

Supplementary Materials

Prediction of disordered region and their roles in the anti-pathogenic and immunomodulatory functions of butyrophilins

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Figure S1. Multiple sequence alignment of human butyrophilin family members by the CLUSTAL Omega (1.2.4) algorithm

sp Q13410 BT1A1_HUMAN	----APFDVIGPPEPILAVVGEDAELPCRLSPNASAEHLELRWFRKKV---SPAVLVHRD	53
sp Q7KYR7 BT2A1_HUMAN	-----QFIVVGPTDPILATVGENTTLRCHLSPEKNAEDMEVRWFRSQF---SPAVFVYKG	52
sp Q8WV5 BT2A2_HUMAN	-----QFTVVG PANPILAMVGENTTLRCHLSPEKNAEDMEVRWFRSQF---SPAVFVYKG	52
sp Q96KV6 BT2A3_HUMAN	-----QVTVVGPTDPILAMVGENTTLRCCLSP EENAEDMEVRWFQSQF---SPAVFVYKG	52
sp O00481 BT3A1_HUMAN	-----QFSVLGSPGPILAMVGEDADLPCHLFPTMSAETMELKWVSSSL---RQVVNVYAD	52
sp P78410 BT3A2_HUMAN	-----QFSVLGSPGPILAMVGEDADLPCHLFPTMSAETMELKWVSSSL---RQVVNVYAD	52
sp O00478 BT3A3_HUMAN	-----QFSVLGSPGPILAMVGEDADLPCHLFPTMSAETMELRWVSSSL---RQVVNVYAD	52
sp Q9UIR0 BTN12_HUMAN	-----DFRVIGPAHPILAGVGEDALLTCQLLPKRTTMHVEVRWYRSEP---STPVFVHRD	52
sp Q6UXE8 BTN13_HUMAN	-----QWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQF---HAVVHLYRD	52
sp Q6UX41 BTN18_HUMAN	-----QWQVFGPDKPVQALVGEDAAAFSCFLSPKTNAEAMEVRFFRGQF---SSVVHLYRD	52
sp Q6UXG8 BTN19_HUMAN	---SSEVKVLGPEYPILALVGEEVEFPCHLWPQLDAQQMEIRWFRSQT---FNVVHLYQE	54
sp A8MVZ5 BTNLA_HUMAN	SIWKADFVDTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP---SLAVHMHER	57
sp Q96PL5 ERMAP_HUMAN	-----HAGDAGKFHVALLGTAELLCP LSLWPGTVPKEVRLRSPFPQRSQAVHIFRD	53
sp Q16653 MOG_HUMAN	----GQFRVIGPRHPIRALVGDEVELPCRISPGKNATGMEVGWYRPPF---SRVVHLYRN	53
	. . * * . : * : : * : : * :	
sp Q13410 BT1A1_HUMAN	GREQEAEQMPEYRGRATLVQDGIAGKGRVALRIRGVRVSDDGEYTCFFREDGSYEEALVHL	113
