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The complex of TFII-I, PARP1 and SFPQ proteins regulates the *DYX1C1* gene implicated in neuronal migration and
Dyslexia

Supplementary Data File

MS-Digest Search Results

Masses from in gel digestion MS are shown in red

Short Peptide sequences identified by MS/MS qTOF are underlined

Acc P09874 Poly [ADP-ribose] polymerase 1, Protein MW: 11308

1	MAESSDKLYR	VEYAKSGRAS	CKKCESEIPK	DSLRLAIMVQ	SPMFDGKVPH	WYHFSFCWKV	GHSIRHPDVE	VDGFSELRWD
81	DQQKVKKTAE	AGGVVTGKGQD	GIGSKAEKTL	GDFAAEYAKS	NRSTCKGCME	KIEKGQVRLS	KKMVDPEKPO	LGMIDRWYHP
161	GCFVKNREEL	GFRPEYSASQ	LKGFSLATE	DKEALKKQLP	GVKSEGKRKG	DEVGDVDEVA	KKKSKKEKDK	DSKLEKALKA
241	QNDLIWNIKD	ELKKVCSTND	LKELLIFNKQ	QVPSGESAIL	DRVADGMVFG	ALLPCEECSE	QLVFKSDAYY	CTGDVTAATK
321	CMVKTQTPNR	KEWVTPKEFR	EISYLKCLKV	KKQDRIFPPE	TSASVAATPP	PSTASAPAAV	NSSASADKPL	SNMKILTLGK
401	LSRNKDEVKA	MIKLGGLT	GTANKASLCI	STKKEVEKMN	KKMEEVKEAN	IRVVEDFLQ	DVSASTKSLQ	ELFLAHILSP
481	WGAEVKAEPV	EVVAPRGKSG	AALSCKSKGQ	VKEEGINKSE	KRMKLTLLKGG	AAVDPDGSLG	HSAHVLEKGG	KVFSATLGLV
561	DIVKGTNSYY	KLQLEDDKE	NRYWIFRSWG	RVGTVIGSNK	LEQMPSKEDA	IEHFMKLYEE	KTGNAWHSKN	FTKYPKKFYP
641	LEIDYGDDEE	AVKKLTVNPG	TKSKLKPVPQ	DLIKMIFDVE	SMKKAMVEYE	IDLQKMPGK	LSKRQIQAAV	SILSEVQQAV
721	SQGSSDSQIL	DLSNRFYTLI	PHDFGMKPP	LLNNADSVQA	KVEMLDNLLD	IEVAYSLLRG	GSDDSSKDP	DVNYEKLKTD
801	IKVVDRDSEE	AEIIRKYVKN	THATTHNAYD	LEVIDIFKIE	REGECQRYKP	FKQLHNRLL	WHGSRTTNFA	GILSQGLRIA
881	PPEAPVTGYM	FGKGIYFADM	VSKSANYCHT	SQGDPIGLIL	LGEVALGNMY	ELKHASHISK	LPKGKHSVKG	LGKTTDPDSA
961	NISLDGVDVP	LGTGISSGVN	DTSLLYNEYI	VYDIAQVNLK	YLLKLFNFK	TSLW		

Acc P23246 Splicing Factor, Proline- and Glutamine-rich SFPQ (PTB-associated-splicing factor) (PSF) Protein MW: 76150

