Table S1. Candidate Tcl1 protein partners isolated through mass spectrometry

Protein	**Accession no. In Pub Med / HUGO gene name**	**Mr KDa**	**Peptide sequences**	**Protein Mascot score**
T-cell leukemia/lymphoma protein 1	NP_001092195.1 TCL1A	13	R.REDVVLGRPMTPTQIGPSLLPIMWQLYPDGR.Y M.AECPTLGEAVTDHPDR.L K.QHAWLPLTIEIK.D	68
Heterogeneous nuclear ribonucleoprotein K (hnRNP K)	NP_002131.2 HNRNPK	51	K.RPAEDMEEEQAFKR.S	178
Heat shock 70 kDa protein 1 (HSP70.1)	NP_005336.3 HSPA1A	70	R.DAKLDKAQIHDLVLVGGSTR.I K.NQVALNPQNTVFDAK.R R.TTPSYVAFTDTER.L	162
Non-POU domain-containing octamer-binding protein (NonO protein)	NP_001138881.1 NONO	54	R.FACHSASLTVRNLPQYVSNELLEEAFSVFGQVER.A R.NLPQYVSNELLEEAFSVFGQVER.A R.FACHSASLTVR.N K.GIVEFSGKPAAR.K R.HEHQVMLMR.Q	107
DAZ-associated protein 1 (Deleted in azoospermia-associated protein 1)	NP_733829.1 DAZ1	43	EYFKKFGVVTEVVMIYDAEK.Q K.FGVVTEVVMIYDAEK.Q	85
Peroxiredoxin-4	NP_006397.1 PRDX4	31	VSVADHSLHLSK.A	80
60S ribosomal protein L8	NP_150644.1 RPL8	28	R.ASGNYATVISHNPETK.K	75
Eukaryotic initiation factor 4A-I	NP_001407.1 EIF4A1	46	R.KGVAINMVTEEDKR.T	72
60S acidic ribosomal protein P2	NP_000995.1 RPLP2	12	K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEEK.K	71
CAD protein	NP_004332.2 CAD	245	R.VLGTPVETIELTEDR.R R.YGVRVLGTPVETIELTEDR.R	66
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily C member 1	NP-003065.3 SMARCA1	123	K.TLAGLVVQLLQFQEDAFGK.H K.HVTNPAFTKLPAK.C R.RFDLQNPSR.M K.TPEIYLAYR.N	58
Spectrin alpha chain	NP_003117.2 SPTA1	285	R.MQHNLEQQIQAR.N K.LGESQTLQQFSR.D	55
Peptidyl-prolyl cis-trans isomerase A	NP_066953.1 FKBP2	18	R.IIPGFMCQGGDFTR.H K.KITIADCGQLE.-	51
Peroxiredoxin-1	NP_859048.1 PRDX1	22	K.ATAVMPDGQFK.D R.TIAQDYGVLK.A	51
Serine-protein kinase ATM(Ataxia telangiectasia mutated) (A-T, mutated)	NP_000042.3 ATM	355	K.SLHLHMYLMLLK.E	43
Tropomyosin-1 alpha chain	NP_001018005.1 TPM1	33	R.IQLVEEELDR.A	42
BAG family molecular chaperone regulator 4 BAG-4)	NP_004865.1 BAG4	50	R.AGGSHQEQPPYPSYNSNYWNSTAR.S	41
Immunoglobulin superfamily member 21 precursor	NP_116269.3 IGFS21	52	HPALSMPMQAEVTLVAPKGPK.I K.HPALSMPMQAEVTLVAPK.G	37