sp Q7KYR7 BT2A1_HUMAN	GRERTEEQMEEYRGRITTFVSKDISRGSVALVIHNITAQENGTYRCYFQEGRSYDEAILHL	112
sp Q8WV5 BT2A2_HUMAN	GRERTEEQMEEYRGRITTFVSKDINRGSVALVIHNVTAQENGIYRCYFQEGRSYDEAILRL	112
sp Q96KV6 BT2A3_HUMAN	GRERTEEQKEEYRGRITTFVSKD-SRGSVALIHNVTAE DNGIYQCYFQEGRSCNEAILHL	111
sp O00481 BT3A1_HUMAN	GKEVEDRQSAPYRGRTSILRDGITAGKAALRIHNV TASDSGKYLCYFQDGD FYEKALVEL	112
sp P78410 BT3A2_HUMAN	GKEVEDRQSAPYRGRTSILRDGITAGKAALRIHNV TASDSGKYLCYFQDGD FYEKALVEL	112
sp O00478 BT3A3_HUMAN	GKEVEDRQSAPYRGRTSILRDGITAGKAALRIHNV TASDSGKYLCYFQDGD FYEKALVEL	112
sp Q9UIR0 BTN12_HUMAN	GVEVTEMQMEEYRGWVEWIENGIAGKNVALKIHNIQPSDNGQYWCHFQDGN YCGETSLLL	112
sp Q6UXE8 BTN13_HUMAN	GEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEEATWEL	112
sp Q6UX41 BTN18_HUMAN	GKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCR ISSQSYYQKAIWEL	112
sp Q6UXG8 BTN19_HUMAN	QQELPGRQMPAFRNRTKLVKDDIAYGSVVLQLHSIIPSDKGT YGCRFHS DNFSGEALWEL	114
sp A8MVZ5 BTNLA_HUMAN	GMDMDGEQKWQYRGRITTFMSDHVAR GKAMVRSHRVTTFDNRTYCCR FKDG VKFGEATVQV	117
sp Q96PL5 ERMAP_HUMAN	GKDQDEDLMPEYKGR TVLVRDA-QEGSVTLQILDVRLEDQGSYRCLIQVGNLSKEDTVIL	112
sp Q16653 MOG_HUMAN	GKDQDGDQAPEYRGRTELLKDAIGEGKVTLRIRNVRFSD EGGFTCCFRDHSYQEEAAMEL	113
	: :. : . * : : : : * : :	
sp Q13410 BT1A1_HUMAN	KVAALGSDPHISMQVQENGEICLECTSVGWYPEPQVQWRTSKGEKFPST-SESRNPDEEG	172
sp Q7KYR7 BT2A1_HUMAN	VVAGLGSKPLISMRGHEDGGIRLECISR GWYPKPLTVWRDPYGGVAPAL-KEVSMPDADG	171
sp Q8WV5 BT2A2_HUMAN	VVAGLGSKPLIEIKAQEDGSIWLECISGGWYPEPLTVWRDPYGEVVPAL-KEVSIADADG	171
sp Q96KV6 BT2A3_HUMAN	VVAGLDSEPVIEMRDHEDGGIQLECISGGWYPKPLTVWRDPYGEVVPAL-KEVSTPDADS	170
sp O00481 BT3A1_HUMAN	KVAALGSDLHVDVKGYKDGGIHLECRSTGWYPQPQIQWSNNKGENIPTV-EAPVVADGVG	171

