

Table S1. Representative proteins specifically identified as a binding partner of *Tcea3* in mESCs

Gene accession no	Protein name	Amino acid sequences by MS/MS analysis			
		Peptide MW (expt)	Peptide MW (calc)	Score	Peptide Sequence
IPI00320034	DNA-directed RNA polymerase II subunit RPB2	942.5246	942.5247	79.63	AGVSQVLNR
		1136.6782	1136.6778	37.83	ARGPIQILNR
		1403.5812	1403.5809	49.37	DGAPSPMMPNEAR
		1773.854	1773.8533	81.27	GEIGDATPFNDAVNVQK
		1325.6364	1325.6364	66.87	GNEVLYNGFTGR
		909.5395	909.5396	56.1	GPIQILNR
		953.439	953.4389	54.1	GTCGIQYR
		1230.6716	1230.6721	62.85	IPQIGDKFASR
		1686.8232	1685.8777	63.74	ITSQIFIGPTYQR
		1016.6275	1016.627	45	IVATLPYIK
		2798.3607	2796.3566	44.23	IVEDAPPIDLQAEAQHASGEVEEPPR
		1708.844	1708.842	69.76	KGFDQEEVFEKPTR
		1239.6457	1239.6459	55.76	LDDDGLIAPGVR
		1259.6225	1259.622	62.22	MATNTVYVFAK
		1057.6241	1057.6244	41.17	NKTQISLVR
		1596.841	1596.8399	69.55	NLTYSAPLYVDITK
		1212.7225	1212.723	54.52	QEVPIIVFR
		1894.9751	1894.9748	50.37	TVIKEGEEQLQTQHQQ
		2274.1327	2273.1288	105.4	VSANKGEIGDATPFNDAVNVQK

		1001.539	1001.5393	51.55	VSGDDVIIGK
		1338.6208	1338.6204	85.54	YSLATGNWGDQK
IPI00317794	Nucleolin	843.5067	843.5065	42.23	ALELTGLK
		1122.5439	1122.5444	38.48	ETLEEVFEK
		1560.6738	1560.6733	68.01	GFGFVDFNSEEDAK
		939.5064	939.5065	50.35	GIAYIEFK
		1002.5093	1002.5094	59.84	LELQGSNSR
		999.5348	999.5349	71.6	NDLAVVDVR
		1361.631	1361.631	45.62	SEADAENKLEEK
		2188.0255	2188.0243	46.2	SEADAENKLEEKQGAIDGR
		1145.5609	1145.5604	42.01	SVSLYTGK
		1486.7414	1486.7416	67.91	SVSLYTGKQGR
		1372.7428	1372.7422	78.45	TIRLELQGSNSR
		1395.7622	1395.7609	91.18	TLVLSNLSYSATK
		2287.148	2287.1485	85.68	VEGSEPTTFFNLFIGNLNPNK
IPI00109401	RNA polymerase II- Associated protein 3	1551.8485	1551.8481	46.53	GIAADRTNALLPANR
		1675.7726	1674.7672	76.26	GMDADPYNPVLPTNR
		1698.8794	1698.8788	103.83	IEAVSDTSAPQAQGVK
		968.5409	968.5403	43.42	TNALLPANR
		1888.9234	1888.9214	78.45	VLELEPDNFEATNELR
IPI00230035	ATP-dependent RNA helicase DDX3X	1127.6445	1127.6438	55.97	DLLDLLVEAK
		1237.5431	1237.5431	72.09	DLMACAQTGSGK
		1794.78	1794.7769	68.83	DYRQSSGASSSFSSSR
		1549.6688	1549.6685	66.52	GFYDKDSSGWSSSK
		1121.5216	1121.5214	60.9	GRGDYDGIGGR

