

Predicted Sequences

Aedes aegypti SID (Refseq: XP_001658947.1)

Aedes aegypti RBD (Refseq: XP_001661740.1)

Anolis carolinensis SBP2

MASERETSOGIKLSAEVKPFVPKYAAVTVAWSEPSEACVFPRYYTTCYPYVODPSVDKHOVYTO
DLPWDSTSTLPHYVSONVMGCTSLGEYTSSPYTPDAAPNVYTVPNFRSENNNSKLFSSSSROGRD
YAKOTPVSRKEAAYHPRRRPRDFEPKLESKRPDGSDSPNRSTESSSYTALHGRNPIKSEPAFEV
NLSDFPKLOSTRSCNLLNFOKOTWGPLGSAEGDKMPRKPEKAVSALVTKEGEECLKRNLPTRP
FTSPDPDGVSOVHLDYFTETPKSCATVLSOTPKRTVSTPAASPSTNHYENKKGQGVLEDRKSEP
KGNASDSEPEEIVEKKKKKKRNKKKAKASSETENVPNKSIIYQEPPIREVQIFIFLVISRFLCS
LPGITGQFGVCRNSGITMAYNETSKSGGKKSHLPVOLDLGNMLAALEOKOOAEKTKHSPKPVVL
SVGGTVTLPSKEPMNOTKNOQLNOGNSPHNPLDSSSPLIKKGKOREVPKAKKPTSLKKIILRER
EORKOOHLLLEOMATPKDSDAAODAESTAENOGYSEDNKAESLEDTSIDPDILAODGPEVDLKCT
ELNGSYTESVLDPVOLKSNLPKIHRRFRDYCTOVLSKEVDSCVTDLLKELVRFODRLYOKDPV
KAKTKRRLVMGLREVLKHLKLKKLKCVIISPNCCKIQSKGGLDETLHLIIDSACEONIPFVFAL
NRKALGRCLNKAVPVSVVGIFSYDGAODYFHKMVELTMEAROAYKDMISALERESAEEESGSDC
TPSKNPYSESRLDTEVEVPPPESEEDVPDYKIWKOKLEEEYKPYMLELEKOLTAEMLEPMGFEEP
Q

Anolis carolinensis SBP2L

NVKLSAEVEPFIPQKKGPDLSLMPMALPNENGGVNGVEAAPIPSYLITCYPFVQENQSNRQLPL
YNNDIRWQQPNPNPAGPYLAYPILSAQPPVSTEYTTYQLMPAPCAQVMGFYHFPAPYSAPFQT
ASAMNTVTTECTDRPTQPNQVFPMCSQRSRSASRGSIQKQQQPLQTHIKSKRPPVKSVATQKE
TCASGPETRPKIVLLVDACQQTDFPSEIASKSLSSESMSTMHWKPKTRRRRSSHPAESSEQGAS
EADIDSDSGYCSPKHSNQAAVTSRSVESAAGNILEPSVHPAGATWANVSSQATQKKPWMERTP
AFSRGGRQAEQHNSSQDEEFPELNSDSGNSKGGNMQLKNAPKVLDDLPENSPINIVQTPIPIT
TSVPKRAKSQKKKALAAALATAQEYSEISMEQRKLQEAVSKAAGKKSKTPVQDLGDMLAALEK
QQQAMKARQITNTRPLSYTVGNAAPFHTKESTNRKSLAKGQPSVGCLNPLDSTSPKVKGKERE
LSKLKRPTALKKIIILKEREKKGRLSVDHTIVGADEEQEVDLNLTPNQSEELASQEEPGLSVPS
DTSLSPASQNSPYCMTVPVSQGPASSGIGSPMASSTITKIHSKRFRREYCNQVLSKEIDEVTLTLL
LQELVSFQEQIYQKDPMRKAKRRLVMGLREVTKHMKLSKIKCVIISPNCCKIQSKGGLDEALY
NVIAMAREQEIPFVFALGRKALGRCVNKLVPVSVVGIFNYSGAENLFNKLVSLEEARAYRDM
VAAMEQEQQEALKNVKKVPHMHGHSRNPASAASISFCSVISEPISEVNEKEYETNWRSMVETSD
GLEASENEREASFSAVPEKPGNSNKVIVNKLSLAAGVVTVSAQVKAPSGKEEVKPDNDLEW
ASQQSTDTGSLDGSCRDILNSSMTSTTSTLVPGMLEEEDEDEDEDDYTHEPISEEVLNSRI
ESWVSETQRTMETLQLGKSLSGGEDDNAEQSEDEELETPEQVESVVESEEWTAEKHSNKAQQKP
AVSTSLDTPMDSNYIP

