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Supplemental Table S1

Detailed mass spectrometry data and IR scores for human TAP interactions. Annotated spectra for proteins identified on the basis of a single peptide are presented in supplemental Table S4 and supplemental Figure S1.

Bait	Prey	Accession Number	Unique Peptide Match	Sequence Coverage %	Protein Mascot Score	IR score
CCT4	CCT2	CAG33352	12	29.3	630	0.8824
CCT4	CCT3	CAI14168	14	25.3	708	0.8557
CCT4	CCT5	AAH02971	10	19.3	487	0.9342
CCT4	CCT6A	BAD92965	13	25.1	610	0.8458
CCT4	CCT6B	Q92526	4	6.6	188	0.7654
CCT4	CCT7	NP_006420	12	27.3	638	0.8553
CCT4	CCT8	EAX09924	15	30.0	811	0.8671
CCT4	HIST1H1E	ABN72276	2	10.5	118	0.7566
CCT4	HSPA6	BAD97082	3	6.7	213	0.8148
CCT4	TCP1	CAA37064	12	25.4	628	0.8331
CCT5	BAT2D1	CAB51071	12	4.9	556	0.7507
CCT5	CAND1	AAH26220	2	2.0	145	0.7494
CCT5	CCT2	NP_006422	28	64.5	1890	0.8740
CCT5	CCT3	CAI14168	20	43.3	1142	0.8659
CCT5	CCT4	NP_006421	30	53.4	1678	0.9336
CCT5	CCT6A	BAD92965	25	48.4	1588	0.8824
CCT5	CCT6B	Q92526	5	9.1	272	0.7613
CCT5	CCT7	EAW99740	24	58.1	1524	0.8993
CCT5	CCT8	BAD96210	32	54.0	2001	0.9062
CCT5	CKAP5	NP_055571	11	5.9	492	0.7728
CCT5	DDX42	EAW94278	5	5.9	312	0.7829
CCT5	EEF1A2	AAA91835	2	4.6	90	0.7414
CCT5	HNRNPU	NP_114032	13	16.8	638	0.7850
CCT5	INF2	EAW81874	5	5.3	294	0.7720
CCT5	KHSRP	AAH85004	9	20.3	487	0.7750
CCT5	KPNA2	AAH67848	2	7.9	120	0.8414
CCT5	LONP1	AAI09219	2	2.6	128	0.7688
CCT5	PCBP1	NP_006187	4	13.8	182	0.7539
CCT5	PCBP2	NP_001092090	4	16.3	180	0.7818
CCT5	PDCD5	NP_004699	7	46.4	378	0.9611
CCT5	RP11-631M21.2	EAW69700	2	28.6	88	0.7351
CCT5	TCP1	NP_110379	24	44.1	1546	0.8830
CCT5	TUBA1A	CAA25855	18	46.1	1132	0.8993
CCT5	TUBA1B	NP_035784	18	46.1	1158	0.7924
CCT5	TUBA1C	NP_116093	18	46.3	1132	0.8097
CCT5	TUBB3	AAH01678	11	29.6	784	0.7792
CCT5	TUBB6	NP_080749	9	20.4	575	0.8173
CCT5	XPO1	NP_003391	1	1.1	67	0.7444
GPN1	BAT1	NP_542165	2	5.1	86	0.7525
GPN1	CCT3	NP_005989	4	7.7	193	0.7872
GPN1	CCT4	NP_006421	10	23.6	479	0.8551
GPN1	CCT5	NP_036205	2	2.4	80	0.8242
GPN1	CCT6A	NP_001753	4	7.5	152	0.7946
GPN1	CCT7	NP_006420	4	11.2	263	0.7991

GPN1	CCT8	NP_006576	6	15.3	271	0.7775
GPN1	GPN3	AAH31024	3	14.4	230	0.9571
GPN1	GRINL1A	BAC11313	3	11.1	139	0.8311
GPN1	HIST1H2BM	NP_003512	2	19.0	92	0.7435
GPN1	HNRNPU	NP_004492	7	13.4	312	0.7979
GPN1	HSP90AB1	NP_031381	2	3.6	105	0.7744
GPN1	HSPA1L	AAH63507	9	18.1	544	0.8052
GPN1	HSPA8	NP_006588	15	25.9	763	0.8490
GPN1	KPNA2	NP_002257	1	2.8	50	0.8097
GPN1	PDRG1	AAH01856	3	25.6	144	0.8120
GPN1	PFDN2	AAH47042	3	22.7	207	0.8643
GPN1	PFDN6	AAH59783	5	34.1	174	0.8299
GPN1	PIH1D1	NP_060386	3	11.0	154	0.8319
GPN1	POLR1C	AAH08118	6	21.3	297	0.8085
GPN1	POLR2A	NP_000928	8	4.6	341	0.8417
GPN1	POLR2B	AAH23503	28	24.8	1331	0.8909
GPN1	POLR2C	CAA11843	3	9.8	131	0.7860
GPN1	POLR2D	AAY14877	1	17.9	69	0.7721
GPN1	POLR2E	AAH04441	10	45.2	482	0.8306
GPN1	POLR2H	AAA91458	2	18.0	101	0.8194
GPN1	RPAP1	NP_056355	18	12.6	812	0.9470
GPN1	RPAP2	AAH39014	6	10.1	233	0.8510
GPN1	RPAP3	AAH56415	8	15.2	326	0.8894
GPN1	RUVBL1	ABF13334	5	15.0	223	0.8369
GPN1	RUVBL2	Q9WTM5	10	26.1	512	0.8298
GPN1	TCOF1	NP_000347	3	3.6	116	0.7427
GPN1	TCP1	NP_110379	8	17.6	339	0.8193
GPN1	TUBA1A	BAE27586	4	11.5	235	0.8456
GPN1	TUBA1C	NP_116093	5	16.0	276	0.7986
GPN1	TUBB	ABE96641	2	12.0	48	0.8092
GPN1	UXT	CAI42449	2	21.7	74	0.8037
GPN1	WDR92	BAB71143	5	13.7	142	0.7823
GPN1	XPO1	NP_003391	1	1.3	38	0.7337
GPN2	ARID3A	AAW30734	2	4.6	159	0.7594
GPN2	CKAP5	NP_055571	6	3.5	322	0.7542
GPN2	DDX3Y	NP_004651	2	3.2	101	0.7428
GPN2	GTF2I	AAB48826	3	2.8	105	0.7416
GPN2	INF2	EAW81874	6	6.6	269	0.7494
GPN2	POLR2B	NP_000929	6	5.0	201	0.7782
GPN2	RPAP1	EAW92503	8	6.6	385	0.7950
GPN3	GPN1	EAX00557	1	4.1	89	0.8901
GPN3	HNRNPU	NP_004492	11	14.0	494	0.7528
GPN3	HSPA6	BAD97082	5	9.8	286	0.7696
GPN3	POLR1A	O95602	18	11.2	775	0.7766
GPN3	POLR1C	CAI42628	3	12.7	156	0.7666
GPN3	POLR2A	CAA52862	8	4.9	376	0.8577
GPN3	POLR2B	NP_000929	7	5.9	277	0.7917
GPN3	POLR2C	NP_116558	2	8.4	107	0.7737
GPN3	POLR2E	AAH34144	4	19.5	203	0.8311
GPN3	POLR2H	NP_006223	2	10.7	123	0.7951
GPN3	RPAP2	EAW73096	6	10.6	218	0.8853
GPN3	TUBA1A	CAA25855	11	32.4	569	0.8131

GPN3	TUBB2C	EAW88369	10	20.6	506	0.7685
GPN3	TUBB3	BAD96759	6	20.7	301	0.7658
GRINL1A	EIF4A2	AAH15842	2	5.7	123	0.7721
GRINL1A	Gcom1	CAB43263	2	15.2	181	0.8535
GRINL1A	POLR2A	NP_000928	5	3.0	219	0.8544
GRINL1A	POLR2B	AAH23503	21	19.8	971	0.7627
GRINL1A	POLR2C	AAH28157	9	32.0	590	0.8333
GRINL1A	POLR2D	2C35	5	32.9	259	0.8372
GRINL1A	POLR2E	AAH04441	13	80.0	796	0.8116
GRINL1A	POLR2H	AAA91458	6	42.0	397	0.8205
GRINL1A	RPAP2	AAH39014	4	7.0	151	0.8469
HSPA8	HSPA5	AAF13605	3	4.4	265	0.7983
HSPA8	TUBA1A	CAA25855	9	26.2	462	0.8245
KPNA2	ACTB	BAD96752	13	31.2	793	0.8362
KPNA2	ACTBL2	NP_001017992	5	11.7	265	0.7963
KPNA2	ACTG1	AAH17450	8	23.7	415	0.8260
KPNA2	ACTL6A	NP_004292	12	35.0	685	0.8178
KPNA2	ARID2	BAB55236	2	8.5	114	0.7573
KPNA2	ARS2	AAI09118	8	9.4	368	0.7534
KPNA2	C12orf45	NP_689531	9	41.1	526	0.8326
KPNA2	C17orf49	NP_777553	3	20.9	232	0.7997
KPNA2	C20orf20	NP_060740	3	17.2	190	0.7528
KPNA2	CCAR1	EAW54300	12	12.7	563	0.7803
KPNA2	CD3EAP	AAI08890	3	13.2	202	0.7794
KPNA2	CDK2AP1	EAW98399	3	29.0	202	0.7991
KPNA2	CHD4	NP_001264	16	9.6	818	0.8041
KPNA2	CTDSPL2	AAH18623	3	28.0	182	0.7525
KPNA2	DPF2	NP_006259	2	5.9	124	0.7717
KPNA2	GATAD2A	CAB99095	3	24.3	178	0.7477
KPNA2	GATAD2B	BAA86464	4	10.2	246	0.7413
KPNA2	HDAC1	BAA08909	5	8.5	200	0.7487
KPNA2	HDAC2	EAW48252	5	10.9	286	0.8255
KPNA2	HNRNPC	EAW66397	2	12.1	100	0.7592
KPNA2	HNRNPU	AAH07950	8	14.0	274	0.8212
KPNA2	KIFC1	Q9BW19	22	35.4	1130	0.8370
KPNA2	KPNB1	NP_002256	51	61.2	3597	0.9322
KPNA2	MBD2	NP_003918	6	12.9	236	0.7584
KPNA2	MBD3	NP_003917	12	38.1	693	0.8438
KPNA2	MDC1	NP_055456	4	3.0	238	0.7516
KPNA2	MTA2	NP_004730	24	35.3	1275	0.8555
KPNA2	NCBP1	NP_002477	15	21.8	629	0.7799
KPNA2	NCBP2	NP_031388	12	48.7	484	0.7589
KPNA2	NHP2L1	NP_004999	2	18.8	131	0.7393
KPNA2	NOLC1	AAH06769	19	22.5	961	0.8208
KPNA2	NOP58	CAB55989	4	11.3	199	0.7420
KPNA2	NUMA1	AAD16994	5	18.7	231	0.8132
KPNA2	NUP153	AAH52965	14	11.4	693	0.7896
KPNA2	NUP50	NP_705931	19	56.4	1295	0.8228
KPNA2	PBRM1	BAB71210	26	28.7	1233	0.8635
KPNA2	PHAX	NP_115553	6	20.1	308	0.7388
KPNA2	PHF10	CAI12317	10	31.5	426	0.8105
KPNA2	POLR1C	CAI42628	2	6.4	93	0.7675