sp P78410 BT3A2_HUMAN	KVAALGSNLHVEVKGYEDGGIHLECRSTGWYPQPQIQWSNAKGENIPAV-EAPVVADGVG	171
sp O00478 BT3A3_HUMAN	KVAALGSDLHIEVKGYEDGGIHLECRSTGWYPQPQIKWSDTKGENIPAV-EAPVVADGVG	171
sp Q9UIR0 BTNL2_HUMAN	KVAGLGSAPSIHMEGPGESGVQLVCTARGWFPPEPQVYWEDIRGEKLLAV-SEHRIQDKDG	171
sp Q6UXE8 BTNL3_HUMAN	RVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSD-SRA-NADGYS	170
sp Q6UX41 BTNL8_HUMAN	QVSALGSVPLISITGYVDRDIQLLQSSGWFPPTAKWKGPQGQDLSTD-SRT-NRDMHG	170
sp Q6UXG8 BTNL9_HUMAN	EVAGLGSDPHLSLEGFKEGGIQLRLRSSGWYPKPKVQWRDHQGCPLPE-FEAIWDAQD	173
sp A8MVZ5 BTNLA_HUMAN	QVAGLGREPRIQVTDQQD-GVRAECTSAGCFKPSWVERRDFRGQARPAV-TNLSASATTR	175
sp Q96PL5 ERMAP_HUMAN	QVAAPSV-----	119
sp Q16653 MOG_HUMAN	KVEDPF-----YWVSPGVLVLLAVLPVLLLQITVG	143
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sp Q13410 BT1A1_HUMAN	LFTVAASVVIIRDTSAKNVSCYIQNLLLGQEKKV-EISIPASSLPR--LTPWIVAVAVIL-	228
sp Q7KYR7 BT2A1_HUMAN	LFMVTTAVIIRDKSVRNMSCSINNTLLGQKKES-VIFIPESFMPS--VSPCAVALPIIV-	227
sp Q8WV5 BT2A2_HUMAN	LFMVTTAVIIRDKYVRNVSCSVNNTLLGQKET-VIFIPESFMPS--ASPWMVALAVILT	228
sp Q96KV6 BT2A3_HUMAN	LFMVTTAVIIRDKSVRNVSISINDTLLGQKKES-VIFIPESFMPS--RSPCVVILPVIM-	226
sp O00481 BT3A1_HUMAN	LYAVAASVIMRGSSGEGVSCITRSSLGLEKTA-SISIADPFFRS--AQRWIAALAGTL-	227
sp P78410 BT3A2_HUMAN	LYEVAASVIMRGSSGEGVSCIIRNSLLGLEKTA-SISIADPFFRS--AQPWIAALAGTL-	227
sp O00478 BT3A3_HUMAN	LYAVAASVIMRGSSGGGVSCIIRNSLLGLEKTA-SISIADPFFRS--AQPWIAALAGTL-	227
sp Q9UIR0 BTNL2_HUMAN	LFYAEATLVVRNASAESVSCLVHNPVLTTEKGS-VISLPEKLQTE--LASLKVNGPSQP-	227
sp Q6UXE8 BTNL3_HUMAN	LYDVEISIIQENAG-SILCSIHLAEQSHEVES-KVLIGETFFQP---SPWRLASI----	221
sp Q6UX41 BTNL8_HUMAN	LFDVEISLTVQENAG-SISCSMRHAHLSREVES-RVQIGDTFFEP---ISWHLATK----	221
sp Q6UXG8 BTNL9_HUMAN	LFSLETSVVVRAGALSNVSVSIQNLLLSQKKEL-VVQIADVFPVG--ASAWKSAFVATL-	229
sp A8MVZ5 BTNLA_HUMAN	LWAVASSLTLDRAVEGLSCSISPLLPERRKVAESHLPATFSRSSQFTAWKAALPLIL-	234
sp Q96PL5 ERMAP_HUMAN	-----GS--LSPSAVALAVIL-	133
sp Q16653 MOG_HUMAN	LIFLCLQYRLRG-----KLRAE-IENLHRTFDPH-----FLR	174
sp Q13410 BT1A1_HUMAN	-----MVLGLLTIGSIFFTWRLYNERPRER-----RNE---	256
sp Q7KYR7 BT2A1_HUMAN	-----VILMIPIAVCIYWINKLQKEKKILSGEKEFERETREIALKELEKERVQ	275
sp Q8WV5 BT2A2_HUMAN	ASPWMVSMTVILAVFIIFMAVSICCIKKLQREKKILSGEKKVEQEEKE-----	276
sp Q96KV6 BT2A3_HUMAN	-----IILMIPIAICIYWINNLOKEKKDSHL-----	252
sp O00481 BT3A1_HUMAN	-----PVLLLLLGGAGYFLWQQQEEKKTQFRKKKREQELREMAWSTMKQE---	272
sp P78410 BT3A2_HUMAN	-----PILLLLLLAGASYFLWRQQKEITALSSEIESEQEMKEMGYAATERE---	272
sp O00478 BT3A3_HUMAN	-----PISLLLLLAGASYFLWRQQKEKIALSRETEREREMKEMGYAATEQE---	272
sp Q9UIR0 BTNL2_HUMAN	-----ILVRVGEDIQ-LTCYLSP-----	244
sp Q6UXE8 BTNL3_HUMAN	-----LLGLLCGALCGVVMGM-----	237
sp Q6UX41 BTNL8_HUMAN	-----VLGILCCGLFFGIVGL-----	237
sp Q6UXG8 BTNL9_HUMAN	-----PLLLVLAALALGVLRKQRRSREKLRKQAEKR-----	260
sp A8MVZ5 BTNLA_HUMAN	-----VAMGLVIAGGICIFWKQRQREKNKASLEEERE-----	265

