog	37878	114	5%	1	114	2.10E-07	K.VGAsLDDPDEEEEDKGK.L	N/100	P8
9	AAP06500.1	hypothetical protein	47262	211	10%	2	140	1.30E-09	K.RLsIDTTGEDEPDKENNANLSLPNVR.S	12.9/94.37	P9
10	AAW24532.1	sorting nexin 6	47576	67	3%	1	67	8.20E-03	K.SIPMPDIKsPTTR.Q	10.6/87.16	P10
11	AAW24704.1	sjchgc02374 protein	24307	150	13%	0	110	9.20E-07	R.AMsHFETNSIENSLPR.V	22.1/99.39	P11
12	AAW25147.1	troponin T	38926	128	8%	2	113	6.80E-07	M.sDDEQsPQPSPAFIPKDEEHDDGKSEAK.I	9.1/86.41	P12
13	AAW26183.1	troponin I	26129	114	11%	1	72	4.40E-03	K.YALEEKDEVANtPK.-	N/100	P13
14	AAW26298.1	adducin related protein	20407	101	9%	1	101	7.10E-06	R.SDTsGAEASHDDTEKETR.K	0/48	P14
15	AAW26505.1	sjchgc02563 protein	35545	146	6%	1	65	2.40E-02	R.VRsVSNFELENNR.E	N/100	P15
16	AAW26588.1	sjchgc01243 protein	38311	219	13%	0	91	5.60E-05	K.NHNITDsPVMSNKPK.L	16/95.72	P16
						0	78	9.40E-04	R.HFsPVAIASSTPK.L	55.3/100	P17
17	AAW26770.1	sjchgc06242 protein	21453	107	8%	0	107	1.90E-06	R.NNPFTTMsPLLNELER.D	21.3/99.21	P18
18	AAW27091.1	cAMP-dependent protein kinase type ii regulatory subunit	19623	90	13%	2	90	1.40E-04	R.RQsVAAESFDPEKDSDDNNEEER.Q	21.4/99.28	P19

19	AAW27136.1	prothymosin alpha-B	14949	80	12%	2	80	7.60E-04	R.KEAGDNASDDKAHsPDSR.H	9.8/88.14	P20
20	AAW27228.1	sjchgc02220 protein	45497	101	10%	0	92	6.00E-05	R.VNVYNSDNTSTIYsPQR.K	35.6/99.97	P21
21	AAW27231.1	B-cell receptor-associated protein-associated bap	28074	85	9%	1	87	2.30E-04	K.VNDSDtEDVYPDTVEALKDELLK.L	0/50	P22
22	AAX25934.2	endothelin-converting enzyme 1	26673	97	6%	0	97	1.50E-05	K.SDsPTNSLNLGQNFK.Y	12.9/95.04	P23
23	AAX27349.2	sjchgc06768 protein	52587	320	23%	0	82	2.90E-04	K.SMDDLsDTLVDLNNLTR.H	11.9/90.77	P24
24	AAX27369.2	ferm domain containing 3	35115	70	6%	0	71	7.40E-03	K.IYLPISTGATGNSsPSTNVK.E	1.5/56.15	P25
25	AAX30518.2	major vault protein	12169	71	11%	2	71	5.80E-03	R.KRTsDAIDNIDTK.-	9.1/89.55	P26
26	CPRT0000000132	cold shock domain protein A	23801	78	5%	0	79	2.60E-06	R.DNYHNEDGsPDMR.D	13.8/96.02	P27
27	CPRT0000000345	alkaline phosphatase	204906	51	0%	0	51	1.90E-03	R.LTTDsGSAATAFLSGAK.G	15/84.78	P28
28	CPRT0000000366	Hydrocephalus-inducing protein homolog	111656	110	1%	1	110	2.70E-09	R.KVsFSDLPIVSGVEER.N	30/98.34	P29
29	CPRT0000000412	filamin	146136	44	0%	1	44	9.90E-03	R.KMsQPQRPACDPK.Q	N/100	P30
30	CPRT0000000616	talin 2	316513	191	2%	1	133	2.40E-11	R.KQTDLTQAAVEFNQATGDLLSSYsPGTFR.R	9.2/89.32	P31
						0	56	7.80E-04	R.AGsRPEMHNAENFTPLR.E	51.8/100	P32
31	CPRT0000000669	arginine serine-rich splicing factor	31746	253	18%	1	61	1.60E-04	R.sRsPLGAPVGR.L	N/100	P33
						1	99	5.20E-08	R.NSsYDGHRYPDHDQFSSFR.S	9/89.56	P34
32	CPRT0000001007	dynein cytoplasmic 1 intermediate chain 2	68240	62	2%	0	62	2.00E-04	R.ELEsPSHDVNDSILQR.N	35/99.99	P35
33	CPRT0000001123	lethal giant larvae homolog 1	150057	90	1%	1	90	3.30E-07	R.SLRPDtPKLEEQVEPSLPVPPAPR.I	13.3/95.54	P36
34	CPRT0000001254	peptidyl-prolyl isomerase G	117498	234	9%	0	62	1.70E-04	K.LISLPTTTHEQsPK.L	39/99.54	P37
						0	61	1.70E-04	R.GTsPSKPIIVITK.K	9/94.35	P38
						0	59	2.50E-04	K.SQVsPQLHLR.I	12.4/94.52	P39
						1	41	2.10E-02	K.YQSKsPILMIsPK.L	14/95.67	P40
35	CPRT0000001365	scaffold attachment factor B	83496	88	4%	1	85	1.60E-06	R.sRsPPIFQSVQHRPEILEYGHR.S	23.9/99.58	P41
36	CPRT0000001534	coatomer protein subunit beta 2	74897	86	5%	0	88	4.20E-07	R.SNsPSVDQELQFR.N	24/98.76	P42
37	CPRT0000001632	eukaryotic translation initiation factor 5A	17852	50	13%	1	51	2.90E-03	M.StFEDEEFATGESGASKTEPK.Q	0/50	P43

38	CPRT0000002152	CDC37 cell division cycle 37-like	45458	127	6%	0	129	6.80E-11	K.WDHIEVsDDEDDTHPNIDTPSLFR.W	14/89.67	P44
39	CPRT0000002185	eukaryotic translation initiation factor 4E binding protein 2	13182	57	20%	2	57	9.70E-04	R.NsPAARSPPPDMIFLPEKAPNSDDK.T	3.2/67.38	P45
40	CPRT0000002239	phosphofurin acidic cluster sorting protein 1	125562	116	1%	0	116	5.40E-10	R.NIsPESTSHGTISAPR.S	52.8/100	P46
41	CPRT0000002347	14-3-3 family protein	25816	108	11%	2	110	5.40E-09	R.DNLNLWNPCNDGEKDTAAsPKGEEK.-	14/90.21	P47
42	CPRT0000002428	glyceraldehyde 3-phosphate dehydrogenase	36566	79	7%	0	79	5.80E-06	K.VINDNFEIVEGLMTTVHSFTAtQK.T	12.5/94.67	P48
43	CPRT0000002762	arginine serine-rich splicing factor	24795	41	21%	1	34	7.70E-02	R.RHsPPGYER.N	N/100	P49
44	CPRT0000002916	phosphate cytidylyltransferase ethanolamine	47612	49	4%	1	45	5.80E-03	R.RTQsLDSVLK.N	4.5/64.49	P50
45	CPRT0000003382	tensin 3	91281	82	3%	0	83	1.50E-06	R.GVQDLDSHVGsLTTLAR.G	27.8/99.71	P51
46	CPRT0000003603	sjchgc09241 protein	39546	303	15%	1	117	5.30E-10	K.KSsFIDESITVAPEATR.S	9/87.34	P52
47	CPRT0000003866	solute carrier family sodium bicarbonate cotransporter- member 10	152092	74	4%	0	72	1.70E-05	R.ITINPPSNQGsPETSR.R	25.6/99.55	P53
48	CPRT0000003998	cytosolic purine 5-nucleotidase	56064	166	10%	0	91	2.80E-07	R.APAMLMPHESTVSHGDsPK.D	29.9/99.9	P54
49	CPRT0000004133	vacuolar protein sorting-associated protein	383946	96	1%	1	97	4.10E-08	R.KTsLTTVADELR.S	13/92.92	P55
50	CPRT0000004177	tensin 4	37269	58	4%	0	59	3.50E-04	R.QNsQYEATPLVANR.S	36.2/99.97	P56
51	CPRT0000004202	heat shock protein hsp 90-alpha	82188	329	6%	2	142	3.20E-12	K.EVsDDEAEKEETKNESEEAEDKPK.V	30.6/99.91	P57
52	CPRT0000004798	eukaryotic translation initiation factor subunit D	47998	87	6%	1	89	6.60E-07	K.TYSFPEENPFKDDEDEDsDNPNPSHNR.N	41/100	P58
53	CPRT0000004561	fragile x mental retardation 1	69914	65	5%	1	65	1.40E-04	R.RGsEDsDIVEPNNIPDGTPGDR.A	16/85.12	P59
54	CPRT0000004986	sjchgc02101 protein	30544	102	4%	1	103	1.30E-08	R.RSsNTNSEESPVTR.R	17/96.47	P60
55	CPRT0000004960	sh3 domain-binding glutamic acid-rich-like protein	38619	52	7%	1	52	1.10E-03	R.KtSDQPVESIR.K	8.3/89.14	P61
56	CPRT0000005000	alpha fucosyltransferase	218756	64	3%	1	56	4.40E-04	R.IAISRLsPTAGR.S	3.2/65.43	P62

57	CPRT0000005165	myosin heavy chain	204958	1404	19%	1	55	6.60E-04	R.ARKPTAsLAPEEE.-	12.2/94.37	P63
58	CPRT0000005313	thymidylate kinase	25311	72	6%	1	72	1.80E-05	R.DSsGGNKFETMDFQK.R	9/89.41	P64
59	CPRT0000005334	hypothetical protein	53707	85	8%	0	87	6.30E-07	K.MQTGKPASSVHFsPTR.V	12.9/95.02	P65
60	CPRT0000005420	pleckstrin homology domain family c member 1 isoform 2	77049	76	1%	0	77	4.30E-06	R.DIsPIGGYLHTGR.Y	65/100	P66
61	CPRT0000005681	coatomer protein subunit beta 1	120852	50	1%	0	74	3.60E-04	R.SHsPVNTLLNSH.-	23.4/99.53	P67
62	CPRT0000005690	sjchgc00797 protein	18016	98	11%	0	99	4.20E-08	K.QVPVYNALsPSPGPLNFER.Y	17/95.63	P68
63	CPRT0000005797	calnexin	65986	131	7%	0	54	1.40E-03	R.DNsEEEAPNEFEGNENVPAAK.Q	N/100	P69
64	CPRT0000006031	calcium-regulated heat stable protein 1	13101	112	16%	1	112	1.60E-09	R.NRTEsQSESASTGEHGVGR.I	11.3/92.84	P70
65	CPRT0000006039	flotillin 2	42889	61	9%	1	58	3.30E-04	R.KAsFDQEVNTAR.A	67.5/100	P71
66	CPRT0000006118	p38 MAPK	29378	204	8%	1	111	2.00E-09	K.sKSPGPPPTEEVASSISAPLK.K	2.3/62.56	P72
67	CPRT0000006130	Phosphofructokinase	86159	75	1%	1	77	3.70E-06	R.RGtELLPGMEGK.Y	N/100	P73
68	CPRT0000006221	RNA-binding protein 4	26526	129	22%	1	130	4.10E-11	R.YGPAWDDGYGGPYAPPPRNsPR.G	N/100	P74
69	CPRT0000006370	eukaryotic translation initiation factor 2 alpha subunit	34474	78	4%	0	79	2.90E-06	K.NIGGMILHSELsR.R	22.2/99.4	P75
70	CPRT0000006676	dentin sialophosphoprotein precursor	85411	71	5%	0	48	3.00E-03	K.GIAsPGNYGDAR.R	41.5/100	P76
71	CPRT0000006702	sjchgc01166 protein	39554	59	9%	1	59	2.20E-04	R.RQsLQNLLR.L	N/100	P77
72	CPRT0000006771	wd-40 repeat protein	61284	133	5%	0	94	1.20E-07	R.LIKPPLsVNNYPVGHNHR.L	N/100	P78
						0	41	1.90E-02	R.IDQPVMDDLsAR.Q	N/100	P79
73	CPRT0000007051	plasminogen activator inhibitor 1RNA-binding protein	45889	98	5%	1	98	6.30E-08	R.VSRsPNANEPPPVVFEDVQITSAK.E	21/98.92	P80
74	CPRT0000007295	sjchgc05354 protein	25195	46	3%	1	47	2.90E-03	R.RYsFSTQR.N	23.8/99.43	P81
75	CPRT0000007659	placenta-specific protein 8 protein	13424	69	11%	1	70	2.40E-05	MEsPTTKQPYAVR.Q	22/99.05	P82
76	CPRT0000007759	sjchgc05800 protein	66670	365	16%	1	88	3.80E-07	R.RTsELSTDLANLK.L	14.9/96.86	P83
						0	81	4.10E-06	K.HPASNLGDITITQGPDSHFRPFTPDQsPK.T	14.8/96.64	P84
						0	74	1.00E-05	K.HLSDDVHFtPFDR.K	67/100	P85

						0	57	3.80E-04	K.SGsASEIAADIHK.N	1.7/59.31	P86
77	CPRT0000007774	heat shock protein 60	63630	185	8%	1	34	9.70E-02	R.NVIIESSWKsPK.I	19.8/98.76	P87
78	CPRT0000007860	glycogen synthase kinase 3	56751	64	2%	0	65	8.60E-05	K.EMVPGTANVSyISSR.Y	N/100	P88
79	CPRT0000008289	ubx domain-containing protein 4	48307	63	3%	0	64	1.10E-04	R.LSHMPDNsDDEQAR.W	21/98.71	P89
80	CPRT0000008409	af287985_1synapsin isoform	36298	72	4%	2	73	1.40E-05	R.RFSsGDLQGELADKR.M	9/88.82	P90
81	CPRT0000008664	lamin	38122	38	7%	0	38	2.20E-02	R.SSsPLTISR.S	0/41.19	P91
82	CPRT0000008751	glucose transport protein	56955	97	3%	0	97	5.90E-08	K.QGNTDGPAsESLLHSR.N	31.5/99.92	P92
83	CPRT0000008924	transcription elongation regulator 1	37650	74	7%	1	64	6.50E-05	R.KLDDSPtVR.E	10.7/92.12	P93
84	CPRT0000008975	rhoptry associated membrane antigen	73359	66	2%	0	66	5.80E-05	R.IPtPDISNNEVESAK.L	40.4/99.99	P94
85	CPRT0000009359	sjchgc04698 protein	55791	65	4%	0	38	7.10E-02	K.IAEEISPTEVFGEGAsEGETVVK.K	35.3/99.97	P95
86	CPRT0000009893	ATP-binding sub-family c member 2	127765	56	1%	1	56	5.40E-04	K.KLsLETPDSFSR.F	14/95.62	P96
87	CPRT0000009921	sjchgc09590 protein	180556	632	7%	1	207	9.60E-19	K.QEALLAEQVDDIPKEHLFVEsDEER.Y	N/100	P97
						1	71	1.80E-05	R.KLEEELEEVDsR.A	N/100	P98
88	CPRT0000010244	Hypothetical protein	13926	45	6%	0	46	4.10E-03	K.LPsPEYYR.E	N/100	P99
89	CPRT0000010408	venom allergen-like 6 protein	15415	37	14%	0	39	5.50E-02	R.sRPTSFANNDDIHYKPVYTR.S	5.7/65.17	P100
90	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	23045	216	13%	1	119	6.70E-10	K.AASENRPNKANEsDEDEDEEPMPMPPQR.V	14/93.78	P101
91	CPRT0000012199	importin 7	116719	112	1%	0	114	1.20E-09	K.ALGsDEDEVDEESVR.Y	72/100	P102

1, Protein IDs were obtained from NCBInr or LSBI-Sjr ((http://lifecenter.sgst.cn/schistosoma/).

2, The underlined phosphopeptides were also identified in our previous study by using an IMAC-based phosphoproteomic method. For a phosphopeptide with MD score < 9, the second ranked phosphosite was framed in a phosphopeptide.

3, “N/100” in the column of “MD score/ Phospho site probability (%)” indicated 100% probability of a phosphosite identified in a phosphopeptide.

Supplementary Table 4 Scansite prediction at high stringency and low stringency for kinase phosphorylation and binding motifs from the phosphoprotein data set of schistosomula (14 d) of *Schistosoma japonicum*

Protein ID	Phospholyated Peptides	High strigency (0.2%)	Low strigency (5%)
CAX69413.1	R.QISVsPTYYHDTSPR.N	N	N
CAX70460.1	R.QTNQLNHQPDSVsPTR.I	N	S666/Cdc2 Kinase/Erk1 Kinase/Cdk5 Kinase
CAX73031.1	R.AGALDNDSHYHDINDsMLISR.A	N	N
	R.YVNLGDSTFGMNRsPK.I	N	S434/Cdk5 Kinase
CAX73091.1	R.KESsSDLLSR.Y	N	N
CAX74150.1	R.HTPHHPPPPPTsPSFFVGR.G	S73/Erk1 Kinase	S73/Erk1 Kinase/p38 MAPK
CAX74794.1	M.sDQEsDAEQDVLDDTVVNKYK.M	N	N
CAX83069.1	R.IKtPPLAPLVTSFR.R	N	T826/14-3-3 Mode 1
	R.ESSLATGDDAVPSEsPKGDR.G	N	S673/Cdk5 Kinase
	R.RDHtPLsPTAPRPSAGYATHMER.S	N	S429/Erk1 Kinase/Cdk5 Kinase/Cdc2 Kinase
AAP05964.1	R.KLsTSGESLFHVLR.V	N	N
AAP06040.1	K.VGAsLDDPDEEEEDKGK.L	N	S59/ATM Kinase/GSK3 Kinase/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase
AAP06130.1	R.ITSDFDDKLsPER.S	N	S331/Casein Kinase 2/Cdk5 Kinase
AAW24704.1	R.AMsHFETNSIENSLPR.V	N	S35/14-3-3 Mode 1/PKC epsilon/Clk2 Kinase
AAW25147.1	M.sDDEQsPQPSPAFIPKDEEHDDGKSEAK.I	N	N
AAW25812.1	R.IESRPLHLssDEEDIKR.I	N	S29/Clk2 Kinase/ATM Kinase/Casein Kinase 2,S30/DNA PK/Casein Kinase 2/
AAW26418.1	K.DNQEVHsDIDEMEKEFVIPYQR.N	N	S179/Casein Kinase 2
AAW26505.1	R.VRsVSNFELENNR.E	N	S42/Casein Kinase 2
AAW26588.1	K.NHNITDsPVMSNKPK.L	N	N
	R.HFsPVAIASSTPK.L	N	N
AAW26771.1	R.NNPFTTMsPLLNELER.D	S103/Casein Kinase 2	S103/14-3-3 Mode 1/PKC epsilon/Clk2 Kinase/Casein Kinase 2,S105/ATM

			Kinase/DNA PK/Casein Kinase 2
AAW26771.1	K.TVIAEEsEDDEEPDASGLSEK.D	N	N
AAW27129.1	.MLGSGLSFGGQSFHGVSsVSR.F	N	N
AAW27091.1	R.RQsVAAESFDPEKDSDDNNEEER.Q	S56/Protein Kinase A/PKC epsilon	S56/14-3-3 Mode 1/Protein Kinase A/PKC epsilon/PKC mu/PKC delta/Calmodulin dependent Kinase 2/Akt Kinase
AAW27136.1	R.HAEAEsEEDGTDDDASQDTK.G R.KEAGDNASDDKAHsPDSR.H	S73/Casein Kinase 2, N	S73/Clk2 Kinase/DNA PK/Casein Kinase 2, S63/Cdk5 Kinase/Cdc2 Kinase
AAW27151.1	K.RPIPVGsDDsDAETESNVLCNNELK.T	N	S37/DNA PK/Casein Kinase 2,S40/Casein Kinase 2
P91800.1	K.LIAANPSGEEGQEEVsDSTER.V	N	S113/DNA PK/Casein Kinase 2
AAX27349.2	K.SMDDLsDTLVDLNNLTR.H R.HRPAsVSGYLDECGLNR.S R.DIKNEHTLDDDQNIDLsPTIGNDEQIHHQSDHLIQHR.S	N N N	S186/Casein Kinase 2 S308/14-3-3 Mode 1/Akt Kinase/Calmodulin dependent Kinase 2 N
AAX27846.2	R.GGGASsMIEGLSHIDDHQHPR.A	N	N
CPRT0000000132	R.DNYHNEDGsPDMR.D	N	N
CPRT0000000218	K.EFHLGDsGEPSSTYTK.I	N	S143/ATM Kinase
CPRT0000000284	R.DAVsPQSYVIGSNK.S	N	N
CPRT0000000366	R.KVsFSDLPIVSGVEER.N	N	S310/14-3-3 Mode 1/rotein Kinase A/PKC mu/
CPRT0000000669	R.sRsPLGAPVGR.L R.NSsYDGHRYPDHDQFSSFR.S	S204/Protein Kinase A N	S204/14-3-3 Mode 1/Protein Kinase A/AMP-activated protein kinase/Clk2 Kinase/Akt Kinase/GSK3 Kinase/,S206/14-3-3 Mode 1/Protein Kinase A/Akt Kinase/Clk2 Kinase/Erk1 Kinase/Cdk5 Kinase/Cdc2 Kinase S119/Calmodulin dependent Kinase 2/Protein Kinase A/Akt Kinase/PKC zeta/Clk2 Kinase/
CPRT0000000835	K.KEFDsDEDVPLSNLTSTK.V	N	S332/DNA PK/Casein Kinase 2/
CPRT0000001216	R.EAsFEEHQIMR.D	N	N
CPRT0000001254	K.LISLPTTTHEQsPK.L	N	S525/Cdk5 Kinase