1	MSRDRFRSRG	GGGGGFHRRG	GGGGRGGLHD	FRSPPPGMGL	NQNRGPMGPG	PGQSGPKPPI	PPPPPHQQQQ	QPPPPQPPPPQ
81	QPPPHQPPPH	PQPHQQQPP	PPPQDSSKPV	VAQGGPAPAG	VGSAPPASS	APPATPPTSG	APPGSGPGPT	PTPPPAV TSA
161	PPGAPPPTPP	SSGVPTTPPQ	AGGPPPPAA	VPGGPGPKQ	GPGGGPKGG	KMPGGPKPGG	GPGLSTPGGH	PKPPHRGGGE
241	PRGGRQHHP	YHQHHQGGP	PGGGGRSEE	KISDSEGFKA	NLSLLRRPGE	KTYTQRCRLF	VGNLPADITE	DEFKRLFAKY
321	GEPGEVFIN	GKGFIFIKLE	SRALAEIAKA	ELDDTPMRGR	QLRVRFATHA	AALSVRNLS	YVSNELLEEA	FSQFGPIERA
401	VVIVDDRGRS	TGKGIVEFAS	KPAARKAFER	CSEGVFLLTT	TPRPVIVEPL	EQLDDEDGLP	EKLAQKNPMY	QKERETPPRF
481	AQHGTFEY	SQRWKSLEDEM	EKQREQVEK	NMKDAKDKLE	SEMEDAYHEH	QANLLRQDLM	RRQEELRME	ELHNQEMQKR
561	KEMQLRQEEE	RRRREEMMI	RQREMEEQMR	RQREESYSRM	GYMDPRERDM	RMGGGGAMNM	GDPYGGGQK	FPPLGGGGGI
641	GYEANPGVPP	ATMSGSMMS	DMRTERFGQG	GAGPVGQGP	RGMGPGTPAG	YGRGREEYEG	PNKKPRF	

Acc P78347 General transcription factor II-I, GTFII-I, TFII-I (Bruton tyrosine kinase-associated protein 135) (Williams-Beuren syndrome chromosome region), Protein MW: 112417

1	MAQVAMSTLP	VEDESSER	MVVTFLMSAL	ESMCKELAKS	KAEVACIAVY	ETDVFVVGTE	RGRAFVNTRK	DFQKDFVKYC
81	VEEEKAEM	HMKSTTQAN	RMSVDAVEIE	TLRKTVEDYF	CFCYGKALGK	STVVPVPEK	MLRDQSAVVV	QGLPEGVAFK
161	HPENYDLATL	KWILENKAGI	SFIKRPFLE	KHVGGVRM	VTDADR SILS	PGGSCGPIKV	KTEPTEDSGI	SLEMAAVTVK
241	EESEDPDYYQ	YNIQAGPSET	DDVDEKQPLS	KPLQGS SHSS	EGNEGTEMEV	PAEDSTQHVP	SETSEDPEVE	VTIEDDDYSP
321	PSKRPKANEL	PQPPVPEPAN	AGKRKVREFN	FEKWNARITD	LRKQVEELFE	RKYAQAIKAK	GPVTIPYPLF	QSHVEDLYVE
401	GLPEGIPFRR	PSTYGIPRLE	RILLAKERIR	FVIKKHELLN	STREDLQLDK	PASGVKEEWY	ARITKLRKMV	DQLFCCKFAE
481	ALGSTEA KAV	PYQKFEAHPN	DLYVEGLPEN	IPFRSPSWYG	IPRLEKIQV	GNRIKFVIKR	PELLTHSTTE	VTQPRTNTPV
561	KEDWNV RITK	LRKQVEEIFN	LKFAQALGLT	EAVKVPYPVF	ESNPEFLYVE	GLPEGIPFRS	PTWFGIPRLE	RIVRGSNKIK
641	FVVKPELVI	SYLPPGMASK	INTKALQSPK	RPRSPGSNSK	VPEIEVTVEG	PNNNNPQ TSA	VRTPTQTNGS	NVPFKPRGRE
721	FSFEAWN AKI	TDLKQKVENL	FNEKCGEALG	LKQAVKVPFA	LFESFPEDFY	VEGLPEGVPF	RRPSTFGIPR	LEKILRNKAK
801	IKFIIKPEM	FETAIKESTS	SKSPRKINS	SPNVNTTASG	VEDLNIIQVT	IPDDDNERLS	KVEKARQLRE	QVNDLFSRK
881	GEAIGMGFPV	KVPYRKITIN	PGCVVDGMP	PGVSFKAPSY	LEISSMRIL	DSAEFIKFTV	IRFPGLVIN	NQLVDQSESE
961	GPVIQESAEP	SQLEVPATEE	IKETDGSSQI	KQEPDPTW				