KPNA2	POLR1D	NP_057056	1	8.3	49	0.7451
KPNA2	POLR1E	NP_071935	1	2.1	57	0.8587
KPNA2	POLR2E	AAB19339	2	39.6	86	0.8503
KPNA2	POLR2H	NP_006223	5	32.7	262	0.8074
KPNA2	POLR2K	NP_005025	1	12.1	45	0.7374
KPNA2	PSME3	EAW60891	2	9.8	161	0.7933
KPNA2	RBBP4	BAD96499	14	27.8	735	0.8153
KPNA2	RBBP7	CAI41284	13	25.2	677	0.8209
KPNA2	RUVBL1	BAD96295	9	27.0	559	0.8229
KPNA2	RUVBL2	NP_006657	5	12.3	365	0.7858
KPNA2	SART3	NP_055521	20	23.7	1019	0.8413
KPNA2	SMARCA2	P51531	19	13.1	849	0.8091
KPNA2	SMARCA4	EAW84167	28	18.0	1347	0.8638
KPNA2	SMARCB1	CAA76639	8	25.6	421	0.7828
KPNA2	SMARCC1	AAI17214	29	23.8	1376	0.8303
KPNA2	SMARCC2	NP_620706	33	26.8	1887	0.8446
KPNA2	SMARCD1	NP_620710	4	9.3	246	0.7832
KPNA2	SMARCD2	Q92925	8	16.0	401	0.7779
KPNA2	SMARCD3	AAS02031	4	13.0	165	0.7601
KPNA2	SMARCE1	NP_003070	11	27.0	739	0.7943
KPNA2	TAF10	NP_006275	2	15.6	178	0.8638
KPNA2	TAF1L	NP_722516	3	1.8	184	0.8297
KPNA2	TAF4	AAC50901	3	4.2	273	0.8223
KPNA2	TAF5	EAW49646	2	3.1	111	0.7809
KPNA2	TAF6	NP_620835	5	10.3	289	0.7918
KPNA2	TAF9	NP_003178	8	31.4	385	0.7765
KPNA2	TAF9B	NP_057059	7	24.3	348	0.7748
KPNA2	TBP	AAI09055	2	6.9	95	0.7495
KPNA2	TUBB	CAI41893	17	47.2	1128	0.8360
KPNA2	TUBB2A	NP_001060	13	34.4	825	0.8417
KPNA2	TUBB2C	EAW88369	16	42.6	973	0.8201
KPNA2	TUBB3	AAH01678	10	26.8	712	0.8305
KPNA2	TUBB4	CAA25318	11	30.0	669	0.8510
KPNA2	TUBB6	EAX01553	6	17.9	303	0.7911
PDRG1	C19orf2	AAH26184	4	7.8	174	0.8142
PDRG1	HSPA5	AAF13605	4	7.4	142	0.7896
PDRG1	LONP1	AAI09219	2	2.6	80	0.7427
PDRG1	PFDN1	BAD97114	5	30.3	262	0.7833
PDRG1	PFDN2	AAF36151	5	46.2	262	0.9235
PDRG1	PFDN5	EAW96684	2	27.1	93	0.7492
PDRG1	PFDN6	NP_055075	11	58.1	472	0.9525
PDRG1	PIH1D1	NP_060386	3	12.8	123	0.8543
PDRG1	POLR2E	EAW69550	4	33.3	212	0.8105
PDRG1	RPAP3	AAH56415	8	13.0	415	0.9110
PDRG1	RUVBL1	BAD96295	5	15.1	383	0.8075
PDRG1	RUVBL2	AAD34041	5	11.8	296	0.7915
PDRG1	SNRPD3	NP_004166	2	15.1	113	0.7676
PDRG1	UXT	NP_004173	4	21.7	259	0.9469
PFDN2	C19orf2	AAH26184	4	8.6	207	0.8543
PFDN2	HNRNPA2B1	NP_112533	2	8.8	154	0.8225
PFDN2	HNRNPU	AAH07950	3	4.5	139	0.7891
PFDN2	KIN	NP_036443	2	2.0	90	0.7827

PFDN2	PDRG1	AAH01856	2	20.2	153	0.9555
PFDN2	PFDN1	BAD97114	11	61.5	638	0.8167
PFDN2	PFDN4	AAB17063	6	45.4	429	0.9337
PFDN2	PFDN5	NP_002615	11	69.5	890	0.8907
PFDN2	PFDN6	NP_055075	21	74.4	1130	0.9371
PFDN2	PIH1D1	NP_060386	2	7.6	88	0.8279
PFDN2	POLR2E	AAB19339	2	39.6	76	0.7645
PFDN2	RPAP3	AAH56415	6	13.3	251	0.8366
PFDN2	RUVBL1	BAD96295	3	9.6	178	0.8348
PFDN2	RUVBL2	AAD34041	2	4.3	104	0.8325
PFDN2	TUBA1B	NP_035784	8	26.8	581	0.8109
PFDN2	TUBB	CAI41893	8	24.9	347	0.8058
PFDN2	TUBB2C	EAW88369	6	17.4	241	0.8034
PFDN2	UXT	NP_004173	4	22.9	246	0.9406
PFDN2	VBP1	AAC50617	16	44.0	828	0.8313
PFDN6	C19orf2	NP_003787	26	41.7	1483	0.9080
PFDN6	CCT2	CAG33352	2	6.0	115	0.7942
PFDN6	HNRNPD	BAA09524	2	10.2	80	0.7340
PFDN6	HSPA2	NP_068814	4	7.8	198	0.7699
PFDN6	HSPA5	AAF13605	2	3.1	99	0.7885
PFDN6	KIN	NP_036443	2	2.0	120	0.7825
PFDN6	PDRG1	AAH01856	7	49.6	462	0.9629
PFDN6	PFDN1	NP_002613	19	88.5	1017	0.8270
PFDN6	PFDN2	NP_036526	15	77.3	1003	0.9521
PFDN6	PFDN4	AAB17063	12	59.2	836	0.9554
PFDN6	PFDN5	NP_002615	10	59.7	793	0.8807
PFDN6	PIH1D1	AAH01108	6	30.7	389	0.9267
PFDN6	POLR2E	NP_002686	9	41.4	422	0.8489
PFDN6	RP11-631M21.2	EAW69700	2	28.6	95	0.7840
PFDN6	RPAP3	EAW57937	35	49.6	1846	0.9340
PFDN6	RUVBL1	BAD96295	9	27.9	647	0.7928
PFDN6	RUVBL2	NP_006657	9	19.9	656	0.8374
PFDN6	TUBA1A	CAA25855	12	33.7	788	0.8438
PFDN6	TUBA1B	NP_035784	12	33.7	834	0.8193
PFDN6	TUBA1C	NP_116093	8	28.1	480	0.8010
PFDN6	TUBA4B	EAW70721	2	16.6	137	0.7801
PFDN6	TUBB	CAI41893	12	27.5	783	0.8203
PFDN6	TUBB2A	NP_001060	9	2.2	562	0.8235
PFDN6	TUBB2C	EAW88369	12	24.3	724	0.8162
PFDN6	UXT	NP_004173	3	17.2	191	0.9329
PFDN6	VBP1	P61758	26	68.5	1380	0.8581
PFDN6	WDR92	NP_612467	9	26.3	364	0.8906
PIH1D1	C19orf2	NP_003787	12	19.4	702	0.8745
PIH1D1	HSPA5	AAF13605	2	3.1	99	0.7871
PIH1D1	PDRG1	AAH01856	3	30.2	172	0.8340
PIH1D1	PFDN2	AAF36151	4	39.6	192	0.9283
PIH1D1	PFDN6	NP_055075	9	64.3	429	0.8715
PIH1D1	POLR2E	NP_002686	10	41.4	406	0.8101
PIH1D1	RP11-631M21.2	EAW69700	2	28.6	72	0.7619
PIH1D1	RPAP3	EAW57937	32	51.4	1675	0.9014
PIH1D1	RUVBL1	BAD96295	10	30.9	702	0.7701
PIH1D1	RUVBL2	NP_006657	8	19.2	560	0.8321

