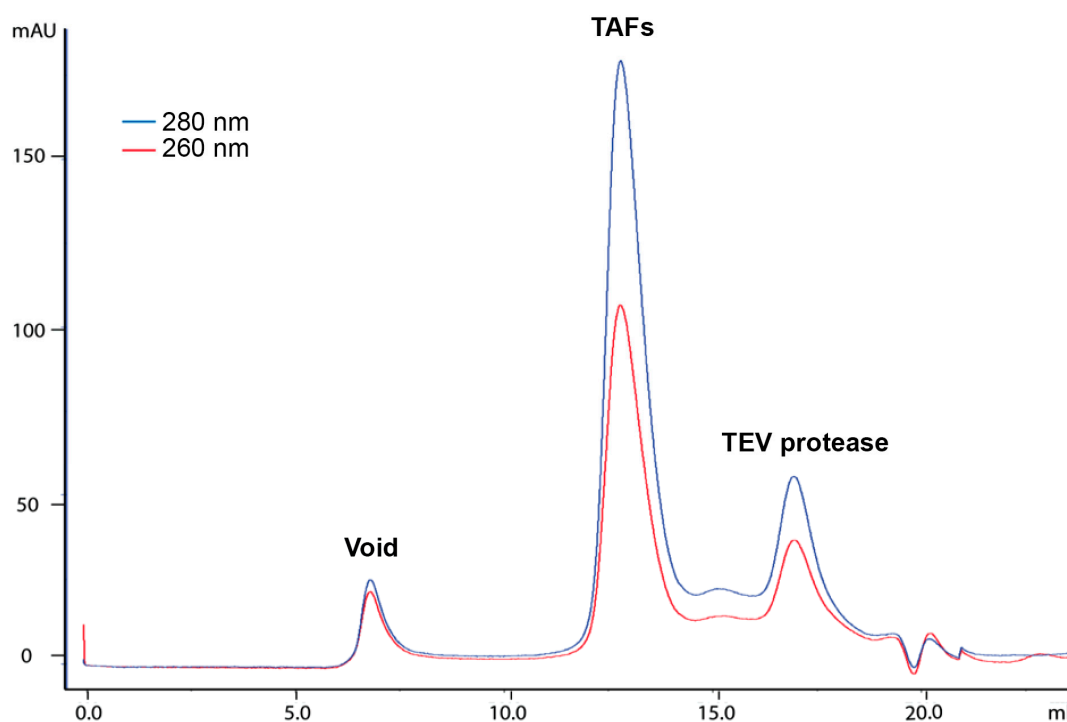


SUPPLEMENTARY MATERIALS accompanying the manuscript “The TAFs of TFIID bind and rearrange the topology of the TATA-less *RPS5* promoter”

SUPPLEMENTARY FIGURE LEGENDS



Supplementary Figure S1. A size-exclusion chromatography profile of the TAF complex purification.