CPRT0000001365	R.sRsPPIFQSVQHRPEILEYGHR.S	S658/14-3-3 Mode 1	S658/14-3-3 Mode 1/Protein Kinase A/Cdk5 Kinase/Erk1 Kinase
CPRT0000001534	R.SNsPSVDQELQFR.N	N	S578/14-3-3 Mode 1/Akt Kinase/Cdk5 Kinase/Erk1 Kinase/Cdc2 Kinase
CPRT0000001619	R.AAtLPSGVAPESQVTSSSSASGK.K	T655/14-3-3 Mode 1	T655/14-3-3 Mode 1/PKC delta/Akt Kinase/Protein Kinase A
CPRT0000001788	R.NLsDHAIIQSR.R	N	S205/Protein Kinase A/Akt Kinase
CPRT0000001895	R.SKsEIINQYMNQADK.S	N	S355/14-3-3 Mode 1/Calmodulin dependent Kinase 2
CPRT0000002080	K.ILDLVSPTKsQDELQIK.S	S731/DNA PK	S731/DNA PK/ATM Kinase
CPRT0000002152	M.SCLNYSKWDHIEVsDDEDDTHPNIDTPSLFR.W	N	S15/Clk2 Kinase/Casein Kinase 2/
CPRT0000002239	R.NIsPESTSHGTISAPR.S	N	S833/Calmodulin dependent Kinase 2/Cdc2 Kinase
CPRT0000002347	R.DNLNLWNPCNDGEKDTAAsPKGEEK.-	N	N
CPRT0000002522	K.HStPPILSSK.R	N	T387/14-3-3 Mode 1/Cdk5 Kinase/Cdc2 Kinase
CPRT0000002551	R.RTDQsIELR.K	N	S25/PKC alpha/beta/gamma/PKC zeta/Clk2 Kinase
CPRT0000002705	K.DKPDAESDLFAsDsEDDKEAER.I	N	S134/DNA PK/ATM Kinase/Casein Kinase 2,S132/Casein Kinase 2
CPRT0000002762	R.RHsPPGYER.N	N	S46/14-3-3 Mode 1/Protein Kinase A/Cdk5 Kinase/Cdc2 Kinase
CPRT0000002896	K.QGKLsPNTPK.M	N	S9/Erk1 Kinase
CPRT0000003012	R.DRNPHTVsFDNTPSYR.N	N	N
CPRT0000003210	K.RLsIDTTGEDEPDKENNANLSLPNVR.S	S136/Calmodulin dependent Kinase 2	S136/Protein Kinase A/Calmodulin dependent Kinase 2/PKC epsilon/PKC delta/PKC alpha/beta/gamma/ATM Kinase
CPRT0000003479	M.VSVVENNPsPDSAFTVVR.M	N	S10/ATM Kinase/Erk1 Kinase/
CPRT0000003518	R.SLPDKWQHDMFQDARsPK.G	N	S65/Cdk5 Kinase/Cdc2 Kinase/
CPRT0000003603	K.AADTsVVKR.D K.EFtPPPDGVAVGILESNPKPR.A K.KSsFIDESITVAPEATR.S	N N S202/PKC epsilon	S277/PKC alpha/beta/gamma/ T134/Erk1 Kinase/Cdk5 Kinase/Cdc2 Kinase/PDK1 Binding/14-3-3 Mode 1 S202/PKC epsilon/Protein Kinase A/Calmodulin dependent Kinase 2
CPRT0000003639	R.SIKYEDSEsPDIPSR.G	N	S453/Casein Kinase 1/Casein Kinase 2/Cdk5 Kinase/
CPRT0000003765	R.sVDKYDHHGSR.Q	N	N

CPRT0000003898	R.GSHsPISLTER.F	N	S102/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase
CPRT0000004133	R.KTsLTTVADELR.S	N	S2193/14-3-3 Mode 1/Protein Kinase A/PKC epsilon/PKC delta
CPRT0000004202	K.EVsDDEAEKEETKNESEEAEDKPK.V	N	S225/PKC epsilon/DNA PK/Casein Kinase 2
CPRT0000004561	R.RGsEDsDIVEPNNIPDGTPGDR.A	N	N
CPRT0000004658	R.QSNLsGGGMHPHIESR.N	N	S349/Protein Kinase A
CPRT0000004688	R.SLNGISSTsPNLNISR.E	N	N
CPRT0000004690	R.GGsIENTYATGLR.A	N	S341/Protein Kinase A/PKC mu
CPRT0000004960	R.KTsDQPVESIR.K	N	S298/Protein Kinase A/PKC mu
CPRT0000004986	R.RSsNTNSEESPVTR.R	N	N
CPRT0000005165	R.GVsVAPGAAPGHGNR.A	N	N
	R.ARKPTAsLAPEEE.-	N	N
CPRT0000005313	R.DSsGGNKFETMDFQK.R	N	N
CPRT0000005336	R.GLMAAsPSGVNLTR.R	N	N
CPRT0000005420	R.DIsPIGGYLHTGR.Y	N	N
CPRT0000005690	K.QVPVYNALsPSPGPLNFER.Y	N	S80/GSK3 Kinase/Erk1 Kinase/
CPRT0000005681	R.SHsPVNTLLNSH.-	N	S1062/14-3-3 Mode 1/
CPRT0000005797	R.DNsEEEAPNEFEGNENVPAAK.Q	S553/DNA PK	S553/14-3-3 Mode 1/Protein Kinase A/Casein Kinase 2/
CPRT0000006118	K.SKsPGPPPTEEVASSISAPLKKPR.L	S176/Erk1 Kinase	S176/14-3-3 Mode 1/GSK3 Kinase/Erk1 Kinase/Cdk5 Kinase/Cdc2 Kinase
CPRT0000006130	R.RGtELLPGMEGK.Y	N	T11/14-3-3 Mode 1/Protein Kinase A/PKC zeta/Akt Kinase/
CPRT0000006131	R.KRsDPVNLGLSEPFSTSLVATTTLMSGMNDFISK.S	N	S1724/14-3-3 Mode 1/Protein Kinase A/
CPRT0000006221	R.YGPAWDDGYGGPYAPPPRNsPR.G	N	S135/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase/
CPRT0000006463	M.AALEVESYPRRsPK.Y	N	S13/Cdk5 Kinase/Cdc2 Kinase/
CPRT0000006620	R.NKAsDDEDYAR.S	N	S105/Casein Kinase 2/PKC zeta/
CPRT0000006676	K.GIAsPGNYGDAR.R	N	N

	R.MHsIsPPYNDR.S	S425/Akt Kinase/Calmodulin dependent Kinase 2	S425/Akt Kinase/Calmodulin dependent Kinase 2/PKC delta
	K.NTHsPANNTESLREPPHTR.S	N	N
CPRT0000006702	R.RQsLQNLLR.L	S277/Protein Kinase A	S277/14-3-3 Mode 1/Protein Kinase A/Akt Kinase
CPRT0000007051	R.VSRsPNANEPPPVVFEDVQITSAK.E	N	S86/Cdk5 Kinase/Cdc2 Kinase/
CPRT0000007240	R.FIsETDSVYR.T	N	S521/14-3-3 Mode 1/Akt Kinase/
CPRT0000007300	R.SSsPSEDIELIMDR.A	N	S334/14-3-3 Mode 1/Protein Kinase A/Akt Kinase/Clk2 Kinase/GSK3 Kinase/Erk1 Kinase/Cdk5 Kinase/Cdc2 Kinase/
CPRT0000007395	.MENPFADPVARLtPTQSHDNSQVSR.V	N	T13/GSK3 Kinase/Erk1 Kinase/
CPRT0000007659	.MEsPTTKQPYAVR.Q	N	N
CPRT0000007759	R.RTsELSTDLANLK.L	N	S258/Protein Kinase A/PKC epsilon/
	K.HLSDDVHFtPFDR.K	N	T163/Cdk5 Kinase/Cdc2 Kinase/
	R.QSVNIsPTSDLHSQGK.F	N	S198/GSK3 Kinase/
CPRT0000007860	K.EMVPGTANVSyISSR.Y	N	N
CPRT0000008142	R.ERRDsDDEFDEFGR.K	S115/Akt Kinase/Clk2 Kinase	S115/Protein Kinase A/Akt Kinase/PKC epsilon/Clk2 Kinase/Calmodulin dependent Kinase 2/ATM Kinase/DNA PK/Casein Kinase 2
CPRT0000008289	R.LSHMPDNsDDEQAR.W	N	S414/Casein Kinase 2
CPRT0000008409	R.RFsSGDLQGELADKR.M	N	S11/Calmodulin dependent Kinase 2/Akt Kinase/
CPRT0000008586	K.QLLQEIEtPPSLK.H	N	T51/Erk1 Kinase/Cdk5 Kinase/Cdc2 Kinase/
CPRT0000008924	R.KLDDSPtVR.E	N	T62/PKC alpha/beta/gamma/PKC zeta/Casein Kinase 1/Casein Kinase 2
CPRT0000008950	R.KLSsPQGGVDDR.N	N	S63/Cdk5 Kinase
CPRT0000009359	K.IAEEISPTEVFGEGAsEGETVVK.K	N	S138/Casein Kinase 2
CPRT0000009445	K.NSREsEEsGGEDEFQVEK.I	N	S135/DNA PK/Casein Kinase 2
CPRT0000009921	K.QEALLAEQVDDIPKEHLFVEsDEER.Y	N	N
	K.VIKENNMLAEEsDEQsNNELECELK.Q	N	S325/Casein Kinase 1/,S321/Casein Kinase 2

CPRT0000010982	K.ANEsDEDEDEEPMPMPPQR.V	S57/Casein Kinase 2	S57/DNA PK/Casein Kinase 2
	K.AASENRPNKANEsDEDEDEEPMPMPPQR.V	S57/Casein Kinase 2	S57/DNA PK/Casein Kinase 2
CPRT0000012199	K.ALGsDEDEVDEESVR.Y	N	S896/DNA PK/Casein Kinase 2/

Supplementary Table 5 Scansite prediction at high stringency and low stringency for kinase phosphorylation and binding motifs from the phosphoprotein data set of adult female (35 d) of *Schistosoma japonicum*

Protein ID	Phospholyated Peptides	High strigency (0.2%)	Low strigency (5%)
CAX70460.1	R.QTNQLNHQPDSVsPTR.I	N	N
CAX73244.1	R.RGsEDsDIVEPNNIPDGTPGDR.A	N	S629/14-3-3 Mode 1/Protein Kinase A,S632/Casein Kinase 2
AAX25971.2	R.YVNLGDSTFGMNRsPK.I	N	S196/Cdk5 Kinase/Cdc2 Kinase
CAX73605.1	R.RHsVAAESFNPATVNDLEPVVHPK.S	S57/Protein Kinase A/PKC epsilon	S57/14-3-3 Mode 1/Protein Kinase A/PKC epsilon/PKC mu/Akt Kinase/Clk2 Kinase
CAX74259.1	K.ALQLVTIDKsPQVPEEQVKPVNAESGSK.L	N	S624/Cdk5 Kinase
	K.IANtPEAEDGFESMGPK.N	N	N
CAX83069.1	R.IKtPPLAPLVTSFR.R	N	T826/14-3-3 Mode 1
AAP05964.1	R.KLsTSGESLFHVLR.V	N	N
AAP06040.1	K.VGAsLDDPDEEEEDKGK.L	N	S143/Calmodulin dependent Kinase 2/DNA PK/ATM Kinase/Casein Kinase 2
AAP06130.1	R.ITSDFDDKLsPER.S	N	S59/ATM Kinase/GSK3 Kinase/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase
AAP06472.1	.MLGSGLSFGGQSFHGVSsVSR.F	N	N
AAW24532.1	K.SIPMPDIKsPTTR.Q	N	S376/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase
AAW27136.1	K.EAGDNASDDKAHsPDSR.H	N	S63/Cdk5 Kinase/Cdc2 Kinase
	R.HAEAEsEEDGtDDDASQDTK.G	S73/Casein Kinase 2,T78/Casein Kinase 2	S73/Clk2 Kinase/DNA PK/Casein Kinase 2,T78/DNA PK/ATM Kinase/Casein Kinase 2/Casein Kinase 1
AAW27231.1	K.VNDsDTEDVYPDTVEALKDELLK.L	N	S160/Casein Kinase 2
AAW27390.1	R.KLDDSPtVR.E	N	T185/PKC alpha/beta/gamma/PKC zeta/Casein Kinase 1/Casein Kinase 2

AAX26240.2	R.LVVTSFFsPNSYHR.R	N	S249/Erk1 Kinase
AAX27349.2	K.SMDDLsDTLVDLNNLTR.H	N	S186/Casein Kinase 2
AAX30518.2	R.KRTsDAIDNIDTK.-	N	S102/Protein Kinase A/PKC epsilon
CPRT0000000132	R.DNYHNEDGsPDMR.D	N	N
CPRT0000000345	R.LTTDsGSAATAFLSGAK.G	N	N
CPRT0000000366	R.KVsFSDLPIVSGVEER.N	N	S310/14-3-3 Mode 1/rotein Kinase A/PKC mu
CPRT0000000669	R.NsSYDGHRYPDHDQFSSFR.S	N	S119/Calmodulin dependent Kinase 2/Protein Kinase A/Akt Kinase/PKC zeta/Clk2 Kinase
CPRT0000000687	R.VGTGLGEYTFDKETLHGEsD.-	N	N
CPRT0000000835	K.EFDsDEDVPLSNLTSTK.V	N	S332/DNA PK/Casein Kinase 2
CPRT0000001007	R.ELEsPSHDVNDSILQR.N	N	S70/Cdk5 Kinase/Cdc2 Kinase /Erk1 Kinase
CPRT0000001178	R.NDsQNGYNDEQDDVK.I	S600/Akt Kinase	S600/Akt Kinase/Calmodulin dependent Kinase 2/DNA PK
CPRT0000001254	K.LISLPTTTHEQsPK.L	N	S525/Cdk5 Kinase
	K.YQSKsPILMIsPK.L	N	N
	K.SQVsPQLHLR.I	N	N
CPRT0000001534	R.SNsPSVDQELQFR.N	N	S578/14-3-3 Mode 1/Akt Kinase/Cdk5 Kinase/Erk1 Kinase/Cdc2 Kinase
CPRT0000001619	R.AAtLPSGVAPESQVTSSSSASGK.K	T655/14-3-3 Mode 1	T655/14-3-3 Mode 1/PKC delta/Akt Kinase/Protein Kinase A
CPRT0000001788	R.NLsDHAIIQSR.R	N	S205/Protein Kinase A/Akt Kinase
CPRT0000002152	K.WDHIEVsDDEDDTHPNIDTPSLFR.W	N	S15/Clk2 Kinase/Casein Kinase 2/
CPRT0000002347	R.DNLNLWNPCNDGEKDTAAsPKGEE K.-	N	N
CPRT0000002428	K.VINDNFEIVEGLMTTVHSFTAtQK.T	N	T183/14-3-3 Mode 1/PKC alpha/beta/gamma/ATM Kinase/DNA PK/
CPRT0000002551	R.RTDQsIELR.K	N	S25/PKC alpha/beta/gamma/PKC zeta/Clk2 Kinase
CPRT0000002705	K.DKPDAESDLFAsDsEDDKEAER.I	N	S134/DNA PK/ATM Kinase/Casein Kinase 2/,S132/Casein Kinase 2
CPRT0000002762	R.RHsPPGYER.N	N	S46/14-3-3 Mode 1/Protein Kinase A/Cdk5 Kinase/Cdc2 Kinase
CPRT0000003234	R.QKsPELSPEER.D	S82/Calmodulin	S82/Calmodulin dependent Kinase 2/Protein Kinase A/Clk2 Kinase/GSK3 Kinase/Cdk5 Kinase/Cdc2

		dependent Kinase 2	Kinase
CPRT0000003518	R.SLPDKWQHDMFQDARsPK.G	N	S65/Cdk5 Kinase/Cdc2 Kinase
CPRT0000004133	R.KTsLTTVADELR.S	N	S2193/14-3-3 Mode 1/Protein Kinase A/PKC epsilon/PKC delta
CPRT0000004202	R.TKEVsDDEAEKEETKNESEEAEDKP K.V	N	S225/PKC epsilon/DNA PK/Casein Kinase 2
CPRT0000004798	K.TYSFPEENPFKDDEDEDsDNPNPSHN R.N	N	S168/Casein Kinase 2/Casein Kinase 1
CPRT0000005165	R.ARKPTAsLAPEEE.- R.GVsVAPGAAPGHGNR.A	N N	N N
CPRT0000005313	R.DSsGGNKFETMDFQK.R	N	N
CPRT0000005420	R.DIsPIGGYLHTGR.Y	N	N
CPRT0000005681	R.SHsPVNTLLNSH.-	N	S1062/14-3-3 Mode 1
CPRT0000005718	R.TEFISMIKsNEsLHR.S	N	S563/PKC alpha/beta/gamma/,s560/ATM Kinase
CPRT0000005797	R.DNsEEEAPNEFEGNENVPAAK.Q	S553/DNA PK	S553/14-3-3 Mode 1/Protein Kinase A/Casein Kinase 2
CPRT0000006130	R.RGtELLPGMEGK.Y	N	T11/14-3-3 Mode 1/Protein Kinase A/PKC zeta/Akt Kinase
CPRT0000006218	K.RLEEAAIAtPPKPIIPQSDPSDR.N	N	N
CPRT0000006221	R.YGPAWDDGYGGPYAPPPRNsPR.G	N	S135/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase
CPRT0000006676	K.GIAsPGNYGDAR.R	N	N
CPRT0000006702	R.RQsLQNLLR.L	S277/Protein Kinase A	S277/14-3-3 Mode 1/Protein Kinase A/Akt Kinase
CPRT0000007051	R.VSRsPNANEPPPVVFEDVQITSAK.E	N	S86/Cdk5 Kinase/Cdc2 Kinase
CPRT0000007069	K.LIAANPSGEEGQEEVsDSTER.V	N	S60/Casein Kinase 2
CPRT0000007295	R.RYsFSTQR.N	N	S44/14-3-3 Mode 1/Protein Kinase A/Calmodulin dependent Kinase 2/Akt Kinase/PKC alpha/beta/gamma/Clk2 Kinase/PDK1 Binding
CPRT0000007659	MEsPTTKQPYAVR.Q	N	N

CPRT0000007759	R.QSVNIsPTSDLHSQGK.F	N	S198/GSK3 Kinase
	R.RTsELSTDLANLK.L	N	N
CPRT0000007860	K.EMVPGTANVSyISSR.Y	N	N
CPRT0000008142	R.ERRDsDDEFDEFGR.K	S115/Akt Kinase/Clk2 Kinase	S115/Protein Kinase A/Akt Kinase/PKC epsilon/Clk2 Kinase/Calmodulin dependent Kinase 2/ATM Kinase/DNA PK/Casein Kinase 2
CPRT0000008289	R.LSHMPDNsDDEQAR.W	N	S414/Casein Kinase 2
CPRT0000008664	R.SEAsPTSFSR.S	N	S54/Clk2 Kinase/Casein Kinase 1/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase
CPRT0000009445	K.NSREsEEsGGEDEFQVEK.I	N	S135/DNA PK/Casein Kinase 2
CPRT0000009893	K.KLsLETPDSFSR.F	N	S416/Protein Kinase A/PKC mu/Calmodulin dependent Kinase 2/ATM Kinase
CPRT0000009921	K.QEALLAEQVDDIPKEHLFVEsDEER.Y	N	N
CPRT0000010982	K.AASENRPNKANEsDEDEDEEPMPMPPQR.V	S57/Casein Kinase 2	S57/DNA PK/Casein Kinase 2
CPRT0000012199	K.ALGsDEDEVDEESVR.Y	N	S896/DNA PK/Casein Kinase 2

Supplementary Table 6 Scansite prediction at high stringency and low stringency for kinase phosphorylation and binding motifs from the phosphoprotein data set of adult male (35 d) of *Schistosoma japonicum*

Protein ID	Phospholyated Peptides	High strigency (0.2%)	Low strigency (5%)
CAX73031.1	R.YVNLGDSTFGMNRsPK.I	N	S434/Cdk5 Kinase/Cdc2 Kinase
CAX73091.1	R.KEsSSDLLSR.Y	N	S10/14-3-3 Mode 1/Protein Kinase A/Clk2 Kinase/Akt Kinase/
CAX73605.1	R.RHsVAAESFNPATVNDLEPVVHPK.S	S57/Protein Kinase A/PKC epsilon	S57/14-3-3 Mode 1/Protein Kinase A/PKC epsilon/PKC mu/Akt Kinase/Clk2 Kinase
CAX74259.1	K.IANtPEAEDGFESMGPK.N	N	N
CAX75242.1	R.QTNQLNHQPDSVsPTR.I	N	N
CAX83069.1	R.IKtPPLAPLVTSFR.R	N	T826/14-3-3 Mode 1
AAP06040.1	K.VGAsLDDPDEEEEDKGK.L	N	S143/Calmodulin dependent Kinase 2/DNA PK/ATM Kinase/Casein Kinase 2
AAP06500.1	K.RLsIDTTGEDEPDKENNANLSLPNVR.S	S209/Calmodulin dependent Kinase 2	S209/Protein Kinase A/Calmodulin dependent Kinase 2/PKC epsilon/PKC delta/PKC alpha/beta/gamma/ATM Kinase
AAW24532.1	K.SIPMPDIKsPTTR.Q	N	S376/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase
AAW24704.1	R.AMsHFETNSIENSLPR.V	N	S35/14-3-3 Mode 1/PKC epsilon/Clk2 Kinase
AAW25147.1	M.sDDEQSPQPSPAFIPKDEEHDDGKSEAK.I	N	N
AAW26183.1	K.YALEEKDEVANtPK.-	N	N
AAW26505.1	R.VRsVSNFELENNR.E	N	S42/Casein Kinase 2
AAW26588.1	K.NHNITDsPVMSNKPK.L R.HFsPVAIASSTPK.L	N N	S233/Cdk5 Kinase/Cdc2 Kinase S88/Protein Kinase A/Cdk5 Kinase/Cdc2 Kinase
AAW26770.1	R.NNPFTTMsPLLNELER.D	N	S119/Erk1 Kinase/PDK1 Binding
AAW27091.1	R.RQsVAAESFDPEKDSDDNNEEER.Q	S56/Protein Kinase	S56/14-3-3 Mode 1/Protein Kinase A/PKC epsilon/PKC mu/PKC delta/Calmodulin dependent Kinase