PIH1D1	TUBA1A	CAA25855	6	20.8	384	0.8133
PIH1D1	UXT	NP_004173	3	24.2	214	0.9348
PIH1D1	WDR92	NP_612467	9	26.3	456	0.8608
POLR1E	ARF6	AAV38671	2	12.0	124	0.7364
POLR1E	ARID3A	AAW30734	11	26.1	609	0.8097
POLR1E	CAND1	AAH26220	4	3.9	216	0.7550
POLR1E	CD3EAP	NP_036231	16	40.8	841	0.7987
POLR1E	GCN1L1	NP_006827	17	7.8	932	0.8018
POLR1E	HSPA5	AAF13605	2	3.1	75	0.7539
POLR1E	HSPA6	BAD97082	5	9.8	277	0.7770
POLR1E	IPO5	EAX08979	4	4.7	159	0.7363
POLR1E	KPNA2	AAH67848	5	9.6	229	0.8909
POLR1E	KPNB1	EAW94809	2	3.2	107	0.7656
POLR1E	PARP1	EAW69785	4	4.7	266	0.7515
POLR1E	PCBP2	NP_001092090	4	16.3	254	0.7823
POLR1E	PHGDH	AAD51414	5	14.1	326	0.7816
POLR1E	POLR1A	NP_056240	104	61.6	5345	0.9757
POLR1E	POLR1B	AAI10834	44	40.4	2274	0.8897
POLR1E	POLR1C	AAH08118	12	42.9	689	0.8199
POLR1E	POLR1D	NP_057056	3	32.3	192	0.8099
POLR1E	POLR2E	NP_002686	10	41.9	487	0.8362
POLR1E	POLR2H	NP_006223	6	41.3	371	0.8030
POLR1E	POLR2L	NP_066951	2	29.9	84	0.7362
POLR1E	POLR3A	NP_008986	2	1.3	80	0.7404
POLR1E	TUBA1A	CAA25855	16	39.0	957	0.8173
POLR1E	TUBB	CAI41893	17	43.2	1095	0.7904
POLR1E	TUBB1	NP_110400	5	15.5	240	0.7358
POLR1E	TUBB2A	NP_001060	13	28.5	749	0.8143
POLR1E	TUBB2C	AAN87335	17	41.3	1074	0.7867
POLR1E	TUBB3	AAH01678	11	28.1	743	0.7919
POLR1E	TUBB4	CAA25318	12	26.4	722	0.8058
POLR1E	TWISTNB	NP_001002926	7	21.9	306	0.8807
POLR2A	BAG2	NP_004273	8	48.8	437	0.7663
POLR2A	C19orf2	AAD08679	5	12.4	232	0.8214
POLR2A	CCT2	AAB67249	2	12.4	134	0.8120
POLR2A	CCT4	NP_006421	4	7.4	187	0.8307
POLR2A	CTDP1	Q9Y5B0	40	45.4	2175	0.8996
POLR2A	DDX26B	CAI56763	6	6.7	307	0.7704
POLR2A	DNAJA1	AAO31694	6	23.9	257	0.7584
POLR2A	GPN1	EAX00557	2	7.4	136	0.8988
POLR2A	GRINL1A	NP_056347	20	60.6	997	0.9741
POLR2A	GTF2B	AAB23144	22	70.7	1493	0.8931
POLR2A	GTF2F1	CAG33079	22	36.6	1340	0.8823
POLR2A	GTF2F2	NP_004119	22	85.9	1259	0.8789
POLR2A	HSP90AB1	NP_031381	10	18.4	537	0.7999
POLR2A	HSPA1A	AAA52697	19	34.5	957	0.8579
POLR2A	HSPA1B	P08107	37	59.9	2244	0.8575
POLR2A	HSPA1L	BAA32521	16	27.8	1128	0.8463
POLR2A	HSPA2	NP_068814	2	4.2	54	0.7520
POLR2A	HSPA6	BAD97082	12	16.5	704	0.8389
POLR2A	HSPA8	NP_006588	34	46.9	2065	0.9102
POLR2A	HSPA9	BAD96478	3	4.1	112	0.7465

POLR2A	INTS1	AAF99604	6	21.6	329	0.8794
POLR2A	INTS3	NP_075391	27	37.1	1341	0.9004
POLR2A	INTS4	NP_291025	11	14.1	713	0.8366
POLR2A	INTS5	NP_085131	17	26.0	992	0.8614
POLR2A	INTS6	NP_001035026	18	25.1	905	0.8144
POLR2A	INTS7	EAW93406	21	26.9	1038	0.8668
POLR2A	INTS9	EAW63505	2	5.0	153	0.7640
POLR2A	KIAA1967	NP_066997	23	30.0	1298	0.8381
POLR2A	KPNA2	AAH67848	1	3.8	79	0.8328
POLR2A	MATR3	NP_061322	10	17.2	329	0.7861
POLR2A	MED15	CAH10580	2	11.6	136	0.7859
POLR2A	MED24	NP_001072986	10	15.1	580	0.8043
POLR2A	MED27	AAF37290	3	13.6	168	0.7513
POLR2A	MED30	NP_542382	3	16.3	150	0.7347
POLR2A	MED4	AAF37289	3	14.8	145	0.7478
POLR2A	MED8	NP_963836	6	37.3	287	0.8377
POLR2A	OBFC2B	NP_076973	4	32.7	249	0.7884
POLR2A	PDRG1	AAH01856	4	41.1	227	0.8810
POLR2A	PFDN2	NP_036526	5	42.2	245	0.8551
POLR2A	PFDN6	NP_055075	5	33.3	162	0.7738
POLR2A	PIH1D1	AAH01108	7	36.6	368	0.9439
POLR2A	POLR2B	NP_000929	81	68.5	5202	0.9006
POLR2A	POLR2C	NP_116558	20	68.4	1428	0.8907
POLR2A	POLR2D	NP_004796	14	83.8	972	0.8785
POLR2A	POLR2E	NP_002686	17	72.9	1084	0.7648
POLR2A	POLR2F	NP_068809	5	15.7	185	0.7600
POLR2A	POLR2G	NP_002687	12	85.5	873	0.9732
POLR2A	POLR2H	NP_006223	11	73.3	743	0.8717
POLR2A	POLR2I	NP_006224	7	77.6	506	0.8393
POLR2A	PPP2R1A	2NYL	5	12.7	273	0.7906
POLR2A	PPP2R1B	NP_002707	3	9.2	201	0.7679
POLR2A	RECQL5	AAH63440	16	19.9	611	0.7612
POLR2A	RFC2	NP_002905	2	10.6	152	0.7547
POLR2A	RFC3	NP_853536	2	8.5	121	0.7880
POLR2A	RFC4	EAW78171	3	13.2	151	0.7791
POLR2A	RP11-631M21.2	EAW69700	2	28.6	88	0.8496
POLR2A	RPAP2	EAW73096	8	18.8	479	0.9372
POLR2A	RPAP3	NP_078880	27	48.0	1304	0.9514
POLR2A	RPL23	AAH03518	3	28.4	161	0.8254
POLR2A	RPRD1A	NP_060640	24	71.2	1488	0.8500
POLR2A	RPRD1B	AAH01696	9	37.7	637	0.8245
POLR2A	RUVBL1	BAD96295	14	40.8	784	0.8273
POLR2A	RUVBL2	NP_006657	12	26.8	730	0.8296
POLR2A	TCEA2	CAD11900	6	19.6	234	0.8952
POLR2A	TUBA1A	CAA25855	28	63.9	1870	0.9172
POLR2A	TUBA1B	XP_001107503	30	69.5	1977	0.8704
POLR2A	TUBA4B	EAW70721	3	16.6	215	0.8115
POLR2A	TUBB	AAN87335	31	75.7	2117	0.8293
POLR2A	TUBB2A	NP_001060	26	57.8	1763	0.8842
POLR2A	TUBB2C	AAH24038	32	75.7	2137	0.8396
POLR2A	TUBB3	NP_006077	16	33.1	1184	0.8443
POLR2A	TUBB4	NP_006078	25	63.5	1537	0.8449

POLR2A	TUBB6	EAX01553	9	20.3	514	0.8087
POLR2A	UXT	NP_004173	5	26.1	267	0.8646
POLR2A	WDR92	NP_612467	7	28.6	303	0.8436
POLR2E	ARID3A	AAW30734	4	10.7	111	0.7408
POLR2E	C19orf2	NP_003787	29	53.6	1493	0.9123
POLR2E	CAND1	AAH26220	5	5.5	256	0.7859
POLR2E	CKAP5	NP_055571	27	16.1	1474	0.8613
POLR2E	DDX5	CAE11890	2	4.9	87	0.7543
POLR2E	EIF4A1	NP_001407	5	15.3	192	0.7577
POLR2E	GTF2I	CAA75163	17	19.1	735	0.8186
POLR2E	HNRNPU	AAH15782	11	17.7	500	0.8093
POLR2E	HSP90AA1	AAI08696	5	9.6	234	0.7974
POLR2E	HSP90AB1	AAF82792	4	7.8	195	0.8053
POLR2E	HSPA1A	AAA52697	30	45.6	1652	0.8865
POLR2E	HSPA1B	P08107	30	45.6	1652	0.8720
POLR2E	HSPA8	NP_006588	8	12.5	353	0.8498
POLR2E	IPO5	EAX08979	4	5.0	161	0.7707
POLR2E	PCBP1	NP_006187	5	18.0	272	0.7960
POLR2E	PCBP2	2AXY	3	43.8	155	0.8062
POLR2E	PDRG1	AAH01856	7	55.0	405	0.9694
POLR2E	PFDN2	NP_036526	12	71.4	720	0.9296
POLR2E	PFDN6	NP_055075	17	74.4	840	0.9484
POLR2E	PHGDH	CAI22213	7	17.4	335	0.7868
POLR2E	PIH1D1	AAH01108	17	69.0	953	0.9490
POLR2E	PTBP1	EAW61158	4	13.6	135	0.7438
POLR2E	RP11-631M21.2	EAW69700	2	28.6	86	0.8100
POLR2E	RPAP3	EAW57937	53	71.7	2705	0.9599
POLR2E	RUVBL1	BAD96295	18	45.6	1200	0.8115
POLR2E	RUVBL2	NP_006657	30	55.1	1971	0.8721
POLR2E	SMARCA4	EAW84167	4	2.7	182	0.7733
POLR2E	TRIP12	EAW70907	2	2.0	111	0.7714
POLR2E	TUBA4B	EAW70721	2	5.8	161	0.8212
POLR2E	TUBB2A	NP_001060	10	32.8	495	0.8434
POLR2E	TUBB4	CAA25318	13	32.0	785	0.8581
POLR2E	TUBB4Q	EAX04599	3	14.1	157	0.7411
POLR2E	UXT	NP_004173	10	44.6	547	0.9405
POLR2E	WDR92	NP_612467	17	51.5	985	0.9284
POLR2E	XPO1	NP_003391	2	2.1	106	0.7627
POLR2G	CCT4	NP_006421	3	4.1	92	0.7501
POLR2G	CKAP5	NP_055571	21	11.0	973	0.8052
POLR2G	GCN1L1	EAW98168	13	6.6	671	0.7842
POLR2G	GRINL1A	BAD97291	4	12.5	187	0.7975
POLR2G	HNRNPU	CAA46472	5	6.9	245	0.7594
POLR2G	KPNB1	EAW94809	3	4.3	156	0.7603
POLR2G	MAP2K2	NP_109587	3	7.2	125	0.7441
POLR2G	PCBP2	NP_001092090	2	7.3	116	0.7666
POLR2G	POLR2A	NP_000928	72	37.0	3591	0.9389
POLR2G	POLR2B	NP_000929	14	14.1	689	0.8356
POLR2G	POLR2C	NP_116558	7	31.6	403	0.8159
POLR2G	POLR2D	NP_004796	12	72.5	816	0.8374
POLR2G	POLR2H	NP_006223	4	30.0	269	0.8151
POLR2G	PRPF31	CAB43677	5	12.0	196	0.7373