TAF5 YEAST Mass: 89426 Score: 1049 Matches: 30(26) Sequences: 25(23) emPAI: 1.74

Transcription initiation factor TFIID subunit 5 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF5 PE=1 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 50	496.2864	990.5582	990.5750	-16.88	0	47	0.031	1	U	R.IVLEYLNK.K
<input checked="" type="checkbox"/> 55	506.2456	1010.4766	1010.4920	-15.29	0	52	0.0054	1	U	K.YLLSGSSEDK.L
<input checked="" type="checkbox"/> 73	537.7444	1073.4742	1073.4890	-13.79	0	43	0.016	1	U	K.DFHGSEINR.L
<input checked="" type="checkbox"/> 92	573.2864	1144.5582	1144.5764	-15.89	0	61	0.00082	1	U	K.NAIYLSYSK.E
<input checked="" type="checkbox"/> 110	587.3151	1172.6156	1172.6302	-12.45	0	50	0.017	1	U	R.SNLALAGGAFRP.-
<input checked="" type="checkbox"/> 139	626.7771	1251.5396	1251.5554	-12.65	0	68	4.7e-005	1	U	R.MWDVSTGDSVR.L
<input checked="" type="checkbox"/> 146	632.7916	1263.5687	1263.5844	-12.39	0	43	0.027	1	U	R.SNGPFSASDLNR.I
<input checked="" type="checkbox"/> 162	642.3332	1282.6518	1282.6557	-3.06	0	72	7e-005	1	U	R.IAAAGFQDSYIK.I
<input checked="" type="checkbox"/> 189	673.8178	1345.6211	1345.6262	-3.83	0	63	0.00029	1	U	K.ENEVASAFQSHK.Y
<input checked="" type="checkbox"/> 208	694.8590	1387.7034	1387.7095	-4.41	0	74	5.1e-005	1	U	R.LEGLNAPENYIR.A
<input checked="" type="checkbox"/> 244	729.3942	1456.7738	1456.7885	-10.13	0	68	0.00019	1	U	K.TAKPISNPTNLSSK.R
<input checked="" type="checkbox"/> 272	762.8820	1523.7494	1523.7692	-13.01	0	55	0.0035	1	U	K.EGNVLISGGADHTVR.V
<input checked="" type="checkbox"/> 304	821.4386	1640.8627	1640.8662	-2.10	0	92	7.3e-007	1	U	R.TVIPTSDLVASFYTK.K
<input checked="" type="checkbox"/> 366	925.9168	1849.8191	1849.8303	-6.02	0	81	2.7e-006	1	U	K.QLNQQTAGDNYSGANNR.T
<input checked="" type="checkbox"/> 380	935.9650	1904.8732	1904.9089	-18.76	0	34	0.19	1	U	K.QSTNQNGNTHQPPVK.N
<input checked="" type="checkbox"/> 407	998.9779	1995.9412	1995.9538	-6.33	0	(47)	0.014	1	U	K.TLVGHSSTVYSTSFSPDNK.Y
<input checked="" type="checkbox"/> 408	666.3210	1995.9412	1995.9538	-6.33	0	66	0.00015	1	U	K.TLVGHSSTVYSTSFSPDNK.Y
<input checked="" type="checkbox"/> 414	1012.0349	2022.0552	2022.0721	-8.33	0	(32)	0.48	1	U	R.LFLGHTAFVSIACVDPGR.W
<input checked="" type="checkbox"/> 415	675.0257	2022.0554	2022.0721	-8.27	0	46	0.02	1	U	R.LFLGHTAFVSIACVDPGR.W
<input checked="" type="checkbox"/> 448	1074.5279	2147.0413	2147.0535	-5.68	0	(11)	66	1	U	R.WLSTGSEDGIINVWDIGTGK.R
<input checked="" type="checkbox"/> 449	1074.5291	2147.0436	2147.0535	-4.60	0	119	1e-009	1	U	R.WLSTGSEDGIINVWDIGTGK.R
<input checked="" type="checkbox"/> 450	716.6885	2147.0436	2147.0535	-4.60	0	(65)	0.00026	1	U	R.WLSTGSEDGIINVWDIGTGK.R
<input checked="" type="checkbox"/> 580	900.0725	2697.1958	2697.2200	-8.96	0	41	0.017	1	U	R.TNNAAGANSQQPQQSQSQSQGGR.S
<input checked="" type="checkbox"/> 626	1026.8220	3077.4442	3077.4717	-8.93	0	62	0.00022	1	U	K.ATTEPSAEPDEPFTIGYLGVDVTSINQDIK.E
<input checked="" type="checkbox"/> 629	627.6931	3133.4294	3133.4543	-7.97	0	(106)	5.4e-009	1	U	K.GHNHPVWDVFSPLGHYFATASHDQTR.L
<input checked="" type="checkbox"/> 630	784.3650	3133.4309	3133.4543	-7.48	0	112	1.6e-009	1	U	K.GHNHPVWDVFSPLGHYFATASHDQTR.L
<input checked="" type="checkbox"/> 633	1048.8174	3143.4302	3143.4465	-5.19	1	80	2.2e-006	1	U	K.IWSLDGSSLNPNIALNNDDKEDPTCK.T
<input checked="" type="checkbox"/> 641	1069.5186	3205.5341	3205.5667	-10.17	1	65	0.00013	1	U	K.KATTEPSAEPDEPFTIGYLGVDVTSINQDIK.E
<input checked="" type="checkbox"/> 680	971.2566	3880.9973	3881.0405	-11.14	0	54	0.00084	1	U	K.NWVDSLEIYKPELSYIMYPIFYLFNLVAK.N
<input checked="" type="checkbox"/> 708	1146.5968	4582.3582	4581.4061	208	1	1	1e+002	1	U	K.NWVDSLEIYKPELSYIMYPIFYLFNLVAKNPVYAR.R

TAF2 YEAST Mass: 162851 Score: 701 Matches: 26(17) Sequences: 24(16) emPAI: 0.52

Transcription initiation factor TFIID subunit 2 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF2 PE=1 SV=3