sp Q96PL5 ERMAP_HUMAN	-----PVLVLLIMVCLCLIWKQRRAKEKLLYEHVTEVDNLLS---DHA---KE	175
sp Q16653 MOG_HUMAN	VPCWKITLFFVIVPVLGPLVALIICYNWLHRRLAGQFLEELRNP-----	218
sp Q13410 BT1A1_HUMAN	----FSSKERLLEELKW-----KKATLHAVDVTLDPDTAHPHLFLYE	294
sp Q7KYR7 BT2A1_HUMAN	KEEELQVKEKLQEELRW-----RRTFLHAVDVVLDPDTAHPDLFLSE	317
sp Q8WV5 BT2A2_HUMAN	-----IAQQQLQEELRW-----RRTFLHAADVLDPDTAHPDLFLSE	312
sp Q96KV6 BT2A3_HUMAN	-----MTFNLCLSLAGW-----RRTFLHAANVVLDQDTGHPYLFVSE	289
sp O00481 BT3A1_HUMAN	----QSTRVKLLEELRWRSIQYASRGERHSAYNEWKKALFKPADVILDPKTANPILLVSE	328
sp P78410 BT3A2_HUMAN	----ISLRESLQEELKRKKIQYLTRGEESSSDTNKSA-----	305
sp O00478 BT3A3_HUMAN	----ISLREKLQEELKWRKIQYMARGEKSLAYHEWKMALFKPADVILDPDTANAILLVSE	328
sp Q9UIR0 BTN12_HUMAN	-----KANASMEVRWDRS-----HRYPAVHVYMDGDHVGAGEQMAEY	281
sp Q6UXE8 BTN13_HUMAN	IIVFFKSKGKIQAELDWRR-----KHGQAEALRDARKHAVEVTLDPETAHPKLCVSD	288
sp Q6UX41 BTN18_HUMAN	KIFFSKFQWKIQAELDWRR-----KHGQAEALRDARKHAVEVTLDPETAHPKLCVSD	288
sp Q6UXG8 BTN19_HUMAN	QEKLTAELEKLQTELDWRR-----AEGQAEWRAAQKYAVDVTLDPASAHPSLEVSE	311
sp A8MVZ5 BTNLA_HUMAN	-----	265
sp Q96PL5 ERMAP_HUMAN	KGKLHKAVKKLRSELKLR-----AAANSWRRARLHFVAVTLDPDTAHPKLIILSE	226
sp Q16653 MOG_HUMAN	-----	218
sp Q13410 BT1A1_HUMAN	DSKSVRLDS-RQ-----KLPEKTERFDSWPCVLGRETFTSGRHYWEVEVGDRTDWAIG	347
sp Q7KYR7 BT2A1_HUMAN	DRRSVRRCPF-RH--L-GESVPDNPERFDSQPCVLGRESFASGKHYWEVEVENVIEWTVG	373
sp Q8WV5 BT2A2_HUMAN	DRRSVRRGPY-RQ-----RVPDNPERFDSQPCVLGWESFASGKHYWEVEVENVMVWTVG	365
sp Q96KV6 BT2A3_HUMAN	DKRSVTLDPS-R-----ESIPGNPERFDSQLCVLGQESFASGKHYLEVDVENVIEWTVG	342
sp O00481 BT3A1_HUMAN	DQRSVQRAKE-PQ-----DLPDNPERFNWHYCVLGCESFISGRHYWEVEVGDRKEWHIG	381
sp P78410 BT3A2_HUMAN	-----	305
sp O00478 BT3A3_HUMAN	DQRSVQRAEE-PR-----DLPDNPERFEWRYCVLGCENFTSGRHYWEVEVGDRKEWHIG	381
sp Q9UIR0 BTN12_HUMAN	RGRTVLVSDAIDEGRLTLQILSARPSDDGQYRCLFE-----KDDVYQEASLDLK-VVSLG	335
sp Q6UXE8 BTN13_HUMAN	LK-TVTHRKA-PQ-----EVPHSEKRFTRK-SVVASQGFQAGKHYWEVDVGQNVGWYVG	339
sp Q6UX41 BTN18_HUMAN	LK-TVTHRKA-PQ-----EVPHSEKRFTRK-SVVASQSFGAGKHYWEVDGGHNKRWRVG	339
sp Q6UXG8 BTN19_HUMAN	DGKSVSRRGAPPG-----PAPGHPQRFSEQTALSLERFSAGRHYWEVHVGRSRWFLG	365
sp A8MVZ5 BTNLA_HUMAN	-----	265
sp Q96PL5 ERMAP_HUMAN	DQRCVRLGDR-RQ-----PVPDNPQRFDFVVSILGSEYFTTGCHYWEVYVGDKTKWILG	279
sp Q16653 MOG_HUMAN	-----	218
sp Q13410 BT1A1_HUMAN	VCRE-NVM--K-KGFDPMTPENGFWAVELY-----GNGYWALTPL	383
sp Q7KYR7 BT2A1_HUMAN	VCRD-SVE--R-KGEVLLIPQNGFWTLEMH-----KGQYRAVSSP	409
sp Q8WV5 BT2A2_HUMAN	VCRH-SVE--R-KGEVLLIPQNGFWTLEMF-----GNQYRALSSP	401