POLR2G	TUBA4B	EAW70721	2	16.6	157	0.7999
POLR2G	TUBB2A	NP_001060	14	36.2	789	0.8148
POLR2G	TUBB2C	EAW88369	17	44.4	1006	0.7836
POLR2G	TUBB3	AAH01678	11	31.5	643	0.7997
POLR2G	TUBB4	NP_006078	14	35.1	860	0.7896
POLR2G	TUBB6	EAX01553	7	20.1	436	0.7923
POLR2J	CTDP1	Q9Y5B0	38	43.1	1907	0.8918
POLR2J	GPN1	CAA09376	6	28.5	360	0.8987
POLR2J	GPN2	AAH08634	3	13.9	200	0.7772
POLR2J	GRINL1A	NP_056347	23	66.0	1324	0.9403
POLR2J	GTF2B	AAB23144	18	59.5	1062	0.8692
POLR2J	GTF2F1	P35269	28	43.5	1769	0.9012
POLR2J	GTF2F2	NP_004119	18	73.5	1028	0.8985
POLR2J	PIH1D1	AAH01108	3	13.8	121	0.8303
POLR2J	POLR1C	CAI42628	4	16.2	137	0.7457
POLR2J	POLR2A	NP_000928	109	61.1	7377	0.9813
POLR2J	POLR2B	NP_000929	85	70.4	5598	0.9798
POLR2J	POLR2C	NP_116558	24	82.9	1752	0.8965
POLR2J	POLR2D	NP_004796	7	54.9	493	0.8775
POLR2J	POLR2E	NP_002686	14	71.0	813	0.8352
POLR2J	POLR2F	NP_068809	3	12.6	106	0.7345
POLR2J	POLR2G	NP_002687	9	51.7	622	0.9284
POLR2J	POLR2H	NP_006223	6	50.7	455	0.8451
POLR2J	POLR2I	NP_006224	7	71.2	431	0.8425
POLR2J	POLR2J2	CAC18329	5	45.2	269	0.7569
POLR2J	POLR2K	NP_005025	4	56.9	158	0.7482
POLR2J	POLR2L	NP_066951	2	29.9	103	0.7647
POLR2J	RECQL5	AAG22469	3	6.7	95	0.7577
POLR2J	RP11-631M21.2	EAW69700	2	28.6	100	0.8128
POLR2J	RPAP1	EAW92504	47	44.3	2823	0.9522
POLR2J	RPAP2	EAW73096	25	40.4	1186	0.9345
POLR2J	RPAP3	AAH56415	11	20.1	549	0.8685
POLR2J	RPRD1A	NP_060640	15	51.0	999	0.8249
POLR2J	RUVBL1	BAD96295	5	14.7	392	0.7798
POLR2J	RUVBL2	AAD34041	3	8.6	199	0.8090
POLR2J	TUBA1A	CAA25855	17	50.1	1322	0.8225
POLR2J	TUBA4A	EAW70718	2	7.4	157	0.7743
POLR2J	TUBA4B	EAW70721	3	16.6	191	0.8066
POLR2J	TUBA8	NP_061816	8	7.1	618	0.8047
POLR2J	TUBB	AAH20946	28	66.2	2131	0.7989
POLR2J	TUBB2A	NP_001060	21	54.4	1452	0.8462
POLR2J	TUBB3	NP_006077	15	31.1	1039	0.8028
POLR2J	TUBB4	NP_006078	18	45.3	1142	0.8125
POLR2J	TUBB6	EAX01553	7	17.9	474	0.7796
POLR3G	HNRNPU	AAH07950	5	8.1	227	0.7579
POLR3G	HSPA6	BAD97082	6	11.4	346	0.7710
POLR3G	POLR1C	CAI42628	8	35.4	471	0.7914
POLR3G	POLR1D	NP_057056	2	21.8	109	0.7391
POLR3G	POLR2E	NP_002686	8	41.0	433	0.8032
POLR3G	POLR2H	NP_006223	6	42.0	360	0.7826
POLR3G	POLR3B	NP_060552	4	3.1	131	0.7382
POLR3G	POLR3C	NP_006459	35	66.3	2054	0.8707

POLR3G	POLR3D	AAM18216	6	14.6	269	0.7711
POLR3G	POLR3E	BAB14481	10	14.0	432	0.7530
POLR3G	POLR3F	BAD97018	8	28.2	403	0.7602
POLR3G	POLR3H	NP_001018062	3	32.6	185	0.9381
POLR3H	HSPA5	AAF13605	3	6.3	176	0.7520
POLR3H	MYLK2	CAI12816	2	5.2	112	0.7342
POLR3H	PCBP2	CAA55015	4	15.1	180	0.7625
POLR3H	POLR1C	AAH08118	7	24.6	404	0.7883
POLR3H	POLR1D	AAH00889	2	18.0	122	0.7585
POLR3H	POLR2E	P19388	2	11.0	66	0.7768
POLR3H	POLR2H	AAA91458	4	37.3	214	0.7726
POLR3H	POLR3A	NP_008986	9	7.4	293	0.7402
POLR3H	POLR3B	NP_060552	14	13.0	623	0.7814
POLR3H	POLR3C	NP_006459	7	15.0	336	0.7632
POLR3H	POLR3D	AAH04484	9	26.1	377	0.8010
POLR3H	POLR3E	BAB14481	8	14.6	271	0.7579
POLR3H	POLR3F	AAH12588	8	23.7	395	0.7841
POLR3H	POLR3G	NP_006458	5	18.9	211	0.7730
RPAP1	CCT5	Q9BU08	2	3.9	65	0.7651
RPAP1	CCT6A	NP_001753	4	7.2	135	0.7555
RPAP1	ELAVL1	NP_001410	4	12.9	213	0.7540
RPAP1	GPN1	CAA09376	8	26.0	301	0.8622
RPAP1	HSPD1	NP_002147	10	19.0	532	0.7595
RPAP1	KPNA2	NP_002257	3	8.7	165	0.8468
RPAP1	POLR2B	Q8CFI7	30	28.4	1235	0.8312
RPAP1	POLR2C	AAC14355	11	45.8	520	0.7892
RPAP1	POLR3B	NP_060552	6	5.4	195	0.7425
RPAP1	RUVBL1	NP_003698	3	6.1	117	0.8338
RPAP2	ACTL6A	NP_829888	3	8.0	116	0.7346
RPAP2	C19orf2	NP_604431	5	9.7	233	0.8130
RPAP2	EIF4A2	NP_001958	4	11.1	151	0.7780
RPAP2	GPN1	NP_009197	10	20.3	444	0.9188
RPAP2	GPN3	NP_057385	3	10.9	133	0.8144
RPAP2	GRINL1A	NP_056347	15	37.8	511	0.9582
RPAP2	HSPA5	NP_005338	2	3.5	112	0.7855
RPAP2	HSPA8	NP_006588	11	17.3	511	0.8339
RPAP2	INTS1	XP_379767	8	2.8	272	0.7559
RPAP2	INTS3	NP_075391	4	6.0	129	0.7569
RPAP2	INTS4	NP_291025	8	8.6	239	0.7364
RPAP2	INTS7	NP_056249	6	6.4	276	0.7459
RPAP2	MED24	NP_055630	3	3.3	109	0.7351
RPAP2	PDRG1	NP_110442	3	15.0	137	0.8254
RPAP2	PFDN2	NP_036526	4	28.6	214	0.8476
RPAP2	PHGDH	NP_006614	3	6.6	147	0.7412
RPAP2	PIH1D1	NP_060386	5	19.0	219	0.8311
RPAP2	POLR2A	NP_000928	43	17.7	1547	0.8785
RPAP2	POLR2B	NP_000929	34	25.3	1343	0.8029
RPAP2	POLR2C	NP_002685	3	9.8	148	0.7904
RPAP2	POLR2E	NP_002686	7	34.3	282	0.8073
RPAP2	POLR2G	NP_002687	3	19.2	143	0.8043
RPAP2	POLR2H	NP_006223	5	33.3	259	0.8366
RPAP2	POLR3A	NP_008986	12	7.6	372	0.7744

RPAP2	POLR3B	NP_060552	5	4.3	217	0.7448
RPAP2	RFC3	NP_002906	2	7.9	128	0.7687
RPAP2	RPAP3	NP_078880	12	20.6	454	0.8199
RPAP2	RUVBL1	NP_003698	12	27.2	513	0.8470
RPAP2	RUVBL2	NP_006657	21	32.6	1049	0.8725
RPAP2	TOPBP1	NP_008958	2	2.0	104	0.7374
RPAP2	WDR92	NP_612467	6	18.5	231	0.8295
RPAP2	YBX1	NP_004550	2	12.0	107	0.7545
RPAP3	C19orf2	NP_604431	3	6.5	100	0.8007
RPAP3	EIF4A1	NP_001407	3	8.6	147	0.7742
RPAP3	GPN1	NP_009197	1	3.5	67	0.8889
RPAP3	HSP90AA1	NP_005339	4	6.1	249	0.7972
RPAP3	HSP90AB1	NP_031381	3	3.5	113	0.7676
RPAP3	HSPA1B	NP_005337	4	7.6	135	0.7657
RPAP3	PFDN2	NP_036526	3	18.8	157	0.8714
RPAP3	PFDN6	NP_055075	2	16.3	69	0.7648
RPAP3	PIH1D1	NP_060386	2	5.5	65	0.7508
RPAP3	POLR1A	NP_056240	6	3.1	226	0.7522
RPAP3	POLR2A	NP_000928	3	1.3	80	0.7712
RPAP3	POLR2E	NP_002686	8	38.1	320	0.8167
RPAP3	POLR3A	NP_008986	4	2.7	115	0.7542
RPAP3	RUVBL1	NP_003698	7	15.6	279	0.8557
RPAP3	RUVBL2	NP_006657	11	27.4	562	0.8456
RPAP3	TRIP12	NP_008958	2	1.4	82	0.7683
RPAP3	WDR92	NP_612467	10	24.6	346	0.9055
RUVBL1	C12orf45	AAH32326	6	22.9	285	0.7729
RUVBL1	C1orf57	CAI22244	3	18.4	143	0.7779
RUVBL1	CAPNS1	AAV40829	6	20.9	263	0.7437
RUVBL1	CASP14	AAI03869	2	8.7	126	0.7730
RUVBL1	DMAP1	CAD97886	2	6.5	106	0.7632
RUVBL1	ELAVL1	AAP88795	3	10.1	188	0.8133
RUVBL1	HSPA1A	AAD21816	3	5.6	176	0.8119
RUVBL1	HSPA8	NP_006588	7	15.0	365	0.8566
RUVBL1	RP11-529I10.4	NP_056263	4	19.7	266	0.8915
RUVBL1	RUVBL2	AAH00428	25	45.4	1706	0.8384
RUVBL1	YEATS4	CAC01935	2	9.9	82	0.7601
RUVBL2	ACTL6A	NP_829888	5	13.2	301	0.8088
RUVBL2	C12orf45	AAH32326	5	22.3	274	0.7839
RUVBL2	C19orf2	NP_003787	7	14.2	370	0.8612
RUVBL2	C1orf57	CAI22244	4	26.3	265	0.8057
RUVBL2	C8orf41	AAH07387	5	13.0	316	0.7770
RUVBL2	CCDC95	AAH47712	3	15.2	176	0.7763
RUVBL2	DDX42	AAC32396	2	3.0	64	0.7354
RUVBL2	DMAP1	CAD97886	3	8.6	135	0.7715
RUVBL2	EFTUD2	AAH02360	6	6.8	292	0.8033
RUVBL2	H2AFV	AAH04274	3	25.4	139	0.7822
RUVBL2	HNRNPU	AAP97707	2	4.3	93	0.8297
RUVBL2	HSP90AA2	AAH23006	3	5.5	126	0.7394
RUVBL2	HSPA1A	CAI18466	12	20.3	613	0.8470
RUVBL2	KIAA0406	AAH13755	27	24.5	1594	0.9421
RUVBL2	KIAA1967	NP_954675	3	3.8	107	0.7490
RUVBL2	KPNB1	NP_002256	4	4.2	123	0.7943