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 41	481.7412	961.4679	961.4902	-23.22	0	48	0.021	1	U	R.LAACEALSK.Y
<input checked="" type="checkbox"/> 56	506.2532	1010.4918	1010.5073	-15.36	0	49	0.014	1	U	K.VVGEEGFFK.S
<input checked="" type="checkbox"/> 59	510.7541	1019.4936	1019.5135	-19.47	0	27	2.7	1	U	R.TSESNELK.Q
<input checked="" type="checkbox"/> 104	581.8168	1161.6191	1161.6394	-17.45	0	35	0.48	1	U	K.ELPHFDLTK.K
<input checked="" type="checkbox"/> 119	601.8460	1201.6774	1201.6958	-15.29	0	36	0.35	1	U	R.LLYPLEVIDK.A
<input checked="" type="checkbox"/> 124	607.2935	1212.5725	1212.6099	-30.81	0	63	0.00037	1	U	K.SSVQSVHNEVK.N
<input checked="" type="checkbox"/> 150	636.8050	1271.5954	1271.6106	-11.91	0	60	0.00069	1	U	R.NIEESNNPSLR.D
<input checked="" type="checkbox"/> 169	648.3343	1294.6540	1294.6744	-15.71	0	36	0.28	1	U	K.LYFLQCNIK.Y
<input checked="" type="checkbox"/> 172	651.3455	1300.6764	1300.6921	-12.11	0	83	7.6e-006	1	U	R.QNISGLIQLCR.D
<input checked="" type="checkbox"/> 173	651.7880	1301.5614	1301.5744	-10.01	0	22	1.6	1	U	R.TECFTGSMIR.I
<input checked="" type="checkbox"/> 200	680.8173	1359.6200	1359.6347	-10.78	0	58	0.00087	1	U	K.YVYDPDFTGGVK.H
<input checked="" type="checkbox"/> 239	721.3860	1440.7574	1440.7799	-15.62	0	43	0.053	1	U	R.VMYTLINSFVVR.L
<input checked="" type="checkbox"/> 256	742.8691	1483.7236	1483.7381	-9.74	0	63	0.00049	1	U	R.ESFQNEFLMLK.I
<input checked="" type="checkbox"/> 263	750.8417	1499.6688	1499.6780	-6.09	0	78	5.9e-006	1	U	K.FASLNEYPTDSK.S
<input checked="" type="checkbox"/> 266	753.3569	1504.6993	1504.6915	5.18	0	47	0.014	1	U	K.HMDFALGICNTR.L
<input checked="" type="checkbox"/> 292	793.8572	1585.6998	1585.7116	-7.46	0	55	0.00099	1	U	R.DVIVCCSEYSNIK.E
<input checked="" type="checkbox"/> 381	955.4742	1908.9339	1907.9629	509	0	10	83	2	U	K.QFLDLIVYNENGENK.Y
<input checked="" type="checkbox"/> 384	639.6462	1915.9167	1915.9428	-13.64	0	54	0.0032	1	U	R.IHEHDTPTYEHIVEIK.D
<input checked="" type="checkbox"/> 392	979.4905	1956.9665	1956.9832	-8.53	0	69	0.00012	1	U	R.YENLVNWLSSYESLIK.T
<input checked="" type="checkbox"/> 422	1028.0936	2054.1726	2054.1928	-9.82	0	0	3.4e+002	1	U	K.ILLWDVLNLPVLSLYQR.K
<input checked="" type="checkbox"/> 435	704.9803	2111.9190	2111.9357	-7.94	0	53	0.0011	1	U	K.SEDDIELFLSGHYVDDMK.I
<input checked="" type="checkbox"/> 443	1070.5364	2139.0582	2139.0789	-9.68	0	95	2.4e-007	1	U	K.LENFFNEWVYSGVPILR.V
<input checked="" type="checkbox"/> 444	714.0267	2139.0582	2139.0789	-9.68	0	(84)	3.3e-006	1	U	K.LENFFNEWVYSGVPILR.V
<input checked="" type="checkbox"/> 446	716.3739	2146.0999	2146.1157	-7.37	0	(20)	8.2	1	U	K.ISLEDANALSNTYPTIPSIK.T
<input checked="" type="checkbox"/> 447	1074.0572	2146.0999	2146.1157	-7.37	0	81	7.5e-006	1	U	K.ISLEDANALSNTYPTIPSIK.T
<input checked="" type="checkbox"/> 699	1055.4923	4217.9400	4217.9713	-7.41	0	33	0.067	1	U	R.CDQFHDPLQTNLGLTSQNVLYSDNSIEQSHFLR.S

TAF14 YEAST Mass: 27423 Score: 605 Matches: 13(11) Sequences: 9(8) emPAI: 2.53

Transcription initiation factor TFIID subunit 14 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF14 PE=1 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 33	455.7332	909.4518	909.4596	-8.53	0	25	3.6	1	U	K.SLWDYVK.K
<input checked="" type="checkbox"/> 282	777.3662	1552.7178	1552.7217	-2.51	0	106	1.6e-008	1	U	K.SGSTEETTANTGTIGK.R
<input checked="" type="checkbox"/> 317	560.2915	1677.8527	1677.8739	-12.64	0	69	0.00015	1	U	K.VIYHLHPTFANPNR.T
<input checked="" type="checkbox"/> 372	944.9662	1887.9178	1887.9248	-3.73	0	149	1.2e-012	1	U	K.LNEDDLVGVMVMDNK.F
<input checked="" type="checkbox"/> 373	630.3138	1887.9197	1887.9248	-2.72	0	(74)	3.6e-005	1	U	K.LNEDDLVGVMVMDNK.T
<input checked="" type="checkbox"/> 430	700.7105	2099.1097	2099.1164	-3.17	0	77	1.6e-005	1	U	K.TQQHILPEVPPVENFPVR.Q
<input checked="" type="checkbox"/> 431	1050.5637	2099.1129	2099.1164	-1.64	0	(18)		12	U	K.TQQHILPEVPPVENFPVR.Q
<input checked="" type="checkbox"/> 485	759.7246	2276.1521	2276.1729	-9.15	0	(50)	0.0084	1	U	R.IEEQMGQFPPLDISVFLEK.A
<input checked="" type="checkbox"/> 486	1139.0833	2276.1521	2276.1729	-9.14	0	55	0.0022	1	U	R.IEEQMGQFPPLDISVFLEK.A
<input checked="" type="checkbox"/> 572	887.1247	2658.3522	2658.3792	-10.17	1	60	0.00059	1	U	R.QWSIEIVLLDDEGEIPATIFDK.V
<input checked="" type="checkbox"/> 635	1055.5184	3163.5335	3163.5635	-9.48	0	88	5.8e-007	1	U	K.TPMNVTNNVEGEFIIDLYSLPEGLLK.S
<input checked="" type="checkbox"/> 689	1000.2885	3997.1249	3997.1564	-7.89	1	(44)	0.0073	1	U	R.KIPHDNLFLQSEYEVEHVQIPLNPKLLTEELAK.S
<input checked="" type="checkbox"/> 690	800.4322	3997.1249	3997.1564	-7.88	1	47	0.0034	1	U	R.KIPHDNLFLQSEYEVEHVQIPLNPKLLTEELAK.S