		A/PKC epsilon	2/Akt Kinase
AAW27136.1	R.KEAGDNASDDKAHsPDSR.H	N	S63/Cdk5 Kinase/Cdc2 Kinase
AAW27228.1	R.VNVYNSDNTSTIYsPQR.K	S289/Cdk5 Kinase/Cdc2 Kinase/	S289/Cdk5 Kinase/Cdc2 Kinase
AAX25934.2	K.SDsPTNSLNLGQNFK.Y	N	S10/Cdk5 Kinase/Cdc2 Kinase
AAX27349.2	K.SMDDLsDTLVDLNNLTR.H	N	S186/Casein Kinase 2
AAX30518.2	R.KRTsDAIDNIDTK.-	N	S102/Protein Kinase A/PKC epsilon
CPRT0000000132	R.DNYHNEDGsPDMR.D	N	N
CPRT0000000345	R.LTTDsGSAATAFLSGAK.G	N	N
CPRT0000000366	R.KVsFSDLPIVSGVEER.N	N	S310/14-3-3 Mode 1/rotein Kinase A/PKC mu
CPRT0000000412	R.KMsQPQRPACDPK.Q	N	S586/14-3-3 Mode 1
CPRT0000000616	R.KQTDLTQAAVEFNQATGDLLSSYs PGTFR.R	N	N
	R.AGsRPEMHNAENFTPLR.E	N	S2264/14-3-3 Mode 1
CPRT0000000669	R.sRsPLGAPVGR.L	S204/Protein Kinase A	S204/14-3-3 Mode 1/Protein Kinase A/AMP-activated protein kinase/Clk2 Kinase/Akt Kinase/GSK3 Kinase/,S206/14-3-3 Mode 1/Protein Kinase A/Akt Kinase/Clk2 Kinase/Erk1 Kinase/Cdk5 Kinase/Cdc2 Kinase
	R.NSsYDGHRYPDHDQFSSFR.S	N	S119/Calmodulin dependent Kinase 2/Protein Kinase A/Akt Kinase/PKC zeta/Clk2 Kinase
CPRT0000001007	R.ELEsPSHDVNDSILQR.N	N	S70/Cdk5 Kinase/Cdc2 Kinase /Erk1 Kinase
CPRT0000001123	R.SLRPDtPKLEEQVEPSLPVPPAPR.I	N	N
CPRT0000001254	K.LISLPTTTHEQsPK.L	N	S525/Cdk5 Kinase/
	R.GTsPSKPIIVITK.K	N	N
	K.SQVsPQLHLR.I	N	S663/Cdk5 Kinase/
	K.YQSKsPILMIsPK.L	N	N
CPRT0000001365	R.sRsPPIFQSVQHRPEILEYGHR.S	S658/14-3-3 Mode 1	S658/14-3-3 Mode 1/Protein Kinase A/Cdk5 Kinase/Erk1 Kinase/

CPRT0000001534	R.SNsPSVDQELQFR.N	N	S578/14-3-3 Mode 1/Akt Kinase/Cdk5 Kinase/Erk1 Kinase/Cdc2 Kinase/
CPRT0000002152	K.WDHIEVsDDEDDTHPNIDTPSLFR.W	N	S15/Clk2 Kinase/Casein Kinase 2/
CPRT0000002239	R.NIsPESTSHGTISAPR.S	N	S833/Calmodulin dependent Kinase 2/Cdc2 Kinase
CPRT0000002347	R.DNLNLWNPCNDGEKDTAAsPKGEEK.-	N	N
CPRT0000002428	K.VINDNFEIVEGLMTTVHSFTAtQK.T	N	T183/14-3-3 Mode 1/PKC alpha/beta/gamma/ATM Kinase/DNA PK
CPRT0000002762	R.RHsPPGYER.N	N	S46/14-3-3 Mode 1/Protein Kinase A/Cdk5 Kinase/Cdc2 Kinase/
CPRT0000003382	R.GVQDLDSHVGsLTTLAR.G	N	N
CPRT0000003603	K.KSsFIDESITVAPEATR.S	S202/PKC epsilon	S202/PKC epsilon/Protein Kinase A/Calmodulin dependent Kinase 2
CPRT0000003866	R.ITINPPSNQGsPETSR.R	N	S1353/GSK3-improved/GSK3 Kinase/Cdk5 Kinase/Cdc2 Kinase
CPRT0000003998	R.APAMLMPHESTVSHGDsPK.D	N	S425/GSK3-improved/GSK3 Kinase/Cdk5 Kinase
CPRT0000004133	R.KTsLTTVADELR.S	N	S2193/14-3-3 Mode 1/Protein Kinase A/PKC epsilon/PKC delta
CPRT0000004177	R.QNsQYEATPLVANR.S	N	S10/14-3-3 Mode 1/Calmodulin dependent Kinase 2/ATM Kinase/DNA PK
CPRT0000004202	K.EVsDDEAEKEETKNESEEAEDKPK.V	N	S225/PKC epsilon/DNA PK/Casein Kinase 2
CPRT0000004798	K.TYSFPEENPFKDDEDEDsDNPNPSHNR.N	N	S168/Casein Kinase 2/Casein Kinase 1
CPRT0000004561	R.RGsEDsDIVEPNNIPDGTPGDR.A	N	S571/14-3-3 Mode 1/Akt Kinase/Protein Kinase A /,S574/Casein Kinase 2
CPRT0000004986	R.RSsNTNSEESPVTR.R	N	N
CPRT0000005165	R.ARKPTAsLAPEEE.-	N	N
CPRT0000005313	R.DSsGGNKFETMDFQK.R	N	N
CPRT0000005334	K.MQTGKPASSVHFsPTR.V	N	S151/cdk5/cdc2
CPRT0000005420	R.DIsPIGGYLHTGR.Y	N	N
CPRT0000005681	R.SHsPVNTLLNSH.-	N	S1062/14-3-3 Mode 1

CPRT0000005690	K.QVPVYNALsPSPGPLNFER.Y	N	S80/GSK3 Kinase/Erk1 Kinase
CPRT0000005797	R.DNsEEEAPNEFEGNENVPAAK.Q	S553/DNA PK	S553/14-3-3 Mode 1/Protein Kinase A/Casein Kinase 2
CPRT0000006031	R.NRTEsQSESASTGEHGVGR.I	N	S26/14-3-3 Mode 1/Akt Kinase/Calmodulin dependent Kinase 2/Clk2 Kinase/DNA PK
CPRT0000006039	R.KAsFDQEVNTAR.A	N	S176/Protein Kinase A/Calmodulin dependent Kinase 2/Akt Kinase/Clk2 Kinase
CPRT0000006130	R.RGtELLPGMEGK.Y	N	T11/14-3-3 Mode 1/Protein Kinase A/PKC zeta/Akt Kinase
CPRT0000006221	R.YGPAWDDGYGGPYAPPPRNsPR.G	N	S135/Cdk5 Kinase/Cdc2 Kinase/Erk1 Kinase
CPRT0000006370	K.NIGGMILHsELSR.R	N	N
CPRT0000006676	K.GIAsPGNYGDAR.R	N	N
CPRT0000006702	R.RQsLQNLLR.L	S277/Protein Kinase A	S277/14-3-3 Mode 1/Protein Kinase A/Akt Kinase
CPRT0000006771	R.LIKPPLsVNNYPVGHNHR.L R.IDQPVMDDLsAR.Q	N N	S274/Erk1 Kinase N
CPRT0000007051	R.VSRsPNANEPPPVVFEDVQITSAK.E	N	S86/Cdk5 Kinase/Cdc2 Kinase
CPRT0000007295	R.RYsFSTQR.N	N	S44/14-3-3 Mode 1/Protein Kinase A/Calmodulin dependent Kinase 2/Akt Kinase/PKC alpha/beta/gamma/Clk2 Kinase/PDK1 Binding
CPRT0000007659	MEsPTTKQPYAVR.Q	N	N
CPRT0000007759	R.RTsELSTDLANLK.L K.HPASNLGDITITQGPDSHFRPFTPDQsPK.T K.HLSDDVHFtPFDR.K	N N N	S258/Protein Kinase A/PKC epsilon/ S250/Cdc2 Kinase/Cdk5 Kinase/Cdc2 Kinase T163/Cdk5 Kinase/Cdc2 Kinase/
CPRT0000007774	R.NVIIESSWKsPK.I	N	S68/Cdk5 Kinase/Cdc2 Kinase/
CPRT0000007860	K.EMVPGTANVSyISSR.Y	N	N
CPRT0000008289	R.LSHMPDNsDDEQAR.W	N	S414/Casein Kinase 2
CPRT0000008409	R.RFSsGDLQGELADKR.M	N	S11/Calmodulin dependent Kinase 2/Akt Kinase
CPRT0000008751	K.QGNTDGPAsESLLHSR.N	N	N

CPRT0000008924	R.KLDDSPtVR.E	N	T62/PKC alpha/beta/gamma/PKC zeta/Casein Kinase 1/Casein Kinase 2
CPRT0000008975	R.IPtPDISNNEVESAK.L	N	N
CPRT0000009359	K.IAEEISPTEVFGEGAsEGETVVK.K	N	S138/Casein Kinase 2
CPRT0000009893	K.KLsLETPDSFSR.F	N	S416/Protein Kinase A/PKC mu/Calmodulin dependent Kinase 2/ATM Kinase
CPRT0000009921	K.QEALLAEQVDDIPKEHLFVEsDEER.Y	N	N
	R.KLEEELEEVDsR.A	N	N
CPRT0000010244	K.LPsPEYYR.E	N	S11/Cdk5 Kinase/Erk1 Kinase/Cdc2 Kinase
CPRT0000010982	K.AASENRPNKANEsDEDEDEEPMPMPPQR.V	S57/Casein Kinase 2	S57/DNA PK/Casein Kinase 2
CPRT0000012199	K.ALGsDEDEVDEESVR.Y	N	S896/DNA PK/Casein Kinase 2

Supplementary Table 7 Evolutionary conservation of phosphorylation sites of the data set of phosphoproteins identified in the present study

Samples	Protein ID	Description	Phosphopeptides	*Homo sapiens*	*Mus musculus*	*Drosophila melanogaster*	*Caenorhabditis elegans*	*Saccharomyces cerevisiae*
SS	CAX74794.1	proliferation-associated protein 2G4	**M.sDQEsDAEQDVLDDTVVNKYK.M**	Q9UQ80[2]	P50580[2]			
SS	AAP05964.1	cysteine string protein	**R.KLsTSGESLFHVLR.V**	Q9H3Z4[10]	P60904[10]			
SS	AAW25812.1	eukaryotic translation initiation factor subunit C	**R.IESRPLHLs(1)s(2)DEEDIKR.I**	Q99613[39(1)]	Q8R1B4[39(1)]	A1ZAX1[34(1)]		P32497[103(2)]
SS	AAW26771.1	nascent polypeptide-associated complex subunit alpha	**K.tVIAEESEDDEEPDASGLSEKDIEL IMQQAGVSR.S**	Q13765[159]	Q60817[159]			
SS	AAW27091.1	cAMP-dependent protein kinase type ii regulatory subunit	**R.RQsVAAESFDPEKDSDDNNEEER.Q**	P31323[114]	P31324[112]	P81900[84]		P07278[145]
SS	CPRT0000000835	Protein DEK	**K.KEFDsDEDVPLSNLTSTK.V**	P35659[307]	Q7TNV0[308]			
SS	CPRT0000001365	scaffold attachment factor B	**R.s(1)Rs(2)PPIFQSVQHRPEILEYGHR.S**	Q9UQ35 [1958(1),1960(2)]	Q8BTI8[1958(2)]			
SS	CPRT0000001619	beta chain spectrin	**R.AAtLPSGVAPESQVTSSSSASGK.K**	Q01082[2328]	Q62261[2327]			
SS	CPRT0000002152	CDC37 cell division cycle 37 homolog	**K.WDHIEVsDDEDDTHPNIDTPSLFR.W**	Q16543[13]	Q61081[13]	Q24276[13]		P06101[14]
SS	CPRT0000004202	heat shock protein 90	**K.EVsDDEAEKEETKNESEEAEDKPK.V**	P07900[231]	P07901[252]	P02828[219]		
SS	CPRT0000007240	programmed cell death-involved	**R.FIsETDSVYR.T**	Q53EL6[457]	Q61823[457]			
SS	CPRT0000007860	glycogen synthase kinase 3	**K.EMVPGTANVSyISSR.Y**	P49840[279]	Q9WV60[216]	P18431[767]		P38615[199]
SS	CPRT0000009445	heterochromatin protein 1	**K.NSREsEEsGGEDEFQVEK.I**	P45973[11]	Q61686[11]	P05205[15]		
SS	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	**K.ANEsDEDEDEEPMPMPPQR.V**	P13861[78]	P31324[85]			
SS	CPRT0000012199	importin 7	**K.ALGsDEDEVDEESVR.Y**	O95373[903]	Q9EPL8[903]			

SF	CAX73605.1	cAMP-dependent protein kinase R2	**R.RHsVAAESFNPATVNDLEPVVHPK.S**	P13861[99]	P12367[96]	P81900[84]	P07278[145]
SF	CPRT0000000345	alkaline phosphatase	**R.LTTDsGSAATAFLSGAK.G**	P05186[110]	P09242[110]		P11491[123]
SF	CPRT0000000687	ferritin-1 heavy chain	**R.VGTGLGEYTFDKETLHGEsD.-**	P02794[179]			
SF	CPRT0000000835	Protein DEK	**K.EFDsDEDVPLSNLTSTK.V**	P35659[307]	Q7TNV0[308]		
SF	CPRT0000001619	beta chain spectrin	**R.AAtLPSGVAPESQVTSSSSASGK.K**	Q01082[2328]	Q62261[2327]		
SF	CPRT0000002152	CDC37 cell division cycle 37 homolog	**K.WDHIEVsDDEDDTHPNIDTPSLFR.W**	Q16543[13]	Q61081[13]	Q24276[13]	
SF	CPRT0000002428	glyceraldehyde 3-phosphate dehydrogenase	**K.VINDNFEIVEGLMTTVHSFTAtQK.T**	P04406[184]	P16858[182]		P00359[182]
SF	CPRT0000003234	RNA binding motif protein 39	**R.QKsPELSPEER.D**	Q14498[136]	Q8VH51[136]		
SF	CPRT0000004202	heat shock protein 90	**R.TKEVsDDEAEKEETKNESEEAED KPK.V**	P07900[231]	P07901[252]	P02828[219]	
SF	CPRT0000007860	glycogen synthase kinase 3	**K.EMVPGTANVSyISSR.Y**	P49840[279]	Q9WV60[216]	P18431[767]	P38615[199]
SF	CPRT0000009445	heterochromatin protein 1	**K.NSREsEEsGGEDEFQVEK.I**	P45973[11]	Q61686[11]	P05205[15]	
SF	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	**K.AASENRPNKANEsDEDEDEEPMPMP PQR.V**	P13861[78]	P31324[85]		
SM	CAX73605.1	cAMP-dependent protein kinase R2	**R.RHsVAAESFNPATVNDLEPVVHPK.S**	P13861[99]	P12367[96]	P81900[84]	P07278[145]
SM	P15845.2	20 kda calcium-binding protein	**R.GQEKIsTTDLGPAFR.A**				P06787[29];
SM	AAP05964.1	cysteine string protein (DnaJ)	**R.KLsTSGESLFHVLR.V**	Q9H3Z4[10]	P60904[10]		
SM	AAW27091.1	cAMP-dependent protein kinase type ii regulatory subunit	**R.RQsVAAESFDPEKDSDDNNEEER.Q**	P31323[114]	P31324[112]	P81900[84]	P07278[145]
SM	CPRT0000000835	Protein DEK	**K.EFDsDEDVPLSNLTSTK.V**	P35659[307]	Q7TNV0[308]		
SM	CPRT0000001365	scaffold attachment factor B	**R.s(1)Rs(2)PPIFQSVQHRPEILEYGHR.S**	Q9UQ35 [1958(1),1960(2)]	Q8BTI8[1958(2)]		
SM	CPRT0000002152	CDC37 cell division cycle 37 homolog	**K.WDHIEVsDDEDDTHPNIDTPSLFR.W**	Q16543[13]	Q61081[13]	Q24276[13]	P06101[14]

SM	CPRT0000002185	eukaryotic translation initiation factor 4E binding protein 2	**R.NsPAARSPPPDMIFLPEKAPNSDDK.T**	Q13542[65]	M/P70445[65]		
SM	CPRT0000002428	glyceraldehyde 3-phosphate dehydrogenase	**K.VINDNFEIVEGLMTTVHSFTAtQK.T**	P04406[184]	P16858[182]		P00359[182]
SM	CPRT0000004202	heat shock protein hsp 90-alpha	**K.EVsDDEAEKEETKNESEEAEDKPK.V**	P07900[231]	P07901[252]	P02828[219]	
SM	CPRT0000006031	calcium-regulated heat stable protein 1	**R.NRTEsQSESASTGEHGVGR.I**	Q9Y2V2[52]	Q9CR86[53]		
SM	CPRT0000006370	eukaryotic translation initiation factor 2 alpha subunit	**K.NIGGMILHsELSR.R**	P05198[49]	Q6ZWX6[49]		
SM	CPRT0000007774	heat shock protein 60	**R.NVIIESSWKsPK.I**	P10809[70]	P63038[70]		
SM	CPRT0000007860	glycogen synthase kinase 3	**K.EMVPGTANVSyISSR.Y**	P49840[279]	Q9WV60[216]	P18431[767]	P38615[199]
SM	CPRT0000009445	heterochromatin protein 1	**K.NSREsEEsGGEDEFQVEK.I**	P45973[11]	Q61686[11]	P05205[15]	
SM	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	**K.AASENRPNKANEsDEDEDEEPMPMPPQR.V**	P13861[78]	P31324[85]		
SM	CPRT0000012199	importin 7	**K.ALGsDEDEVDEESVR.Y**	O95373[903]	Q9EPL8[903]		

Supplementary Table 8 Summary of the phosphoproteins co-identified in schistosomula (14d), adult female (35 d) and adult male (35 d) schistosomes of *Schistosoma japonicum*

#	Description	worms	Protein ID	Sequence Coverage	Ion score	Expect	Peptides
1	Cysteine string protein	SS	AAP05964.1	7%	114	2.80E-07	**R.KLsTSGESLFHVLR.V**
		SM	AAP05964.1	6%	115	2.30E-07	**R.KLsTSGESLFHVLR.V**
		SF	AAP05964.1	6%	126	1.90E-08	**R.KLsTSGESLFHVLR.V**
2	Nuclear distribution gene c homolog	SS	AAP06040.1	7%	89	9.60E-05	**K.VGAsLDDPDEEEEDKGK.L**
		SM	AAP06040.1	5%	114	2.10E-07	**K.VGAsLDDPDEEEEDKGK.L**
		SF	AAP06040.1	5%	103	1.00E-06	**K.VGAsLDDPDEEEEDKGK.L**
3	Prothymosin alpha-b	SS	AAW27136.1	27%	113	4.20E-07	**R.HAEAEsEEDGTDDDASQDTK.G**
		SS	AAW27136.1	27%	94	3.20E-05	**R.KEAGDNASDDKAHsPDSR.H**
		SM	AAW27136.1	12%	80	7.60E-04	**R.KEAGDNASDDKAHsPDSR.H**
		SF	AAW27136.1	14%	112	1.20E-06	**K.EAGDNASDDKAHsPDSR.H**
		SF	AAW27136.1	14%	99	9.00E-06	**R.HAEAEsEEDGtDDDASQDTK.G**
4	B-cell receptor-associated protein-associated bap	SS	AAW27231.1	12%	67	2.40E-02	**K.VNDSDtEDVYPDTVEALKDELLK.L**
		SM	AAW27231.1	9%	87	2.30E-04	**K.VNDSDtEDVYPDTVEALKDELLK.L**
		SF	AAW27231.1	9%	201	2.00E-15	**K.VNDsDTEDVYPDTVEALKDELLK.L**
5	Transcription elongation regulator 1	SS	CPRT0000008924	9%	42	1.10E-02	**R.KLDDSPtVR.E**
		SM	CPRT0000008924	7%	64	6.50E-05	**R.KLDDSPtVR.E**
		SF	AAW27390.1	2%	68	1.70E-02	**R.KLDDSPtVR.E**
6	Epidermal growth factor receptor pathway substrate 8	SS	CAX73031.1	8%	92	5.90E-05	**R.YVNLGDSTFGMNRsPK.I**
		SS	CAX73031.1	8%	159	1.40E-11	**R.AGALDNDSHYHDINDsMLISR.A**
		SM	CAX73031.1	12%	90	5.30E-05	**R.YVNLGDSTFGMNRsPK.I**
		SF	AAX25971.2	6%	106	2.20E-06	**R.YVNLGDSTFGMNRsPK.I**