RUVBL2	MATR3	NP_954659	2	3.1	112	0.7856
RUVBL2	NOP58	AAH09306	5	12.6	219	0.7832
RUVBL2	PCBP1	CAA55016	5	20.2	263	0.8100
RUVBL2	PCBP2	CAA55015	5	18.9	265	0.8200
RUVBL2	PDRG1	AAH01856	3	31.0	161	0.8644
RUVBL2	PFDN6	AAH59783	9	57.4	383	0.8658
RUVBL2	PIH1D1	NP_060386	5	16.2	269	0.8841
RUVBL2	POLR2B	NP_000929	2	1.6	69	0.8028
RUVBL2	POLR2E	AAH04441	9	36.2	327	0.8178
RUVBL2	POLR2H	AAA91458	2	21.3	80	0.8115
RUVBL2	RFC4	AAH24022	3	7.7	122	0.7815
RUVBL2	RFC5	CAG28579	2	5.3	89	0.7577
RUVBL2	RP11-529I10.4	NP_056263	16	47.8	915	0.9650
RUVBL2	RPAP3	AAH56415	22	39.0	1197	0.9313
RUVBL2	RPL23	AAH03518	3	24.6	115	0.7641
RUVBL2	RUVBL1	BAD96295	36	60.3	2658	0.8555
RUVBL2	SRCAP	NP_006653	21	7.3	831	0.7874
RUVBL2	TFPT	AAH07776	3	11.9	193	0.7389
RUVBL2	TUBB2A	CAA23844	6	14.2	275	0.8331
RUVBL2	UCHL5	CAI10834	3	15.2	109	0.7385
RUVBL2	UXT	NP_004173	6	40.1	333	0.9462
RUVBL2	WDR92	BAB71143	13	36.1	592	0.8989
RUVBL2	YEATS4	CAC01935	9	39.5	498	0.9245
RUVBL2	ZNHIT2	BAD97078	8	22.6	413	0.7988
TUBA1A	CCT2	CAG33352	6	14.6	286	0.8381
TUBA1A	CCT3	CAI14168	7	12.3	357	0.8184
TUBA1A	CCT4	NP_006421	10	17.3	413	0.8675
TUBA1A	CCT5	AAH09454	4	10.6	149	0.9103
TUBA1A	CCT6A	BAD92965	6	10.4	255	0.8005
TUBA1A	CCT7	EAW99740	3	4.8	166	0.7658
TUBA1A	CCT8	AAH12584	7	16.3	532	0.8354
TUBA1A	TCP1	CAA37064	7	11.5	389	0.8101
TUBA1A	TUBB4	NP_006078	9	21.6	509	0.8466
TWISTNB	CD3EAP	NP_036231	18	37.8	1133	0.8466
TWISTNB	KPNA2	AAH67848	6	11.7	240	0.8349
TWISTNB	POLR1A	EAW99467	115	65.8	6798	0.9668
TWISTNB	POLR1B	NP_061887	22	20.4	972	0.8036
TWISTNB	POLR1C	AAH08118	17	54.7	1067	0.8340
TWISTNB	POLR1D	NP_057056	7	58.6	357	0.8088
TWISTNB	POLR1E	AAH14331	21	46.8	1194	0.9630
TWISTNB	POLR2E	NP_002686	13	58.1	708	0.8042
TWISTNB	POLR2H	NP_006223	7	59.3	512	0.7938
TWISTNB	POLR2K	NP_005025	2	13.8	84	0.7404
TWISTNB	POLR2L	NP_066951	4	31.3	221	0.7696
TWISTNB	POLR3A	NP_008986	2	1.3	91	0.7477
TWISTNB	RRN3	CAC07955	16	24.1	736	0.7891
TWISTNB	TCOF1	EAW61738	19	11.5	871	0.7881
UXT	BAT1	CAI18284	3	6.1	150	0.7786
UXT	BAT2	CAB51071	23	8.4	1183	0.7353
UXT	C19orf2	NP_003787	19	31.0	1004	0.8892
UXT	CAND1	CAD38737	2	3.4	134	0.7882
UXT	INF2	NP_116103	2	7.7	118	0.7578

UXT	KIF5B	EAW85976	5	5.9	210	0.7565
UXT	LRRC41	AAH04953	4	11.5	139	0.7574
UXT	PCBP1	CAA82631	2	8.0	111	0.7632
UXT	PDRG1	AAH01856	7	49.6	317	0.8946
UXT	PFDN2	AAF36151	6	53.8	255	0.9490
UXT	PFDN6	NP_055075	16	72.9	620	0.9478
UXT	PIH1D1	AAH01108	7	35.5	332	0.9136
UXT	POLR2E	EAW69550	7	49.6	286	0.8641
UXT	RPAP3	EAW57937	25	36.5	1351	0.9256
UXT	RUVBL1	BAD96295	11	33.3	660	0.7923
UXT	RUVBL2	NP_006657	9	20.5	510	0.8241
UXT	SF3B2	EAW74495	5	7.4	210	0.7393
UXT	SMARCC1	AAC50693	5	4.0	225	0.7482
UXT	SMARCC2	NP_620706	4	3.2	128	0.7375
UXT	TUBB	CAI41893	8	19.7	464	0.8137
UXT	TUBB2C	EAW88369	6	13.7	416	0.7940
UXT	WDR92	NP_612467	2	7.8	118	0.8145
WDR92	ALB	AAG35503	5	10.0	239	0.7426
WDR92	C19orf2	NP_003787	13	21.3	593	0.8532
WDR92	CCT2	NP_006422	7	18.9	365	0.8350
WDR92	CCT3	CAI14168	8	17.2	410	0.7987
WDR92	CCT4	NP_006421	10	20.4	426	0.8638
WDR92	CCT5	AAH02971	6	11.3	390	0.8936
WDR92	CCT6A	NP_001009186	7	15.6	294	0.8024
WDR92	CCT7	EAW99740	5	11.8	238	0.8770
WDR92	CCT8	AAH12584	7	16.3	556	0.8340
WDR92	HSPA6	BAD97082	6	11.7	373	0.8015
WDR92	HSPA8	NP_694881	3	6.5	148	0.8081
WDR92	PDRG1	AAH01856	3	30.2	130	0.7799
WDR92	PFDN2	NP_036526	9	48.1	363	0.8792
WDR92	PFDN6	NP_055075	11	52.7	473	0.8491
WDR92	PIH1D1	AAH01108	16	69.3	1039	0.9319
WDR92	POLR2E	AAB19339	2	39.6	73	0.8545
WDR92	POLR3A	NP_008986	3	2.5	138	0.8039
WDR92	RPAP3	EAW57937	52	71.9	2728	0.9358
WDR92	RUVBL1	BAD96295	14	39.0	948	0.8211
WDR92	RUVBL2	NP_006657	16	31.3	999	0.8460
WDR92	TCP1	CAA37064	7	14.7	327	0.8231
WDR92	TUBA1A	CAA25855	7	25.5	473	0.8620
WDR92	TUBB	CAI41893	9	21.4	472	0.8228
WDR92	UXT	NP_004173	5	26.1	287	0.9200

Supplementary Table S2

Detailed mass spectrometry data for yeast TAP interactions. Annotated spectra for proteins identified on the basis of a single peptide are presented in supplemental Table S5 and supplemental Figure S2. ND: not determined.

Yeast Standard Name	Yeast systematic Name	Human protein Name	Accession number	Yeast Unique Peptide Match	Sequence Coverage %	Yeast Protein Mascot Score
Rpb2	YOR151C	POLR2B	AAA68096	16	12	780
Rpb1	YDL140C	POLR2A	CAA26904	12	7	531
Rpb7	YDR404C	POLR2G	2B8K_G	4	15	320
Hsp60	YLR259C	HSPD1	NP_013360	2	5	142
Rpap2	YER139C	RPAP2	NP_011066	3	21	214
Hsp70	YDL229W	ND	NP_010052	2	4	145
Rpb3	YIL021W	POLR2C	AAA34889	3	9	137
Rpb8	YOR224C	POLR2H	NP_014867	3	17	134
Rpb5	YBR154C	POLR2E	AAC60556	2	8	130
Rvs167	YDR388W	ND	NP_010676	2	1	44
Rpb12	YHR143W-A	POLR2K	NP_012013	1	38	45
Rpc1	YOR116C	POLR3C	NP_014759	2	3	39
Rpb6	YPR187W	POLR2F	NP_015513	1	12	30

Supplemental Table S3.
Yeast strains and plasmids used in this study

Strain/Plasmid	Description	Source
Yeast strains		
BY4347-22250	*MATa/α his3Δ1/his3Δ1 leu2Δ0/leu2Δ0 met15Δ0/MET15 ura3Δ0/ura3Δ0 lys2Δ0/LYS2 npa3::kanMX/NPA3*	Invitrogen
BCY74	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3*	This study
BCY93	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415	This study
BCY75	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*NPA3*	This study
BCY86	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-K16R	This study
BCY87	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-K16A	This study
BCY89	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-K16I	This study
BCY127	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-D40A	This study
BCY129	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-D40E	This study
BCY110	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-G70A	This study
BCY111	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-P71A	This study
BCY112	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-N72A	This study
BCY113	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-N72Q	This study
BCY163	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-D106A	This study
BCY237	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-D106E	This study
BCY148	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-P108A	This study
BCY164	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-G109A	This study
BCY155	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-Q110A	This study
BCY160	*MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 lys2Δ0 npa3::kanMX* pRS316-*NPA3* pRS415-*npa3*-Q110N	This study
Plasmids		
pRS316	*URA3, ampR, CEN6, ARSH4*	Sikorski and Heiter, 1989
pRS415	*LEU2, ampR, CEN6, ARSH4*	Sikorski and Heiter, 1989

Supplemental Table S4

Annotation for human proteins identified on the basis of a single peptide.