TAF6 YEAST Mass: 57980 Score: 550 Matches: 17(11) Sequences: 13(9) emPAI: 1.29

Transcription initiation factor TFIID subunit 6 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF6 PE=1 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 77	546.7649	1091.5153	1091.5347	-17.76	0	43	0.043	1	U	R.DVLTTDDVSK.A
<input checked="" type="checkbox"/> 93	573.3041	1144.5936	1144.6088	-13.25	0	53	0.008	1	U	K.GVSVLEGESIR.F
<input checked="" type="checkbox"/> 94	573.3052	1144.5958	1144.6088	-11.38	0	(32)	0.92	1	U	K.GVSVLEGESIR.F
<input checked="" type="checkbox"/> 100	578.3486	1154.6827	1154.6910	-7.22	0	58	0.001	2	U	R.ILEIIEQAVK.F
<input checked="" type="checkbox"/> 122	604.2895	1206.5645	1206.5743	-8.15	0	50	0.0087	1	U	R.VFGTYGCLK.G
<input checked="" type="checkbox"/> 136	622.8315	1243.6484	1243.6747	-21.20	0	32	0.9	1	U	R.CGVGTIGPHLK.R
<input checked="" type="checkbox"/> 193	676.3407	1350.6669	1350.6833	-12.11	0	42	0.069	1	U	R.FFLGNLNNWR.L
<input checked="" type="checkbox"/> 194	677.8587	1353.7028	1353.7180	-11.25	0	78	1.9e-005	1	U	R.DFAASLLDYVLK.K
<input checked="" type="checkbox"/> 298	807.8664	1613.7183	1613.7321	-8.58	0	48	0.0063	1	U	K.DDSPQIEHFLEK.T
<input checked="" type="checkbox"/> 401	662.0466	1983.1180	1983.1503	-16.31	0	(29)	0.58	1	U	K.EETQILVDTVISALLVLK.K
<input checked="" type="checkbox"/> 402	992.5731	1983.1316	1983.1503	-9.44	0	92	2.7e-007	1	U	K.EETQILVDTVISALLVLK.K
<input checked="" type="checkbox"/> 403	662.0516	1983.1329	1983.1503	-8.78	0	(72)	2.5e-005	1	U	K.EETQILVDTVISALLVLK.K
<input checked="" type="checkbox"/> 423	1030.0014	2057.9883	2057.9946	-3.06	0	75	2.1e-005	1	U	R.VLNVEPLYGYDQSEVVK.A
<input checked="" type="checkbox"/> 606	948.1187	2841.3342	2841.3417	-2.64	0	132	2.5e-011	1	U	R.LVFNMSGITLDNIEEHLNDSNPTR.T
<input checked="" type="checkbox"/> 607	711.3415	2841.3370	2841.3417	-1.64	0	(67)	7.6e-005	1	U	R.LVFNMSGITLDNIEEHLNDSNPTR.T
<input checked="" type="checkbox"/> 634	790.1714	3156.6565	3156.6720	-4.90	0	21	2.7	1	U	R.LPTFTTHLAVGVQPAIIQNPNLDIR.V
<input checked="" type="checkbox"/> 717	1010.3225	5046.5759	5046.6110	-6.95	0	32	0.065	1	U	R.GAIVTALNDSLQTFVTSTASAVTDTGASQHLNPKVQNTVEVKPLVK..

TAF1 YEAST Mass: 120849 Score: 537 Matches: 15(11) Sequences: 13(10) emPAI: 0.45

Transcription initiation factor TFIID subunit 1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF1 PE=1 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 80	551.2828	1100.5511	1100.5713	-18.37	0	56	0.003	1	U	K.INNLELEK.Q
<input checked="" type="checkbox"/> 163	642.3735	1282.7324	1282.7496	-13.37	0	39	0.099	1	U	K.LLQLELANLEK.S
<input checked="" type="checkbox"/> 166	645.8135	1289.6125	1289.6324	-15.42	0	37	0.19	1	U	K.NNLLQSNSSASR.R
<input checked="" type="checkbox"/> 171	433.8928	1298.6567	1298.6942	-28.90	1	32	0.67	1	U	R.KANEQDTLRPK.L
<input checked="" type="checkbox"/> 190	673.8454	1345.6763	1345.6878	-8.53	0	46	0.037	1	U	K.HDISGDTFLTK.S
<input checked="" type="checkbox"/> 259	746.4012	1490.7878	1490.8093	-14.40	0	71	9.9e-005	1	U	K.LPVGETHVLGVQDK.S
<input checked="" type="checkbox"/> 260	497.9366	1490.7879	1490.8093	-14.39	0	(40)	0.11	1	U	K.LPVGETHVLGVQDK.S
<input checked="" type="checkbox"/> 283	778.9121	1555.8097	1555.8246	-9.58	0	58	0.0017	1	U	K.SLEENLLPWNIK.N
<input checked="" type="checkbox"/> 336	579.6605	1735.9598	1735.9985	-22.26	1	41	0.054	1	U	R.RGLIHVSIDELFPK.E
<input checked="" type="checkbox"/> 342	889.8990	1777.7835	1777.7966	-7.38	0	123	1.7e-010	1	U	R.TENSVDNGSDLAGVTDGK.A
<input checked="" type="checkbox"/> 405	996.4696	1990.9246	1990.9371	-6.30	0	83	3.1e-006	1	U	K.TISEDLLIATDDWQEK.I
<input checked="" type="checkbox"/> 490	765.7499	2294.2278	2294.2481	-8.87	0	(66)	0.00017	1	U	K.QQLDSSNLILPLNETILQOK.F
<input checked="" type="checkbox"/> 491	1148.1212	2294.2278	2294.2481	-8.87	0	92	4.3e-007	1	U	K.QQLDSSNLILPLNETILQOK.F
<input checked="" type="checkbox"/> 498	774.3663	2320.0770	2320.0981	-9.08	0	78	7.1e-006	1	U	R.AMIQIHGVDPTGCGEGFSLK.T
<input checked="" type="checkbox"/> 555	856.0997	2565.2774	2565.2976	-7.86	0	87	1.1e-006	1	U	R.NINHLFTVGQTFVVEIIPGNRSR.K