		851.4209	851.4211	47.67	IGLDFCK
		1172.575	1172.5747	44.51	IVEQDTMPPK
		1484.7657	1484.7657	56.82	IVEQDTMPPKGVR
		1484.8712	1484.8715	62	KQYPISLVLAPTR
		1367.6218	1367.6214	50.32	MLDMGFEPQIR
		1360.586	1360.5855	47.96	QSSGASSSSFSSSR
		1356.7773	1356.7765	63.14	QYPISLVLAPTR
		1328.6761	1328.6758	50	RIVEQDTMPPK
		1640.8663	1640.8668	42.41	RIVEQDTMPPKGVR
		926.4608	926.461	50.98	SGFGKFER
		1439.8465	1439.846	57.49	SGKSPILVATAVAAR
		1168.701	1167.6975	104.83	SPILVATAVAAR
		1523.7738	1523.7732	78.51	VGNLGLATSEFFNER
		1901.9995	1900.9942	70.32	VRPCVVYGGAEIGQQIR
		1271.687	1271.6874	54.59	VWVVEEIDKR
IPI00307837	Elongation factor 1-alpha 1	1331.7262	1331.7231	46.71	DMRQTVAVGVK
		1313.7346	1313.7343	61.37	EHALLAYTLGVK
		1154.5271	1154.5277	42.93	FEKEAAEMGK
		1024.6017	1024.603	63.64	IGGIGTVPVGR
		3600.6612	3598.6537	50.29	IGYNPDTVAFVPISGWNGDNMLEPSANMPWFK
		3122.6497	3121.6441	67.78	KDGSASGTTLEALDCILPPTRPTDKPLR
		3728.7541	3726.7487	50.23	KIGYNPDTVAFVPISGWNGDNMLEPSANMPWFK
		974.545	974.5437	55.47	LPLQDVYK
		1297.5494	1297.5496	53.71	MDSTEPPYSQK
		1453.6515	1453.6507	52.83	MDSTEPPYSQKR

		2926.4381	2924.426	60.82	NMITGTSQADCAVLIVAAGVGEFEAGISK
		869.534	869.5334	44.7	QLIVGVNK
		2150.0819	2149.0725	71.37	QLIVGVNKMDSTEPPYSQK
		2306.1891	2305.1736	51.26	QLIVGVNKMDSTEPPYSQKR
		913.5617	913.5597	60.7	QTVAVGVK
		1755.9464	1755.9407	82.96	RYEEIVKEVSTYIK
		3027.3953	3026.3824	73.56	SGDAAIVDMVPGKPMCVESFSDYPPLGR
		1119.5937	1119.5924	51.08	STTTGHLIYK
		1625.7995	1625.797	72.97	TIEKFEKEAAEMGK
		2530.3751	2530.3717	45.08	VETGVLKPGMVVTFAPVNVTTTEVK
		1599.8441	1599.8396	81.42	YEEIVKEVSTYIK
		1727.9387	1727.9345	94.75	YEEIVKEVSTYIKK
		1403.7208	1403.7197	62.76	YYVTIIDAPGHR
		1907.9992	1906.9941	59	YYVTIIDAPGHRDFIK
IPI00318841	Elongation factor 1-gamma	2357.0257	2356.0198	70.45	AAAPAPEEEMDECEQALAAEPK
		1540.7329	1540.731	39.83	AAGTLYTYPENWR
		1693.9405	1692.9311	65.89	AFKALIAAQYSGAQVR
		1122.622	1122.6186	40.29	AKDPFAHLPK
		1346.7311	1346.7306	88.53	ALIAAQYSGAQVR
		1714.8003	1713.7787	64.88	EYFSWEGTFQHVGK
		805.3971	805.397	41.8	FAESQPK
		2688.2394	2686.234	51.65	GQELAFPLSPDWQVDYESYTW
		1121.6821	1121.6808	76.43	ILGLLDTHLK
		2501.1273	2500.1097	75.32	KAAAPAPEEEMDECEQALAAEPK
		1571.8159	1571.8155	42.48	KLDPGSEETQTLVR
		1443.7213	1443.7205	80.88	LDPGSEETQTLVR

		946.4612	946.4621	50.74	QAFPNTNR
		2537.2093	2537.2386	42.29	QAFPNTNRWFLTCINQPQFR
		1245.6205	1245.6201	50.11	QATENAKEEVK
		1401.7217	1401.7212	48.73	QATENAKEEVKR
		1277.7834	1277.7819	62.78	RILGLLDTHLK
		1240.6449	1240.6452	56.28	STFVLDEFKR
		821.4485	820.4443	38.29	TFLVGER
		1077.5957	1077.5931	41.92	TRTFLVGER
		1707.8786	1706.8641	63.32	VLSAPPHFHFGQTNR
		1608.7875	1608.7871	62.47	WFLTCINQPQFR
IPI00226073	Isoform 1 of Heterogeneous nuclear ribonucleoprotein F	1996.9555	1995.969	66.83	ATENDIYNFFSPLNPVR
		1615.6803	1615.6759	69.32	DLSYCLSGMYDHR
		1629.7165	1629.7132	88.93	HSGPNSADSANDGFVR
		1868.9437	1866.9363	90.05	ITGEAFVQFASQELAEK
		1780.8092	1780.8003	72.99	QSGEAFVELESEDDVK
		1400.6877	1400.6871	39.41	SHRTEMDWVLK
		2207.0112	2207.0052	52.89	VTGEADVEFATHEEAVAAMSK
		2227.9515	2226.9423	47.41	YGDSEFTVQSTTGHCVHMR