sp Q96KV6 BT2A3_HUMAN	ICRD-NVE--R-KWEVPLLPQNGFWTLEMH-----KRKYWALTSL	378
sp O00481 BT3A1_HUMAN	VCSK-NVQ--R-KGWVKMTPENGFWTMGLT-----D-GNKYRTLTEP	418
sp P78410 BT3A2_HUMAN	-----	305
sp O00478 BT3A3_HUMAN	VCSK-NVE--RKKGWVKMTPENGYWTMGLT-----D-GNKYRALTEP	419
sp Q9UIR0 BTNL2_HUMAN	SSPLITVEGQEDGEMQPMCSSDGWFPPHPVWRDMEGKTIPSSSQALTQGSHGLFHVQTL	395
sp Q6UXE8 BTNL3_HUMAN	VCRD-DVD--RGKNNVTLSPPNGYWVLRLT-----T-EHLYFTFNPH	377
sp Q6UX41 BTNL8_HUMAN	VCRD-DVD--RRKEYVTLSPDHGYWVLRLN-----G-EHLYFTLNPR	377
sp Q6UXG8 BTNL9_HUMAN	ACLA-AVP--RA-GPARLSPAAGYWVLGLW-----N-GCEYFVLAPH	402
sp A8MVZ5 BTNLA_HUMAN	-----	265
sp Q96PL5 ERMAP_HUMAN	VCSE-SVS--R-KGKVTASPANGHWLLRQS-----R-GNEYEALTSP	316
sp Q16653 MOG_HUMAN	-----	218
sp Q13410 BT1A1_HUMAN	R--TPLPLAGPPRRVGIFLDYESGDISFYNMNDGSDIYTFSNVTFSGPLRPFFCLW----	437
sp Q7KYR7 BT2A1_HUMAN	D--RILPLKESLCRVGVFLDYEAGDVSFYNMRRSHIYTCPRSAFSVPVRPFFRLG----	463
sp Q8WV5 BT2A2_HUMAN	E--RILPLKESLCRVGVFLDYEAGDVSFYNMRRSHIYTCPRSAFTVPVRPFFRLG----	455
sp Q96KV6 BT2A3_HUMAN	K--WILSLEEPLCQVGIFLDYEAGDVSFYNMRRSHIYTFPHSAFSVPVRPFFSLG----	432
sp O00481 BT3A1_HUMAN	R--TNLKLKPKPKKVGFLDYETGDISFYNAVDSHIHTFLDVSFSEALYPVFRIL----	472
sp P78410 BT3A2_HUMAN	-----	305
sp O00478 BT3A3_HUMAN	R--TNLKLPEPPRKVGIFLDYETGEISFYNATDGSHIYTFPHASFSEPLYPVFRIL----	473
sp Q9UIR0 BTNL2_HUMAN	LRVTNISAVDVTCSISI-----PFL---GEEKIATFSLSGW-----	428
sp Q6UXE8 BTNL3_HUMAN	F--ISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLTCQFEGLLRPYIQH-AMVD	434
sp Q6UX41 BTNL8_HUMAN	F--ISVFPRTPTTKIGVFLDYECGTISFFNINDQSLIYT-LTCRFEGLLRPYIEY-PSYN	433
sp Q6UXG8 BTNL9_HUMAN	R--VALTLRVPPRRLGVFLDYEAGELSFFNVSDGSHIFTFH-DTFSGALCAYFRPRAHDG	459
sp A8MVZ5 BTNLA_HUMAN	-----	265
sp Q96PL5 ERMAP_HUMAN	Q--TSFRLKEPPRCVGIFLDYEAGVISFYNVTKSHIFTFT-HNFSGPLRPFFEPCLHDG	373
sp Q16653 MOG_HUMAN	-----	218
sp Q13410 BT1A1_HUMAN	SSGKKPLTICPIADGPERVTVIANAQDLSKE-----IPLSPMGEDSAPRDADTLH	487
sp Q7KYR7 BT2A1_HUMAN	C-EDSPIFICPALTGANGVTVP EEGTLHRV-GTHQSL-----	499
sp Q8WV5 BT2A2_HUMAN	S-DDSPIFICPALTGASGMVPEEGLKLHRV-GTHQSL-----	491
sp Q96KV6 BT2A3_HUMAN	S-YDSQILICSAFTGASGVTVPEEGWTLHRA-GTHSPQNQFP SLTAMETSPGHLSSHCT	490
sp O00481 BT3A1_HUMAN	TLEPTALTICPA-----	484
sp P78410 BT3A2_HUMAN	-----	305
sp O00478 BT3A3_HUMAN	TLEPTALTICPIPKVESSPD PDLVPDHSLE-----TPLTPGLANESGEPQAEVT	523
sp Q9UIR0 BTNL2_HUMAN	-----	428
sp Q6UXE8 BTNL3_HUMAN	EEKGTPIFICPVSWG-----	449
sp Q6UX41 BTNL8_HUMAN	EQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATT PFLPRG-----	481