TAF3 YEAST Mass: 40385 Score: 444 Matches: 13(9) Sequences: 13(9) emPAI: 1.03

Transcription initiation factor TFIID subunit 3 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF3 PE=1 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 34	464.3041	926.5937	926.6164	-24.54	0	43	0.021	1	U	R.ISILQLLK.A
<input checked="" type="checkbox"/> 199	454.2053	1359.5941	1359.6280	-24.94	0	51	0.0023	1	U	R.HHHTTITNEDR.M
<input checked="" type="checkbox"/> 250	737.8634	1473.7123	1473.7252	-8.78	0	63	0.00047	1	U	M.TTNDFYFALLR.I
<input checked="" type="checkbox"/> 313	835.9597	1669.9049	1669.9138	-5.32	0	86	2.7e-006	1	U	R.ITALPTVELLQSEK.E
<input checked="" type="checkbox"/> 316	839.9336	1677.8527	1677.8760	-13.86	0	2	6.8e+002	1	U	R.ARPSTLVDMTDLAK.F
<input checked="" type="checkbox"/> 322	846.4618	1690.9089	1690.9254	-9.70	0	109	1.2e-008	1	U	K.FLSLLASEVSSIAQAR.C
<input checked="" type="checkbox"/> 387	968.4576	1934.9007	1934.9109	-5.27	0	77	1.2e-005	1	U	R.DEDALTEIQENPFTSK.L
<input checked="" type="checkbox"/> 436	1058.0212	2114.0278	2114.0531	-11.97	0	55	0.0026	1	U	K.TELIEDLINNGLDQWK.L
<input checked="" type="checkbox"/> 453	1079.5466	2157.0786	2157.0953	-7.76	0	9	1e+002	1	U	K.ESDPLSAIPDYLNLQLNK.G
<input checked="" type="checkbox"/> 478	748.3780	2242.1120	2242.1481	-16.09	1	10	75	1	U	R.KTELIEDLINNGLDQWK.L
<input checked="" type="checkbox"/> 602	940.4421	2818.3045	2818.3396	-12.44	0	75	9.8e-006	1	U	R.LENITLSFEDEELESLEGEVGNQK.S
<input checked="" type="checkbox"/> 676	953.2489	3808.9664	3808.9985	-8.44	1	15	7.4	1	U	R.ITALPTVELLQSEKESDPLSAIPDYLNLQLNK.G
<input checked="" type="checkbox"/> 707	1141.7995	4563.1689	4563.2174	-10.62	0	100	1.2e-008	1	U	R.CQDDTIALQDITALENIGIVKPTNVLVDYDENSELSSSR.G

TAF12 YEAST Mass: 61150 Score: 425 Matches: 14(10) Sequences: 14(10) emPAI: 0.69

Transcription initiation factor TFIID subunit 12 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF12 PE=1 SV=1

☐ Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 28	437.7330	873.4514	873.4708	-22.29	0	52	0.012	1	U	K.TPAFVAYR.S
<input checked="" type="checkbox"/> 76	545.7853	1089.5561	1089.5720	-14.53	0	30	1.5	1	U	K.LWQNFQVR.H
<input checked="" type="checkbox"/> 84	560.7793	1119.5441	1119.5560	-10.65	0	61	0.00086	1	U	R.IPGYSADEIR.S
<input checked="" type="checkbox"/> 114	596.8126	1191.6107	1191.6248	-11.84	0	68	0.00022	1	U	K.QVYDALTLNR.R
<input checked="" type="checkbox"/> 137	623.8084	1245.6023	1244.6109	797	0	12	67	2	U	K.NNGNNVASLNTK.K
<input checked="" type="checkbox"/> 138	625.2900	1248.5654	1248.5809	-12.34	0	53	0.0028	1	U	K.LPPYEMDTQR.V
<input checked="" type="checkbox"/> 147	632.8101	1263.6056	1263.6208	-11.96	0	71	7.6e-005	1	U	K.FLQESTQQQR.V
<input checked="" type="checkbox"/> 220	703.8354	1405.6562	1405.6738	-12.51	1	13	39	1	U	R.KWNPSQNYNQK.L
<input checked="" type="checkbox"/> 295	803.8773	1605.7401	1605.7522	-7.52	0	64	0.00024	1	U	K.QVLTPEENQEYK.L
<input checked="" type="checkbox"/> 301	814.4290	1626.8434	1626.8464	-1.89	0	5	3.3e+002	1	U	K.QTEPAIPISINISTK.T
<input checked="" type="checkbox"/> 356	914.9431	1827.8717	1827.8823	-5.82	0	92	4.7e-007	1	U	K.SQQQQNTITATNNPR.G
<input checked="" type="checkbox"/> 379	951.9817	1901.9488	1901.9582	-4.94	0	70	0.0001	1	U	K.ISSSNSTEIPSVTGPDAK.S
<input checked="" type="checkbox"/> 513	787.7267	2360.1582	2360.1754	-7.28	0	98	1e-007	1	U	R.SNRPTITGGSAMNASALNTPATK.L
<input checked="" type="checkbox"/> 695	1025.7227	4098.8617	4098.9104	-11.87	0	59	0.00016	1	U	K.TVGIDEGDGETVIDGDVEELLDLADDFVTNVTAFSCR.L

