

UniprotKB ID	Entry name	organism	full name	oglnacscore	oglnac sites	phosphorylation sites	PMIDS	sequence
Q9UPA5	BSN_HUMAN	Homo sapiens	Protein bassoon	23.165899	S286;S1322;S1328;S1375;T1380;T1383;T1384;S1455;S1457;T1501;S1515;T1560;S1563;S1646;S1647;T1651;S1652;T1663;T1680;S1767;T1783;T1819;S1912;T1916;S1922;S1927;S1937;S1938;S1982;S1983;T1987;S2012;S2018;S2022;S2024;S2041;T2043;S2086;S2091;T2093;T2094;S2107;S2183;T2184;T2197;S2230;T2234;T2239;S2240;S2272;S2297;T2313;T2314;T2315;S2534;T2676;T2691;T2809;S2810;S2814;T2896;T2932;T2936;S3013;S3015;T3122;T3127;S3149;S3186;S3347;S3394;S3499;T3807;T3829;T3912;S3916	S145;S244;S248;S970;S1040;S1041;S1090;T1092;S1098;S1104;S1226;S1477;S1486;S1488;S1985;S2041;S2570;T2587;T2614;S2802;S2851;S2857;S3013;S3291;S3373	28657654;30379171;38253038;20563614;37340703	MGNEVSLEGGAGDGPLPPGGAGPG PGPGPGGAGKPPSAPAGGGQLPAA GAARSTAVPPVPGPGPGPGPGPG STSRRLDPKPEPLGNQRAASPTPKQA SATTPGHESPRETROAGPAGQEQADG PRRTLQVDSRTQSRGRSPVSPDRG STPTSPYVQIAPLPSSTLCPICKTS DLTSTPSQPNFNCTQCHNKVCNQ CGFNPNPHLTQVKEWLCCLNCQMQR ALGMDMTTAPRSKSSQQLHSPALSP AHSFAKQPLGKPDQERSRGPGGPQP GSRQAETARATSVPGPAQAAAPPEV GRVSPQPPQPTKPTAEP RPPEGEAP AKSATAVPAGLGATEQTQEGLTGKL FGLGASLLTQASTLMSVQPEADTQG QPAPSKGTPKIVFNDASKEAGPKPLG SGPGPGPAPGAKTEPGARMGPGSGP GALPKTGGTSPKHGRAEHQAASKA AAKPKTMPKERAICPLCQAEALNVGS KSPANYNCTTCRLQVCNLCGFNPT PHLVEKTEWLCCLNCQTKRLLGSLG EPTPLPPPTSQPPV GAPHRASGTSP LKQKGPQGLGQPSGLPAKASPLST KASPLPSKASPQAKPLRASEPSKTPS SVQEKTRVPTKAEMP KPPPETTPT PATPKVKSGVRRRAEPATPVVKAVPEA PKGGEAEDLVGKPYSDASRSQSL SDTGYSSDGISSSQSEITGVVQQEVE QLDSAGVTGPHPPSPSEIHKVGS RPLLQAQGLAPSERSKPLSSGTGEE QKQRPHSLSITPEAFDSDELEDILE EDED SAEWRRRREQD TAESSDDF GSQLRHDYVEDSSEGLSPLPPQPP ARAAELTDEDFMRRQILEMSAEEDN LEEDDTATSGRGLAKHGTQKGGPRP RPEPSQEPALPKRRLPHNATTGYE ELLPEGGS AEATDGSGLTQGG LRRF KTIELNSTGSGHELDLGGQPDPSL DREPELEMESLTGSPEDRSRGEHSS TLPASTPSYTSGTSP TSLSSLEEDSDS SPSRRQRLEEAKQQRKARHRSHG LPTIEDSSEEEELREEEELLREQEK REVEQQRIRSTARKTRRDKEELRAQ RRRERSKTPPSNLSPIEDASPTIELR QAAEMEELHRSSCSEYSPSPSLDSE AEALDGGPSRLYKSGSEYNLPTFMS LYSPTETPSGSSTTPSSGRPLKSAEE AYEEMMRKAELLQRQGGQAAGARG PHGGPSQPTGPRGLGSFEYQD TDR EYQAAQPA AEGTPASLGA AVYEEIL QTSQSIVRMRQASSRDLAFAEDKKK EKQFLNAESAYMDPMKQNGGGLTP GTSPTQLAAPVSFSTPTSSDSSGGRV IPDVRVTQHFAKETQDPLKLHSSPAS PSSASKEIGMPFSQGPATTA VAP CPAGLPRGYMTPASPAGSERSPSPSS TAHSYGHSPPTANYGSQTEDLPQAP SGLAAAGRAAREKPLSASDGE GGT QPSRAYSIFASSPPLSPSPSPSEPTF SPGKMGPRATAEFSTQTPSPAPASD MPRSPGAPTPSPMVAQGTQTPHRPS