sp Q6UXG8 BTNL9_HUMAN	GEHPDPLTICPLPVRGT-----GVPEENDSDTWL---QPYEPAD-----	495
sp A8MVZ5 BTNLA_HUMAN	-----	265
sp Q96PL5 ERMAP_HUMAN	GKNTAPLVICSELHKSEESIVPRPEGKGHAN--GDVSLKVNSSLPPKAPEL-----K	424
sp Q16653 MOG_HUMAN	-----	218

sp Q13410 BT1A1_HUMAN	SKLIPTQPSQGAP-----	500
sp Q7KYR7 BT2A1_HUMAN	-----	499
sp Q8WVV5 BT2A2_HUMAN	-----	491
sp Q96KV6 BT2A3_HUMAN	MPLVEDTPSS---PLVTQENIFQLPLSHPLQTS-APVHLLIRCGFSSSFSGCNYGMESRHR	546
sp O00481 BT3A1_HUMAN	-----	484
sp P78410 BT3A2_HUMAN	-----	305
sp O00478 BT3A3_HUMAN	SLLLPAHPGAEVSPSATTNQ-----NHKLQAR-TEAL-----Y-----	555
sp Q9UIR0 BTNL2_HUMAN	-----	428
sp Q6UXE8 BTNL3_HUMAN	-----	449
sp Q6UX41 BTNL8_HUMAN	-----EM-----	483
sp Q6UXG8 BTNL9_HUMAN	-----PALDWW-----	501
sp A8MVZ5 BTNLA_HUMAN	-----	265
sp Q96PL5 ERMAP_HUMAN	DIILSLPPDLG--P-----ALQELKAPSF-----	446
sp Q16653 MOG_HUMAN	-----	218