MS-Fit results upper band

21/38 matches (55%) **Blue** Acc P09874 Poly [ADP-ribose] polymerase 1 (PARP-1) (ADPRT) (NAD(+) ADP-ribosyltransferase 1)
 Index: 138653 MW: 113085 Da
 pl: 9.0
 10/38 matches (26%) **Red** Acc P78347 General transcription factor II-I (GTFII-I)
 Index: 78631 MW: 112417 Da (Bruton tyrosine kinase-associated protein 135)(Williams-Beuren syndrome region)
 pl: 6.1

m/z Submitted Mass value [H+]	MH+ Matched	Delta Da	Modifications	Start	End	Missed Cleavages	Sequence
784.412012	784.4141	-0.0021		583	587	0	(R) YWIFR (S)
800.375467							
816.407432							
819.411271	819.3632	0.048		79	84	0	(R) WDDQKQ (V)
853.387985	853.3839	0.0041		457	462	0	(K) EEWYAR (I)
868.468917	868.4788	-0.0099		859	865	0	(R) LLWHGSR (T)
900.449751	900.4322	0.018		622	629	0	(K) TGNAWHSK (N)
996.490005							
1030.567024	1030.5792	-0.012		782	790	0	(R) RPSTFGIPR (L)
1049.528843	1049.5262	0.0026		364	371	0	(K) QVEELFER (K)
1060.549799	1060.5574	-0.0076		620	628	0	(R) SPTWFGIPR (L)
	1060.6626	-0.11		427	434	2	(K) ERIRFVIK (K)
1061.539657	1061.5109	0.029		807	815	0	(R) DSEEAEIIR (K)
1064.529731	1064.5405	-0.011		254	262	1	(K) KVCSTNDLK (E)
1092.535279	1092.5208	0.014		788	796	0	(K) DPIDVNYEK (L)
1107.535687	1107.5429	-0.0072		870	878	0	(R) EQVNDLFSR (K)
1118.525009	1118.6092	-0.084		131	140	0	(K) STVVPVPYEK (M)
1130.540423	1130.5551	-0.015		894	903	0	(K) GIYFADMVSK (S)
1185.577210	1185.5786	-0.0014		109	119	0	(K) TLGDFAAEYAK (S)
1193.592242	1193.5561	0.036		157	165	0	(R) WYHPGCFVK (N)
1193.5922	1193.6235	-0.031		807	816	0	(K) KPETFETAIK (E)
1341.663966	1341.7274	-0.063		8	18	2	(K) LYRVEYAKSGR (A)
1365.658871							
1372.673976	1372.7067	-0.033		572	582	1	(K) LQLEDDKENR (Y)
1377.723683	1377.7485	-0.025		866	878	0	(R) TTNFAGILSQGLR (I)
1399.712268	1399.7176	-0.0053		270	282	0	(K) QQVPSGESAILDR (V)
1399.7123	1399.7427	-0.030		444	456	0	(R) EDLQLDKPASGVK (E)
1401.700508							
1475.753122							
1499.6966	1499.8250	-0.13		207	221	1	(R) SILSPGGSCGPIKVK (T)
1499.696560	1499.7125	-0.016		66	78	0	(R) HPDVEVDGFSCLR (W)
1593.767989	1593.7981	-0.030	1Met-ox	879	893	0	(R) IAPPEAPVTGYMFGK (G)
1624.787880	1624.8065	-0.019		453	467	0	(R) VVSEDFLQDVSASTK (S)
1643.8046	1643.8500	-0.045		703	717	0	(R) TPTQTNGSNVFPKPR (G)
1646.809258							
1714.866711							
1753.823795	1753.8755	-0.052		168	182	0	(R) EELGFRPEYSASQLK (G)
1964.934371	1964.9092	0.025	2Met-ox	601	616	1	(K) LEQMPSKEDIAEHFMK (L)
1988.990917	1988.9672	0.024		529	548	0	(K) GGAAVDPDSGLEHSAHVLEK (G)
2023.960594	2024.0196	-0.059		166	182	1	(K) NREELGFRPEYSASQLK (G)
2044.914146							
2365.088272							

