

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
Q12830	BPTF_HUMAN	Homo sapiens	Nucleosome-remodeling factor subunit BPTF	44.796723	S1617;S1626;T1709;T1712;T1716;T1738;S1741;S1742;T1743;S1749;T1750;T1753;T1754;T1755;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	S216;S572;S763;S817;T1064;S1231;S1300;T1303;S1310;S2098;S2465	27114449;35289036;31637018;29237092;32574038;33214551;34846842;21158410;34725712;35254053;31492838;32119511;22661428;29249144;20068230;30379171;36240223;30620550;29351928;35132862;30059200;34019948;34065225;28657654;20305658;34931806	MRGRRGRPPKQPAAPAAERCAPAPP PPPPPTSGPIGGLRSRHRGSSRGR WAAQAQEVAPKTRLSFRGGSSRR KPPPPPPAPPSTAPGRGGRGGGGG RTGGGGGGGHLARTTAARRAVNKV VYDDHESEEEEEEDMVSEEEEEEE DGDAAEETQSEDEDEMEEDDDDD SDYPEEMEDDDDDASYCTESSFRSH STYSSTPGRRKPRVHRPRSPILEEKD IPPLEFPKSSEDLMPVNEHIMNVIAI YEVLRNFGTVLRLSPFRFEDFCAALV SQEQCTLMAEMHVLLKAVLREED TSNTTFGPADLKDSVNSTLYFIDGM TWPEVLRVYCESDKEYHHVLPYQEA EDYPYPVENVKIKVLQFLVDQFLTTN IAREELMSEGVIQYDDHCRVCHKLG DLLCCETCSAVYHLECVKPPLEEVPE DEWQCEVCVAHKVPGVTDCAEIQK NKPYIRHEPIGYDRSRRKYWFLNRR LIIEDTENENEKKIWIYYSTKVQLAE LIDCLDKDYWEAELCKILEEMREEIH RHMDITEDLTNKARGSNKSFLAAAN EEILESIRAKKGDIDNVKSPEETEKD KNETENDSKDAEKNREEFEDQSLSE KDSDDKTPDDDDPEQKSEEPTEVGD KGNSVSANLGDNTTATSEETSPSE GRSPVGCSETPDSSNMAEKKVASE LPQDVPEEPNKTCESSNTSATTTSIQ PNLENSNSSELNSSQSESAKAADD PENGERSHTPVSIQEEIVGDFKSEK SNGELSESPGAGKGAGSTRIITRLR NPDSKLSQLKSQQVAAAHEANKLF KEGKVLVNSQGEISRLSTKKEVIM KGNINNYFKLGQEGKYRVYHNQYST NSFALNKHQHREDHDKRRHLAHKF CLTPAGEFKWNGSVHGSKVLITISTL RLTITQLENNIPSSFLHPNASHRA NWKAVQMCKSPREFALALALECA VKPVVMLPIWRESLGHTRLHRMTSI EREKEKVKKKEKKQEEEEETMQQA TWVKYTFPVKHQVWKQKGEYRVT GYGGWSWISKTHVYRFVPLPGNTN VNYRKSLEGTKNMMDENMDESDK RKCSRSPKKIKIEPDSEKDEVKGSDA AKGADQNEMDISKITEKKDQDVKEL LDSDSKPKKEEPMEVDDDMKTES HVNCQESSQVDVVNVSEGFHLRTSY KKKTKSSKLDGLLERRIKQFTLEEKQ RLEKIKLEGGIKGIGTSTNSSKNLS ESPVITKAKEGCQSDSMRQEQSPNA NNDQPEDLIQGCSESDSSVLRMSDP SHTTNKLYPKDRVLDDVSIRSPEKTC PKQNSIENDIEKVSIDLASRGQEPSK SKTKGNDFIDDSKLASADDIGTLIC KNKKPLIQEESDTIVSSSKSALHSSV PKSTNDRDATPLSRAMDFEGKLGCD SESNSTLENSSDTVSIQDSSEEDMIV QNSNESISEQFRTRREQDVEVLEPLK CELVSGESTGNCEDRLPVKGTEANG KKPSQQKLEERPVNKCSQDIKLN TTDKNNENRESEKKGQRTSTFQIN GKDNKPKIYLKGECLKEISESRVVS NVEPKVNNINKIIPENDIKSLTVKES

AIRPFINGDVMEDFNERNSSSETKS  
HLLSSDAEGNYRDSLETLPSTKES  
DSTQTTTPSASCPESSNSVNQVEDME  
IETSEVKVTSSPITSEEEESNLSNDFI  
DENGLPINKNENVNGESKRRTVITE  
VTTMTSTVATESKTIVIKVEKGDQTV  
VSSTENCAKSTVTTTTTTVTKLSTPS  
TGGSDIISVKEQSKTVTTTTVTDLSL  
TTGGTLVTSMTVSKEYSTRDKVKLM  
KFSRPKTRSGTALPSYRKFVTKSSK  
KSIFVLPNDDLKKLARKGGIREVPYF  
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EKQAACKRKRRESVEQKRKQKQATK  
LSALLFKHKEQLRAEILKRALDKD  
LQIEVQEELKRDLEKKEKDLMLQA  
QATAVAAPCPPVTPAPPAPPAPPSP  
PPPAVQHTGLLSTPTLPAASQKRKR  
EEEKSSSKSKKKMISTTSKETKK  
DTKLYCICKTPYDESKFYIGCDRCQN  
WYHGRCVGLQSEALIDEYVCPQC  
QSTEDAMTVLTPLEKDYEGLKRVL  
RSLQAHKMAWPFLEPVDNDAPDY  
YGVIKEPMDLATMEERVQRRYKEL  
TEFVADMTKIFDNCRYNPSDSPFY  
QCAEVLESFFVQKLGFKASRSHNN  
KLQSTAS