sp Q13410 BT1A1_HUMAN	-----	500
sp Q7KYR7 BT2A1_HUMAN	-----	499
sp Q8WVV5 BT2A2_HUMAN	-----	491
sp Q96KV6 BT2A3_HUMAN	ELVVPQLPARKKV	559
sp O00481 BT3A1_HUMAN	-----	484
sp P78410 BT3A2_HUMAN	-----	305
sp O00478 BT3A3_HUMAN	-----	555
sp Q9UIR0 BTNL2_HUMAN	-----	428
sp Q6UXE8 BTNL3_HUMAN	-----	449
sp Q6UX41 BTNL8_HUMAN	-----	483
sp Q6UXG8 BTNL9_HUMAN	-----	501
sp A8MVZ5 BTNLA_HUMAN	-----	265
sp Q96PL5 ERMAP_HUMAN	-----	446
sp Q16653 MOG_HUMAN	-----	218

Figure S2. Percent Identity Matrix created by Clustal 2.1 for human butyrophilin family members

sp Q13410 BT1A1_HUMAN	100.00	49.14	50.33	44.99	50.89	47.78	49.10	32.82	39.07	35.46	40.69	36.51	42.05	35.53
sp Q7KYR7 BT2A1_HUMAN	49.14	100.00	84.52	78.63	44.18	42.51	45.34	31.55	39.72	35.46	39.53	38.52	40.92	29.56
sp Q8WVV5 BT2A2_HUMAN	50.33	84.52	100.00	74.03	46.36	44.57	46.40	31.63	38.64	35.04	38.10	37.35	43.27	30.56
sp Q96KV6 BT2A3_HUMAN	44.99	78.63	74.03	100.00	41.63	39.10	40.47	30.59	36.15	31.81	35.19	37.45	36.63	28.57
sp O00481 BT3A1_HUMAN	50.89	44.18	46.36	41.63	100.00	82.30	85.74	26.65	38.44	36.70	41.18	35.02	37.63	32.02
sp P78410 BT3A2_HUMAN	47.78	42.51	44.57	39.10	82.30	100.00	89.84	33.59	36.02	32.18	37.94	35.41	28.35	33.00
sp O00478 BT3A3_HUMAN	49.10	45.34	46.40	40.47	85.74	89.84	100.00	28.10	38.32	34.84	41.20	37.35	37.97	32.51
sp Q9UIR0 BTNL2_HUMAN	32.82	31.55	31.63	30.59	26.65	33.59	28.10	100.00	24.61	25.19	25.95	31.95	22.37	32.98
sp Q6UXE8 BTNL3_HUMAN	39.07	39.72	38.64	36.15	38.44	36.02	38.32	24.61	100.00	74.33	43.18	29.66	36.36	32.61
sp Q6UX41 BTNL8_HUMAN	35.46	35.46	35.04	31.81	36.70	32.18	34.84	25.19	74.33	100.00	40.72	29.24	34.90	34.24
sp Q6UXG8 BTNL9_HUMAN	40.69	39.53	38.10	35.19	41.18	37.94	41.20	25.95	43.18	40.72	100.00	29.34	37.63	31.03
sp A8MVZ5 BTNLA_HUMAN	36.51	38.52	37.35	37.45	35.02	35.41	37.35	31.95	29.66	29.24	29.34	100.00	31.06	30.54
sp Q96PL5 ERMAP_HUMAN	42.05	40.92	43.27	36.63	37.63	28.35	37.97	22.37	36.36	34.90	37.63	31.06	100.00	38.41
sp Q16653 MOG_HUMAN	35.53	29.56	30.56	28.57	32.02	33.00	32.51	32.98	32.61	34.24	31.03	30.54	38.41	100.00

