

Table S1. SPRY4-IT1-binding Proteins Identified by Mass Spectrometry

Lipin 2 shows the highest spectral counts (83).

Number	Gene Symbol	Gene description	Subcellular location	Molecular function	Biological process	Peptide sequence	Nondegenerative sequence?	Instances observed	Total instances per gene	
1	<i>ILF2</i>	Interleukin enhancer-binding factor 2	cytoplasm, nucleolus, nucleolus, nuc	ATP binding, DNA binding, double-str immune response, positive regulatio	ILPTLEAVAALGNK	Yes	1	1		
2	<i>GPR37</i>	Probable G-protein coupled receptor 37	endoplasmic reticulum, endoplasmic	G-protein coupled receptor activity, G-protein coupled receptor signaling	LAVIIVWVALLLALP	Yes	12	12		
3	<i>SLC25A5</i>	ADP/ATP translocase 2	MMXD complex, integral to plasma	adenine transport, chromosome seg	YFPTQALNFAFK	Yes	1	1		
4	<i>RPLP1</i>	60S acidic ribosomal protein P1	cytoplasm, cytosol, cytosolic large	rRNA binding, protein binding, struct	RNA metabolic process, cellular prot	AAGVNVPEFWPLFLAK	Yes	2	2	
5	<i>IGF2BP1</i>	Insulin-like growth factor 2 mRNA-binding protein 1	CRD-mediated mRNA stability compl	mRNA-UTR binding, mRNA-UTR bin	CRD-mediated mRNA stabilization, R	MVIITGPPEAQFK	Yes	2	2	
6	<i>RPS3</i>	40S ribosomal protein S3	cytoplasm, cytosol, cytosol, cytosolic	DNA-(apurinic or pyrimidinic site) ly	RNA metabolic process, activation of	FGFPEGSVELYAEK GGKPEPPAMPQVPVPTA	No Yes	2 2	4	
7	<i>RPS6</i>	40s ribosomal protein S6	cytoplasm, cytosol, cytosolic small	rR protein binding, protein kinase	BIND RNA metabolic process, T cell	differe	DIPGLTDTTVPR	Yes	2	2
8	<i>LIPIN2</i>	Phosphatidate phosphatase lipin2	ic reticulum, endoplasmic reticulum	matidate phosphatase activity, transcr	sitive regulation of transcription from	TIFTPS[167]SVKK TIFTSS[167]VKK	Yes Yes	19 83	102	
9	<i>ALB</i>	Uncharacterized protein	basement membrane, cytoplasm, ex	DNA binding, antioxidant activity, ce	bile acid and bile salt transport, bile	-KVPQVSTPTLVEVSR	Yes	3	3	
10	<i>NACA</i>	Nascent polypeptide-associated complex subunit alpha	cytoplasm, nascent polypeptide-assc	DNA binding	interspecies interaction between org	IEDLSQQAAQAAAEK	Yes	2	2	
11	<i>HNRNPCL1</i>	Heterogeneous nuclear ribonucleoprotein c-like 1	nucleus, ribonucleoprotein complex	RNA binding, nucleotide binding		VFIGNLNTLVVK	Yes	3	3	
12	<i>TRAP1</i>	Heat shock protein 75 kDa, mitochondrial	cellular_component, mitochondrion	ATP binding, nucleotide binding, tur	cellular response to oxidative stress, G	VVDESDIPLNSLR	Yes	13	13	
13	<i>TUBB2B</i>	Tubulin beta-2b chain	cytoplasm, cytoskeleton, microtubule,	nucleotide binding, peptide binding	bule-based movement, mitosis, neur	AFVHWYTT[181]GEGM[147]DEME	No	1	70	
						AILVDLEPGTM[147]DSVR	No	15		
						AILVDLEPGTM[147]DSVR	No	1		
						AILVDLEPGTMDSVR	No	11		
						GHYTEGAELVDSVLDVVR	No	1		
						GHYTEGAELVDSVLDVVRK	No	5		
						INVYYNEATGNKYVPR	Yes	4		
						ISEQFTAM[147]FR	No	4		
						ISEQFTAMFR	No	1		
						LAVNM[147]VPFPR	No	10		
LAVNMVPFPR	No	2								
LHFFM[147]PGFAPLTSR	No	5								
LHFFM[147]PGFAPLTSR	No	2								
LTPPTYGDLNHLVSATM[147]SGVTTCLR	No	2								
LTPPTYGDLNHLVSATMSGVTTCLR	No	2								
M[147]SATFIGNSTAIQELFK	No	1								
YLTVAIFR	No	3								
14	<i>RPS8</i>	40S ribosomal protein S8	cytoplasm, cytosol, cytosolic small	rR structural constituent of ribosome, s	RNA metabolic process, cellular prot	IIDVVYNASNELVR	Yes	2	2	
15	<i>HIST1H1B</i>	Histone H15	chromosome, nucleosome, nucleus	DNA binding	nucleosome assembly	ATGPPVSELTK	Yes	1	1	
16	<i>HSPE1</i>	10 kDa heat shock protein, mitochondrial	cytoplasm, mitochondrial matrix, mi	ATP binding, chaperone binding, cha	activation of cysteine-type endopept	VVLDDKDYFLFR	Yes	2	2	
17	<i>DPYSL2</i>	Dihydropyrimidinase-related protein 2	ondrion, neuronal cell body, protein	activity, acting on carbon-nitrogen	[titive regulation of glutamate secretion	GLYDGPVCEVSVTPK	Yes	2	4	
						ILDLDITGPEGHVLSRPEEVEAEAVNR	Yes	1		
						MDENQFVAVSTNAAK	No	1		
18	<i>VCL</i>	Isoform 1 of vinculin	mere, cytoplasm, cytoskeleton, cytos	ienin binding, beta-dystroglycan	bndesion, lamellipodium assembly, mor	AVGT[181]ANKS[167]T[181]VEGIQASVK	Yes	1	14	
						LVQAAQM[147]LQ	No	12		
						AGVNTVTLVENK	No	1		
19	<i>RPL7A</i>	60s ribosomal protein 7a	omal subunit, membrane fraction, p	protein binding, structural constitue	nt process, ribosome biogenesis, transl	LKVPAINQFTQALDR	Yes	1	2	
20	<i>RPL24</i>	60S ribosomal protein L24	cytosol, cytosolic large ribosomal	sul RNA binding, structural constitue	nt (RNA metabolic process, cellular prot	AITGASLADIM[147]AK	Yes	2	12	
21	<i>IGH@</i>	Putative matrix cell adhesion molecule-3				LTM[147]TRDTSTST	Yes	9	10	
						VGPGAHS[167]QVQLVQS[167]GAEVK	No	1		
						ALELALLQGLLG	Yes	1		
22	<i>NYNRIN</i>	Isoform 1 of protein nyrin	:omponent, integral to membrane,	molecular_function, nucleic acid bindi	ng DNA integration, biological_process	LEVT[181]VSHVALTA	Yes	1	8	
						LEVTVS[167]HVALTA	Yes	5		
						LPFTFAGNLFMVPDPLGR	Yes	1		
23	<i>RPSA</i>	Laminin receptor-like protein lamr5	90S preribosome, cytoplasm, cytop	rotein binding, receptor activity, r	ibRNA metabolic process, cell adhesior	AIVAIENPADVSVISR	Yes	1	1	
25	<i>DDX17</i>	Probable atp-dependent rna helicase ddx17 isoform 3	nucleus	ATP binding, ATP-dependent helicase	rNA processing	ELAQQVQVADDDYK	Yes	1	1	