TAF10 YEAST Mass: 23005 Score: 369 Matches: 6(4) Sequences: 5(3) emPAI: 0.97

Transcription initiation factor TFIID subunit 10 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF10 PE=1 SV=1

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Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 51	496.7347	991.4548	990.4883	976	0	34	0.27	1	U	K.NGFNVADV.R
<input checked="" type="checkbox"/> 419	1026.9763	2051.9380	2051.9436	-2.75	0	111	3.3e-009	1	U	R.EAVVDGSENAFGIPEFTR.K
<input checked="" type="checkbox"/> 601	934.1436	2799.4090	2799.4012	2.77	0	107	1.1e-008	1	U	R.QLLGGQQPGVQQISQQHQNEK.T
<input checked="" type="checkbox"/> 610	956.8307	2867.4702	2867.4817	-4.04	0	118	9.4e-010	1	U	K.VVLTVNDLSAVALYGLNIGRDPFYR.-
<input checked="" type="checkbox"/> 611	717.8759	2867.4747	2867.4817	-2.46	0	(102)	3.1e-008	1	U	K.VVLTVNDLSAVALYGLNIGRDPFYR.-
<input checked="" type="checkbox"/> 655	1118.5522	3352.6348	3352.6710	-10.78	1	0	3.2e+002	1	U	K.DKTLLEIEMMDSTPIIPDAVIDYILTK.N

TAF4 YEAST Mass: 42338 Score: 328 Matches: 10(8) Sequences: 10(8) emPAI: 0.83

Transcription initiation factor TFIID subunit 4 OS=Saccharomyces cerevisiae (strain YJM789) GN=TAF4 PE=3 SV=1

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Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 29	444.7412	887.4679	887.4825	-16.41	0	20	21	1	U	R.ASNVTAGLR.A
<input checked="" type="checkbox"/> 49	494.7684	987.5223	987.5461	-24.10	1	56	0.0045	1	U	R.RSEVSAAALR.A
<input checked="" type="checkbox"/> 78	550.2655	1098.5164	1098.5305	-12.84	0	65	0.00023	1	U	K.IDSEETLHR.A
<input checked="" type="checkbox"/> 113	596.2965	1190.5785	1190.5931	-12.31	0	52	0.0076	1	U	K.EQNFNLTPTK.N
<input checked="" type="checkbox"/> 127	607.8511	1213.6877	1213.7030	-12.65	0	65	0.00035	1	U	R.DILTNAIVISR.H
<input checked="" type="checkbox"/> 265	752.8698	1503.7250	1503.7416	-11.01	0	84	3.5e-006	1	U	R.EEALINSSINASK.S
<input checked="" type="checkbox"/> 290	790.9084	1579.8023	1579.8206	-11.55	0	59	0.0015	1	U	K.ASELWSLSPSPQIK.S
<input checked="" type="checkbox"/> 388	646.3383	1935.9930	1936.0054	-6.42	0	90	8.4e-007	1	U	K.QYGLTSSVKNPTSLGAK.S
<input checked="" type="checkbox"/> 469	731.3647	2191.0723	2191.0997	-12.48	0	9	90	1	U	K.IPNHLPLHPEQVSNYMR.K
<input checked="" type="checkbox"/> 499	775.3592	2323.0558	2323.0677	-5.12	0	80	3.7e-006	1	U	K.STAHVSSSTHDAAGNTDDSVLPK.N

TAF9 YEAST Mass: 17361 Score: 312 Matches: 6(5) Sequences: 5(4) emPAI: 1.44

Transcription initiation factor TFIID subunit 9 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF9 PE=1 SV=1

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Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 20	404.7233	807.4321	807.4491	-21.01	0	1	1.3e+003	7	U	R.YTQGVLK.D
<input checked="" type="checkbox"/> 181	657.8446	1313.6746	1313.6914	-12.78	0	66	0.00035	1	U	K.ALQVMGTWGV.R
<input checked="" type="checkbox"/> 427	1037.9741	2073.9337	2073.9451	-5.50	0	111	2.9e-009	1	U	K.NSVGSVSEVGPDSTQETPR.D
<input checked="" type="checkbox"/> 539	834.0529	2499.1368	2499.1514	-5.82	0	123	1.7e-010	1	U	K.DALVYNDYAGSGNSAGSLGVDIR.L
<input checked="" type="checkbox"/> 650	829.6808	3314.6939	3314.7234	-8.88	0	(52)	0.0024	1	U	R.LLHLLASQSIHQYEDQVFLQDMFAHR.Y
<input checked="" type="checkbox"/> 651	663.9461	3314.6940	3314.7234	-8.87	0	59	0.00051	1	U	R.LLHLLASQSIHQYEDQVFLQDMFAHR.Y

TAF7 YEAST Mass: 67571 Score: 263 Matches: 7(7) Sequences: 7(7) emPAI: 0.39

Transcription initiation factor TFIID subunit 7 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF7 PE=1 SV=1