7	Sjchgc06768 protein	SS	AAX27349.2	22%	106	2.40E-06	**K.SMDDLsDTLVDLNNLTR.H**
		SS	AAX27349.2	22%	133	8.70E-09	**R.DIKNEHTLDDDQNIDLsPTIGNDEQIHHQSDHLIQHR.S**
		SS	AAX27349.2	22%	70	8.70E-03	**R.HRPAsVSGYLDECGLNR.S**
		SM	AAX27349.2	23%	82	2.90E-04	**K.SMDDLsDTLVDLNNLTR.H**
		SF	AAX27349.2	10%	90	2.00E-05	**K.SMDDLsDTLVDLNNLTR.H**
8	Fragile x mental retardation 1 isoform 16	SS	CAX70460.1	1%	110	5.20E-07	**R.QTNQLNHQPDSVsPTR.I**
		SM	CAX75242.1	5%	94	3.40E-05	**R.QTNQLNHQPDSVsPTR.I**
		SF	CAX70460.1	1%	80	1.90E-04	**R.QTNQLNHQPDSVsPTR.I**
9	Fragile x mental retardation 1	SF	CPRT0000004561	2%	74	4.70E-03	**R.RGsEDsDIVEPNNIPDGTPGDR.A**
		SS	CPRT0000004561	3%	96	1.10E-07	**R.RGsEDsDIVEPNNIPDGTPGDR.A**
		SM	CPRT0000004561	5%	65	1.40E-04	**R.RGsEDsDIVEPNNIPDGTPGDR.A**
10	Tetratricopeptide repeat domain 14	SS	CAX83069.1	8%	90	1.00E-04	**R.ESSLATGDDAVPSEsPKGDR.G**
		SS	CAX83069.1	8%	63	3.40E-02	**R.IKtPPLAPLVTSFR.R**
		SS	CAX83069.1	8%	93	6.40E-05	**R.RDHtPLsPTAPRPSAGYATHMER.S**
		SM	CAX83069.1	5%	64	2.50E-02	**R.IKtPPLAPLVTSFR.R**
		SF	CAX83069.1	10%	58	1.00E-01	**R.IKtPPLAPLVTSFR.R**
11	Cold shock domain protein A	SS	CPRT0000000132	7%	81	1.80E-06	**R.DNYHNEDGsPDMR.D**
		SM	CPRT0000000132	5%	79	2.60E-06	**R.DNYHNEDGsPDMR.D**
		SF	CPRT0000000132	7%	82	1.50E-06	**R.DNYHNEDGsPDMR.D**
12	Hydrocephalus inducing protein homolog	SS	CPRT0000000366	1%	149	3.60E-13	**R.KVsFSDLPIVSGVEER.N**
		SM	CPRT0000000366	1%	110	2.70E-09	**R.KVsFSDLPIVSGVEER.N**
		SF	CPRT0000000366	2%	85	8.00E-07	**R.KVsFSDLPIVSGVEER.N**
13	Arginine serine-rich splicing factor	SS	CPRT0000000669	23%	104	1.50E-08	**R.NSsYDGHRYPDHDQFSSFR.S**
		SS	CPRT0000000669	23%	60	1.70E-04	**R.sRsPLGAPVGR.L**

		SM	CPRT0000000669		99	5.20E-08	**R.NSsYDGHRYPDHDQFSSFR.S**
		SM	CPRT0000000669	18%	61	1.60E-04	**R.sRsPLGAPVGR.L**
		SF	CPRT0000000669	26%	92	2.60E-07	**R.NsSYDGHRYPDHDQFSSFR.S**
14	Peptidyl-prolyl isomerase G	SS	CPRT0000001254	8%	54	1.00E-03	**K.LISLPTTTHEQsPK.L**
		SM	CPRT0000001254	9%	62	1.70E-04	**K.LISLPTTTHEQsPK.L**
		SM	CPRT0000001254		59	2.50E-04	**K.SQVsPQLHLR.I**
		SM	CPRT0000001254		41	2.10E-02	**K.YQSKsPILMIsPK.L**
		SM	CPRT0000001254		61	1.70E-04	**R.GTsPSKPIIVITK.K**
		SF	CPRT0000001254	6%	64	1.00E-04	**K.LISLPTTTHEQsPK.L**
		SF	CPRT0000001254		62	0.00013	**K.SQVsPQLHLR.I**
		SF	CPRT0000001254		70	2.50E-05	**K.YQSKsPILMIsPK.L**
15	Coatomer protein subunit beta 2	SS	CPRT0000001534	1%	126	6.70E-11	**R.SNsPSVDQELQFR.N**
		SM	CPRT0000001534	5%	88	4.20E-07	**R.SNsPSVDQELQFR.N**
		SF	CPRT0000001534	1%	106	6.00E-09	**R.SNsPSVDQELQFR.N**
16	Eukaryotic translation initiation factor 5A	SS	CPRT0000001632	13%	85	1.20E-06	**M.StFEDEEFATGESGASKTEPK.Q**
		SM	CPRT0000001632	13%	51	2.90E-03	**M.StFEDEEFATGESGASKTEPK.Q**
		SF	CPRT0000001632	13%	76	9.10E-06	**M.StFEDEEFATGESGASKTEPK.Q**
17	CDC37 cell division cycle 37 homolog	SS	CPRT0000002152	16%	65	2.10E-04	**M.SCLNYSKWDHIEVsDDEDDTHPNIDTPSLFR.W**
		SM	CPRT0000002152	6%	129	6.80E-11	**K.WDHIEVsDDEDDTHPNIDTPSLFR.W**
		SF	CPRT0000002152	16%	151	4.10E-13	**K.WDHIEVsDDEDDTHPNIDTPSLFR.W**
18	14-3-3 family protein	SS	CPRT0000002347	11%	145	1.50E-12	**R.DNLNLWNPCNDGEKDTAAsPKGEEK.-**
		SM	CPRT0000002347	11%	110	5.40E-09	**R.DNLNLWNPCNDGEKDTAAsPKGEEK.-**
		SF	CPRT0000002347	11%	127	1.00E-10	**R.DNLNLWNPCNDGEKDTAAsPKGEEK.-**
19	Arginine serine-rich splicing factor	SS	CPRT0000002762	10%	36	4.00E-02	**R.RHsPPGYER.N**

		SM	CPRT0000002762	21%	34	7.70E-02	**R.RHsPPGYER.N**
		SF	CPRT0000002762	16%	36	3.90E-02	**R.RHsPPGYER.N**
20	Phosphate cytidylyltransferase ethanolamine	SS	CPRT0000002916	2%	48	2.70E-03	**R.RTQsLDSVLK.N**
		SM	CPRT0000002916	4%	45	5.80E-03	**R.RTQsLDSVLK.N**
		SF	CPRT0000002916	2%	42	1.00E-02	**R.RTQsLDSVLK.N**
21	Vacuolar protein sorting-associated protein	SS	CPRT0000004133	2%	117	4.20E-10	**R.KTsLTTVADELR.S**
		SM	CPRT0000004133	1%	97	4.10E-08	**R.KTsLTTVADELR.S**
		SF	CPRT0000004133	1%	99	2.40E-08	**R.KTsLTTVADELR.S**
22	Heat shock protein 90	SS	CPRT0000004202	3%	164	1.70E-14	**K.EVsDDEAEKEETKNESEEAEDKPK.V**
		SM	CPRT0000004202	6%	142	3.20E-12	**K.EVsDDEAEKEETKNESEEAEDKPK.V**
		SF	CPRT0000004202	10%	176	1.30E-15	**R.TKEVsDDEAEKEETKNESEEAEDKPK.V**
23	Myosin heavy chain	SS	CPRT0000005165	6%	55	6.80E-04	**R.ARKPTAsLAPEEE.-**
		SS	CPRT0000005165	6%	67	4.40E-05	**R.GVsVAPGAAPGHGNR.A**
		SM	CPRT0000005165	19%	55	6.60E-04	**R.ARKPTAsLAPEEE.-**
		SF	CPRT0000005165	9%	38	3.60E-02	**R.ARKPTAsLAPEEE.-**
		SF	CPRT0000005165		46	5.10E-03	**R.GVsVAPGAAPGHGNR.A**
24	Thymidylate kinase	SS	CPRT0000005313	7%	84	1.00E-06	**R.DSsGGNKFETMDFQK.R**
		SM	CPRT0000005313	6%	72	1.80E-05	**R.DSsGGNKFETMDFQK.R**
		SF	CPRT0000005313	7%	85	9.70E-07	**R.DSsGGNKFETMDFQK.R**
25	Pleckstrin homology domain family c member 1 isoform 2	SS	CPRT0000005420	2%	83	1.10E-06	**R.DIsPIGGYLHTGR.Y**
		SM	CPRT0000005420	1%	77	4.30E-06	**R.DIsPIGGYLHTGR.Y**
		SF	CPRT0000005420	1%	72	1.30E-05	**R.DIsPIGGYLHTGR.Y**
26	Coatomer subunit beta	SS	CPRT0000005681	1%	75	6.80E-06	**R.SHsPVNTLLNSH.-**
		SM	CPRT0000005681	1%	58	3.60E-04	**R.SHsPVNTLLNSH.-**

		SF	CPRT0000005681	2%	66	4.90E-05	**R.SHsPVNTLLNSH.-**
27	Calnexin	SS	CPRT0000005797	9%	66	9.20E-05	**R.DNsEEEAPNEFEGNENVPAAK.Q**
		SM	CPRT0000005797	7%	54	1.40E-03	**R.DNsEEEAPNEFEGNENVPAAK.Q**
		SF	CPRT0000005797	7%	53	2.10E-03	**R.DNsEEEAPNEFEGNENVPAAK.Q**
28	Phosphofructokinase	SS	CPRT0000006130	1%	77	4.30E-06	**R.RGtELLPGMEGK.Y**
		SM	CPRT0000006130	1%	77	3.70E-06	**R.RGtELLPGMEGK.Y**
		SF	CPRT0000006130	1%	61	1.60E-04	**R.RGtELLPGMEGK.Y**
29	RNA-binding protein 4	SS	CPRT0000006221		135	1.50E-11	**R.YGPAWDDGYGGPYAPPPRNsPR.G**
		SM	CPRT0000006221	22%	130	4.10E-11	**R.YGPAWDDGYGGPYAPPPRNsPR.G**
		SF	CPRT0000006221	9%	115	1.50E-09	**R.YGPAWDDGYGGPYAPPPRNsPR.G**
30	Dentin sialophosphoprotein precursor	SS	CPRT0000006676	8%	55	6.90E-04	**K.GIAsPGNYGDAR.R**
		SS	CPRT0000006676	8%	75	1.20E-05	**K.NTHsPANNTESLREPPHTR.S**
		SS	CPRT0000006676	8%	53	1.10E-03	**R.MHsIsPPYNDR.S**
		SM	CPRT0000006676	5%	48	3.00E-03	**K.GIAsPGNYGDAR.R**
		SF	CPRT0000006676	1%	57	3.70E-04	**K.GIAsPGNYGDAR.R**
31	Sjchgc01166 protein	SS	CPRT0000006702		59	2.20E-04	**R.RQsLQNLLR.L**
		SM	CPRT0000006702	9%	59	2.20E-04	**R.RQsLQNLLR.L**
		SF	CPRT0000006702	2%	59	2.20E-04	**R.RQsLQNLLR.L**
32	Plasminogen activator inhibitor 1 rna-binding protein	SS	CPRT0000007051	5%	93	2.20E-07	**R.VSRsPNANEPPPVVFEDVQITSAK.E**
		SM	CPRT0000007051	5%	98	6.30E-08	**R.VSRsPNANEPPPVVFEDVQITSAK.E**
		SF	CPRT0000007051	5%	92	2.60E-07	**R.VSRsPNANEPPPVVFEDVQITSAK.E**
33	Placenta-specific gene 8 protein	SS	CPRT0000007659	11%	91	2.20E-07	**MEsPTTKQPYAVR.Q**
		SM	CPRT0000007659	11%	70	2.40E-05	**MEsPTTKQPYAVR.Q**
		SF	CPRT0000007659	11%	47	4.70E-03	**MEsPTTKQPYAVR.Q**

34	Sjchgc05800 protein	SS	CPRT0000007759	14%	56	6.90E-04	**K.HLSDDVHFtPFDR.K**
		SS	CPRT0000007759	14%	79	3.60E-06	**R.QSVNIsPTSDLHSQGK.F**
		SS	CPRT0000007759	14%	65	6.80E-05	**R.RTsELSTDLANLK.L**
		SM	CPRT0000007759		74	1.00E-05	**K.HLSDDVHFtPFDR.K**
		SM	CPRT0000007759		81	4.10E-06	**K.HPASNLGDITITQGPDSHFRPFTPDQsPK.T**
		SM	CPRT0000007759		57	3.80E-04	**K.SGsASEIAADIHK.N**
		SM	CPRT0000007759	16%	88	3.80E-07	**R.RTsELSTDLANLK.L**
		SF	CPRT0000007759	16%	89	3.30E-07	**R.QSVNIsPTSDLHSQGK.F**
		SF	CPRT0000007759		77	4.60E-06	**R.RTsELSTDLANLK.L**
35	Glycogen synthase kinase 3	SS	CPRT0000007860	2%	59	3.60E-04	**K.EMVPGTANVSyISSR.Y**
		SM	CPRT0000007860	2%	65	8.60E-05	**K.EMVPGTANVSyISSR.Y**
		SF	CPRT0000007860	2%	68	4.20E-05	**K.EMVPGTANVSyISSR.Y**
36	Ubx domain containing 2	SS	CPRT0000008289	8%	56	6.60E-04	**R.LSHMPDNsDDEQAR.W**
		SM	CPRT0000008289	3%	64	1.10E-04	**R.LSHMPDNsDDEQAR.W**
		SF	CPRT0000008289	3%	67	5.50E-05	**R.LSHMPDNsDDEQAR.W**
37	Sjchgc09590 protein	SS	CPRT0000009921	7%	183	2.30E-16	**K.QEALLAEQVDDIPKEHLFVEsDEER.Y**
		SS	CPRT0000009921	7%	41	4.80E-02	**K.VIKENNMLAEEsDEQsNNELECELK.Q**
		SM	CPRT0000009921	7%	207	9.60E-19	**K.QEALLAEQVDDIPKEHLFVEsDEER.Y**
		SM	CPRT0000009921	7%	71	1.80E-05	**R.KLEEELEEVDsR.A**
		SF	CPRT0000009921	2%	201	3.50E-18	**K.QEALLAEQVDDIPKEHLFVEsDEER.Y**
38	cAMP-dependent protein kinase type ii-alpha regulatory subunit	SS	CPRT0000010982	20%	140	6.30E-12	**K.AASENRPNKANEsDEDEDEEPMPMPPQR.V**
		SS	CPRT0000010982	20%	90	3.20E-07	**K.ANEsDEDEDEEPMPMPPQR.V**
		SM	CPRT0000010982	13%	119	6.70E-10	**K.AASENRPNKANEsDEDEDEEPMPMPPQR.V**
		SF	CPRT0000010982	13%	104	2.40E-08	**K.AASENRPNKANEsDEDEDEEPMPMPPQR.V**

		SS	CPRT0000012199	1%	118	4.00E-10	**K.ALGsDEDEVDEESVR.Y**
39	Importin 7	SM	CPRT0000012199	1%	114	1.20E-09	**K.ALGsDEDEVDEESVR.Y**
		SF	CPRT0000012199	4%	127	5.60E-11	**K.ALGsDEDEVDEESVR.Y**

Supplementary Table 9 List of differently identified phosphoproteins being highly repeatable between adult male and adult females

Samples	Protein ID	Description	Protein Score	Miss cleavage	Ion score	Expect	Peptides
SM	CAX73091.1	hypotheticial protein	78	1	78	8.10E-04	R.KEsSSDLLSR.Y
SM	AAW24704.1	sjchgc02374 protein	150	0	110	9.20E-07	R.AMsHFETNSIENSLPR.V
SM	AAW26183.1	troponin I	114	1	72	4.40E-03	K.YALEEKDEVANtPK.-
SM	AAW26505.1	sjchgc02563 protein	146	1	65	2.40E-02	R.VRsVSNFELENNR.E
SM	AAW26770.1	sjchgc06242 protein	107	0	107	1.90E-06	R.NNPFTTMsPLLNELER.D
SM	AAX25934.2	endothelin-converting enzyme 1	97	0	97	1.50E-05	K.SDsPTNSLNLGQNFK.Y
SM	CPRT0000005334	hypothetical protein	85	0	87	6.30E-07	K.MQTGKPASSVHFsPTR.V
SM	CPRT0000005690	sjchgc00797 protein	98	0	99	4.20E-08	K.QVPVYNALsPSPGPLNFER.Y
SM	CPRT0000006771	wd-40 repeat protein	133	0	94	1.20E-07	R.LIKPPLsVNNYPVGHNHR.L
				0	41	1.90E-02	R.IDQPVMDDLsAR.Q
SM	CPRT0000008409	af287985_1synapsin isoform	72	2	73	1.40E-05	R.RFSsGDLQGELADKR.M
SM	CPRT0000008751	glucose transport protein	97	0	97	5.90E-08	K.QGNTDGPAsESLLHSR.N
SM	CPRT0000010244	Hypothetical protein	45	0	46	4.10E-03	K.LPsPEYYR.E
SF	CPRT0000000687	ferritin-1 heavy chain	63	1	64	1.40E-04	R.VGTGLGEYTFDKETLHGEsD.-
SF	CPRT0000003518	disulfide-isomerase precursor	59	2	60	3.90E-04	R.SLPDKWQHDMFQDARsPK.G
SF	CPRT0000007069	translationally-controlled tumor protein homolog	88	0	90	4.10E-07	K.LIAANPSGEEGQEEVsDSTER.V

Supplementary Table 10 List of all phosphopeptides identified in schistosomula (SS), adult females (SF), and adult males (SM) of *S. japoncum* in quintuplicate MS analyses

Worms	#	Protein ID	Description	MW	Protein Score	Sequence Coverage	Miss cleavage	Ion score	Expect	Peptides
SS	1	AAD56715.1	14-3-3 protein	28979	86	14%	1	66	3.40E-02	**R.AFDTsIGELDSLQDDSYKDSTLIMQLLR.D**
SS	2	AAP05957.1	transmembrane protein 55a	26311	67	7%	0	67	1.80E-02	**R.FLQGPATHGTFGsPQSLR.L**
SS	3	AAP05964.1	cysteine string protein	24000	150	7%	1	114	2.80E-07	**R.KLsTSGESLFHVLR.V**
SS	4	AAP06040.1	nuclear distribution gene c homolog	37878	160	7%	1	89	9.60E-05	**K.VGAsLDDPDEEEEDKGK.L**
SS	5	AAP06130.1	rab guanine nucleotide exchange factor 1	17450	105	7%	1	105	2.30E-06	**R.ITSDFDDKLsPER.S**
SS	6	AAP06137.1	n-myc downstream regulated	38028	80	7%	0	62	2.90E-02	**K.LHDEsPINEYDDHNIA.-**
							1	60	5.20E-02	**R.RMsSTIPVAR.N**
SS	7	AAP06201.1	sjchgc01517 protein	31916	108	4%	1	57	0.13	**R.RDsDDEFDEFGR.K**
SS	8	AAP06212.1	fha modulated abc efflux pump with fused atpase and integral membrane subunits	27784	63	8%	2	63	6.20E-02	**R.HKVEEDDGDsNDDLDDNSNSKR.L**
SS	9	AAW24704.1	sjchgc02374 protein	24307	111	7%	0	111	3.60E-07	**R.AMsHFETNSIENSLPR.V**
SS	10	AAW24985.1	chromobox protein homolog 1 (heterochromatin protein 1 homolog beta)	27252	177	13%	0	67	1.50E-02	**R.LTWHTPENRPPGtPR.S**
SS	11	AAW25087.1	troponin	37932	110	5%	2	110	9.00E-07	**M.sDDEQRDEEHDDGKSEAK.I**
SS	12	AAW25147.1	troponin t	38926	126	8%	2	128	2.30E-08	**M.sDDEQsPQPSPAFIPKDEEHDDGKSEAK.I**
SS	13	AAW25178.1	sjchgc09526 protein	31353	151	12%	0	151	1.00E-10	**R.SLDStDNPVLIAADNLVHDVILSATQTHLEETQVSR.I**
SS	14	AAW25812.1	eukaryotic translation initiation factor subunit C	27962	96	7%	1	97	2.00E-05	**R.IESRPLHLssDEEDIKR.I**
SS	15	AAW26271.1	sjchgc09241 protein	49819	341	14%	1	105	2.90E-06	**R.NMEATGGQsIDEENRK.K**
SS	16	AAW26418.1	microtubule-associated protein futsch	105262	107	2%	1	77	2.50E-03	**K.DNQEVHsDIDEMEKEFVIPYQR.N**
SS	17	AAW26505.1	sjchgc02563 protein	35545	97	6%	1	76	1.90E-03	**R.VRsVSNFELENNR.E**

SS	18	AAW26588.1	sjchgc01243 protein	38311	134	8%	0	62	5.30E-02	**K.NHNITDsPVMSNKPK.L**
							0	72	4.10E-03	**R.HFsPVAIASSTPK.L**
SS	19	AAW26700.1	sjchgc01107 protein	21285	101	14%	1	101	3.80E-06	**K.NTDDENANSERDsPEPLPLIPATIWTR.K**
SS	20	AAW26770.1	sjchgc06242 protein	21453	82	8%	0	82	6.00E-04	**R.NNPFTTMsPLLNELER.D**
SS	21	AAW26771.1	nascent polypeptide-associated complex subunit alpha	24461	241	15%	0	112	3.40E-07	**K.TVIAEEsEDDEEPDASGLSEK.D**
							1	129	6.40E-09	**K.tVIAEESEDDEEPDASGLSEKDIELIMQQAGVSR.S**
							1	129	2.10E-08	**K.TVIAEEsEDDEEPDASGLSEKDIELIMQQAGVSR.S**
SS	22	AAW26951.1	myosin regulatory light chain	22748	248	26%	1	116	3.90E-07	**R.ATsNVFGMFPQNQIQEFKEAFSLIDQNR.D**
SS	23	AAW27091.1	cAMP-dependent protein kinase type ii regulatory subunit	19623	91	13%	2	91	1.00E-04	**R.RQsVAAESFDPEKDSDDNNEEER.Q**
SS	24	AAW27129.1	pyruvate kinase	61146	173	7%	0	105	2.90E-06	**.MLGSGLSFGGQSFHGVSsVSR.F**
SS	25	AAW27136.1	prothymosin alpha-b	14949	273	27%	0	113	4.20E-07	**R.HAEAEsEEDGTDDDASQDTK.G**
							2	94	3.20E-05	**R.KEAGDNASDDKAHsPDSR.H**
SS	26	AAW27151.1	sjchgc09494 protein	13854	80	20%	0	80	1.30E-03	**K.RPIPVGsDDsDAETESNVLCNNELK.T**
SS	27	AAW27166.1	calcium-regulated heat stable protein 1	13101	142	34%	1	103	5.10E-06	**R.NRTEsQSESASTGEHGVGR.I**
SS	28	AAW27231.1	B-cell receptor-associated protein-associated bap	28074	146	12%	1	67	2.40E-02	**K.VNDSDtEDVYPDTVEALKDELLK.L**
							2	81	9.90E-04	**R.LLDQSKVNDsDTEDVYPDTVEALKDELLK.L**
SS	29	AAX24429.2	sjchgc08077 protein	25746	90	20%	0	90	7.50E-05	**R.SLsQGSLLAVASLAGLR.H**
SS	30	AAX24643.2	sjchgc07823 protein	23091	66	12%	0	66	2.80E-02	**R.SNQADAHsDDsDDPLDQFMAGINEEVR.T**
SS	31	AAX24755.2	microtubule-associated protein	29239	107	10%	0	107	2.90E-06	**K.SNKPTDTSsPPASLFDFESFLCDMMSK.L**
SS	32	AAX25017.2	sjchgc04120 protein	19296	72	6%	0	72	0.004	**K.EHLFVEsDEER.Y**
SS	33	AAX25098.2	scaffold attachment factor b-related	22094	188	25%	0	97	1.10E-05	**K.VLSsPSQSFRPTNHAFFLSSAYENR.N**
SS	34	AAX25853.2	ubqln1 protein	28521	74	15%	1	74	1.70E-03	**R.ESTRsPNNTPQTGTAGLNTFAGMQQAMQAQVMQNPELLR.N**