Anopheles gambiae SBP2

PAVPGAPRAAMEQETHNRPPQQPQQHQPIPHQSDGEKLSARKARKEAEROKKOAKKYEEOLKKI
RGPKSOKLOI IDESFLEKYRHVOSLPPGPTLTKTKR SKKAPT DVVOINLSECIREOLAGGERME
PKPIVPIVPOOPLLLLHKGKOREVPKEKKLTRLKKDI IRSRTEKGAPGDGOOSAGNAGGAQOPV
PAEGGKGANGLLKSSEATSPSGGGAVDSPFLKAIERCCINDGPPPSRDSSEYONGFPSLRVSA
AVSRPTALRHSRNF RPYCDHFISDELRELAEDVVVKLFSFOSKAYAKNPIKAVANKRFVVG FNE
VLKLELRKVRLVLIAPDLEPNETIDOMVANVKMLCROSOVPYLFALKRRKIGFHLLKKAPISC
VGVLSYAGCDDTVKQMLSVVEQERESYRTLMDGAIPC

Apis mellifera SBP2 (Refseq: XP_001122154.1)

Canis familiaris SBP2 (Refseq: XP_533552.2)

Canis familiaris SBP2L (Refseq: XP_544672.2)

Capitella sp. SBP2L

MFKLSAEAKSFVPRHATPADESGVLPYYVTNCYPFVQTVPEPSNNAQVLSRDAGVRAAWNSCFSP
RESEVASLHGPPRNSRPKNSRGLLG VHPMSVHAAPYTALPFPTPRGFSPGGGAIGMYPRTPPR
WNTDPPPPLGVVPPQRSIWWRGPRPAFASNGVNLKHHPANQPTARKRSKSKTIICMDAAFQTGL
LCIVSAIAHLFCLDFSEEIARYTLAERPNSLYCKSCHVSTDSEEVDSDSGYSSPLHRKNQISNG
TDASPGSLLQSKQRALGAAVSGAPSVMSYSSVVSRAASAKPTQCQRSESGIKTDNSEAEGDPGS
GRKKQRGKRKKRRKSAGDEEVPTEQKPPEQEEHAEELPELNFODEEEFPNLLSGGVPPPAA
PLSYSEVL RHSYSASGOSOESSLSHSTTGGORSADRS HASTPNSFDSKGGKESKSARKRRKRRE
OANTAADNELAEISLEOEVLRELSIVHNMDPKAAAIKOEKSSSRLPPAPVAKOPPSTGKKSKO
PIALNIADMIDALEKAODVPAKKPLKSEKAAPGGAREGVRVANALDASAPVKRGKEREAPRNKK
PSPLKKVILKEREEKRLRLLEETGPISPSETSASASOIOSGLPLDSDLSDGVSSKASSMDCG
TTTPVTVDMSPI SOTSPVMSPLSGSPFASGINSPIACGLAGLGIVPKALDDIDASVLMKIHRS
RYREYCKQVLNKDIDSCCTALLQDLIRFQDRLFHKDPIKARSKRRIVLGLREVTKHLKLKKLRC
VIISPNI LERIQSKGGLDEALNNILQICQEQTVPFVFALGRRALGRACAKLVPVSVVGIFNYEGS
EGNFKKLMDLMGRAREAYDQMVSNIQELQEHRSSSTRTVASSVGTQLFPHMGHSRTPSACSAIS
FTSSILSEPISENYPRSEPETDSRGYEIVKKEEEEEEEEEEEEEEEEEEDOSSVIDKIATLTEID
DGHEADTEEDHYKVKAADLPIDSIHSATLDLSSEILSOHSSKTLELAKSESKSCKVAF AEDVT
SLGGVSGKOAPTSSSVNKDRIELWVADTTKOIEHLGESKO

Ciona intestinalis SBP2L (Refseq: XP_002123233.1)