Figure S3. Phylogenetic Tree created for the human butyrophilin family members by the CLUSTAL Omega (1.2.4) algorithm. This is a Neighbor-joining tree without distance corrections.

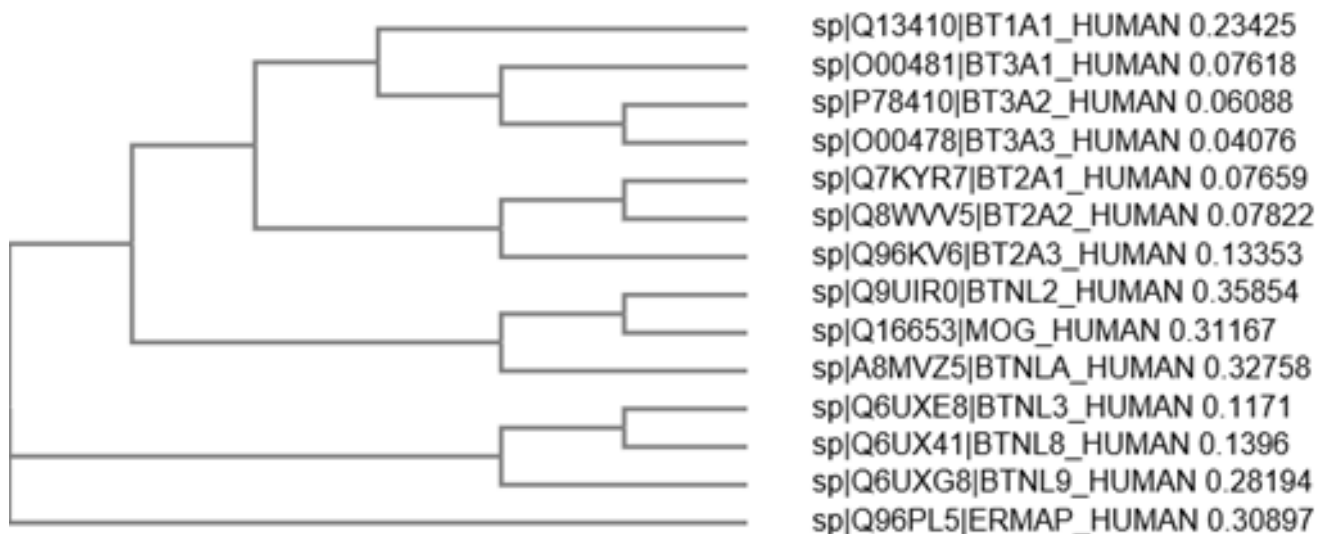


Figure S4. Analysis of the interactivity of the human BTN2A1 (**A**), BTN2A2 (**B**), BTN3A1 (**C**), BTN3A2 (**D**), BTN3A2 (**E**), BTNL2 (**F**), BTNL8 (**G**), BTNL9 (**H**), and MOG (**I**) by STRING platform (<http://string-db.org/cgi/>). STRING produces the network of predicted associations for a particular protein and its interactome. The network nodes are proteins, whereas the edges represent the predicted or known functional associations. There are seven types of evidence used in predicting the associations which are indicated in the resulting network by the differently colored lines, where a red line indicates the presence of fusion evidence; a green line - neighborhood evidence; a blue line – co-occurrence evidence; a purple line - experimental evidence; a yellow line – text mining evidence; a light blue line - database evidence; a black line – co-expression evidence.