MS-Fit results lower band

19/32 matches (59%) **Red** Acc P23246 Splicing factor, proline- and glutamine-rich (Polypyrimidine tract-binding protein-associated-splicing factor)
 Index: 197642 MW: 76150 Da (PTB-associated-splicing factor) (PSF)
 pl: 9.5

m/z Submitted Mass value [H+]	MH+ Matched	Delta Da	Modifications	Start	End	Missed Cleavages	Sequence
830.424266	830.4479	-0.024		543	548	1	(R) QEELRR (M)
	830.4479	-0.024		542	547	1	(R) RQEELR (R)
1054.468566	1054.4912	-0.023		592	599	1	(R) QREESYSR (M)
1143.611661	1143.6269	-0.015		366	376	0	(R) FATHAALSVR (N)
1249.589893	1249.6140	-0.024		573	581	2	(R) RREEMMIR (Q)
1252.600232	1252.5409	0.059	1Met-ox	582	590	1	(R) QREMEEQMR (R)
	1252.6208	-0.021		320	330	0	(K) YGEPGEVFINK (G)
1267.610030	1267.6212	-0.011		33	44	0	(R) SPPPGMGLNQNR (G)
1283.622194	1283.6161	0.0061	1Met-ox	33	44	0	(R) SPPPGMGLNQNR (G)
1323.659926							
1341.635240	1341.6658	-0.031		667	681	0	(R) FGQGGAGPVGGQGPR (G)
1346.647216	1346.6699	-0.023		696	706	1	(R) EEYEGPNKKPR (F)
1360.698201							
1363.665742	1363.6271	0.039	1Met-ox	562	571	1	(K) EMQLRQEER (R)

1403.718543							
1411.746169							
1454.748706							
1556.704490	1556.6767	0.028		600	611	2	(R) MGYMDPRERDMR (M)
1559.762230	1559.7925	-0.030		694	706	2	(R) GREEYEGPNKKPR (F)
1572.716914	1572.6716	0.045	1Met-ox	600	611	2	(R)MGYMDPRERDMR(M)
	1572.7257	-0.0088		549	560	1	(R) MEELHNQEMQKR (K)
	1572.7257	-0.0088		548	559	1	(R) RMEELHNQEMQK (R)
1582.778789							
1588.722591	1588.6665	0.056	2Met-ox	600	611	2	(R)MGYMDPRERDMR(M)
	1588.7206	0.0020	1Met-ox	549	560	1	(R)MEELHNQEMQKR(K)
	1588.7206	0.0020	1Met-ox	548	559	1	(R)RMEELHNQEMQK(R)
1604.739875	1604.6614	0.078	3Met-ox	600	611	2	(R)MGYMDPRERDMR(M)
	1604.7156	0.024	2Met-ox	549	560	1	(R)MEELHNQEMQKR(K)
	1604.7156	0.024	2Met-ox	548	559	1	(R)RMEELHNQEMQK(R)
1707.755841							
1714.846394							
1716.789630	1716.8156	-0.026	1Met-ox	549	561	2	(R)MEELHNQEMQKR(E)
1762.730564	1762.7820	-0.051		480	493	0	(R) FAQHGTFEYEQSR (W)
1782.888574							
1802.868196							
1963.927906	1964.0124	-0.084		299	315	1	(R) LFGVNLPADETEDEFKR (L)
2388.932675							
2403.078269	2403.1351	-0.057		246	267	0	(R) QHHPYHQHHQGGPPGGPGR (S)
2445.125349							
3313.190951							