

UniprotKB ID	Entry name	organism	full name	oglcnacscore	oglcnac sites	phosphorylation sites	PMIDS	sequence
O88737	BSN_MOUSE	Mus musculus	Protein bassoon	51.743608	T308;T329;T412;T1354;S1373;T1384;S1386;T1394;T1395;S1407;S1414;T1417;S1418;S1419;S1423;T1429;S1445;S1472;T1506;T1513;T1517;T1537;S1553;S1655;T1666;T1683;S1707;S1772;T1788;T1824;S1932;T1934;S1943;T1962;S1987;S1988;S1990;S2027;S2029;S2058;S2067;S2068;S2070;S2091;S2096;T2098;T2099;S2122;S2141;S2177;S2188;T2189;S2201;T2210;S2295;S2316;T2317;T2318;S2352;T2488;T2514;T2524;T2662;T2685;S2694;T2700;T2703;S2787;T2818;T2941;T2945;S3158;T3179;T3187;S3197;S3216;T3222;S3830;T3842;T3878	S142;S241;S245;S980;S1050;S1051;S1100;T1102;S1108;S1114;S1236;S1482;S1491;S1493;S1990;S2046;S2578;T2595;T2622;S2811;S2860;S2866;S3022;S3301;S3382	36757814;22645316;33300544;19458039;34678516;26192747;35822049;22826440;22517741	MGNEASLEGGAGEGGLPPGSGGLG PGPGAGKPPSALAGGGQLPVGAAR AAGPPTPGLGPVPGPGPGPGSV RRLDPKEPLGSQRTTSPTPKQASATA PGRESPRETRAQGPSGQEAESPRRT LQVDSRTQRSGRSPSVSPDRGSTPT SPYSVQFIAPLPSSTLCPIKCTSDLTS TPSQPNFNTCTCQHNKVCNQCGFN PNPHLTQVKEWLCCLNCQMQRALG MDMTTAPRSKSSQQQLHSPALSPA HSPAKQPLGKPEQERSPRGPGATQSG PRQAEAAARATSVPGPTQATAPPEVG RVSPQPPLSTKTPSTAEPRPPAGEAQG KSATTVPSPGLGAGEQTQEGLTGKLF GLGASLLTQASTLMSVQPEADTQGO PSPSKGQPKIVFSDASKEAGPRPPGS GPGPGPTPGAktePGARMGPGSGPG ALAKTGGTASPKHGAEHQAAASKAA AKPKTMPKERASACPLCQAEINMG SRGPANYNTCTACKLQVCNLCGFNP TPHLVEKTEWLCCLNCQTKRLEGLS GEPAPLPLPTPQQPPAGVPHRAAGA APLKQKGPQGLGQPSGLPAKASPO ATKASPQATKASPQATKASPQTTKAS PQAKPLRATEPSKTSSSAQEKKTVTS AKAEPVPPPPETTVPPTPKAKSGV KRTDPATPVVKPVPEAPKGGAEPEV PKPYSQDLRSRPSQLSDTYSSDGV SSQSEITGVVQVEVEQLDSAGVTGP RPPSPSELHKVGSRLRPSLEAQAVAP SAEWSKPPRSSSSAVEDQKRRPHSL SITPEAFDSDEELGDILEEDDSLAWG RQREQQDTAESSDDFGSRLRHDYV EDSSEGLSPLPPQPPARADMTDEE FMRRQILEMSAEEDNLEEDDTAVSG RGLAKHSAQKASARPRPSSQEPKR RLPHNATTGYEELLSEAGPAEPTDSS GALQGGLRRFKTIELNSTGSGYHEL DLGQGPDPNLDREPELEMESLTGSP EDRSRGEHSSTLPASTPSYTSPTSPT SLSSLEEDSDSSPSRRQRLEEAKQO RKARHRSHGPLLPTIEDSSEEEELRE EEELLREQEKMREVEQQRIRSTARK TRRDKEELRAQRRRERSKTPPSNLS PIEDASPEELRQAAEMEELHRSSC SEYSPSPSLDSEATLDGGPTRLYKS GSEYNLPAFMSLYSPTETPSGSSTTP SSGRPLKSAEEAYEDMMRKAEMLO RQGGQVAGARGPHGGPSQPTGPRS QGSFEYQDTQDHDYGGRASQPVAES TPAGLGAAYVEEILQTSQSIARMRQA SSRDLGFTEDKKKEKQFLNAESAYM DPMKQNGGPLTPGTSPTQLAAPVSF STSTSSDSSGGRVDPVVRTQHFQAKE PQDPLKLHSSPVSSTLTSKEVGMFT SQGPGSPATTASPTRGYMTPTSPAGS ERSPSTSTIHSYGQPPTTANYGSQT EELPHAPSGPPGSGRAPREKPLSGG DSEVGAPQPSRGYSYFTGSSPPLSPS TPSESPTFSPGKLGPRATAEFSTQTP SLTLSSDIPRSPGPPSPMVAQGTQTP