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Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 140	626.8319	1251.6491	1251.6724	-18.57	0	45	0.041	1	U	K.HGISPPLYNVR.N
<input checked="" type="checkbox"/> 141	627.8289	1253.6432	1253.6615	-14.66	0	64	0.00045	1	U	K.EEITIASAVGK.Q
<input checked="" type="checkbox"/> 175	652.3203	1302.6261	1302.6416	-11.87	0	60	0.001	1	U	K.QLQQTEDSVQK.Q
<input checked="" type="checkbox"/> 182	657.8786	1313.7427	1313.7595	-12.76	0	59	0.0013	1	U	R.ILPDIQLEFVK.N
<input checked="" type="checkbox"/> 211	698.3285	1394.6424	1394.6565	-10.14	0	69	8.9e-005	1	U	K.QAEVSYDLVDK.S
<input checked="" type="checkbox"/> 248	735.3540	1468.6933	1468.7045	-7.61	0	94	3.2e-007	1	U	K.NSLESGDYSIGISIK.W
<input checked="" type="checkbox"/> 522	802.7369	2405.1889	2405.2074	-7.68	0	72	4.9e-005	1	U	R.QHTELLADELNELETTLAHTK.H

TAF8 YEAST Mass: 58007 Score: 256 Matches: 5(5) Sequences: 5(5) emPAI: 0.32
Transcription initiation factor TFIID subunit 8 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF8 PE=1 SV=1

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Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 132	611.3470	1220.6794	1220.6989	-16.02	0	47	0.021	1	U	R.NLHNLTLQR.R
<input checked="" type="checkbox"/> 312	832.9198	1663.8250	1663.8377	-7.63	0	128	1.7e-010	1	U	K.TSESGTGTQSTIVQLR.N
<input checked="" type="checkbox"/> 516	1188.0700	2374.1254	2374.1481	-9.57	0	46	0.014	1	U	R.EFNLDAPSLYQQFQASEFIK.S
<input checked="" type="checkbox"/> 528	820.1125	2457.3156	2457.3366	-8.55	0	67	0.0001	1	U	R.NLPDLTEISHLEIDAPVVEILK.K
<input checked="" type="checkbox"/> 694	1012.4754	4045.8723	4045.9141	-10.31	0	52	0.00098	1	U	K.SLSHISSASNTPPFGLDDEDAIEQQLEIWNALER.K

TAF11 YEAST Mass: 40656 Score: 167 Matches: 7(4) Sequences: 7(4) emPAI: 0.48
Transcription initiation factor TFIID subunit 11 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF11 PE=1 SV=1

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Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 116	599.2755	1196.5365	1196.5244	10.1	0	12	31	3	U	R.TQEGGQGSFMR.-
<input checked="" type="checkbox"/> 137	623.8084	1245.6023	1245.6313	-23.26	0	63	0.00057	1	U	R.TGGTSINNQLNK.Y
<input checked="" type="checkbox"/> 167	645.8388	1289.6630	1289.6827	-15.27	0	47	0.03	1	U	R.ETTLGNSLLQSK.S
<input checked="" type="checkbox"/> 242	726.8643	1451.7140	1451.7521	-26.22	0	10	1e+002	1	U	K.YNNSPLLPEHTR.E
<input checked="" type="checkbox"/> 275	765.4046	1528.7947	1528.8209	-17.16	1	53	0.0066	1	U	K.LLVTNLDKQDTNR.F
<input checked="" type="checkbox"/> 299	808.9257	1615.8368	1615.8529	-9.98	0	84	4.3e-006	1	U	K.LASTVANQTISENIR.V
<input checked="" type="checkbox"/> 363	920.9851	1839.9556	1839.9771	-11.64	0	34	0.36	1	U	K.VNYPPILTIANIFYSTK.Q

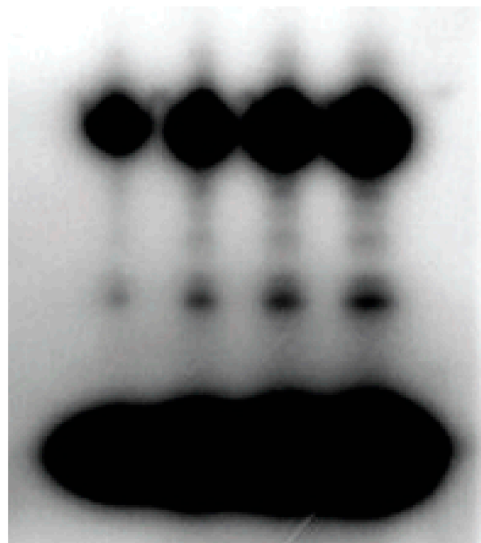
TAF13 YEAST Mass: 19235 Score: 38 Matches: 1(1) Sequences: 1(1) emPAI: 0.18
Transcription initiation factor TFIID subunit 13 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=TAF13 PE=1 SV=2