Affinity Tagged Polypeptides	Interaction Partners	Peptide sequence	Observed precursor m/z	Charge	Protein Mascot Score
CCT5	XPO1	YYGLQILENVIK	726.9174	2	53.56
GPN1	KPNA2	LLGASELPIVTPALR	775.6239	2	49.96
GPN1	POLR2D	AGDVEEDASQLIFPK	809.9060	2	68.74
GPN1	XPO1	EPEVLSTMAIIVNK + Oxidation (M)	780.8839	2	39.28
GPN3	GPN1	SMSLVLDEFYSSLR	823.9111	2	77.12
KPNA2	POLR1D	GTLPAVEPFQR	607.8367	2	49.02
KPNA2	POLR1E	AAETIIDTK	481.2692	2	57.41
KPNA2	POLR2K	LVVFDAR	410.2443	2	45.12
POLR2A	KPNA2	NKNPAPPIDAVEQILPTLVR	1093.1200	2	78.56
RPAP3	GPN1	DMGSVALDAGTAK + Oxidation (M)	626.9589	2	66.52

Supplemental Table S5

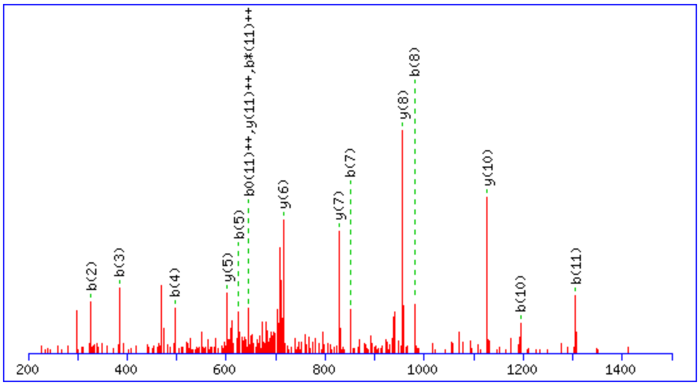
Annotation for yeast proteins identified on the basis of a single peptide.

Yeast Standard Name	Yeast Systematic Name	Peptide sequence	Observed precursor m/z	Charge	Protein Mascot Score
Rvs167	YDR388W	FQELEQETK	576.2864	2	44
Rpb12	YHR143W-A	LVQFEAR	431.7438	2	45
Rpc1	YOR116C	LVRYDNSGCLVK + carbamidomethyl (C)	712.3654	2	32
Rpb6	YPR187W	TIVTGGNGPEDFQQHEQIR	709.3552	3	30

Supplemental Figure S1

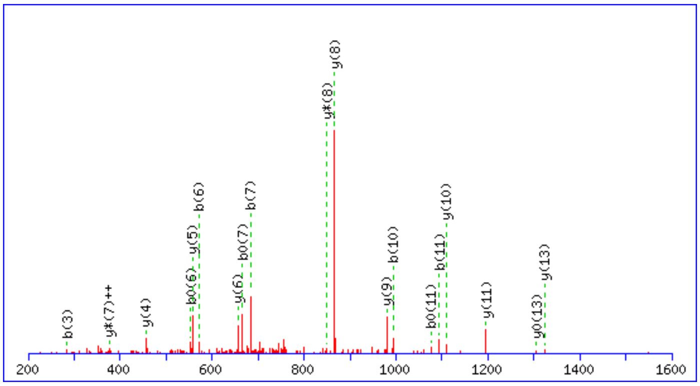
Annotated spectra for proteins identified on the basis of a single peptide.

Affinity tagged polypeptide	***Interaction partner***	***peptide***
CCT5	XPO1	YYGLQILENVIK



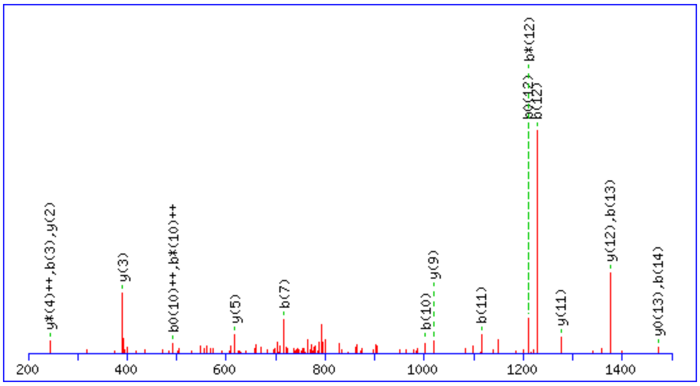
#	b	b^{++}	Seq.	y	y^{++}	#
1	164.071	82.5389	Y			12
2	**327.134**	164.071	Y	1289.75	**645.377**	11
3	**384.155**	192.581	G	**1126.68**	563.845	10
4	**497.24**	249.123	L	1069.66	535.334	9
5	**625.298**	313.153	Q	**956.578**	478.792	8
6	738.382	369.695	I	**828.519**	414.763	7
7	**851.466**	426.237	L	**715.435**	358.221	6
8	**980.509**	490.758	E	**602.351**	301.679	5
9	1094.55	547.78	N	473.308	237.158	4
10	**1193.62**	597.314	V	359.265	180.136	3
11	**1306.7**	653.856	I	260.197	130.602	2
12			K	147.113	74.06	1

GPN1	KPNA2	LLGASELPIVTPALR



#	b	b^{0}	Seq.	y	y^{++}	#
1	114.091		L			15
2	227.175		L	1436.85	718.927	14
3	**284.197**		G	**1323.76**	662.385	13
4	355.234		A	1266.74	633.874	12
5	442.266	424.255	S	**1195.7**	598.356	11
6	**571.309**	**553.298**	E	**1108.67**	554.84	10
7	**684.393**	**666.382**	L	**979.63**	490.319	9
8	781.445	763.435	P	**866.546**	433.777	8
9	894.53	876.519	I	769.493	385.25	7
10	**993.598**	975.587	V	**656.409**	328.708	6
11	**1094.65**	**1076.64**	T	**557.341**	279.174	5
12	1191.7	1173.69	P	**456.293**	228.65	4
13	1262.74	1244.72	A	359.24	180.124	3
14	1375.82	1357.81	L	288.203	144.605	2
15			R	175.119	88.0631	1

GPN1	POLR2D	AGDVEEDASQLIFPK

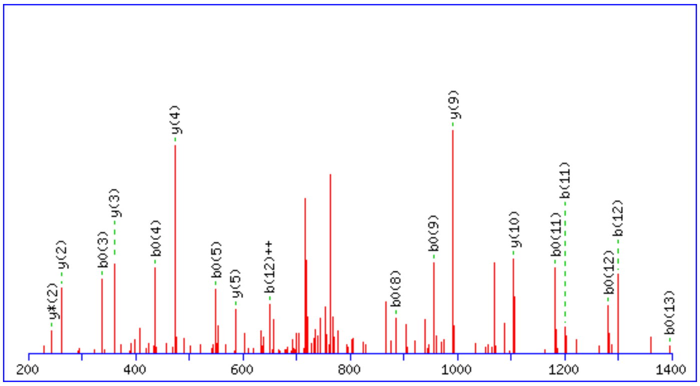


#	b	b^{++}	Seq.	y	y^{++}	#
1	72.0444	36.5258	A			15
2	129.066	65.0366	G	1547.76	774.383	14
3	**244.093**	122.55	D	1490.74	745.872	13
4	343.161	172.084	V	**1375.71**	688.359	12
5	472.204	236.606	E	**1276.64**	638.825	11
6	601.246	301.127	E	1147.6	574.303	10
7	**716.273**	358.64	D	**1018.56**	509.782	9
8	787.31	394.159	A	903.53	452.269	8
9	874.343	437.675	S	832.493	416.75	7
10	**1002.4**	501.704	Q	745.461	373.234	6
11	**1115.49**	558.246	L	**617.402**	309.205	5
12	**1228.57**	614.788	I	504.318	252.663	4
13	**1375.64**	688.322	F	**391.234**	196.121	3
14	**1472.69**	736.849	P	**244.166**	122.586	2
15			K	147.113	74.06	1

Supplemental Figure S1

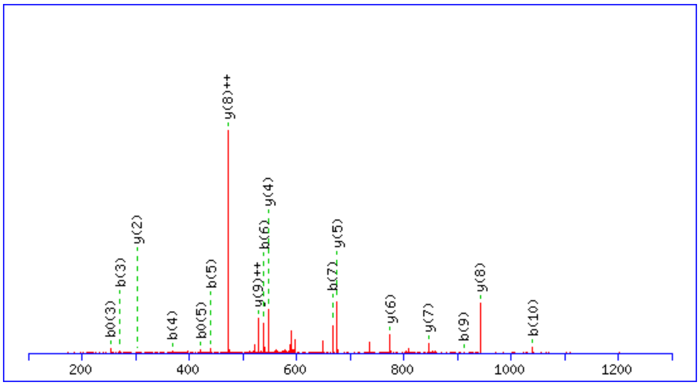
Annotated spectra for proteins identified on the basis of a single peptide.