SS	35	AAX26169.2	adhesion regulating molecule 1	25289	66	15%	0	66	3.50E-02	**R.HLNAGHLDESNVSTSILGAATTPSSGAsPTGSNALR.T**
SS	36	AAX26431.2	sjchgc07306 protein	13244	65	21%	1	62	4.90E-02	**R.KDGsDDHKPSSYQR.K**
SS	37	AAX26939.2	sjchgc08161 protein	26837	62	4%	0	62	0.035	**K.SQVsPQLHLR.I**
SS	38	AAX27349.2	sjchgc06768 protein	52587	348	22%	0	106	2.40E-06	**K.SMDDLsDTLVDLNNLTR.H**
							1	133	8.70E-09	**R.DIKNEHTLDDDQNIDLsPTIGNDEQIHHQSDHLIQHR.S**
							0	70	8.70E-03	**R.HRPAsVSGYLDECGLNR.S**
SS	39	AAX27846.2	tensin 3	50789	138	4%	0	138	1.70E-09	**R.GGGASsMIEGLSHIDDHQHPR.A**
SS	40	AAX28334.2	cytoplasmic dynein intermediate chain 2 (dhic-2)	25952	109	6%	0	109	1.00E-06	**R.ELEsPSHDVNDSILQR.N**
SS	41	AAX28429.2	eukariotic translation initiation factor epsilon subunit	28374	98	8%	1	99	6.00E-06	**R.IEsDADDEQSESFIITELKR.T**
SS	42	ACE06825.1	thymidylate kinase	25311	211	7%	2	127	1.70E-08	**R.DSsGGNKFETMDFQKR.V**
SS	43	CAX69413.1	sjchgc08095 protein	36511	114	11%	0	93	4.60E-05	**R.QISVsPTYYHDTSPR.N**
SS	44	CAX70347.1	eukaryotic translation initiation factor subunit 7 zeta	73563	114	4%	1	115	1.60E-07	**K.TYSFPEENPFKDDEDEDsDNPNPSHNR.N**
SS	45	CAX70460.1	fragile x mental retardation 1 isoform 16	87407	110	1%	0	110	5.20E-07	**R.QTNQLNHQPDSVsPTR.I**
SS	46	CAX72702.1	troponin T	38401	62	0%	1	62	0.081	**M.sDDEQSPQPSPAFIPNDDGKSEAK.I**
SS	47	CAX73031.1	epidermal growth factor receptor pathway substrate 8	57535	303	8%	0	159	1.40E-11	**R.AGALDNDSHYHDINDsMLISR.A**
							1	92	5.90E-05	**R.YVNLGDSTFGMNRsPK.I**
SS	48	CAX73091.1	hypotheticial protein	25814	77	4%	1	77	1.00E-03	**R.KESsSDLLSR.Y**
SS	49	CAX74150.1	zinc c2h2-type domain-containing protein	106115	226	5%	0	68	8.20E-03	**R.HTPHHPPPPPTsPSFFVGR.G**
							0	79	5.30E-04	**R.QSLPMMHsPSSTPR.N**
SS	50	CAX74259.1	cell division cycle and apoptosis regulator protein 1	125508	255	6%	1	90	1.00E-04	**K.ALQLVTIDKsPQVPEEQVKPVNAESGSK.L**

							2	54	2.50E-01	**R.RRsPLDLASTR.H**
SS	51	CAX74794.1	proliferation-associated protein 2G4	42827	82	5%	1	83	6.20E-04	**M.sDQEsDAEQDVLDDTVVNKYK.M**
SS	52	CAX83069.1	tetratricopeptide repeat domain 14	103388	352	8%	1	90	1.00E-04	**R.ESSLATGDDAVPSEsPKGDR.G**
							1	63	3.40E-02	**R.IKtPPLAPLVTSFR.R**
							1	93	6.40E-05	**R.RDHtPLsPTAPRPSAGYATHMER.S**
							1	77	0.0019	**R.RSEsDENLAELDQFVAQLK.A**
							0	60	0.024	**R.sESDENLAELDQFVAQLK.A**
SS	53	P91800.1	translationally-controlled tumor protein homolog	19364	111	12%	0	112	6.00E-07	**K.LIAANPSGEEGQEEVsDSTER.V**
SS	54	CPRT0000000132	cold shock domain protein A	23801	149	7%	0	81	1.80E-06	**R.DNYHNEDGsPDMR.D**
SS	55	CPRT0000000218	phosphatase 2A inhibitor i2pp2a	29186	70	6%	0	71	2.20E-05	**K.EFHLGDsGEPSSTYTK.I**
SS	56	CPRT0000000226	sjchgc09295 protein	304753	78	3%	1	42	1.60E-02	**R.EMQTSESsPRDEIK.L**
								39	4.15E-02	**R.QPHENISTQTDPITQVHVTsPK.T**
SS	57	CPRT0000000284	transducin-like enhancer protein 4	130640	94	2%	0	88	4.10E-07	**R.DAVsPQSYVIGSNK.S**
SS	58	CPRT0000000366	hydrocephalus inducing protein homolog	111656	149	1%	1	149	3.60E-13	**R.KVsFSDLPIVSGVEER.N**
SS	59	CPRT0000000480	splicing arginine serine-rich 2	17962	57	15%	2	29	3.00E-01	**R.YGRsPPRIDGMVSLK.V**
							1	30	1.60E-01	**R.YRLPssPR.H**
SS	60	CPRT0000000616	talin 2	316513	89	2%	1	86	1.20E-06	**R.KQTDLTQAAVEFNQATGDLLSSYsPGTFR.R**
SS	61	CPRT0000000626	splicing factor 3b subunit 1-related	124272	61	5%	1	52	2.70E-03	**R.LLMIsPARVDPFADGDQTPDHR.L**
SS	62	CPRT0000000669	arginine serine-rich splicing factor	31746	291	23%	0	42	0.011	**R.ANYsPPFVR.E**
							1	28	0.28	**R.GRsPPDSYNGR.S**
							1	104	1.50E-08	**R.NSsYDGHRYPDHDQFSSFR.S**
							2	31	0.21	**R.RSsPGRIPFPVNHR.G**
							1	60	1.70E-04	**R.sRsPLGAPVGR.L**
SS	63	CPRT0000000786	pyruvatekinase	58347	69	4%	1	49	0.0043	**R.VVKLEDAETKPIVMVPsITHFDD.-**
SS	64	CPRT0000000835	protein DEK	45498	124	5%	1	64	1.30E-04	**K.KEFDsDEDVPLSNLTSTK.V**

SS	65	CPRT0000000881	troponin I	103135	49	1%	0	50	2.30E-03	**K.KPVLPSKPLsPTSYPTK.I**
SS	66	CPRT0000001123	lethal giant larvae homolog 1	150057	126	3%	0	49	3.80E-03	**R.MLGMsLTSGTGSTSKPEK.D**
							1	77	9.20E-06	**R.sLRPDtPKLEEQVEPSLPVPPAPR.I**
SS	67	CPRT0000001187	elongation factor 2	95305	55	1%	2	31	2.00E-01	**R.FtDtRKDEQER.S**
SS	68	CPRT0000001216	centromeric protein	91005	61	3%	0	61	1.70E-04	**R.EAsFEEHQIMR.D**
SS	69	CPRT0000001254	peptidyl-prolyl isomerase G	117498	259	8%	0	54	1.00E-03	**K.LISLPTTTHEQsPK.L**
							1	34	1.10E-01	**K.YQsKSPILMIsPK.L**
							1	78	5.70E-06	**R.NRNPStSPsSFAGVSDNLR.D**
SS	70	CPRT0000001337	zinc c2h2-type domain-containing protein	99949	134	8%	1	74	1.10E-05	**R.DARQsPPPIPPAPER.L**
SS	71	CPRT0000001365	scaffold attachment factor B	83496	206	10%	1	94	2.10E-07	**R.sRsPPIFQSVQHRPEILEYGHR.S**
SS	72	CPRT0000001534	coatomer protein subunit beta 2	74897	124	1%	0	126	6.70E-11	**R.SNsPSVDQELQFR.N**
SS	73	CPRT0000001619	beta chain spectrin	77788	141	7%	0	86	8.60E-07	**R.AAtLPSGVAPESQVTSSSSASGK.K**
SS	74	CPRT0000001632	eukaryotic translation initiation factor 5A	17852	84	13%	1	85	1.20E-06	**M.StFEDEEFATGESGASKTEPK.Q**
SS	75	CPRT0000001698	transformer-2 protein	18426	44	13%	1	33	1.30E-01	**R.YsRDsDIDPIPR.K**
SS	76	CPRT0000001788	regulatory factor x domain containing 2	87924	75	3%	0	70	2.10E-05	**R.NLsDHAIIQSR.R**
SS	77	CPRT0000001848	Nuclear polyadenylated RNA-binding protein NAB2	73363	41	5%	0	42	0.028	**K.LSQQTPQLVVNLNEtDEDEDIATLLAEAER.H**
SS	78	CPRT0000001880	adenylate cyclase-associated protein 1	51932	42	3%	1	42	1.90E-02	**R.TsPIKTSSESGNPLSVK.E**
SS	79	CPRT0000001895	sjchgc06333 protein	59613	73	2%	1	74	1.20E-05	**R.SKsEIINQYMNQADK.S**
SS	80	CPRT0000001920	serine arginine repetitive matrix 1	53515	44	2%	1	44	8.90E-03	**R.StsPSKLEQKPK.S**
SS	81	CPRT0000002080	protein cGMP- type ii	108795	69	1%	1	69	3.60E-05	**K.ILDLVSPTKsQDELQIK.S**
SS	82	CPRT0000002094	short coiled-coil protein	13285	46	24%	1	48	9.30E-03	**K.LRSENQILGQYIENMMANSSVFQSTsPR.V**
SS	83	CPRT0000002108	hla-b-associated transcript 3	151616	41	2%	0	44	2.40E-02	**R.NVFDDDDLHDDDLPFLDAYSDLPSDEIsPPILLK.Q**
SS	84	CPRT0000002121	nuclear receptor coactivator 2	50993	87	4%	0	87	8.50E-07	**M.TAsPEQVDNSFQSIPESETHFR.S**
SS	85	CPRT0000002124	nuclear hormone receptor ftz-f1 beta	101827	44	7%	2	31	2.80E-01	**M.AASEVKsPADIQDDLKDESLK.A**
SS	86	CPRT0000002152	cdc37 cell division cycle 37 homolog	45458	81	16%	0	42	0.03	**K.WDHIEVSDDEDDtHPNIDTPSLFR.W**

							1	65	2.10E-04	**M.SCLNYSKWDHIEVsDDEDDTHPNIDTPSLFR.W**
SS	87	CPRT0000002181	heterogeneous nuclear ribonucleoprotein H	53750	83	6%	0	84	2.20E-06	**R.sPAYNTGGSQGSQYNNYPLHDDMHYADDIR.Y**
SS	88	CPRT0000002239	phosphofurin acidic cluster sorting protein 1	125562	101	1%	0	102	1.60E-08	**R.NIsPESTSHGTISAPR.S**
SS	89	CPRT0000002258	adducin 1	91507	66	8%	0	67	6.20E-05	**M.PsSNVANEVMLSGKPEK.F**
SS	90	CPRT0000002292	SAPK substrate protein 1	82066	134	6%	1	107	1.20E-08	**K.GLEEAMEWIIENDsGDEKEEALDGTGETK.K**
SS	91	CPRT0000002347	14-3-3 family protein	25816	144	11%	2	145	1.50E-12	**R.DNLNLWNPCNDGEKDTAAsPKGEEK.-**
SS	92	CPRT0000002428	glyceraldehyde 3-phosphate dehydrogenase	36566	68	7%	0	66	0.00013	**K.VINDNFEIVEGLMTTVHSFTAtQK.T**
SS	93	CPRT0000002522	tubulin-specific chaperone C	79727	45	1%	0	45	5.00E-03	**K.HStPPILSSK.R**
SS	94	CPRT0000002551	Importin alpha-2 subunit	17579	56	6%	1	47	3.40E-03	**R.RTDQsIELR.K**
SS	95	CPRT0000002705	hypotherical protein	27929	85	8%	1	85	1.50E-06	**K.DKPDAESDLFAsDsEDDKEAER.I**
SS	96	CPRT0000002762	arginine serine-rich splicing factor	24795	46	10%	1	36	4.00E-02	**R.RHsPPGYER.N**
SS	97	CPRT0000002896	ubiquitin specific peptidase 7	97653	47	5%	1	42	1.10E-02	**K.QGKLsPNTPK.M**
SS	98	CPRT0000002916	phosphate cytidylyltransferase ethanolamine	47612	48	2%	1	48	2.70E-03	**R.RTQsLDSVLK.N**
SS	99	CPRT0000003012	eukaryotic translation initiation factor 3 subunit 10	75064	44	2%	1	45	9.10E-03	**R.DRNPHTVsFDNTPSYR.N**
SS	100	CPRT0000003089	abl interactor 2	64196	55	2%	1	55	6.30E-04	**R.RGsSSLSGQLPGR.Q**
SS	101	CPRT0000003155	transformer-2 protein	22830	81	20%	2	41	2.70E-02	**R.RTDsPIASNGYRNsVsPR.G**
SS	102	CPRT0000003210	hypothetical protein	39314	178	19%	2	127	9.30E-11	**K.RLsIDTTGEDEPDKENNANLSLPNVR.S**
							2	56	0.00077	**R.RGsVKHESTTQKPLNQLFK.R**
SS	103	CPRT0000003320	rna binding single stranded interacting protein 3 isoform 1	99442	45	1%	1	45	6.50E-03	**R.KSsPVNNSAEVR.M**
SS	104	CPRT0000003479	RAS-gap sh3 binding protein related	40758	89	4%	0	90	3.10E-07	**M.VSVVENNPsPDSAFTVVR.M**
SS	105	CPRT0000003518	disulfide-isomerase precursor	26123	66	7%	2	92	7.40E-05	**R.SLPDKWQHDMFQDARsPK.G**

SS	106	CPRT0000003603	sjchgc09241 protein	39546	445	21%	1	34	6.20E-02	**K.AADTsVVKR.D**
							0	150	3.70E-13	**K.EFtPPPDGVAVGILESNPKPR.A**
							1	114	1.10E-09	**K.KSsFIDESITVAPEATR.S**
SS	107	CPRT0000003639	myelin expression factor 2	60032	93	2%	1	94	1.10E-07	**R.SIKYEDSEsPDIPSR.G**
SS	108	CPRT0000003713	glycyl-tRNA synthetase	117527	102	4%	1	105	1.90E-08	**K.ATSESHLsADEVNVEVLHDKAESSTLSNNPK.H**
							1	96	4.30E-05	**K.AtSESHLSADEVNVEVLHDKAESSTLSNNPK.H**
SS	109	CPRT0000003724	tetratricopeptide repeat protein 14	91798	180	7%	0	30	3.90E-01	**R.QNHAPDQsPPGFLsPNR.S**
SS	110	CPRT0000003765	RNA-binding protein	74909	48	1%	1	49	2.80E-03	**R.sVDKYDHHGSR.Q**
SS	111	CPRT0000003898	sjchgc07201 protein	53500	78	2%	0	79	2.10E-06	**R.GSHsPISLTER.F**
SS	112	CPRT0000003916	GPI-anchored membrane protein 1	56776	110	7%	0	31	0.37	**K.ATVPCFTNHNLEENNIDQsPITR.M**
							0	92	2.00E-07	**R.SSsPLSSGNINQTISLK.S**
SS	113	CPRT0000004133	vacuolar protein sorting-associated protein	383946	116	2%	1	117	4.20E-10	**R.KTsLTTVADELR.S**
SS	114	CPRT0000004172	sjchgc08522 protein	30379	46	6%	0	34	1.00E-01	**R.sLTGEQNLSHSTTLK.H**
SS	115	CPRT0000004202	heat shock protein 90	82188	323	3%	2	164	1.70E-14	**K.EVsDDEAEKEETKNESEEAEDKPK.V**
SS	116	CPRT0000004239	suppressor of fused	104462	72	4%	0	72	2.00E-05	**K.NNLVNSPtELTNLVGGALGFR.T**
SS	117	CPRT0000004242	protein phosphatase	76968	50	5%	0	53	1.40E-03	**R.VTsLVNLNSPSDTLLR.G**
SS	118	CPRT0000004379	short isoform h	247103	82	2%	1	72	1.50E-05	**R.VGERGEMSLsPEMR.L**
SS	119	CPRT0000004561	fragile x mental retardation 1	69914	95	3%	1	96	1.10E-07	**R.RGsEDsDIVEPNNIPDGTPGDR.A**
SS	120	CPRT0000004658	guanine monphosphate synthetase	58090	103	3%	0	104	1.20E-08	**R.QSNLsGGGMHPHIESR.N**
SS	121	CPRT0000004687	nuclear cap binding protein subunit 80kda	67809	47	2%	2	47	5.40E-03	**R.RRsDsFDDDDFR.F**
SS	122	CPRT0000004688	ankyrin 23 unc44	264545	45	0%	0	47	5.30E-03	**R.SLNGISSTsPNLNISR.E**
SS	123	CPRT0000004690	mucoidy inhibitor A	69128	133	3%	0	70	2.30E-05	**R.GGsIENTYATGLR.A**
							1	64	7.50E-05	**R.RDHsPAIPISR.N**
SS	124	CPRT0000004960	sh3 domain-binding glutamic acid-rich-like protein	38619	80	3%	1	82	1.20E-06	**R.KTsDQPVESIR.K**
SS	125	CPRT0000004986	sjchgc02101 protein	30544	113	4%	1	114	9.70E-10	**R.RSsNTNSEESPVTR.R**

SS	126	CPRT0000005000	alpha fucosyltransferase	218756	60	1%	1	57	3.80E-04	**R.IAISRLsPTAGR.S**
SS	127	CPRT0000005165	myosin heavy chain	204958	349	6%	1	55	6.80E-04	**R.ARKPTAsLAPEEE.-**
							0	67	4.40E-05	**R.GVsVAPGAAPGHGNR.A**
SS	128	CPRT0000005313	thymidylate kinase	25311	211	7%	1	84	1.00E-06	**R.DSsGGNKFETMDFQK.R**
SS	129	CPRT0000005334	Conserved hypothetical protein	53707	86	8%	0	86	7.00E-07	**K.MQTGKPASSVHFsPTR.V**
SS	130	CPRT0000005336	protein cAMP dependent type isoform cra_a	53108	37	5%	0	37	3.90E-02	**R.GLMAAsPSGVNLTR.R**
SS	131	CPRT0000005420	pleckstrin homology domain family c member 1 isoform 2	77049	88	2%	0	83	1.10E-06	**R.DIsPIGGYLHTGR.Y**
SS	132	CPRT0000005681	coatomer subunit beta	120852	74	1%	0	75	6.80E-06	**R.SHsPVNTLLNSH.-**
SS	133	CPRT0000005690	sjchgc00797 protein	18016	131	20%	0	99	4.20E-08	**K.QVPVYNALsPSPGPLNFER.Y**
SS	134	CPRT0000005708	zinc finger protein	90547	53	3%	0	53	2.80E-03	**K.AVEsEDDDDDDDMVPVGEIDDDQPLLTK.S**
SS	135	CPRT0000005797	calnexin	65986	145	9%	0	79	4.80E-06	**K.NAENEELEEsGEDDIVQVSK.G**
							0	66	9.20E-05	**R.DNsEEEAPNEFEGNENVPAAK.Q**
SS	136	CPRT0000005999	transcription initiation factor tfiid subunit 3	32009	47	6%	1	48	5.70E-03	**R.DRsPISTSAQSEQALDAYER.A**
SS	137	CPRT0000006031	calcium-regulated heat stable protein 1 (calcium-regulated heat-stable protein of 24 kda)	13101	142	18%	1	40	0.04	**.MEPPPNPASNLVIPsPIFHKR.N**
SS	138	CPRT0000006118	p38 MAPK	29378	291	9%	2	147	7.50E-13	**K.SKsPGPPPTEEVASSISAPLKKPR.L**
SS	139	CPRT0000006130	Phosphofructokinase	86159	75	1%	1	77	4.30E-06	**R.RGtELLPGMEGK.Y**
SS	140	CPRT0000006131	uncoordinated family member (unc-44)	233254	109	1%	2	111	3.50E-09	**R.KRsDPVNLGLSEPFSTSLVATTTLMSGMNDFISK.S**
SS	141	CPRT0000006221	RNA-binding protein 4	26526	133	15%	1	135	1.50E-11	**R.YGPAWDDGYGGPYAPPPRNsPR.G**
SS	142	CPRT0000006364	glutamate synthase	152392	76	2%	2	72	2.70E-05	**R.QSDsVKDFRDNPTTLSFADLLPADR.R**
SS	143	CPRT0000006463	tat-binding protein 10	48646	39	9%	2	36	5.90E-02	**M.AALEVESYPRRsPK.Y**
SS	144	CPRT0000006530	hsp90 co-chaperone	20909	45	9%	0	45	9.20E-03	**M.sGDHGVAVHPSLLWAQR.N**
SS	145	CPRT0000006564	adenosinetriphosphatase	20127	40	7%	0	40	0.032	**R.FTsNVFSMFNEAQISEFK.E**