Ciona savignyi SBP2L

MKLRTNLRAEVPPFVPRREWTEESMDPQSGRPLPRYVTTTCYPFVQDNQDERRMQHGANFNQRF
TPALRNGTTYANVG YLDSSSNSAAFTNVNQFAMGTVSQNFSGLPFEGNLADTAHITAVYGDSIQ
CQYSPNPSSVVVHKSSSLKTRSRGSSGKRILKRNVTQKEANRGSPSPELVDNCQQTDFPI SIA
SKSLTDHPSLLRKPGRSRRRRETLVYTSGAYDSSSDHADVDSDSGYYSPKHRLVHAKSGGTSTH
GLNARNEKDSVPOVIYITPSNVSAHGPMFOVHPSSATNHLFHNSLSPHVT PPPTSL LGYGOPGP
PIIFSPPPNPMLANRPSPGFPLHPSLIQTSNGNQPIGVALTCGEALFVKQVFLYILCEFR AVEK
KRRALVTFSQQAFLRVHQSMNPAGPAERTIKKKAARLASSGSSTSNWNTNMAFHAGYWSNGPN
PFHHQONFRNP SLDPRSQRKFNF DNRSKSPSYGGHTNHHQMGKSSTMERQLRDDSPIVLNSHN

NPSINGLHLPEDNTLFMLSDNQEFPGGLGGNLYTTSTAPGNVFSYSAAVMGKIPRSSQSNVQNO
VYPPSNSNEKAQAQKSKRRKKAERAAKAADEEYAEISKEHENIQKVFKKTASGRNKS KTPVLD
FSEVMTKLEEKIIDSSQKGGASEKLKDNAAAKKPPLNIROQTAVSMITPMNALDGTAPMIKKGK
EREVPKVKKPSALKKVIKEREKKEHHLKQLTTPVPAPDVPPYPASIYRAINTTDESKGESV
AAPDSVDIIPATVPQIHSRRYREYCCQVLDKRIDETCTMMLQKLVQFQDRLFQKDPMKAKRRR
LVMGLREVTKHLKMKKLRCIFISPNLEKIQAKGGLDDALQQILNLCEEQNVTYVFALGRKALGR
AVSKMVPVSI VGVFDYSGAEQYKQLVELVTEAQVKYKEMVSIYQQEVMEANQPAQTSGGASKR
FAHMTHSRNPSAASCVSFASFISEPISEMNEASNWRVMMDTGEEVSALSPPPEDDASDEEEAEK
DQTESHVRPQEPEVLSRKDSGSTVVERLSEVEHEDQLESTKSNQKEDSIASKDDKDVQDTSANH
RRALDKSFSTCSTTKPDSVIPPPRQSNSDTSSHDVSSQSSAHDRHLWLEDATR SVADLDLNEQ
SDAEQLVSTESVLDTKQEES

Culex quinquefasciatus SBP2 (Refseq: XP_001868539.1)

Daphnia pulex SBP2

MSRRNYGROYFNOPOOAPYGNGDLPDMTFASYTOPYLYODHSYEYYGVPYTPSPNIHTANSYWC
GGGLGYDYSTVSTAPSVVTSSFSSTOSSFSPDAPEFVSROCOOITTGVENASLOPSTKKKKKKK
KKKTPSNNTLSNLICSGDEEKS KSVLSNDEKKSSLPKLTGFOELPEDKKNLGVKSSSKNOSS
KDIKVDSLOEYPPRDKKHFELKTPOILPKTKPSKESKSVRFOESATEDKRSLELKNPOISTTGE
STKGIGSSWPKPFTNVTKSOECIKRPPKMSFADKLKSPVPTKSPFLDWRDORTSAANAPIKFNT
NITESEEKLINOPISISATADKALPPPATAEDGFTTVSRKKTDKKIEKVPEEIAKSLPTKVSVP
AEDAKKKLEKERKKLREKOKKKOAREEKLLAEKLAPKGOKITITPKLMEOFKSGRNANAFSK
PVMKLSDDMFALGKRGGKGNVSESESEWETTEIEVVOKEPAVPPRNVKRS DPIEFDLMALITK
KNTKKKSIQDPTKKGKNRPGIVANVLD RSAPTLSRGKIRNKKRKLSEIRKALLVAKAKKKIARE
SOSFAFPSSGSRPHILHSKKFREYCDOMLTDOIDLLARDMLYHLRMFODRVFKKDPIKARMKKR
LVAGLREVT KOVERN RVKII FLAPDIORCPETGGLDEAVKRL LDAARRLDLP IVYAMSRRKLGR
VLFKKVPVSCCGILNYOATEETWKOLTEAVSLARENYOLKLOELGLAVDLTGKETKTDDENIRN
DVDIAAFTVEKKT DOTDALLELMKLSLKD KH