☐ Check to include this hit in error tolerant search or archive report

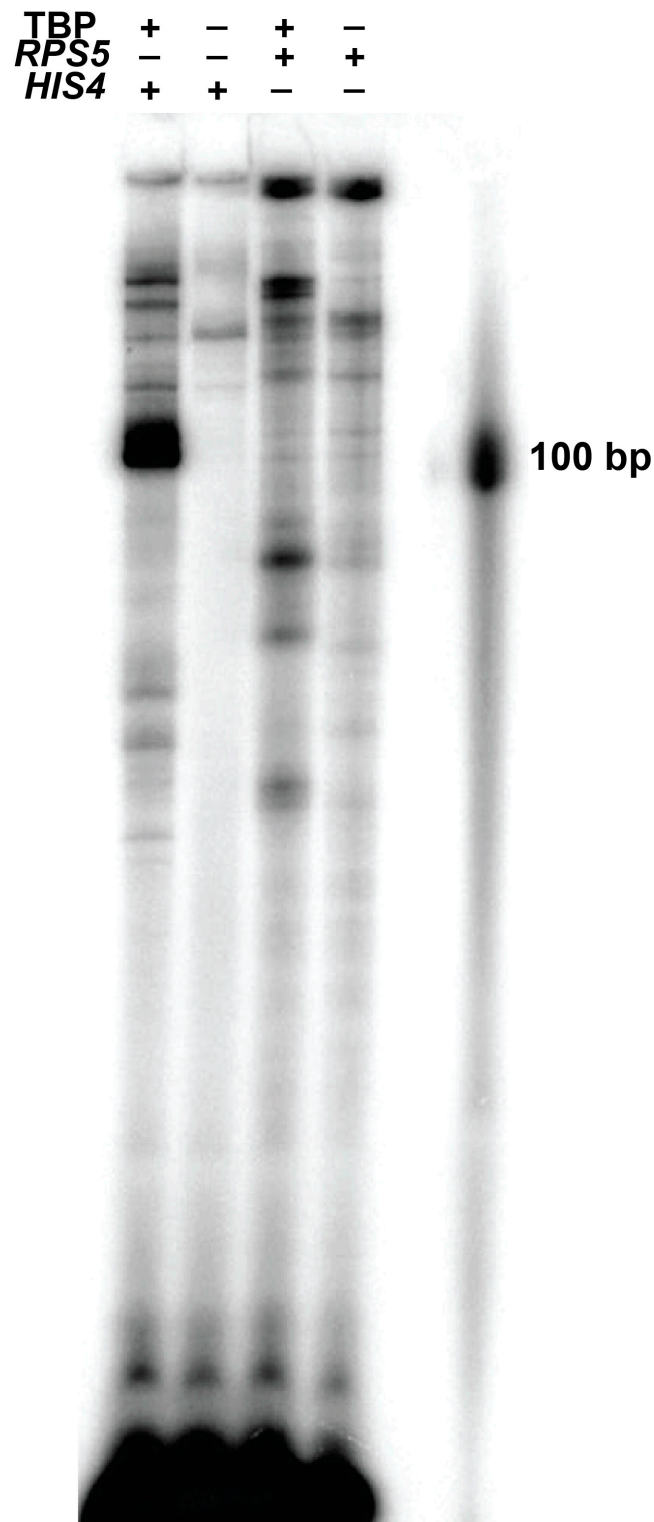
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 719	1049.2987	5241.4572	5241.5023	-8.62	0	38	0.01	1	U	K.DVSSLLYAYGDVFPQLQATVQCCLDELVSGLVDVCTNAFHTAQNSQR.N

Supplementary Figure S2. Mass spectrometry results showing that all 14 TAFs are present in the purified complex.

pmol TBP 1 2 3 4

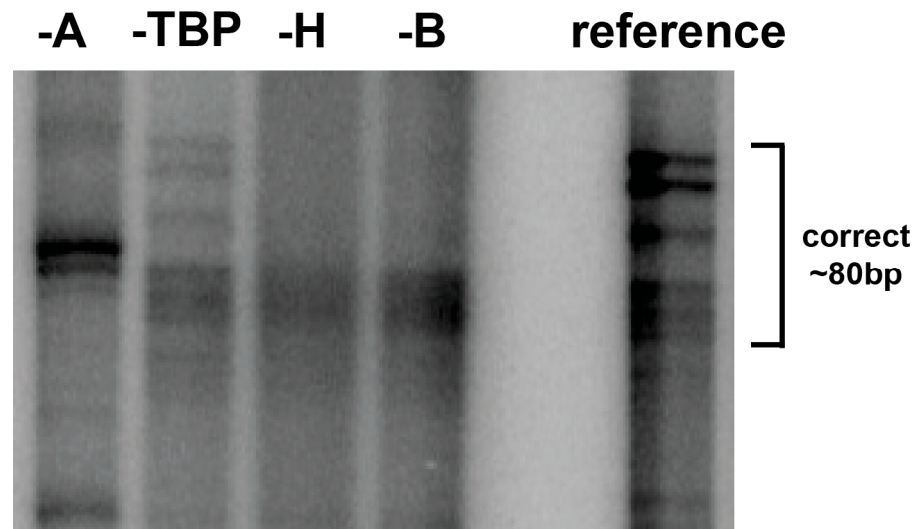


Supplementary Figure S3. EMSA in 2% agarose gel for TBP on RPS5. TBP alone binds RPS5 forming at least two specific complexes with one or more TBP molecules bound.



Supplementary Figure S4. Positive and negative controls for transcription run-off assays. Lane 1: Run-off products from the *HIS4* TATA promoter to assess the activity of purified GTFs without the TAF complex. Lane 2: Negative control; same as Lane 1 minus TBP and TAFs. Lane 3: Run-off products from the *RPS5* TATA-less promoter in the presence of TBP only (minus TAFs). This establishes the TBP-directed transcription background. Lane 4: Negative control to establish *RPS5* background transcription (minus TBP minus TAFs). Comparing Lanes 3 and 4 reveals the strongest top band that is much longer than 100 bp, inconsistent with the mRNA products detected in vivo. This band corresponds to an artificial

transcript from a TSS located approximately 25 bp downstream of the pseudo-TATA box. Rightmost lane: 100 bp ladder.



Supplementary Figure S5. Negative controls for transcription run-off assays on *RPS5* with TAFs present. Lane 1: Omitting TFIIA. Lane 2: Omitting TBP. Lane 3: Omitting TFIIH. Lane 4: Omitting TFIIB. Faint correct bands are observed when TBP is omitted, which we attribute to the 3% contamination of TBP in our TAF complex preparation.