SS	146	CPRT0000006620	upstream activation factor subunit uaf30	25101	51	5%	1	52	1.40E-03	**R.NKAsDDEDYAR.S**
SS	147	CPRT0000006672	elongation factor-2 kinase	70369	53	6%	0	50	5.10E-03	**.MEEGHFGSsPTDLFPQALPVIFSGASGVK.Q**
SS	148	CPRT0000006676	dentin sialophosphoprotein precursor	85411	247	8%	0	55	6.90E-04	**K.GIAsPGNYGDAR.R**
							1	75	1.20E-05	**K.NTHsPANNTESLREPPHTR.S**
							1	39	0.026	**K.SSVKDTsPTVEK.N**
							0	53	1.10E-03	**R.MHsIsPPYNDR.S**
							1	34	0.11	**R.WRtPEDDVNDDHLR.K**
SS	149	CPRT0000006702	sjchgc01166 protein	39554	56	10%	1	59	2.20E-04	**R.RQsLQNLLR.L**
SS	150	CPRT0000006705	sjchgc08095 protein	36566	106	16%	1	46	7.00E-03	**R.RsPsPEDVYVYR.N**
SS	151	CPRT0000006868	sjchgc09526 protein	29640	184	20%	0	184	2.40E-16	**R.SLDstDNPVLIAADNLVHDVILSATQTHLEETR.V**
SS	152	CPRT0000007051	plasminogen activator inhibitor 1 rna-binding protein	45889	93	5%	1	93	2.20E-07	**R.VSRsPNANEPPPVVFEDVQITSAK.E**
SS	153	CPRT0000007240	programmed cell death-involved	58881	80	7%	0	66	4.80E-05	**R.FIsETDSVYR.T**
SS	154	CPRT0000007295	sjchgc05354 protein	25195	37	12%	1	39	2.20E-02	**R.RYsFSTQR.N**
SS	155	CPRT0000007300	Expressed protein	50510	107	6%	0	104	9.40E-09	**R.SSsPSEDIELIMDR.A**
SS	156	CPRT0000007395	secretory carrier membrane protein 2	26211	69	15%	1	68	7.50E-05	**.MENPFADPVARLtPTQSHDNSQVSR.V**
SS	157	CPRT0000007659	placenta-specific gene 8 protein	13424	89	11%	1	91	2.20E-07	**.MEsPTTKQPYAVR.Q**
SS	158	CPRT0000007689	cell division cycle and apoptosis regulator protein 1	28655	103	15%	0	54	0.00082	**R.HSsPTSGLYCR.T**
SS	159	CPRT0000007759	sjchgc05800 protein	66670	275	14%	0	56	6.90E-04	**K.HLSDDVHFtPFDR.K**
							0	43	0.029	**K.HPASNLGDITITQGPDSHFRPFtPDQsPK.T**
							1	37	0.067	**R.KYsDEYENISGHHDQYK.Q**
							0	79	3.60E-06	**R.QSVNIsPTSDLHSQGK.F**
							1	65	6.80E-05	**R.RTsELSTDLANLK.L**
SS	160	CPRT0000007774	heat shock protein 60	63630	171	7%	1	33	0.11	**R.NVIIESSWKsPK.I**
SS	161	CPRT0000007788	cell-cycle and apoptosis regulatory protein	75461	108	6%	0	109	3.40E-09	**K.IANtPEAEDGFESMGPK.N**

			1 isoform 1							
SS	162	CPRT0000007836	sjchgc03741 protein	14820	48	17%	0	48	5.30E-03	**R.TFGNPAsIIDAPLIDVAEINEIK.Q**
SS	163	CPRT0000007860	glycogen synthase kinase 3	56751	58	2%	0	59	3.60E-04	**K.EMVPGTANVSyISSR.Y**
SS	164	CPRT0000007998	testis-specific metallothionein-like protein	57643	90	4%	0	84	1.50E-06	**R.SAHLVPELDDDIMsDEDPVER.A**
SS	165	CPRT0000008142	zinc finger protein	31916	142	4%	2	82	2.00E-06	**R.ERRDsDDEFDEFGR.K**
SS	166	CPRT0000008289	ubx domain containing 2	48307	55	8%	0	56	6.60E-04	**R.LSHMPDNsDDEQAR.W**
SS	167	CPRT0000008409	af287985_1synapsin isoform	36298	55	4%	2	56	7.10E-04	**R.RFsSGDLQGELADKR.M**
SS	168	CPRT0000008438	dip2 disco-interacting protein 2 homolog c	234276	157	3%	0	51	3.40E-03	**K.TADsFEQLAALAEAQLNFHNLGMR.N**
							1	107	1.10E-08	**R.KFsSPAAASGSFGQDISSDANQTTSFVCHNR.V**
SS	169	CPRT0000008530	guanine nucleotide-binding protein subunit beta 1	42092	69	8%	1	70	4.80E-05	**R.AGsIAsAGYNEEISEEEKALDAEILNLK.T**
SS	170	CPRT0000008586	beta thymosin	8688	41	16%	0	41	1.90E-02	**K.QLLQEIEtPPSLK.H**
SS	171	CPRT0000008751	glucose transport protein	56955	63	7%	0	58	0.00041	**K.QGNTDGPAsESLLHSR.N**
SS	172	CPRT0000008913	major egg antigen	39370	142	13%	0	34	0.2	**K.INITNTPGTLLPQTsVPCGMMDFLK.D**
							1	109	5.20E-09	**K.NSGSESSVPLSESTISGsHRR.L**
SS	173	CPRT0000008924	transcription elongation regulator 1	37650	108	9%	1	42	1.10E-02	**R.KLDDSPtVR.E**
							2	50	0.003	**R.KLDDsPTVREDsYTR.K**
SS	174	CPRT0000008950	U2 small nuclear rna auxiliary factor 2	34484	105	7%	1	27	0.51	**R.HRsAsSPtLVYK.Y**
							1	80	2.00E-06	**R.KLSsPQGGVDDR.N**
SS	175	CPRT0000009335	sjchgc02564 protein	11644	49	16%	2	49	4.10E-03	**M.ADKsPEKNHISHPPAVK.A**
SS	176	CPRT0000009359	sjchgc04698 protein	55791	89	4%	0	47	8.00E-03	**K.IAEEISPTEVFGEGAsEGETVVK.K**
SS	177	CPRT0000009445	heterochromatin protein 1	51650	140	3%	1	100	2.90E-08	**K.NSREsEEsGGEDEFQVEK.I**
							0	39	0.032	**R.ESEEsGGEDEFQVEK.I**
SS	178	CPRT0000009494	ribosomal protein LP2	12075	121	14%	2	52	0.0035	**K.AESKPAKTEVKEEsEsEEDMGFGLFD.-**
SS	179	CPRT0000009921	sjchgc09590 protein	180556	417	7%	1	183	2.30E-16	**K.QEALLAEQVDDIPKEHLFVEsDEER.Y**
							1	41	4.80E-02	**K.VIKENNMLAEEsDEQsNNELECELK.Q**

SS	180	CPRT0000010020	z band alternatively spliced pdz-motif protein isoform f	35351	51	6%	0	51	3.00E-03	**K.HNISPLPFGQsPPAPGENFLAK.V**
SS	181	CPRT0000010808	was protein member 3	66022	60	2%	1	60	3.50E-04	**K.MPDVDRNsPLSDETFTR.D**
SS	182	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	23045	234	20%	1	140	6.30E-12	**K.AASENRPNKANEsDEDEDEEPMPMPPQR.V**
							0	90	3.20E-07	**K.ANEsDEDEDEEPMPMPPQR.V**
SS	183	CPRT0000011219	spectrin beta chain	47018	84	3%	1	86	9.90E-07	**K.VGsVNLLSEEMLDKAHPDAEK.I**
SS	184	CPRT0000012199	importin 7	116719	117	1%	0	118	4.00E-10	**K.ALGsDEDEVDEESVR.Y**

Worms	**#**	**Protein ID**	**Description**	**MW**	**Protein score**	**Sequence coverage**	**Miss cleavage**	**Ion score**	**Expect**	**Peptides**
SF	1	AAP05964.1	cysteine string protein	24000	126	6%	1	126	1.90E-08	**R.KLsTSGESLFHVLR.V**
SF	**2**	AAP06040.1	nuclear distribution gene C homolog	37878	103	5%	1	103	1.00E-06	**K.VGAsLDDPDEEEEDKGK.L**
SF	3	AAP06053.1	dek oncogene (dna binding)	39355	83	5%	1	66	3.50E-02	**K.KEFDsDEDVPLSNLTSTK.S**
SF	4	AAP06130.1	rab guanine nucleotide exchange factor 1	17450	86	7%	1	86	1.80E-04	**R.ITSDFDDKLsPER.S**
SF	5	AAP06137.1	n-myc downstream regulated	38028	70	7%	0	63	4.20E-02	**K.LHDEsPINEYDDHNIA.-**
SF	6	AAP06472.1	pyruvate kinase 3	29794	89	7%	0	91	8.30E-05	**.MLGSGLSFGGQSFHGVSsVSR.F**
SF	7	AAW24532.1	sorting nexin-6	47576	69	3%	1	69	2.40E-03	**K.SIPMPDIKsPTTR.Q**
SF	8	AAW24985.1	chromobox protein homolog 1	27252	140	7%	0	62	5.40E-02	**R.ESEEsGGEDEFQVEK.I**
							0	60	5.70E-02	**R.LTWHTPENRPPGtPR.S**
SF	9	AAW25087.1	troponin	37932	88	5%	2	88	0.00014	**M.sDDEQRDEEHDDGKSEAK.I**
SF	10	AAW25147.1	troponin t	38926	117	8%	2	119	1.90E-07	**M.sDDEQsPQPSPAFIPKDEEHDDGKSEAK.I**
SF	11	AAW25812.1	eukaryotic translation initiation factor subunit c	27962	68	7%	1	69	1.30E-02	**R.IESRPLHLssDEEDIKR.I**
SF	12	AAW26271.1	sjchgc09241 protein	49819	142	4%	0	144	9.80E-10	**K.EFtPPPDGVAVGILESNPKPR.A**
SF	13	AAW26273.1	RNA-binding proteins	24591	201	19%	2	68	0.012	**R.RSsPGRIPFPVNHR.G**

							1	61	0.048	**R.sRsPLGAPVGR.L**
SF	14	AAW26588.1	sjchgc01243 protein	38311	117	11%	0	65	1.60E-02	**K.NHNITDsPVMSNKPK.L**
							0	61	1.50E-02	**R.HFsPVAIASSTPK.L**
SF	15	AAW26760.1	dentin sialophosphoprotein precursor	83439	100	4%	1	69	2.20E-02	**R.WRtPEDDVNDDHLR.K**
SF	16	AAW26771.1	nascent polypeptide-associated complex subunit alpha	24461	150	9%	0	150	2.10E-10	**K.TVIAEEsEDDEEPDASGLSEK.D**
SF	17	AAW26781.1	ribosomal large p2	12079	79	22%	2	59	3.70E-01	**K.AESKPAKTEVKEEsEsEEDMGFGLFD.-**
SF	18	AAW27136.1	prothymosin alpha-b	14949	167	12%	1	112	1.20E-06	**K.EAGDNASDDKAHsPDSR.H**
							0	99	9.00E-06	**R.HAEAEsEEDGtDDDASQDTK.G**
SF	19	AAW27231.1	B-cell receptor-associated protein-associated bap	28074	200	9%	1	201	2.00E-15	**K.VNDsDTEDVYPDTVEALKDELLK.L**
							1	76	2.90E-03	**K.VNDSDtEDVYPDTVEALKDELLK.L**
SF	20	AAW27390.1	transcription elongation regulator 1	52564	68	2%	1	68	1.70E-02	**R.KLDDSPtVR.E**
SF	21	AAW27659.1	heat shock protein 90	82166	411	9%	2	123	8.40E-08	**R.TKEVsDDEAEKEETK.N**
SF	22	AAX25017.2	sjchgc04120 protein	19296	73	6%	0	73	0.00084	**K.EHLFVEsDEER.Y**
SF	23	AAX25971.2	epidermal growth factor receptor pathway substrate 8	30090	104	6%	1	106	2.20E-06	**R.YVNLGDSTFGMNRsPK.I**
SF	24	AAX26229.2	myosin heavy chain		315		0	74	7.20E-04	**R.KPTAsLAPEEE.-**
SF	25	AAX26240.2	splicing factor u2af 65 kda subunit	28128	80	5%	0	82	5.30E-04	**R.LVVTSFFsPNSYHR.R**
SF	26	AAX27349.2	sjchgc06768 protein	52587	149	10%	0	90	2.00E-05	**K.SMDDLsDTLVDLNNLTR.H**
							1	63	0.031	**R.KQPsQTEEPISR.Y**
SF	27	AAX30518.2	major vault protein	12169	81	11%	2	81	6.10E-04	**R.KRTsDAIDNIDTK.-**
SF	28	AAX30938.2	sjchgc08909 protein	8064	56	27%	0	58	0.034	**R.GSsPSHDFNHRPYNSTLDNR.R**
SF	29	ABA40479.2	nucleosome assembly protein 1-like 1	44963	62	3%	0	62	4.50E-02	**K.EGGEFsDSAEFHESK.S**
SF	30	CAX70460.1	fragile x mental retardation 1 isoform 16	87407	80	1%	0	80	1.90E-04	**R.QTNQLNHQPDSVsPTR.I**
SF	31	CAX72702.1	Troponin T	38401	82		1	59	0.099	**M.sDDEQSPQPSPAFIPNDDGKSEAK.I**

SF	32	CAX73244.1 /CPRT0000004561	fragile x mental retardation 1	85594	72	2%	1	74	4.70E-03	**R.RGsEDsDIVEPNNIPDGTPGDR.A**
SF	33	CAX73605.1	cAMP-dependent protein kinase R2	40108	73	6%	1	73	7.70E-04	**R.RHsVAAESFNPATVNDLEPVVHPK.S**
SF	34	CAX74259.1	cell division cycle and apoptosis regulator protein 1	125508	209	5%	1	86	2.50E-04	**K.ALQLVTIDKsPQVPEEQVKPVNAESGSK.L**
							0	66	2.20E-02	**K.IANtPEAEDGFESMGPK.N**
SF	35	CAX83069.1	Tetratricopeptide repeat protein 14	103388	215	10%	1	73	0.0048	**R.ESSLATGDDAVPSEsPKGDR.G**
							1	58	1.00E-01	**R.IKtPPLAPLVTSFR.R**
							0	79	0.00012	**R.QNHAPDQsPPGFLsPNR.S**
SF	36	CPRT0000000132	cold shock domain protein A	23801	82	7%	0	82	1.50E-06	**R.DNYHNEDGsPDMR.D**
SF	37	CPRT0000000345	alkaline phosphatase	204906	112	0%	0	112	1.70E-09	**R.LTTDsGSAATAFLSGAK.G**
SF	38	CPRT0000000366	Hydrocephalus-inducing protein homolog	111656	85	2%	1	85	8.00E-07	**R.KVsFSDLPIVSGVEER.N**
SF	39	CPRT0000000480	splicing arginine serine-rich 2	17962	49	15%	2	36	6.80E-02	**R.YGRsPPRIDGMVSLK.V**
SF	40	CPRT0000000616	talin 2	316513	76	2%	1	69	6.00E-05	**R.KQTDLTQAAVEFNQATGDLLSSYsPGTFR.R**
SF	41	CPRT0000000669	splicing arginine serine-rich 7	31746	237	26%	1	92	2.60E-07	**R.NsSYDGHRYPDHDQFSSFR.S**
SF	42	CPRT0000000687	ferritin-1 heavy chain	11618	63	19%	1	64	1.40E-04	**R.VGTGLGEYTFDKETLHGEsD.-**
SF	43	CPRT0000000835	Protein DEK	45498	58	4%	0	59	4.10E-04	**K.EFDsDEDVPLSNLTSTK.V**
SF	44	CPRT0000001007	dynein cytoplasmic 1 intermediate chain 2	68240	108	2%	0	108	5.40E-09	**R.ELEsPSHDVNDSILQR.N**
SF	45	CPRT0000001123	lethal giant larvae homolog 1	15057	40	1%	1	40	4.80E-02	**R.sLRPDTPKLEEQVEPSLPVPPAPR.I**
SF	46	CPRT0000001178	p30 dbc protein	100463	48	1%	0	49	3.30E-03	**R.NDsQNGYNDEQDDVK.I**
SF	47	CPRT0000001254	peptidyl-prolyl isomerase G	117498	295	6%	0	64	1.00E-04	**K.LISLPTTTHEQsPK.L**
							0	62	0.00013	**K.SQVsPQLHLR.I**
							1	70	2.50E-05	**K.YQSKsPILMIsPK.L**
							1	44	0.011	**R.HYTRsPEDIR.Q**
							1	51	2.60E-03	**R.NRNPsTsPSSFAGVSDNLR.D**
SF	48	CPRT0000001337	zinc c2h2-type domain-containing protein	99949	109	5%	1	40	0.028	**R.DARQsPPPIPPAPER.L**

							1	60	0.00014	**R.ELRsPLR.D**
SF	49	CPRT0000001365	scaffold attachment factor B	83496	80	4%	1	69	5.30E-05	**R.sRsPPIFQSVQHRPEILEYGHR.S**
SF	50	CPRT0000001534	coatomer subunit beta	74897	105	1%	0	106	6.00E-09	**R.SNsPSVDQELQFR.N**
SF	51	CPRT0000001619	beta chain spectrin	77788	114	4%	0	61	3.00E-04	**R.AAtLPSGVAPESQVTSSSSASGK.K**
							1	39	3.10E-02	**R.HGRGSsDVGRPAPR.D**
SF	52	CPRT0000001632	eukaryotic translation initiation factor 5A	17852	75	13%	1	76	9.10E-06	**M.StFEDEEFATGESGASKTEPK.Q**
SF	53	CPRT0000001698	transformer-2 protein	18426	42	34%	2	31	3.40E-01	**K.DVEYGYYNPNKDYIsPSKELR.R**
SF	54	CPRT0000001788	regulatory factor x domain containing 2	87924	67	1%	0	68	2.90E-05	**R.NLsDHAIIQSR.R**
SF	55	CPRT0000002152	cdc37 cell division cycle 37 homolog	45458	149	7%	0	151	4.10E-13	**K.WDHIEVsDDEDDTHPNIDTPSLFR.W**
SF	56	CPRT0000002181	heterogeneous nuclear ribonucleoprotein H	53750	97	6%	0	98	9.80E-08	**R.sPAYNTGGSQGSQYNNYPLHDDMHYADDIR.Y**
SF	57	CPRT0000002186	arsenite-resistance protein	10090	79	5%	1	30	1.80E-01	**R.GRsPAAEPPYK.R**
SF	58	CPRT0000002347	14-3-3 family protein	25816	126	11%	2	127	1.00E-10	**R.DNLNLWNPCNDGEKDTAAsPKGEEK.-**
SF	59	CPRT0000002428	glyceraldehyde 3-phosphate dehydrogenase	36566	86	7%	0	86	1.20E-06	**K.VINDNFEIVEGLMTTVHSFTAtQK.T**
SF	60	CPRT0000002551	importin alpha-related	17579	46	6%	1	46	4.50E-03	**R.RTDQsIELR.K**
SF	61	CPRT0000002705	hypotherical protein	27929	110	8%	1	110	4.20E-09	**K.DKPDAESDLFAsDsEDDKEAER.I**
SF	62	CPRT0000002762	Serine/arginine repetitive matrix	24795	101	16%	2	59	0.00039	**R.RHsHEDsRsPIDDSHNESR.N**
							1	36	3.90E-02	**R.RHsPPGYER.N**
SF	63	CPRT0000002916	phosphate cytidylyltransferase ethanolamine	47612	42	2%	1	42	1.00E-02	**R.RTQsLDSVLK.N**
SF	64	CPRT0000003210	hypothetical protein	39314	125	13%	2	129	6.30E-11	**K.RLsIDTTGEDEPDKENNANLSLPNVR.S**
SF	65	CPRT0000003234	RNA binding motif protein 39	50448	53	2%	1	53	1.20E-03	**R.QKsPELSPEER.D**
SF	66	CPRT0000003518	disulfide-isomerase precursor	26123	59	7%	2	89	3.90E-04	**R.SLPDKWQHDMFQDARsPK.G**
SF	67	CPRT0000003603	expressed protein	39546	166	10%	0	37	0.048	**R.NMEATGGQsIDEENR.K**
SF	68	CPRT0000003639	myelin expression factor 2	60032	40	2%	1	42	2.00E-02	**R.SIKYEDsESPDIPSR.G**
SF	69	CPRT0000003724	tetratricopeptide repeat protein 14	91798	46	2%	1	47	1.00E-02	**R.RDHtPLsPTAPRPSAGYATHMER.S**