HRPSTPRLVWQSSQEAPIMVITLAS
DASSQTRMVHASASTSPLCSPTDSQ
PTSHSYSQTTPPSASQMPSEPAGPP
GFPRAPSAGTDGFLALYWGALPAE
NISLCRISSVPGTSRVEPGPRPGTA
VVDLRTAVKPTPIILTDQGMDLTSLA
VEARKYGLALDPVSGRQSTAVQPLVI
NLNAQEQTHTFLATATTVSITMASS
VLMAQQKQPVVYGDPFQSRDFGQ
GSGSPVCLAQVKQVEQAVQTAPYRG
GPRGRPREAKFARYNLPNQVTPLAR
RDILITQMGTAAQGVGLKPGVPEPGA
EPHRATPAELRSHAPPGTRKPHTVV
VQMGEAGTAVTTLPEEPAGALDL
TGMRPESQLACCDMVYKFPFGSSCT
GTFHPAPSADKSVTDTALPGQSSG
PFYSPRDPEPPEPLTFRTQGVVGGP
HEEQRFYPQGLPGRLYSSMSDTNLA
EAGLNYHAQRLGQLFQGPGRDSAV
DLSSLKHSYSLGFADGRYLGQGLQY
GSFTDLRHPTDLLSHPLPLRRYSSVS
NIYSDHRYGPRGDAVGFQEASLAQY
SATTAREISRMCAALNSMDQYGGRR
HGSGSGGPDVQYQPQHGPGLSAP
QGLAPLRSGLGNPTYPEGQPSPGN
LAQYGPAASQATAVRQLLPSTATVRA
ADGMIYSTINTPIAATLPITTQPASVL
RPMVIRGMYRFPYVSGGVTAVPLTSL
TRVPMIAPRVPLGPAGLYRYPAPRFPI
ASSVPPAEGPVYLGKPAAKASGAG
GPPRPELPAGVAREEPFSTTAPAVIK
EAPVAPAPGPAPPPGQKPAGEAVA
GSGSGVLSRPASEKEEASQEDRQRK
QQEQLLQLERERVELEKLRQLRLQE
ELERERVELQRHREEEQLLVQRELQ
ELQTIKQHVLLQQQEEERQAQFALQR
EQLAQQLQLLEQIQQLQQQLQLQLE
EQKQRQKAPFPATCEAPSRGPPPA
TELAQNGQYWPPLTHAAFIAVAGTE
GPGQPREPVLHRGLPSSASDMSLQT
EEQWEAGRSGIKKRHSMPRLRDAC
EPESGPDPTVRRRIADSSVQTDDEEG
EGRYLVTRRRRTRRSADCSVQTDDE
DNADWEQPVRRRRSRLSRHSDSGS
DSKHDATASSTTAAATARAMSSVGI
QTISDCSVQTEPEQLPRVSPAIHITAA
TDPKVEIVRYISAPEKTGRGESLACQ
TEPDGQAQGVAGPQLIGPTAISPYLP
GIQIVTPGALGRFEKPKPDPLEIGYQ
AHLPPESLSQLVSRQPPKSPQVLYSP
VSPLSPHRLDTSFASSERLNKAHV
SPQKQFIADSTLRQOTLPRPMKTLQ
RSLSDPKPLSPTAESAERFSLYQH
QGGLGSQVSALPPNGLVRKVKRTL
SPPPEEAHLPLAGQVPSQLYAASLLQ
RGLAGPTTVPATKASLLRELDRLRL
VEHESTKLRKKQAELEEEKEIDAK
LKYLELGITQRKESLAKDRGGRDYP
LRGLGEHRDYLSSELNQLRLQGCT
TPAGQYVDYPASAAPVATPSGPTAFQ
QPRFPPAAPQYTAGSSGPTQNGFPA
HQAPTYYTGPSTYPAPTYPPGTGYP
PGLPSQPAFHPTGHYAAPTMPPTTQ
SAPFPVQADSRAAHQPRQTSLADL

EQKVPTNYEVIGSPAVTMSSAPPETG
YSGPAVSGSYEQKCAPEHPRGSDRS
SVSQSPAPTYPSDSHYTSLEQNVPR
NYVMIDDISELTKDSTPTASESORLE
PLGPGGVSGRPGKDPGEPAVLEGPT
LPCCYGRGEESEEDSYDPRGKSGH
HRSMESNGRPPSTHYYGDSYRHHGA
RADKYGPGPMGPKHPSKSLAPAAIS
SKRSKHRKQGMEQKISKFSPIEEAK
DVESDLASYPPPTVSSSLTSRGRKFQ
DEITYGLKKNVYEQQRYYGVSSRDA
AEEDERMYGSSSRSMASAYSGEKL
SSHDYSSRGKGYERERDTAERLQKA
GSKPSSLMAHGRARPPMRSQASE
EESPVSPLGRPRPAGGALPPGDTCP
QFCSSHSMPDVQEHVKDGPRAHAY
KREEGYMLDDSHCVVSDSEAYHLG
QEETDWFDPKPRDARSDFRHHGGH
TVSSSQKRGPARHSYHDYDEPPEEG
LWPHDEGGPGRHTSAKEHRHSDH
GRHSGRHAGEEPGRRAAKPHARDM
GRHEARPHPQASPAPAMQKKGQPG
YPSSADYSQSSRAPSAHHASESKK
GSRQAHTGPSALQPKADTQAQPQM
QGRQAAPGPQQSQPPSSRQTPSGTA
SRQPQTQQQQQQQQQQGLGQQAP
QQAPSQARLQPQSQPTRGTAPAAS
QPAGKPQPGPTTAPGPQAGPPRAE
QASSKPPAAKAPQQGRAPQAQTTP
GPGPAGAKPGARPGGTPGAPASQPG
AEGESVFSKILPGGAAEQAGKLTEAV
SAFGKKFSSFW