Dictyostelium discoideum SBP2 (Refseq: XP_641793.1)

Drosophila melanogaster SBP2 (Refseq: NP_648204.1)

Drosophila sechellia SBP2 (Refseq: XP_002029697.1)

Drosophila simulans SBP2 (Refseq: XP_002084094.1)

Drosophila virilis SBP2 (Refseq: XP_002046871.1)

Drosophila yakuba SBP2 (Refseq: XP_002093482.1)

Emiliania huxleyi SBP2

MGDSQTESAPEPAPVSLNANACEFVPSFGAPGAATAASFYWGQAQALSAASACAFGYPGVPPSP
YAGGEPPDFADATGWDYVPLPEPLCGLPLHKRDLAVSQSGGAGAGGRGMGREKDGEAGAGEEQG

GAAGEAMFEAVGAF CGARSGWVFKQGEQGLGYREPAKAKPSRAAGTAATGRPPEVVFALGGCG
GDPSASRRAAASFLRAPLGLQETERRPASEAGSGSGGAVAAPPALVPKRQAESRHPAPAAAAV
SGQESGGAEKSWAALVKPRWGGASQPATASESFPRLGAADDAGGRRKIYIRNAGGAAGGAGATA
GGARDGGAAASAAAPPGGAFPALGAGAPRAAAVTPPSCWTRGGASVAGAAAGSAAGAAAAASP
ASPVAAAATASGGGGEGEFLPVARGSKSARKGGEAAVARVESKPTPSGGAYARCGDTPLASP
KTAPLRLGLHKLSPETVAAMKAGAERAAARGLPMANPPGSKPKPOKNVSLFDFDLAKPGGGVA
TAAKLKPGSAKSAKTPALAAASGRAKSAPRORPGEGLTSGLGRTOKRGKEKEGPKKVRLSQMKK
RILLELLARSEAAAPGGGDGGSGGAGVVLPAYAELEEQGRKRGRGDATWWREGGGEGGGGGGGG
GGGGGEGSGGEGSDDERGGGGGGGGEGKPKRELKRPAEAVANPRLVREYCEQLVVPVNEAACA
LLAEVORFOERLYLRDPLKASOKKRFCVGLREVARALKSNKAKVLIVAHNIERITAEAGLDDMV
SOLITLCAKKOVVYDEAAKASTLOHEDRDKEVLLVFAMTRKALSRALKRSAKTSVVAVLNHDG
ASEOYARLEALTRGARLAYROLTSAGASDSGGDGLPAPADERFLVNYVTGROAAVDPLLMRP
SLCRVDDEEASPCDLGRWLGSLSLAES

Equus caballus SBP2 (Refseq: XP_001493870)

Equus caballus SBP2L (Refseq: XP_001499828.2)*

italicized region was modified from the Refseq entry to match EST data

MSTVIERFSKVKQLCPAREDWLWVIFIDIVHHQGTDRKRPSQILEGLRAVKMGNSSESWNVKL
EVEPFIPQKKNPDTFMIPMALPNENGNVSGVEPTPIPSYLITCYPFVQENQSNRQFPLYNNDIR
WQQPNPNPAGPYLAYPIISAQPPVSTEYTYQLMPAPCAQVMGFYHPFPTPYSNTFQAANAVNT
ITTECTERNQQLGQVFPLSSHRSRNSNRGPVVPKQQLLQOHIKSKRPLVKNVATQKETNAAGPD
NRKIVLLVDASQQTDFPSDIANKSLSESSATMLWWSKGRRRRASHPTAESSEQGASEADIDS
DSGYCSPKHSNNQPAAGALRNPDSSTMSHVESSICTGGVNSNVTCQATQKKPWMEKNQTFSRG
GRQTEQRNNSQVGFRCRGHSTSSERRQNLQKRQDNKQLNPSQSHRGNPNSESLYFEDEDGFREL
NENGNAKDENIQQLSSKVLDDLPENSPINIVQTPITTSVPKRAKSQKKKALAAALATAQEY
SEISMEQKKLQEALSKAAGKKNKTPVQLDLGDMLALEKQQQAMKARQITNTRPLSCTVVTAAS
FHTKDSTNRKPLTKSQPCLTSFNSLDITSSKAKKGKEKEIAKLKRPTALKKVILKEREEKKGR
TVDHNLGSEEPVEMHLDFIDDLQEIVSQEDTGLSMPSDTSLSPASQNSPYCMTVPVSQGPAS
SGIGSPMASSTITKIHSKRFREYCNQVLCKEIDECVTLLLQELVSFQERIYQKDPVRARARRL
VMGLREVTKHMKLNKIKCVIISPNCCKIQSKGGLDEALYNVIAMAREQEIPFVFALGRKALGRC
VNKLVPVSVVGIFNYFGAESLFNKLVALTEEARAYKDMVAALEQEQAEEASKNVKKGPHHMGH
SRNPSAASAI SFCVISEPISEVNEKEYETNWRNMVETS DGLETSENEREISCKHSTSEKPSKA
PFDTAPVGKQPSLVAAGSATSATNP GKATVSEKEEVKPD DLEWASQQSTETGSLDGSCRDLLNS
SITSTTSTLVPGMLEEEDEEEEEEDYTHEPISVEVQLNSRIESWVSETQRTMETLQLGKTLN
GSEEDNAEPSGEEEAPEVLEPRMDSETWTTDHANQEQQKPSSCSSLSTEHS DSHYAPPDP