SF	70	CPRT0000003898	cytosolic purine 5-nucleotidase	53500	40	2%	0	41	2.60E-02	**R.APAMLMPHESTVSHGDsPK.D**
SF	71	CPRT0000003916	GPI-anchored membrane protein 1	56776	92	3%	0	94	1.10E-07	**R.SSsPLSSGNINQTISLK.S**
SF	72	CPRT0000003998	sjchgc07201 protein	53500	51	3%	0	53	1.00E-03	**R.GSHsPISLTER.F**
SF	73	CPRT0000004133	vacuolar protein sorting-associated protein	383946	101	1%	1	99	2.40E-08	**R.KTsLTTVADELR.S**
SF	74	CPRT0000004202	heat shock protein 90	82188	556	10%	3	176	1.30E-15	**R.TKEVsDDEAEKEETKNESEEAEDKPK.V**
SF	75	CPRT0000004242	protein phosphatase	76968	46	2%	0	49	3.50E-03	**R.VTsLVNLNSPSDTLLR.G**
SF	76	CPRT0000004688	ankyrin 23 unc44	264545	38	0%	0	39	3.70E-02	**R.SLNGISSTsPNLNISR.E**
SF	77	CPRT0000004798	eukaryotic translation initiation factor subunit D	47998	140	6%	1	143	2.90E-12	**K.TYSFPEENPFKDDEDEDsDNPNPSHNR.N**
SF	78	CPRT0000005000	alpha fucosyltransferase	218756	37	2%	1	39	2.70E-02	**R.IAISRLsPTAGR.S**
SF	79	CPRT0000005165	myosin heavy chain	204958	505	9%	1	38	3.60E-02	**R.ARKPTAsLAPEEE.-**
							0	46	5.10E-03	**R.GVsVAPGAAPGHGNR.A**
SF	80	CPRT0000005313	thymidylate kinase	25311	123	7%	1	85	9.70E-07	**R.DSsGGNKFETMDFQK.R**
SF	81	CPRT0000005420	pleckstrin homology domain family c member 1 isoform 2	77049	71	1%	0	72	1.30E-05	**R.DIsPIGGYLHTGR.Y**
SF	82	CPRT0000005681	coatomer protein subunit beta 1	120852	66	2%	0	66	4.90E-05	**R.SHsPVNTLLNSH.-**
SF	83	CPRT0000005718	solute carrier family 6 member 5	86218	71	1%	1	73	1.70E-05	**R.TEFISMIKsNEsLHR.S**
SF	84	CPRT0000005797	calnexin	65986	131	7%	0	80	3.60E-06	**K.NAENEELEEsGEDDIVQVSK.G**
							0	53	2.10E-03	**R.DNsEEEAPNEFEGNENVPAAK.Q**
SF	85	CPRT0000005868	myosin regulatory light chain 2	35248	50	5%	0	50	3.20E-03	**R.ATsNVFGMFPQNQIQEFK.E**
SF	86	CPRT0000006118	mitogen-activated protein kinase 14A	29378	181	8%	0	65	8.80E-05	**K.sPGPPPTEEVASSISAPLK.K**
SF	87	CPRT0000006130	phosphofructokinase	86159	59	1%	1	61	1.60E-04	**R.RGtELLPGMEGK.Y**
SF	88	CPRT0000006140	zinc finger protein	119523	48	1%	2	46	0.014	**K.TDAPNALEEsENEESDIIKSDPDKESVPK.V**
SF	89	CPRT0000006218	myosin-7	88487	51	2%	1	54	1.50E-03	**K.RLEEAAIAtPPKPIIPQSDPSDR.N**
SF	90	CPRT0000006221	RNA-binding protein 4	26526	113	9%	1	115	1.50E-09	**R.YGPAWDDGYGGPYAPPPRNsPR.G**
SF	91	CPRT0000006620	upstream activation factor subunit uaf30	25101	57	5%	1	58	3.10E-04	**R.NKAsDDEDYAR.S**

SF	92	CPRT0000006676	dentin sialophosphoprotein precursor	85411	56	1%	0	57	3.70E-04	**K.GIAsPGNYGDAR.R**
SF	93	CPRT0000006702	sjchgc01166 protein	39554	58	2%	1	59	2.20E-04	**R.RQsLQNLLR.L**
SF	94	CPRT0000007051	plasminogen activator inhibitor 1 RNA-binding protein	45889	92	5%	1	92	2.60E-07	**R.VSRsPNANEPPPVVFEDVQITSAK.E**
SF	95	CPRT0000007069	translationally-controlled tumor protein homolog	23826	88	10%	0	90	4.10E-07	**K.LIAANPSGEEGQEEVsDSTER.V**
SF	96	CPRT0000007295	sjchgc05354 protein	25195	44	14%	1	45	4.90E-03	**R.RYsFSTQR.N**
SF	97	CPRT0000007395	secretory carrier membrane protein 2	26211	51	10%	1	51	4.90E-03	**MENPFADPVARLtPTQSHDNSQVSR.V**
SF	98	CPRT0000007659	placenta-specific protein 8 protein	13424	46	11%	1	47	4.70E-03	**MEsPTTKQPYAVR.Q**
SF	99	CPRT0000007689	cell division cycle and apoptosisregul	28655	101	8%	0	43	0.011	**R.HSsPTSGLYCR.T**
							2	60	0.00021	**R.RRsPLDLASTR.H**
SF	100	CPRT0000007759	sjchgc05800 protein	66670	263	11%	0	36	6.70E-02	**K.HLSDDVHFtPFDR.K**
							0	56	1.40E-03	**K.HPASNLGDITITQGPDSHFRPFtPDQsPK.T**
							0	43	6.00E-03	**K.sGSASEIAADIHK.N**
							0	48	3.10E-03	**K.SGsASEIAADIHK.N**
							1	56	1.60E-04	**R.KYsDEYENISGHHDQYK.Q**
							0	89	3.30E-07	**R.QSVNIsPTSDLHSQGK.F**
							1	77	4.60E-06	**R.RTsELSTDLANLK.L**
SF	101	CPRT0000007774	heat shock protein 60	63630	155	9%	1	36	0.057	**R.NVIIESSWKsPK.I**
SF	102	CPRT0000007860	glycogen synthase kinase 3	56751	67	2%	0	68	4.20E-05	**K.EMVPGTANVSyISSR.Y**
SF	103	CPRT0000008142	zinc finger protein	31916	143	4%	2	78	4.10E-06	**R.ERRDsDDEFDEFGR.K**
SF	104	CPRT0000008289	ubx domain-containing protein 4	48307	65	3%	0	67	5.50E-05	**R.LSHMPDNsDDEQAR.W**
SF	105	CPRT0000008664	lamin b2	38122	38	3%	0	38	2.70E-02	**R.SEAsPTSFSR.S**
SF	106	CPRT0000009445	heterochromatin protein 1	51650	166	6%	1	103	1.80E-08	**K.NSREsEEsGGEDEFQVEK.I**
SF	107	CPRT0000009893	ATP-binding sub-family c member 2	127765	62	1%	1	62	1.40E-04	**K.KLsLETPDSFSR.F**
SF	108	CPRT0000009921	sjchgc09590 protein	180556	269	2%	1	201	3.50E-18	**K.QEALLAEQVDDIPKEHLFVEsDEER.Y**

SF	109	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	23045	197	13%	1	104	2.40E-08	**K.AASENRPNKANEsDEDEDEEPMPMPPQR.V**
SF	110	CPRT0000011219	spectrin beta chain	47018	71	9%	0	29	3.20E-02	**K.VGsVNLLSEEMLDK.A**
SF	111	CPRT0000011316	sjchgc06770 protein	58915	146	10%	0	53	1.50E-03	**R.HRPAsVSGYLDECGLNR.S**
SF	112	CPRT0000012071	heat shock protein 4	61196	64	9%	0	64	0.00013	**K.EVEVsVSEDNPVVDGPANSTK.E**
SF	113	CPRT0000012199	importin 7	116719	131	4%	0	127	5.60E-11	**K.ALGsDEDEVDEESVR.Y**

Worms	**#**	**Protein ID**	**Description**	**MW**	**Protein Score**	**Sequence Coverage**	**Miss cleavage**	**Ion score**	**Expect**	**Peptides**
SM	1	AAC82332.1	myosin	92385	983	25%	1	69	8.10E-03	K.AGTLAsLEDLRDEK.L
SM	2	AAD56715.1	14-3-3 protein	28979	64	19%	1	65	1.30E-02	R.AFDTSIGELDSLQDDsYKDSTLIMQLLR.D
SM	3	AAP05964.1	cysteine string protein	24000	115	6%	1	115	2.30E-07	R.KLsTSGESLFHVLR.V
SM	4	AAP06040.1	nuclear distribution gene C homolog	37878	114	5%	1	114	2.10E-07	K.VGAsLDDPDEEEEDKGK.L
SM	5	AAP06053.1	dek oncogene (dna binding)	39335	101	5%	1	62	3.50E-02	K.KEFDsDEDVPLSNLTSTK.S
SM	6	AAP06137.1	similar to NM_078233 ZK1073	38028	88	7%	0	60	0.086	K.LHDEsPINEYDDHNIA.-
SM	7	AAP06237.1	adducin 1		110	6%	1	112	5.30E-07	K.LENVADLKGsLPTIPINDLR.G
SM	8	AAP06500.1	hypothetical protein	47262	211	10%	2	140	1.30E-09	K.RLsIDTTGEDEPDKENNANLSLPNVR.S
							2	72	5.50E-03	R.RGsVKHESTTQKPLNQLFK.R
SM	9	AAW24532.1	sorting nexin 6	47576	67	3%	1	67	8.20E-03	K.SIPMPDIKsPTTR.Q
SM	10	AAW24704.1	sjchgc02374 protein	24307	150	13%	0	110	9.20E-07	R.AMsHFETNSIENSLPR.V
SM	11	AAW24985.1	chromobox protein homolog 1 (heterochromatin protein 1 homolog beta)		80	7%	1	80	8.20E-04	K.NSREsEEsGGEDEFQVEK.I
SM	12	AAW25147.1	troponin T	38926	128	8%	2	113	6.80E-07	M.sDDEQSPQPSPAFIPKDEEHDDGKSEAK.I
SM	13	AAW26183.1	troponin I	26129	114	11%	1	72	4.40E-03	K.YALEEKDEVANtPK.-
SM	14	AAW26271.1	sjchgc09241 protein	49819	291	12%	2	62	0.061	K.DIESGKTDKDAsSERPK.L
SM	15	AAW26298.1	adducin related protein	20407	101	9%	1	101	7.10E-06	R.SDTsGAEASHDDTEKETR.K

SM	16	AAW26418.1	microtubule-associated protein futsch	105262	120	5%	1	66	4.60E-02	K.TSHLTHSYPGEENDGRLPSDMMTtTPPPSATSNTPSK.E
SM	17	AAW26505.1	sjchgc02563 protein		146	6%	0	61	0.046	R.SVsNFELENNR.E
SM	18	AAW26588.1	sjchgc01243 protein	38311	219	13%	0	91	5.60E-05	K.NHNITDsPVMSNKPK.L
							0	78	9.40E-04	R.HFsPVAIASSTPK.L
SM	19	AAW26700.1	elegans protein confirmed by transcript evidence	21285	83	14%	1	83	6.70E-04	K.NTDDENANsERDSPEPLPLIPATIWTR.K
SM	20	AAW26760.1	dentin sialophosphoprotein precursor	83439	128	5%	1	72	4.70E-03	R.WRtPEDDVNDDHLR.K
SM	21	AAW26770.1	sjchgc06242 protein	21453	107	8%	0	107	1.90E-06	R.NNPFTTMsPLLNELER.D
SM	22	AAW26771.1	nascent polypeptide-associated complex subunit alpha	22461	112	9%	0	112	6.90E-07	K.TVIAEEsEDDEEPDASGLSEK.D
SM	23	AAW27091.1	cAMP-dependent protein kinase type ii regulatory subunit	19623	90	13%	2	90	1.40E-04	R.RQsVAAESFDPEKDSDDNNEEER.Q
SM	24	AAW27136.1	prothymosin alpha-B	14949	80	12%	2	80	7.60E-04	R.KEAGDNASDDKAHsPDSR.H
SM	25	AAW27228.1	sjchgc02220 protein	45497	101	10%	0	92	6.00E-05	R.VNVYNSDNTSTIYsPQR.K
SM	26	AAW27231.1	B-cell receptor-associated protein-associated bap	28074	85	9%	1	87	2.30E-04	K.VNDSDtEDVYPDTVEALKDELLK.L
SM	27	AAW27396.1	sjchgc09482 protein	26110	85	14%	0	66	0.012	R.SPKPIsPQPMNK.Q
SM	28	AAW27659.1	heat shock protein 90	82166	535	7%	3	129	1.60E-08	R.TKEVsDDEAEKEETKNESEEAEDKPK.V
SM	29	AAX25017.2	sjchgc04120 protein	19296	130	23%	0	72	0.0028	K.EHLFVEsDEER.Y
SM	30	AAX25098.2	scaffold attachment factor b-related	22094	105	25%	0	69	1.60E-02	K.VLSsPSQSFRPTNHAFFLSSAYENR.N
SM	31	AAX25934.2	endothelin-converting enzyme 1	26673	97	6%	0	97	1.50E-05	K.SDsPTNSLNLGQNFK.Y
SM	32	AAX26229.2	myosin heavy chain	1302	18	23%	0	65	5.90E-02	R.GVsVAPGAAPGHGNR.A
SM	33	AAX26676.1	calnexin	24636	143	18%	0	96	2.40E-05	K.NAENEELEEsGEDDIVQVSK.G
SM	34	AAX26685.2	sjchgc04347 protein	43341	95	9%	1	95	4.80E-05	K.ATSESHLsADEVNVEVLHDKAESSTLSNNPK.H
SM	35	AAX27349.2	heat shock 70kda protein 4	57715	148	10%	0	77	2.30E-03	K.EVEVsVSEDNPVVDGPANSTK.E
SM	36	AAX27349.2	sjchgc06768 protein	52587	320	23%	0	82	2.90E-04	K.SMDDLsDTLVDLNNLTR.H

							1	87	7.40E-05	R.DIKNEHTLDDDQNIDLsPTIGNDEQIHHQSDHLIQHR.S
							0	66	0.015	R.YHTQLGDESEYVLSDFGsLDR.N
SM	37	AAX27369.2	ferm domain containing 3	35115	70	6%	0	71	7.40E-03	K.IYLPISTGATGNSsPSTNVK.E
SM	38	AAX28429.2	eukariotic translation initiation factor epsilon subunit	28374	74	8%	1	75	3.50E-03	R.IEsDADDEQSESFIITELKR.T
SM	39	AAX30518.2	major vault protein	12169	71	11%	2	71	5.80E-03	R.KRTsDAIDNIDTK.-
SM	40	CAX69370.1	cell cycle associated protein 1	58076	99	3%	0	101	6.70E-06	R.SSsPLSSGNINQTISLK.S
SM	41	CAX72987.1	Ezrin-radixin-moesin-binding phosphoprotein 50	21556	117	7%	2	117	1.40E-07	R.KSsDVISAAIKDPIR.C
SM	42	CAX73031.1	epidermal growth factor receptor pathway substrate 8	57535	163	12%	1	90	5.30E-05	R.YVNLGDSTFGMNRsPK.I
SM							1	71	4.20E-03	R.SAEIQLPPMVTKED[sVYs]ESQINR.E
SM	43	CAX73091.1	hypotheticial protein	25814	78	4%	1	78	8.10E-04	R.KEsSSDLLSR.Y
SM	44	CAX73605.1	cAMP-dependent protein kinase r2	40108	72	6%	1	73	5.20E-03	R.RHsVAAESFNPATVNDLEPVVHPK.S
SM	45	CAX74150.1	zinc c2h2-type domain-containing protein	106115	102	3%	1	70	1.10E-02	R.DARQsPPPIPPAPER.L
							0	55	2.90E-01	R.HTPHHPPPPPtSPSFFVGR.G
SM	46	CAX74259.1	cell division cycle and apoptosis regulator protein 1	125508	168	5%	1	67	2.20E-02	K.ALQLVTIDKsPQVPEEQVKPVNAESGSK.L
							0	90	7.90E-05	K.IANtPEAEDGFESMGPK.N
SM	47	CAX75242.1	fragile x mental retardation 1 isoform 16	87421	149	5%	0	94	3.40E-05	R.QTNQLNHQPDSVsPTR.I
SM	48	CAX83069.1	tetratricopeptide repeat domain 14	103388	145	5%	1	64	2.50E-02	R.IKtPPLAPLVTSFR.R
							0	62	0.021	R.DHTPLsPTAPRPSAGYATHMER.S
SM	49	CPRT0000000132	cold shock domain protein A	23801	78	5%	0	79	2.60E-06	R.DNYHNEDGsPDMR.D
SM	50	CPRT0000000218	phosphatase 2a inhibitor i2pp2a	29186	43	6%	0	44	1.00E-02	K.EFHLGDsGEPSSTYTK.I
SM	51	CPRT0000000226	sjchgc09295 protein	304753	151	2%	1	47	0.0057	K.KLQAIIQQPLENISTQTDPITQVHVTsPK.T
SM							0	36	0.11	R.QPLENISTQTDPITQVHVTsPK.T

SM	52	CPRT0000000345	alkaline phosphatase	204906	51	0%	0	51	1.90E-03	R.LTTDsGSAATAFLSGAK.G
SM	53	CPRT0000000366	Hydrocephalus-inducing protein homolog	111656	110	1%	1	110	2.70E-09	R.KVsFSDLPIVSGVEER.N
SM	54	CPRT0000000412	filamin	146136	44	0%	1	44	9.90E-03	R.KMsQPQRPACDPK.Q
SM	55	CPRT0000000480	splicing arginine serine-rich 2	17962	66	19%	2	38	4.00E-02	R.YGRsPPRIDGMVSLK.V
SM	56	CPRT0000000616	talin 2	316513	191	2%	0	56	7.80E-04	R.AGsRPEMHNAENFTPLR.E
							1	133	2.40E-11	R.KQTDLTQAAVEFNQATGDLLSSYsPGTFR.R
SM	57	CPRT0000000669	arginine serine-rich splicing factor	31746	253	18%	0	46	4.20E-03	R.ANYsPPFVR.E
							1	99	5.20E-08	R.NSsYDGHRYPDHDQFSSFR.S
							1	61	1.60E-04	R.sRsPLGAPVGR.L
SM	58	CPRT0000000786	pyruvate muscle	58347	44	9%	0	44	5.00E-02	K.LEDAETKPIVMVPsITHFDD.-
SM	59	CPRT0000000835	protein DEK	45498	37	5%	0	38	0.047	K.EFDsDEDVPLSNLTSTK.V
SM	60	CPRT0000001007	dynein cytoplasmic 1 intermediate chain 2	68240	62	2%	0	62	2.00E-04	R.ELEsPSHDVNDSILQR.N
SM	61	CPRT0000001123	lethal giant larvae homolog 1	150057	90	1%	1	90	3.30E-07	R.SLRPDtPKLEEQVEPSLPVPPAPR.I
SM	62	CPRT0000001254	peptidyl-prolyl isomerase G	117498	234	9%	0	62	1.70E-04	K.LISLPTTTHEQsPK.L
							0	59	2.50E-04	K.SQVsPQLHLR.I
							1	41	2.10E-02	K.YQSKsPILMIsPK.L
							0	61	1.70E-04	R.GTsPSKPIIVITK.K
SM	63	CPRT0000001337	zinc c2h2-type domain-containing protein	99949	45	7%	1	49	0.018	R.ELRsPLR.D
SM	64	CPRT0000001365	scaffold attachment factor B	83496	88	4%	1	85	1.60E-06	R.sRsPPIFQSVQHRPEILEYGHR.S
SM	65	CPRT0000001534	coatomer protein subunit beta 2	74897	86	5%	0	88	4.20E-07	R.SNsPSVDQELQFR.N
SM	66	CPRT0000001619	beta chain spectrin	77788	68	4%	1	39	2.80E-02	R.DSEAGSRLPTVTtPR.H
							1	39	3.10E-02	R.HGRGsSDVGRPAPR.D
SM	67	CPRT0000001632	eukaryotic translation initiation factor 5A	17852	50	13%	1	51	2.90E-03	M.StFEDEEFATGESGASKTEPK.Q
SM	68	CPRT0000001880	adenylate cyclase-associated protein 1	51932	48	3%	1	48	4.30E-03	R.TsPIKTSSESGNPLSVK.E
SM	69	CPRT0000002080	protein cGMP- type ii	108795	47	1%	1	47	4.90E-03	K.ILDLVSPTKsQDELQIK.S
SM	70	CPRT0000002152	CDC37 cell division cycle 37-like	45458	127	6%	0	129	6.80E-11	K.WDHIEVsDDEDDTHPNIDTPSLFR.W

