

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q12830	BPTF_HUMAN	Homo sapiens	Nucleosome-remodeling factor subunit BPTF	44.278554	S1617;S1626;T1709;T1712;T1716;T1738;S1741;S1742;T1743;S1749;T1750;T1752;T1753;T1754;T1755;T1756;T1757;T1759;S1762;T2056;S2057;T2058;T2059;S2060;S2081;S2083;T2085;T2086;T2088;T2094;S2098;T2101;T2103;S2140;S2141;T2144;T2148;T2192;S2229;T2230;S2233;T2237;S2239;S2240;T2241;S2246;S2261;T2338;T2342;T2343;T2345;T2346;S2348;T2349;T2350;T2351;T2352	S216;S572;S763;S817;T1064;S1231;S1300;T1303;S1310;S2098;S2465	32119511;34725712;37217939;35132862;21158410;31637018;29249144;32574038;36240223;22661428;30059200;20068230;35289036;33214551;29237092;30379171;34019948;35254053;20305658;37340703;28657654;34931806;27114449;34065225;34846842;30620550;31492838;29351928	MRGRRRGRPPKQPAAPAAERCAPAPP PPPPPTSGPIGGLRSRHRGSSRRGR WAAAQAQEVAPKTRLSFRGSSRRR KPPPPPPAPPSTAPGRGGRGGGGG RTGGGGGGGHLARTTAARRAVNKV VYDDHESEEEEEEDMVEEEEEEE DGDAAEETQDSDEEDMEEDDDDD SDYPEEMEDDDDDASYCTESSFRSH STYSSTPGRRKPRVHRPRSPILEEKD IPPLEFPKSSEDLMPVNEHIMNVIAI YEVLRNFGTVLRLSPFRFEDFCAALV SQEQCTLMAEMHVLLKAVLREED TSNTTFGPADLKDSVNSTLYFIDGM TWPEVLRVYCESDKEYHHVLPYQEA EDYPYPVENVKIKVLQFLVDQFLTTN IAREELMSEGVIQYDDHCRVCHKLG DLLCCECTCSAVYHLECVKPPLEEVPE DEWQCEVCVAHKVPGVTDCAEIQK NKPYIRHEPIGYDRSRRKYWFLNRR LIIEDTENENEKKIWIYYSTKVQLAE LIDCLDKDYWEAELCKILEEMREEIH RHMDITEDLTNKARGSNKSFLAAAN EEILESIRAKKGDIDNVKSPEETEKD KNETENDSKDAEKNREEFEDQSLSE KDSDDKTPDDDDPEQKSEEPTEVGD KGNVSANLGDNTTATSEETSPSE GRSPVGCSETPDSSNMAEKKVASE LPQDVPEEPNKTCESSNTSATTTSIQ PNLENSNSSSELNSSQSESAKAADD PENGERSHTPVSIQEEIVGDFKSEK SNGELSESPGAGKGAGSTRIITRLR NPDSKLSQLKSQQVAAAHEANKLF KEGKEVLVVNSQGEISRLSTKKEVIM KGNINNYFKLGQEGKYRVYHNQYST NSFALNKHQHREDHDKRRHLAHKF CLTPAGEFKWNGSVHGSKVLITISTL RLTITQLENNIPSSFLHPNASHRA NWKAVQMCKSPREFALALALECA VKPVVMLPIWRESLGHTRLHRMTSI EREKEKVKKKEKKQEEEEETMQQA TWVKYTFPVKHQVWVKQKGEEYRVT GYGGWSWISKTHVYRFVPKLPNGTN VNYRKSLEGTKNMMDENMDESDK RKCSRSPKKIKIEPDSEKDEVKGSDA AKGADQNEMDISKITEKKDQDVKEL LDSDSKPKKEEPMEVDDDMKTES HVNCQESSQVDVVNVSEGFHLRTSY KKKTKSSKLDGLLERRIKQFTLEEKQ RLEKIKLEGGIKGIGKTSTNSSKNLS ESPVITKAKEGCQSDSMRQEQSPNA NNDQPEDLIQGCSESDSSVLRMSDP SHTTNKLYPKDRVLDDVSIRSPETKC PKQNSIENDIEKVSIDLASRGQEPSK SKTKGNDFIDDSKLASADDIGTLIC KNKKPLIQEESDTIVSSSKSALHSSV PKSTNDRDATPLSRAMD FEGKLGCD SESNSTLENSSDTVSIQDSSEEDMIV QNSNESISEQFRTREQDVEVLEPLK CELVSGESTGNCEDRLPVKGTEANG KKPSQQKLEERPVNKCSQIKLKN TTDKNNENRESEKKGQRTSTFQIN GKDNKPKIYLKGECLKEISESRVSG NVEPKVNNINKIIPENDIKSLTVKES

AIRPFINGDVIMEDFNERNSSSETKS  
HLLSSDAEGNYRDSLETLPSTKES  
DSTQTTTPSASCPESENSVNQVEDME  
IETSEVKVTSSPITSEEEENLNSNDFI  
DENGLPINKNENVNGESKRRTVITE  
VTTMTSTVATESKTVIKVEKGDQTV  
VSSTENCAKSTVTTTTTTVTKLSTPS  
TGGSDIISVKEQSKTVTTTTVTDLSL  
TTGGTLVTSMTVSKEYSTRDKVKLM  
KFSRPKTRSGTALPSYRKFVTKSSK  
KSIFVLPNDDLKKLARKGGIREVPYF  
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PETPKETPTPQRKGLRSSALRPKRPE  
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FAERVEKEKAQAVEQQAKRLEQQK  
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LQIEVQEELKRDLEKKEKDLMLQA  
QATAVAAPCPPVTPAPPAPPAPPSP  
PPPAVQHTGLLSTPTLPAASQKRKR  
EEEKSSSKSKKKMISTTSKETKK  
DTKLYCICKTPYDESKFYIGCDRCQN  
WYHGRCVGLQSEALIDEYVCPQC  
QSTEDAMTVLTPLEKDYEGLKRVL  
RSLQAHKMAWPFLEPVDNDAPDY  
YGVIKEPMDLATMEERVQRRYKEL  
TEFVADMTKIFDNCRYNPSDSPFY  
QCAEVLESFFVQKLGFKASRSHNN  
KLQSTAS