Gallus gallus SBP2 (Refseq: XP_424425.2)

Gallus gallus SBP2L (XP_413816.2) *duplication of residues 6-173 in Refseq sequence deleted

MDKADKNVKL SAEVEPFIPQKKG PETLMIPMALPNDSGGINGVEPTPIPSYLITCYPFVQENQ
NRQFPLYNNDIRWQQPNPNPAGPYLAYPIISAQPPVSTEYTYQLMPAPCAQVMGFYHPFP
SAPFQTANAVNTVTTECTERNPPGQVFPLSTQSRSSNRGPIIPKQQQLQMHINKRPPVKNV

ATQKETSSSGPENRSKIVLLVDASQQTDFPSDIANKSLSESASTMLWKS KGRRRRASHPAAESS
SEQGASEADIDSDSGYCS PKHGNNQAAAVTSRNADSCAMNVVEPSINATGVSWTNVNSQATQKK
PWIEKTQTFIRGGRQAEQRNSSQSGFRCRGHSTSSERRQNLQKRHEKPLTTSQSSRAEQSPEPL
YFEDEDEFPELNSDNGNSKSSNIQOKISPKVLDDL PENSPINIVQTPIPITTSVPKRAKSQKKK
ALAAALATAQEYSEISMEQKKLQEALS KAAGKKS KTPVQLDLGDM LAALEKQQQAMKARQITNT
RPLSYTVGSAAPFHTKESANRKS LTKGQPSMGCLNPLDSTAPKV KRGKEREISK LKRPTALKKI
ILKEREKKGRLSVDHSL LGSDEQKQVHISLPTDQSQELASQEETGLSMPSDTSLSPASQNSPY
CMT PVSQGS PASSGIGSPMASSAITKIHSKRFREYCNQVLSKEIDECVTLLLQELVSFQERIYQ
KDPMRAKARRRLVMGLREVTKHMKLNKIKCVIISP NCEKIQSKGGLDEALYNVIAMAREQEIPF
VFALGRKALGRCV NKLVPVSVVGIFNYS GAEDLFNKL VSLTEEARKAYRDMVAAMEQEQAEEAL
KNVKKAPHHMGHSRNP SAAS AISFC SVISEPISEVNEKEYETNWRNMVETSDGLETSENERESS
SQTAVPEKAANGQIAKSTLHKQPPLAATSTTSATNHGKATPGEKEEVKPDNLEWASQQSTETG
SLDGSCRDILNSSMISTTSTLVPGMLEEEDEEDEDEDEDYAHEPISVEVQLNSRIESWVSETQR
TMETLQLGKTLSGAEEDNAEQSEEEIETSEQVDP AVDSEEW TNDK HASNIQH KPTICGSLNKE
HTDSIYMP