SM	71	CPRT0000002154	pap-inositol- -phosphatase	62828	41	3%	0	41	2.40E-02	R.SHGSPtHATVNNAFFPTEVLR.A
SM	72	CPRT0000002185	eukaryotic translation initiation factor 4E binding protein 2	13182	57	20%	2	57	9.70E-04	R.NsPAARSPPPDMIFLPEKAPNSDDK.T
SM	73	CPRT0000002186	arsenite-resistance protein	10090	85	3%	1	31	1.30E-01	R.GRsPAAEPPYK.R
							0	57	7.90E-04	R.GSsPSHDFNHRPYNSTLDNR.R
SM	74	CPRT0000002239	phosphofurin acidic cluster sorting protein 1	125562	116	1%	0	116	5.40E-10	R.NIsPESTSHGTISAPR.S
SM	75	CPRT0000002258	adducin related protein	91507	46	5%	0	47	6.30E-03	M.PsSNVANEVMLSGKPEK.F
SM	76	CPRT0000002292	SAPK substrate protein 1	82066	49	6%	1	50	0.0053	K.GLEEAMEWIIENDsGDEKEEALDGTGETK.K
SM	77	CPRT0000002347	14-3-3 family protein	25816	108	11%	2	110	5.40E-09	R.DNLNLWNPCNDGEKDTAAsPKGEEK.-
SM	78	CPRT0000002428	glyceraldehyde 3-phosphate dehydrogenase	36566	79	7%	0	79	5.80E-06	K.VINDNFEIVEGLMTTVHSFTAtQK.T
SM	79	CPRT0000002490	troponin I	29514	43	12%	2	43	0.0091	K.KVsKTESHMAR.F
SM	80	CPRT0000002762	arginine serine-rich splicing factor	24795	41	21%	1	34	7.70E-02	R.RHsPPGYER.N
SM	81	CPRT0000002916	phosphate cytidylyltransferase ethanolamine	47612	49	4%	1	45	5.80E-03	R.RTQsLDSVLK.N
SM	82	CPRT0000003234	rna binding motif protein 39	50448	40	4%	1	32	1.40E-01	R.QKsPELSPEER.D + Phospho (ST)
SM	83	CPRT0000003382	tensin 3	91281	82	3%	0	83	1.50E-06	R.GVQDLDSHVGsLTTLAR.G
SM	84	CPRT0000003603	sjchgc09241 protein	39546	303	15%	0	129	4.30E-11	K.EFtPPPDGVAVGILESNPKPR.A
							1	117	5.30E-10	K.KSsFIDESITVAPEATR.S
							1	59	4.00E-04	R.NMEATGGQsIDEENRK.K
SM	85	CPRT0000003724	tetratricopeptide repeat domain 14	91798	66	5%	1	67	6.30E-05	R.ESSLATGDDAVPSEsPKGDR.G
SM	86	CPRT0000003767	neuropathy target esterase swiss cheese-related protein		48	0%	0	50	3.00E-03	R.QSSLsWTEGYLESLSR.N
SM	87	CPRT0000003811	pdz and lim domain 7	17761	46	6%	1	46	4.70E-03	R.RAsIDSPWGFR.V
SM	88	CPRT0000003866	solute carrier family sodium bicarbonate cotransporter- member 10	152092	74	4%	0	72	1.70E-05	R.ITINPPSNQGsPETSR.R

SM	89	CPRT0000003998	cytosolic purine 5-nucleotidase	56064	166	10%	0	47	5.60E-03	MDSVVLSQQERPPsVR.V
							0	91	2.80E-07	R.APAMLMPHESTVSHGDsPK.D
SM	90	CPRT0000004133	vacuolar protein sorting-associated protein	383946	96	1%	1	97	4.10E-08	R.KTsLTTVADELR.S
SM	91	CPRT0000004172	sjchgc08522 protein	30379	70	6%	0	36	6.00E-02	R.sLTGEQNLSHSTTLK.H
							1	34	1.30E-01	R.sRSLTGEQNLSHSTTLK.H
SM	92	CPRT0000004177	tensin 4	37269	58	4%	0	59	3.50E-04	R.QNsQYEATPLVANR.S
SM	93	CPRT0000004184	major vault protein	97356	76	8%	2	64	1.00E-04	R.KRtSDAIDNIDTK.-
SM	94	CPRT0000004202	heat shock protein hsp 90-alpha	82188	329	6%	2	142	3.20E-12	K.EVsDDEAEKEETKNESEEAEDKPK.V
SM	95	CPRT0000004239	suppressor of fused	104462	39	1%	0	39	0.05	K.NNLVNSPtELTNLVGGALGFR.T
SM	96	CPRT0000004242	protein phosphatase	76968	45	4%	0	47	0.0048	R.VTsLVNLNSPSDTLLR.G
SM	97	CPRT0000004561	fragile x mental retardation 1	69914	65	5%	1	65	1.40E-04	R.RGsEDsDIVEPNNIPDGTPGDR.A
SM	98	CPRT0000004749	dynactin subunit 1	157056	56	1%	0	31	0.21	R.RPsLDDDVLSGVLAGK.R
SM	99	CPRT0000004798	eukaryotic translation initiation factor subunit D	47998	87	6%	1	89	6.60E-07	K.TYSFPEENPFKDDEDEDsDNPNPSHNR.N
SM	100	CPRT0000004960	sh3 domain-binding glutamic acid-rich-like protein	38619	52	7%	1	52	1.10E-03	R.KtSDQPVESIR.K
SM	101	CPRT0000004986	sjchgc02101 protein	30544	102	4%	1	103	1.30E-08	R.RSsNTNSEESPVTR.R
SM	102	CPRT0000005000	alpha fucosyltransferase	218756	64	3%	1	56	4.40E-04	R.IAISRLsPTAGR.S
SM	103	CPRT0000005165	myosin heavy chain	204958	1404	19%	1	55	6.60E-04	R.ARKPTAsLAPEEE.-
							0	37	0.034	R.KPTAsLAPEEE.-
SM	104	CPRT0000005313	thymidylate kinase	25311	72	6%	1	72	1.80E-05	R.DSsGGNKFETMDFQK.R
SM	105	CPRT0000005334	hypothetical protein	53707	85	8%	0	87	6.30E-07	K.MQTGKPASSVHFsPTR.V
SM	106	CPRT0000005420	pleckstrin homology domain family c member 1 isoform 2	77049	76	1%	0	77	4.30E-06	R.DIsPIGGYLHTGR.Y
SM	107	CPRT0000005681	coatomer protein subunit beta 1	120852	50	1%	0	74	3.60E-04	R.SHsPVNTLLNSH.-
						1%	0	51	1.60E-03	R.sHSPVNTLLNSH.-

SM	108	CPRT0000005690	sjchgc00797 protein	18016	98	11%	0	99	4.20E-08	K.QVPVYNALsPSPGPLNFER.Y
SM	109	CPRT0000005797	calnexin	65986	131	7%	0	54	1.40E-03	R.DNsEEEAPNEFEGNENVPAAK.Q
SM	110	CPRT0000005868	myosin regulatory light chain 2	35248	43	5%	0	43	0.02	R.ATsNVFGMFPQNQIQEFK.E
SM	111	CPRT0000006031	calcium-regulated heat stable protein 1	13101	112	16%	1	112	1.60E-09	R.NRTEsQSESASTGEHGVGR.I
SM	112	CPRT0000006039	flotillin 2	42889	61	9%	1	58	3.30E-04	R.KAsFDQEVNTAR.A
SM	113	CPRT0000006118	p38 MAPK	29378	204	8%	1	111	2.00E-09	K.sKSPGPPPTEEVASSISAPLK.K
							0	93	1.60E-07	K.sPGPPPTEEVASSISAPLK.K
SM	114	CPRT0000006130	Phosphofructokinase	86159	75	1%	1	77	3.70E-06	R.RGtELLPGMEGK.Y
SM	115	CPRT0000006131	uncoordinated family member (unc-44)	233254	44	1%	1	47	8.90E-03	K.ITGTLKQEsEVEDAFQSQQPESYHK.E
SM	116	CPRT0000006221	RNA-binding protein 4	26526	129	22%	1	130	4.10E-11	R.YGPAWDDGYGGPYAPPPR
SM	117	CPRT0000006370	eukaryotic translation initiation factor 2 alpha subunit	34474	78	4%	0	79	2.90E-06	K.NIGGMILHSELsR.R
SM	118	CPRT0000006672	elongation factor-2 kinase	70369	37	7%	0	35	1.50E-01	MEEGHFGSsPTDLFPQALPVIFSGASGVK.Q
SM	119	CPRT0000006676	dentin sialophosphoprotein precursor	85411	71	5%	0	48	3.00E-03	K.GIAsPGNYGDAR.R
SM	120	CPRT0000006702	sjchgc01166 protein	39554	59	9%	1	59	2.20E-04	R.RQsLQNLLR.L
SM	121	CPRT0000006705	sjchgc08095 protein	36566	39	3%	1	41	2.00E-02	R.RsPsPEDVYVYR.N
SM	122	CPRT0000006771	wd-40 repeat protein	61284	133	5%	0	41	1.90E-02	R.IDQPVMDDLsAR.Q
							0	94	1.20E-07	R.LIKPPLsVNNYPVGHNHR.L
SM	123	CPRT0000007015	20 kda calcium-binding protein (antigen sm20)	65770	71	5%	1	43	1.40E-02	R.GQEKIStTDLGPAFR.A
SM	124	CPRT0000007051	plasminogen activator inhibitor 1RNA-binding protein	45889	98	5%	1	98	6.30E-08	R.VSRsPNANEPPPVVFEDVQITSAK.E
SM	125	CPRT0000007295	sjchgc05354 protein	25195	46	3%	1	47	2.90E-03	R.RYsFSTQR.N
SM	126	CPRT0000007395	secretory carrier membrane protein 2	26211	83	10%	1	83	2.30E-06	MENPFADPVARLtPTQSHDNSQVSR.V
SM	127	CPRT0000007435	k-cl cotransporter	65594	38	5%	0	33	1.10E-01	R.KPSsADIYQPDIVK.S
SM	128	CPRT0000007659	placenta-specific protein 8 protein	13424	69	11%	1	70	2.40E-05	MEsPTTKQPYAVR.Q

							0	49	0.0027	R.HSsPTSGLYCR.T
							2	47	0.0041	R.RRsPLDLASTR.H
SM	129	CPRT0000007759	sjchgc05800 protein	66670	365	16%	0	74	1.00E-05	K.HLSDDVHFtPFDR.K
							0	81	4.10E-06	K.HPASNLGDITITQGPDSHFRPFTPDQsPK.T
							0	57	3.80E-04	K.SGsASEIAADIHK.N
							1	57	7.80E-04	R.KYsDEYENISGHHDQYK.Q
							1	88	3.80E-07	R.RTsELSTDLANLK.L
SM	130	CPRT0000007774	heat shock protein 60	63630	185	8%	1	34	9.70E-02	R.NVIIESSWKsPK.I
SM	131	CPRT0000007860	glycogen synthase kinase 3	56751	64	2%	0	65	8.60E-05	K.EMVPGTANVSyISSR.Y
SM	132	CPRT0000007964	junctophilin cg4405- isoform a	88211	39	1%	0	39	3.50E-02	R.EFsPEFVQLGLMWEK.Q
SM	133	CPRT0000007965	hypothetical protein	23568	50	15%	0	50	2.60E-03	K.SYLIEsIIHLPGDVK.E
SM	134	CPRT0000008111	dynein light intermediate chain	124613	41	2%	0	43	1.30E-02	R.HIsPLLDTESDIR.T
SM	135	CPRT0000008142	Zinc finger Ran-binding domain-containing protein 2	31916	60	4%	2	60	3.00E-04	R.ERRDsDDEFDEFGR.K
SM	136	CPRT0000008289	ubx domain-containing protein 4	48307	63	3%	0	64	1.10E-04	R.LSHMPDNsDDEQAR.W
SM	137	CPRT0000008409	af287985_1synapsin isoform	36298	72	4%	2	73	1.40E-05	R.RFSsGDLQGELADKR.M
SM	138	CPRT0000008545	dynactin 1 isoform 3	48742	42	12%	2	41	1.90E-02	R.RQEPLANVNDTSDKENIPSPtQEQKPSTLPQILR.D
SM	139	CPRT0000008664	lamin	38122	38	7%	0	38	2.20E-02	R.SSsPLTISR.S
SM	140	CPRT0000008751	glucose transport protein	56955	97	3%	0	97	5.90E-08	K.QGNTDGPAsESLLHSR.N
SM	141	CPRT0000008913	major egg antigen	39394	68	13%	0	40	3.10E-02	K.INITNTPGTLLPQTsVPCGMMDFLK.D
							1	38	3.50E-02	K.NSGSESSVPLSESTISGsHRR.L
SM	142	CPRT0000008924	transcription elongation regulator 1	37650	74	7%	1	64	6.50E-05	R.KLDDSPtVR.E
SM	143	CPRT0000008950	U2 small nuclear rna auxiliary factor 2	34484	63	7%	1	63	0.0001	R.KLSsPQGGVDDR.N
SM	144	CPRT0000008975	rhoptry associated membrane antigen	73359	66	2%	0	66	5.80E-05	R.IPtPDISNNEVESAK.L
SM	145	CPRT0000009359	sjchgc04698 protein	55791	65	4%	0	38	7.10E-02	K.IAEEISPTEVFGEGAsEGETVVK.K
SM	146	CPRT0000009392	ke (drosophila actin-binding) homolog family member		253	9%	0	53	2.20E-03	M.ASPEVGMAYQLPSQFsPQSGNLATSTK.V

			(ketn-1)							
							0	166	1.20E-14	R.NsVSVDEASGPPQFVVHPVGQLTIAEGEPANITAR.V
							0	140	1.40E-09	R.NSVsVDEASGPPQFVVHPVGQLTIAEGEPANITAR.V
							0	36	4.00E-02	R.VGtPGEFNIK.A
SM	147	CPRT0000009445	heterochromatin protein 1	51650	53	2%	0	40	0.03	R.ESEEsGGEDEFQVEK.I
SM	148	CPRT0000009452	Alpha-adducin	38225	54	6%	0	54	0.0018	K.ANSDsGDIPWTPAELEFEAEMR.V
SM	149	CPRT0000009893	ATP-binding sub-family c member 2	127765	56	1%	1	56	5.40E-04	K.KLsLETPDSFSR.F
SM	150	CPRT0000009905	sjchgc02563 protein	35659	79	6%	1	53	1.40E-03	R.VRsVsNFELENNR.E
SM	151	CPRT0000009921	sjchgc09590 protein	180556	632	7%	0	55	1.10E-03	K.GELVSPPLPPPVAQDIsPNDELK.S
							1	207	9.60E-19	K.QEALLAEQVDDIPKEHLFVEsDEER.Y
							1	71	1.80E-05	R.KLEEELEEVDsR.A
SM	152	CPRT0000010020	z band alternatively spliced pdz-motif protein isoform f	35351	54	7%	0	43	0.021	K.HNISPLPFGQsPPAPGENFLAK.V
SM	153	CPRT0000010244	hypothetical protein	13926	45	6%	0	46	4.10E-03	K.LPsPEYYR.E
SM	154	CPRT0000010273	sjchgc02220 protein		105	17%	1	53	2.50E-03	R.KIENSSNWNPSsPIYPAYPAYMDK.S
SM	155	CPRT0000010408	venom allergen-like 6 protein	15415	37	14%	0	39	5.50E-02	R.sRPTSFANNDDIHYKPVYTR.S
SM	156	CPRT0000010982	cAMP-dependent protein kinase type ii-alpha regulatory subunit	23045	216	13%	1	119	6.70E-10	K.AASENRPNKANEsDEDEDEEPMPMPPQR.V
SM	157	CPRT0000011219	spectrin beta chain	47018	161	3%	1	40	0.038	K.VGsVNLLSEEMLDKAHPDAEK.I
SM	158	CPRT0000011316	sjchgc06768 protein		162	13%	0	46	7.90E-03	R.HRPAsVSGYLDECGLNR.S
							1	57	0.00063	R.KWsIASDYQYSPIHHSK.T
SM	159	CPRT0000012199	importin 7	116719	112	1%	0	114	1.20E-09	K.ALGsDEDEVDEESVR.Y
SM	160	CPRT0000012397	calcium-dependent secretion	423767	54	1%	0	51	1.90E-03	R.sLSQGSLLAVASLAGLR.H

Supplementary Table 11 The primers used for real time RT-PCR analysis

Part 1

The following primers were used to investigate RNAi effect of SjHsp90 silencing on the expression of putative SjHsp90 clients.

1) Protein ID: AAW27231.1
Forward 5` ATGTTGGTATGTGTGTTAGC3`
Reverse 5` CATCCGCATTAAGTAGAGTG3`

2) Protein ID: AAP06040.1
Forward 5` TGAAGAAGAGGAAGACAAGG3`
Reverse 5` GACATCACGGCACTTAATG3`

3) Protein ID: CPRT0000002152
Forward 5` GTCTTGGTCCTGGTGGTCTG3`
Reverse 5` CGGTGTTGTCGCTGTTTGG3`

4) Protein ID: CPRT0000002347
Forward 5` TCACAGTCACTCATCCTATTCG3`
Reverse 5` GGGTTCCACAAATTAAGATTATCTC3`

5) Protein ID: CPRT0000005797
Forward 5` CCTTGGCTTATCGTTGTAGTTG3`
Reverse 5` AGAGTCATCAGGAGTGAATGTG3`

6) Protein ID: CPRT0000010982
Forward 5`GGTCTAAGGGAACTATTACAGGAG3`
Reverse 5`CTTCATCTTCATCACTTTCATTTGC3`

7) Protein ID: CPRT0000006130
Forward 5`GAACAGAATTACTGCCTGGTATG3`
Reverse 5`ACCCGACATCCACAATATATCC3`

8) Protein ID: CPRT0000009921
Forward 5` AGAACAGAAGCCAGACTATG3`
Reverse 5` ACGAATCTCCTTGTGAATAATC3`

9) Protein ID: CPRT0000007860
Forward 5`ACTAATTTACCGTTATTCTCAGAGG3`
Reverse 5`GGACCATAGTATCTTCATTAACCAG3`

Part 2

The following primers were used to determine the mRNA transcripts of the genes encoding the phosproteins specifically detected in adult females.

1) Protein ID: CPRT0000000687
Forward 5`TATCAGCACCTCCTCAACTTTC3`
Reverse 5`CTCCGTGTAAGGTTTCTTTATCG3`

2) Protein ID: CPRT0000003518
Forward 5` TGGCAGCACGATATGTTTCAAG 3`
Reverse 5` GTACCCAGAGAACGACCACTTC 3`

4) Protein ID: CPRT0000007069
Forward 5`TGCTAATCCATCAGGTGAAGAAG3`
Reverser 5`GCCAATGTAGTGCTCATAATCG3`

Part 3
The following primers were used to determine the mRNA transcripts of the genes encoding the phosproteins specifically detected in adult males.

1) Protein ID: AAW24704.1
Forward 5` ATGGGTTACCGCCTGTTGTAC 3`
Reverse 5` TCGACGCTCAGCTTGCATATC 3`

2) Protein ID: AAW26183.1
Forward 5` AGGTAGCTCAAGAAAGACAGCG 3`
Reverse 5` TGTCGGCGTTTCATCTCAGC 3`

3) Protein ID: AAW26505.1
Forward 5` CATAGGTCGTGTACGCTCAG 3`
Reverse 5` TTTCAATTGTTCGACGTTTAGC 3`

4) Protein ID: AAW26700.1
Forward 5` GAAATCAAATCAGCCTTGGTGC 3`
Reverse 5` GCTGTTGTTGATGAGCAAGTTG 3`

5) Protein ID: CAX73091.1
Forward 5` TCAGGATATCGCAAGCATACGC 3`
Reverse 5` ACAAGATTCAGATGGCACTCGG 3`

6) Protein ID: CPRT0000010244
Forward 5` TGCCCTCACCTGAATACTACAG 3`
Reverse 5` ACTAATCCCTTCCCATAGCCTC 3`

7) Protein ID: CPRT0000005334

Forward 5` AGGCCACCTCCTCCAAGTAG 3`
Reverse 5` ATGTATGGGTTCGGTCCTTTCC3`

8) Protein ID: CPRT0000005690
Forward 5` AGTGCATTAAGACAAGTCGCAG 3`
Reverse 5` AGGTGATGGTGACAGAGCATTG3`

9) Protein ID: CPRT0000006771
Forward 5`CCATTACCAGAAGTATTACCAGAAG3`
Reverse 5`CCAGATTAAGGCGGAAATTAGTAG3`

10) Protein ID: CPRT0000008751
Forward 5`CCACGAGGTGCTGCCTATTC3`
Reverse 5`TCCAGAGCTGTAGTACGTTTGC3`

11) Protein ID: AAX25934
Forward 5`ATGGGAACGAGTAAACAGTATG3`
Reverse 5`ACTAGACGCTAGAAGACACTC3`

12) Protein ID: CPRT0000008409
Forward 5` AGAAGCTATTGGGCGATTGGG 3`
Reverse 5` CGCTTGGATGTTGTCGTATCAG 3`

Supplementary method:

Expression and Purification of Recombinant WD40 Protein

The cloning, expression of a partial fragment of the WD40 protein, and its purification was performed according to the standard molecular procedures. Briefly, expression plasmids containing partial fragment of SjWD40 were constructed by PCR-based amplification and subsequent insertion of the corresponding fragment into a pET28a (+) expression vector (Novagen). Restriction recognition sites of E*coR* Ⅰ(5′ -end) and H*ind* Ⅲ (3′ -end) were introduced by PCR using specific primers (Forward primer, 5`CCG AAT TCG TCT CAG TGG ACG GTT CAC 3`; Reverse primer, 5`GCA AGC TTG CTG AGT ATC CCA TAC TTG T3`) with cDNA derived from total RNA as template. Recombinant SjWD40 were expressed in transformed *E. coli* BL21 (DE3) cells carrying its corresponding vectors with an induction of 1.0 mM IPTG at 37℃. Soluble recombinant SjWD40 were purified by a Ni-NTA His*Band Purification Kit following the manufacturer's instructions (Novagen). The eluted protein fractions were analyzed by 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE).

Generation of the Antiserum for Recombinant SjWD40

Approximately 1mg purified recombinant SjWD40 was emulsified with equal amount of 206 adjuvant (Sigma-Aldrich). Three mice were intramuscularly immunized with the emulsified mixture, followed by two boosts at 3-weeks interval. Seven days after the last boost, mice were bled and the sera were collected and stored at −20℃.

Western Blot Analysis for SjWD40 Protein

The protein lysates of schistosomes (35 d) were prepared by using Tris buffer (pH=7.8), separated in 10% SDS-PAGE, and then electrotransferred onto polyvinylidene difluoride membrane (Sino-American Biotechnology, China). Non-specific protein–protein interactions were blocked using 5% non-fat dry milk in potassium phosphate buffer (PBS, pH=7.4) containing 0.1% Tween 20 (Sigma-Aldrich). Membranes were incubated in the sera against SjWD40 (1:500 dilution) for 1 h at room temperature, and washed five times for 5 min each time in 0.1% PBST. The secondary antibodies (Sino- American Biotechnology, China) were horseradish peroxidase (HRP) conjugated goat anti-mouse IgG and the membrane was incubated with the secondary antibodies (1:2,500 dilution) for 1 h. Upon the completion of five-time wash using PBST, the membrane was developed using Enhanced HRP-DAB Western blot Detection Kit according to manufacturer's instrument (Tiangen, China).