Affinity tagged polypeptide	***Interaction partner***	***peptide***
GPN1	XPO1	EPEVLSTMAIIVNK +Oxidation M



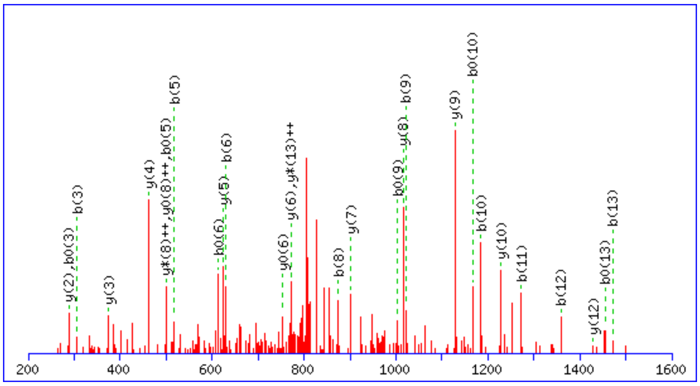
#	b	b^0	Seq.	y	y^{++}	#
1	130.05	112.039	E			14
2	227.103	209.092	P	1430.79	715.9	13
3	356.145	**338.135**	E	1333.74	667.373	12
4	455.214	**437.203**	V	1204.7	602.852	11
5	568.298	**550.287**	L	**1105.63**	553.318	10
6	655.33	637.319	S	**992.545**	496.776	9
7	756.377	738.367	T	905.512	453.26	8
8	903.413	**885.402**	M	804.465	402.736	7
9	974.45	**956.439**	A	657.429	329.218	6
10	1087.53	1069.52	I	**586.392**	293.7	5
11	**1200.62**	**1182.61**	I	**473.308**	237.158	4
12	**1299.69**	**1281.68**	V	**360.224**	180.616	3
13	1413.73	**1395.72**	N	**261.156**	131.082	2
14			K	147.113	74.06	1

GPN3	GPN1	SMSLVLDEFYSSLR



#	b	b^0	Seq.	y	y^{++}	#
1	88.0393	70.0287	S			14
2	219.08	201.069	M	1559.78	780.392	13
3	**306.112**	**288.101**	S	**1428.74**	714.872	12
4	419.196	401.185	L	1341.7	671.356	11
5	**518.264**	**500.254**	V	**1228.62**	614.814	10
6	**631.348**	**613.338**	L	**1129.55**	565.28	9
7	746.375	728.365	D	**1016.47**	508.738	8
8	**875.418**	857.407	E	**901.441**	451.224	7
9	**1022.49**	**1004.48**	F	**772.399**	386.703	6
10	**1185.55**	**1167.54**	Y	**625.33**	313.169	5
11	**1272.58**	1254.57	S	**462.267**	231.637	4
12	**1359.61**	1341.6	S	**375.235**	188.121	3
13	**1472.7**	**1454.69**	L	**288.203**	144.605	2
14			R	175.119	88.0631	1

KPNA2	POLR1D	GTLPAVEPFQR

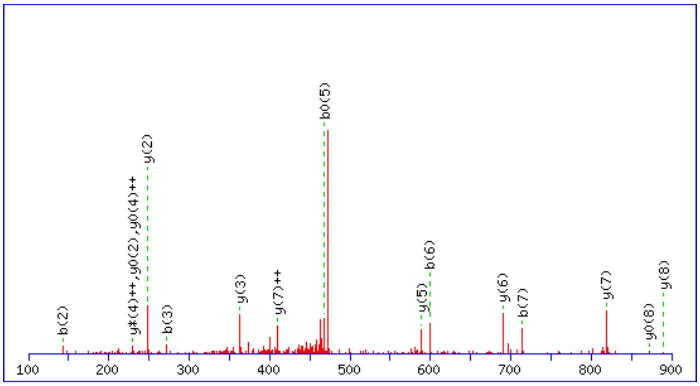


#	b	b^{++}	Seq.	y	y^{++}	#
1	58.0287	29.518	G			11
2	159.076	80.0418	T	1157.63	579.319	10
3	**272.161**	136.584	L	1056.58	**528.796**	9
4	**369.213**	185.11	P	**943.5**	**472.253**	8
5	**440.25**	220.629	A	**846.447**	423.727	7
6	**539.319**	270.163	V	**775.41**	388.209	6
7	**668.361**	334.684	E	**676.341**	338.674	5
8	765.414	383.211	P	**547.299**	274.153	4
9	**912.483**	456.745	F	450.246	225.627	3
10	**1040.54**	520.774	Q	**303.178**	152.092	2
11			R	175.119	88.0631	1

Supplemental Figure S1

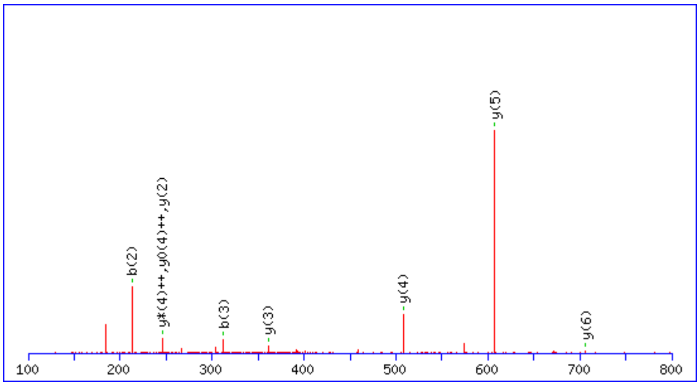
Annotated spectra for proteins identified on the basis of a single peptide.

Affinity tagged polypeptide	***Interaction partner***	***peptide***
KPNA2	POLR1E	AAETIIDTK



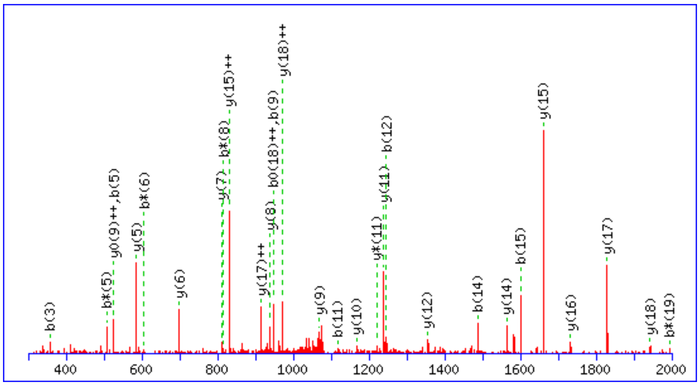
#	b	b^{++}	Seq.	y	y^{++}	#
1	72.0444	36.5258	A			9
2	**143.082**	72.0444	A	**890.483**	445.745	8
3	**272.124**	136.566	E	**819.446**	**410.227**	7
4	373.172	187.09	T	**690.403**	345.705	6
5	486.256	243.632	I	**589.356**	295.181	5
6	**599.34**	300.174	I	476.272	238.639	4
7	**714.367**	357.687	D	**363.187**	182.097	3
8	815.415	408.211	T	**248.161**	124.584	2
9			K	147.113	74.06	1

KPNA2	POLR2K	LVVFDAR



#	b	b^{++}	Seq.	y	y^{++}	#
1	114.091	57.5493	L			7
2	**213.16**	107.084	V	**706.388**	353.698	6
3	**312.228**	156.618	V	**607.32**	304.164	5
4	459.297	230.152	F	**508.251**	254.629	4
5	574.324	287.665	D	**361.183**	181.095	3
6	645.361	323.184	A	**246.156**	123.582	2
7			R	175.119	88.0631	1

POLR2A	KPNA2	NKNPAPPIDAVEQILPTLVR

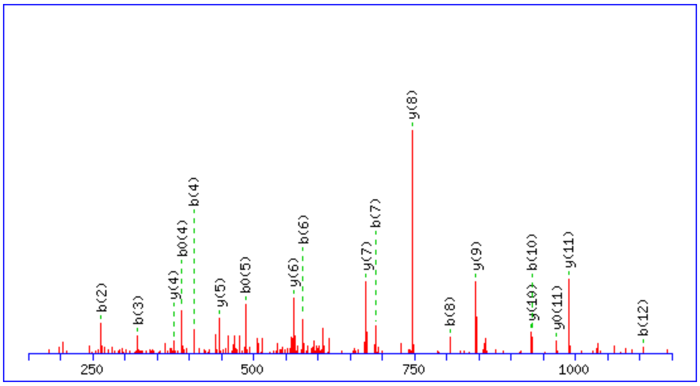


#	b	b^{++}	Seq.	y	y^{++}	#
1	115.05	58.0287	N			20
2	243.145	122.076	K	2071.19	1036.1	19
3	**357.188**	179.098	N	**1943.1**	**972.052**	18
4	454.241	227.624	P	**1829.05**	**915.03**	17
5	**525.278**	263.143	A	**1732**	866.504	16
6	622.331	311.669	P	**1660.96**	**830.985**	15
7	719.384	360.195	P	**1563.91**	782.459	14
8	832.468	416.737	I	1466.86	733.933	13
9	**947.495**	474.251	D	**1353.77**	677.39	12
10	1018.53	509.769	A	**1238.75**	619.877	11
11	**1117.6**	559.304	V	**1167.71**	584.358	10
12	**1246.64**	623.825	E	**1068.64**	534.824	9
13	1374.7	687.854	Q	**939.599**	470.303	8
14	**1487.79**	744.396	I	**811.54**	406.274	7
15	**1600.87**	800.938	L	**698.456**	349.732	6
16	1697.92	849.465	P	**585.372**	293.19	5
17	1798.97	899.989	T	488.319	244.663	4
18	1912.05	956.531	L	387.271	194.139	3
19	2011.12	1006.06	V	274.187	137.597	2
20			R	175.119	88.0631	1

Supplemental Figure S1

Annotated spectra for proteins identified on the basis of a single peptide.