TPRLVWQESSQEAPFMVITLASDAS  
SQTRMVHASASTSPLCSPTTETQPTT  
HGYSQTTPPSVSQLPPEPPGPPGFPR  
VPSAGADGPLALYGGALPAENISL  
CRISSVPGTSRVEPGPRTPGTAVVDL  
RTAVKPTPIILTDQGMDLTSLAVEAR  
KYGLALDPIGRQSTAVQPLVINLNA  
QEHTFLATATTVSITMASSVFMAQQ  
KQPVVYGDYQSRDLDFGQGGGSPVC  
LAQVKQVEQAVQTAPYRSGPRGRPR  
EAKFARYNLPNQVAPLARRDVLITQ  
MGTAQSIGLKPVPPEPGAEPHRAT  
PAELRSHALPGARKPHTVVVVQMGEG  
TAGTVTTLLPEEPAGALDLTGMRPES  
QLACCDMVYKLPFGSSCTGTFHPAP  
SVPEKSMADAAPPQSSSPFYGPRD  
PEPPEPPTYRAQGVVGGPHEEQRP  
YPOGLPGRLYSSMSDTNLAEAGLNY  
HAQRIGQLFQGPGRDSAMDLSLKH  
SYSLGFADGRYLGQGLQYGSVTDLR  
HPTDLLAHPLMRRYSSVSNISYDH  
RYGPRGDAVGFQEAASLAQYSATTAR  
EISRMCAALNSMDQYGGRHGSGGG  
GPDLVQYQPQHGPGLSAPQSLVPLR  
PGLLGNPTFFEGHPSPGNLAQYGA  
AGQGTAVRQLLPSTATVRAADGMIV  
STINTPIAATLPITTPASVLRPMVVRG  
GMYRYPYASGGITAVPLTSLTRVPMIA  
PRVPLGPTGLYRYPAPSRFPIASSVPP  
AEGPVYLGKPAAAKAPGAGGSRPE  
MPVGAAREEPLPTTTPAAIKEAAGAP  
APAPLAGQKPADAAPGGGSGALS  
PGFEKEEASQEERQRKQEQQLLQLE  
RERVELEKLRQLRLQEELERERVEL  
QRHREEEQLLVQRELQELQTIKHHV  
LQQQEEERQAQFALQREQLAQQL  
QLEIQQLQQQLQQQLEEQKQRQK  
APFPAACEAPGRGPPLAAAELAQNG  
QYWPLTHAAFIAMAGPEGLGQPRE  
PVLHRGLPSSASDMSLQTEEQWEAS  
RSGIKKRHSMPRLRDACELESSTEP  
CVVRIADSSVQTDDEDEDGESRYLLSR  
RRRARRSADCSVQTDDEDSAWEQ  
PVRRRRSRLPRHSDSGSDSKHDATA  
SSSSAAATVRAMSSVGIQTISDCSVQ  
TEPDQLPRVSPAHIHITAATDPKVEIVR  
YISAPEKTGRGESLACQTEPDGQAO  
GVAGPQLVGPTAISPYLPGIQTIVTGP  
LGRFEKPPKSPQVLYSPVSPHRL  
LDTSFASSERLNKAHVSPQKHFTAD  
SALRQQTLPKMTLQRSLSDPKPL  
SPTAEESAKERFSLYQHQQGLGSQV  
SALPPNSLVRKVKRTLPSPPPEEAHL  
PLAGQASPQLYAASLLQRGLTGPTTV  
PATKASLLRELDRLRLVEHESTKLR  
KKQAELEDEEKEIDAKLYLELGITQ  
RKESLAKDRGGRDYPPRLRGLGEHRD  
YLSSELNQLRLQGCTTPAGQFVDF  
PATAAAPATPSGPTAFQPPRFQPPAP  
QYSAGSGGPTQNGFPAHQAPTYPGP  
STYPAPAFPPGASYPAPGLPNQAF  
RPTGHYAGQTPMPTTQSTLFPVPAD  
SRAPLQKPRQTSLADLEQKVPTNYE

VIASPVPMSSAPSETSYSQPAVSSG  
YEQGVPEVPRAGDRGSVSQSPAPT  
YPSDSHYTSLEQNVPRNYVMIDDISE  
LTKDSTSTAPDSQRLEPLGPGSSGRP  
GKEPGEVGLDGPPLCCYARGEEE  
SEEDSYDPRGKGGHLRSMESNGRP  
ASTHYYGSDYRHGARVEKYGPGPM  
GPKHPSKSLAPAAISSKRSKHKRQG  
MEQKISKFSPIEEAKDVESDLASYPP  
PAVSSSLVSRGRKFQDEITYGLKKNV  
YEQQKYGMSSRDAVEDDRIYGGSS  
RSRAPSAYSGEKLSHDFSGWGKGY  
EREREAVERLQKAGPKPSSLSMAHS  
RVRPMPRSQASEEESPVSPGRPRP  
AGGPLPPGGDTCPQFCSSHSMPDVQ  
EHVKDGPRAHAYKREEGYILDDSHC  
VVDSEAYHLGQEETDWFDPKPRDA  
RSDRFRHHGGHAVSSSSQKRGPAR  
HSYHDYDEPPEEGLWPHDEGGPGR  
HASAKEHRHGDHGRHSGRHTGEEP  
GRRAAKPHARDLGRHEARPHSQPSS  
APAMPKKGQPGYPSSAEYSQPSRAS  
SAYHHASDSKKGSRQAHSQPAALQS  
KAEFQAQPQLQGRQAAPGQQSQSP  
SSRQIPSGAASRQPQTQQQQGLGL  
QPPQALQTARLQQSQPTTRGSAP  
AASQPAGKPPGPSTATGPPAGPP  
RAEQTNKSGTAKAPQQGRAPQAQP  
APGPGPAGVKAGARPGGTPGAPAGQ  
PGADGESVFSKILPGGAAEQAGKLTE  
AVSAFGKKFSSFW