Table S1. Proteins detected by ESI LC/MS and MSMS

Protein name	Uniprot accession no.	ID category[a]	Protein MW, Da	Sequence Coverage, %[b]	Best peptide mascot "score"[c]	Best peptide	Peptide mass error, Da
La-related protein 7	Q4G0J3	[ID2+]	67,143	34	135	SSSEDAESLAPR	-0.0
Bicoid-interacting protein 3 homolog	Q7L2J0	[ID2+]	74,937	23	84	DAPQPYELNTAINCR	-0.14
Polyadenylate-binding protein 1	P11940	[ID2+]	70,508	19	57	SKVDEAVAVLQAHQAK	-0.10
Heterogenous nuclear ribonucleoprotein K	P661978	[ID2+]	47,756	13	56	IITITGTQDQIQNAQYLLQNSVK	-0.18
Heterogeneous nuclear ribonucleoprotein H	P31943	[ID1]	49,352	9	49	EEIVQFFSGLEIVPNGITLPVDFQGR	-0.10
Lupus La protein	P05455	[ID1]	47,919	3	61	LTTDFNVIVQALSK	-0.04
Heat shock protein HSP 90-beta	P08238	[ID2+]	83,423	66	104	GVVDSEDLPLNISR	-0.04
Cyclin-T1	O60563	[ID2+]	81,034	30	76	TYSLSSSFSSSSSTR	-0.04
Cyclin T2	Q29R66	[ID2+]	74,149	16	94	SPVGLSSDGISSSSSSSR	-0.03
Cell division protein kinase 9	P50750	[ID2+]	43,149	75	96	NPATTNQTEFER	-0.09
Hexamethylene bis-acetamide-inducible protein 1	O94992	[ID2+]	40,884	33	77	LGAPAAGGEEEWGQQQR	-0.06
Hexamethylene bis-acetamide-inducible protein 2	Q96MH2	[ID1]	32,741	6	66	QVEELAAEVQR	-0.05
Hsp90 co-chaperone Cdc37	Q16543	[ID2+]	44,953	32	76	QYMEGFNDELEAFK	-0.07

[a]Protein identification is based on 1 and 2 or more peptides for [ID1] and [ID2+] categories, respectively.

[b]Unique nonoverlapping peptides were used to calculate protein sequence coverage defined as the ratio between the sum of amino acids encompassed by the confidently matched peptides (%CI >95%) and the number of amino acids in a polypeptide sequence.

[c]Ions score is -10*Log(P), where P is the probability that the observed match is a random event. Ions scores above N, the mascot significance level calculated for $p < 0.05$, are considered to be statistically nonrandom.