Affinity tagged polypeptide	***Interaction partner***	***peptide***
RPAP3	GPN1	DMGSVALDAGTAK+Oxidation M

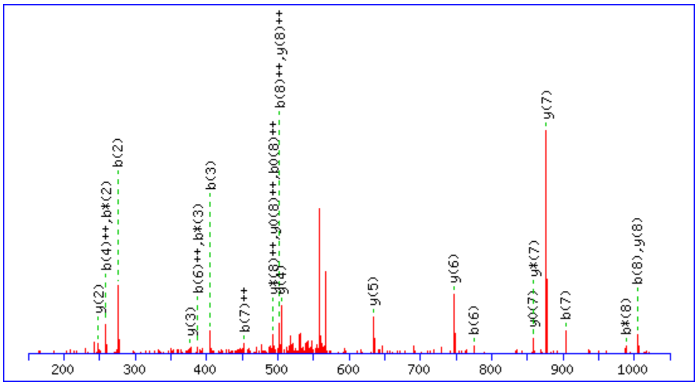


#	b	b^{++}	Seq.	y	y^{++}	#
1	116.034	58.5207	**D**			**13**
2	**263.07**	132.038	**M**	1136.56	568.784	**12**
3	**320.091**	160.549	**G**	**989.526**	495.267	**11**
4	**407.123**	204.065	**S**	**932.505**	466.756	**10**
5	506.192	253.599	**V**	**845.473**	423.24	**9**
6	**577.229**	289.118	**A**	**746.404**	373.706	**8**
7	**690.313**	345.66	**L**	**675.367**	338.187	**7**
8	**805.34**	403.173	**D**	**562.283**	281.645	**6**
9	876.377	438.692	**A**	**447.256**	224.132	**5**
10	**933.398**	467.203	**G**	**376.219**	188.613	**4**
11	1034.45	517.727	**T**	319.198	160.102	**3**
12	**1105.48**	553.245	**A**	218.15	109.579	**2**
13			**K**	147.113	74.06	**1**

Supplemental Figure S2

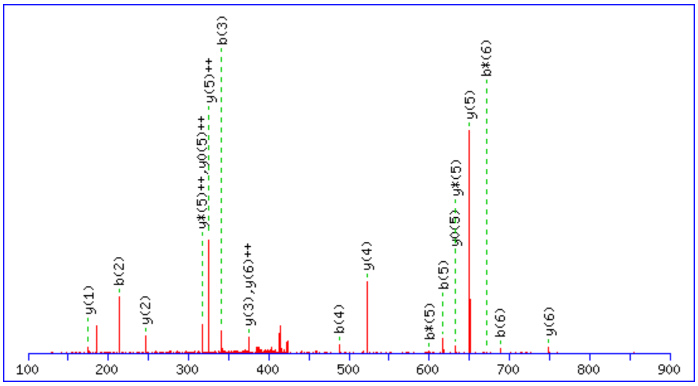
Annotated spectra for proteins identified on the basis of a single peptide.

Yeast standard name	***Yeast systematic name***	***peptide***
Rvs167	YDR388W	FQELEQETK



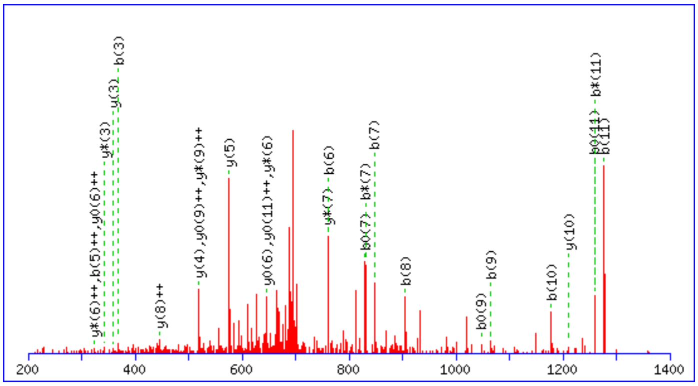
#	b	b^{++}	Seq.	y	y^{++}	#
1	148.08	74.54	F			9
2	276.13	138.57	Q	1004.49	502.75	8
3	405.18	203.09	E	876.43	438.72	7
4	518.26	259.63	L	747.39	374.20	6
5	647.30	324.16	E	634.30	317.66	5
6	775.36	388.18	Q	505.26	253.13	4
7	904.40	452.71	E	377.20	189.11	3
8	1005.45	503.23	T	248.16	124.58	2
9			K	147.11	74.06	1

Rpb12	YHR143W-A	LVQFEAR



#	b	b^{++}	Seq.	y	y^{++}	#
1	114.09	57.55	L			7
2	213.16	107.08	V	749.39	375.20	6
3	341.22	171.11	Q	650.33	325.67	5
4	488.29	244.65	F	522.27	261.64	4
5	617.33	309.17	E	375.20	188.10	3
6	688.37	344.69	A	246.16	123.58	2
7			R	175.12	88.06	1

Rpc1	YOR116C	LVRYDNSGCLVK

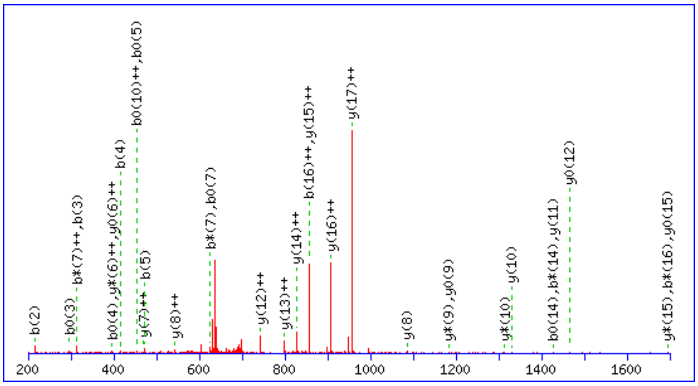


#	b	b^{++}	Seq.	y	y^{++}	#
1	114.09	57.55	L			12
2	213.16	107.08	V	1310.65	655.83	11
3	369.26	185.13	R	1211.58	606.30	10
4	532.32	266.67	Y	1055.48	528.25	9
5	647.35	324.18	D	892.42	446.71	8
6	761.39	381.20	N	777.39	389.20	7
7	848.43	424.72	S	663.35	332.18	6
8	905.45	453.23	G	576.32	288.66	5
9	1065.48	533.24	C	519.30	260.15	4
10	1178.56	589.78	L	359.27	180.14	3
11	1277.63	639.32	V	246.18	123.59	2
12			K	147.11	74.06	1

Supplemental Figure S2

Annotated spectra for proteins identified on the basis of a single peptide.

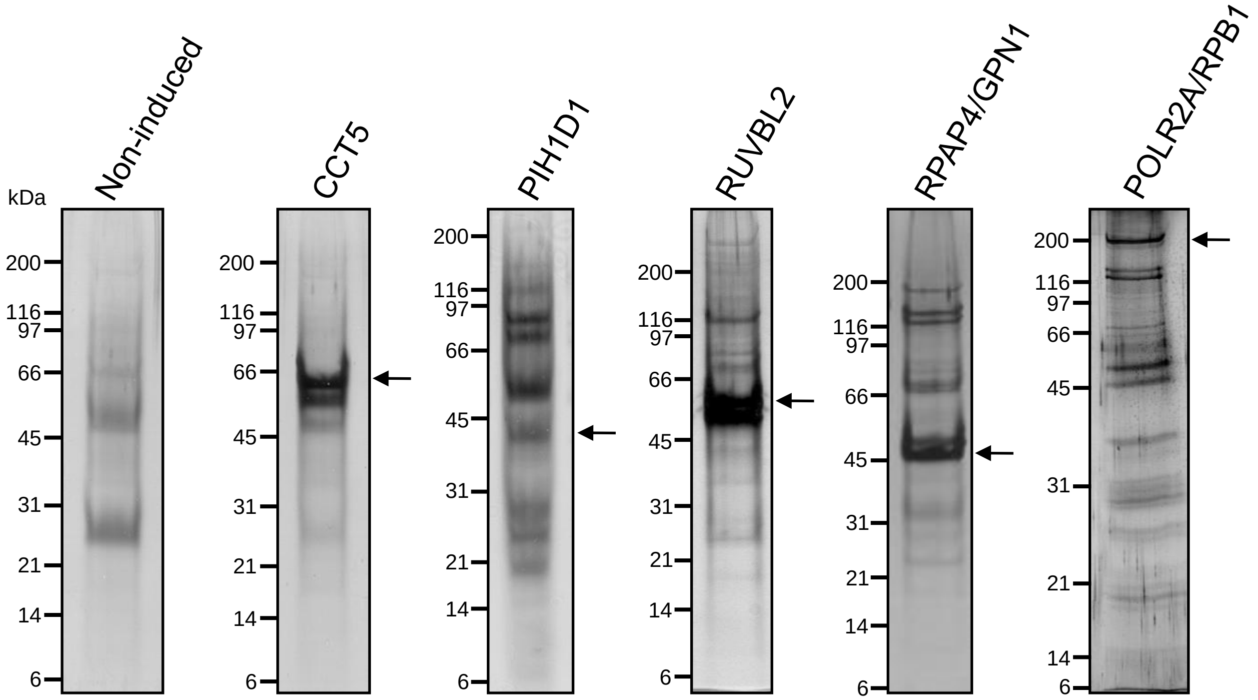
Yeast standard name	***Yeast systematic name***	***peptide***
Rpb6	YPR187W	TIVTGGNGPEDFQQHEQIR



#	b	b^{++}	Seq.	y	y^{++}	#
1	102.06	51.53	T			19
2	**215.14**	108.07	I	2024.98	1012.99	18
3	**314.21**	157.61	V	1911.89	**956.45**	17
4	**415.26**	208.13	T	1812.83	**906.92**	16
5	**472.28**	236.64	G	1711.78	**856.39**	15
6	529.30	265.15	G	1654.76	**827.88**	14
7	643.34	322.17	N	1597.74	**799.37**	13
8	700.36	350.68	G	1483.69	**742.35**	12
9	797.42	399.21	P	**1426.67**	713.84	11
10	926.46	463.73	E	**1329.62**	665.31	10
11	1041.48	521.25	D	1200.58	600.79	9
12	1188.55	594.78	F	**1085.55**	**543.28**	8
13	1316.61	658.81	Q	938.48	**469.74**	7
14	1444.67	722.84	Q	810.42	405.71	6
15	1581.73	791.37	H	682.36	341.69	5
16	1710.77	**855.89**	E	545.30	273.16	4
17	1838.83	919.92	Q	416.26	208.63	3
18	1951.91	976.46	I	288.20	144.61	2
19			R	175.12	88.06	1

Supplemental Figure S3

Representative silver-stained gels of the CCT5-, PIH1D1-. RUVBL2-, RPAP4/GPN1-, POLR2A/RPB1-TAP eluates. A typical non-induced eluate is also shown. The position of molecular weight markers is indicated. Arrows indicate the position of the bait.



Supplemental Figure S4

Representative images of immunofluorescence experiments showing the intracellular localization of POLR2A/RPB1, POLR2B/RPB2, POLR2C/RPB3 and POLR2F/RPB6 following treatment with RPAP4 and control siRNA, leptomycin B (LMB) and benomyl. In each case, the location of DNA is shown (TO-PRO®-3 iodide). An anti-FLAG antibody was used to localize FLAG-POLR2B,C and F. In this figure, endogenous POLR2A was localized using the 8WG16 antibody (the location of FLAG-POLR2A is identical (not shown)).