Gasterosteus aculeatus SBP2

MKLVLVILSPSTQTSKGN SGVHAEGRVVGKNSLDPOOKGLRGGRSLPNSAEPDLVPFEVKMTDF
PELAVGSLGKGD PPIOKESRGPTIPSSSPOMRIAASSWKSVRKGPPTOTDPROTGNNDV PDS PA
ESPGHLGGTSWANVASOPPKKVPK EKTINEOTEETA AOREEGAPGKRKRKKKKKAKGAVEDAE
EESEEPAMYQELPKFEDEEEFPGLSPA VTRTERLKTSSYAAKLCNEENOREGFOROSADHKEKA
PAETHKKGOKVEKVSGKSKVPVOLDIGNMLVALEMKOSOKVKPDAKPVILSVGGGLTVVQKQK
KLPSHQDKIAHNPLDSTCPLVKKGKQREVPKAKKPSPLKKVILKEREERKLKRLL EERGLPLEC
EFTPANDGDVDAAEEGGPVETNATASDEVGSPKEELED RSDFNGAEQV VNKADEEADKDKIVEQ
RTISPVPCPASRPKIHSRKF RDYCSQMLSKDVDECVTALLKELVRFODRLYOKDPMKARMKRRI
VMGLREVLKHLKLRKVKCVILSPNCERIOSK GGLDEALYTIIDTCREOGVPFVFALS RKALGRC
VNKAVPVSLVGIFNYDGAODFYHKMIELSSEARRAYEVMVSSLEOTGOADPESVEEKLOISSAA
EEAELGRDITPPEEPEYMKIWK KMLEKDYNHKFLNFEEQLSSMHLDSVCAENTDEDDKS

Gasterosteus aculeatus SBP2L

MAVHLSLVQDVKLSAEVEPFIPQKKMEGSQVSM SLSGEAGGGSGGGSGGVETTPIPSYLITC
YPFVQENQPNRQH PMYNGGELRWQQPNPSPGGSYLAYPILSSPQPPVSN DYAYYQIMPAPCPPV
MGFYQPFPGPYAGPVQAGV VNPVSAEVGERPLPLGPAYGMNSQRGRGMVRPNVPPNVQKQQLGV
CQPLRGRRP PTRSVAVQKEVCTLGP DGRTKTVMLVDAAQQTDFPGEVSGRCAAERASPQLWKNK
TKRRRASHPAENYSEQGASEADIDSDSGYCS PKHNQAAGVTQ RSAENTAAPTAVETG VMTGTWV
NVA SQATQSWGDRNGHFHRADQRKNSEQRNFSQEFHTGYAGRGPPGLSHQRPQPAVVSGTQVSP
HPLYFEDEDEFD LASGGAQRCTKAESTSAQTHA QPKLPKNLLDNLPENSPINIVQTPIPITT
SVPKRAKSQRKKAMAAALATAQEYSEISMEQKKLQEAFTKAAGKKS KTSVELDLGDM LAALEKH
QQAMKARQLNNTKPLSFTVGT TAPFHGSGLVSLPSALKGHQQPYSVPHNSLDSTAPRIKRGKER
EIPKVKRPTALKKIILKEREKKGKTSVEQE SSGQEEHADESLHFTDDLAREPASQEETGLSMP
SDASLSPASQNSPYSITPVSQGS PASSGIGSPMASNAITKIHSRRFREYCNQVLSKEIDESVTM
LLQELVRFQERIYQKDPTKAKTKRRLVMGLREVTKHMKLNKIKCVLISP NCEKIQAKGGLDEAL
YNVIAMARDQEIPFVFALGRKALGRCV NKLVPVSVVGIFNYS GAEGLFNRLVSLTEEARKAYKD
MVSAL EQEQAEEAQKNDKKLPHHMGHSRNHSAAS AISFC SIFSEPISEVNEKEYETNWRSMVEN

SDALEPVESEPRRPAPPTSTPKVGEAAAATPPATSASTATPSSTAPQTARTAPPTLTQNGNERD
EVRVDDRLELASQQSTETGSLDGSCRGPLNSSITSTTSTLVPGLAEEDDYTPPIAVEVP
TLSSRIEYVWSKTLENLQLGKSQESTEEDEDEEEEEERGHSEEEEDLDSADIAETRSEDKD
QVEVKKPLDTRNNLRLNSFRLQRFWEQVLEMGNCSPLAEEEGT

Homo sapiens SBP2 (Refseq: NP_076982.3)

Homo sapiens SBP2L (GenBank: AAH33001.1)

Ixodes scapularis SBP2 (GenBank: EEC14282)

Lottia gigantea SBP2L

MDQIYYQNIRMVRPNMGYPNQIGGTRHPRPPVNVTHTMHGVVPMHVWANGPPVRNHYPMVAPD
HLSHKNVTDITESRPTKPLMCNTESQTDFPKEIADLHLKELPNSLYLHKDKVKPENINGVKKTE
GTSNOLLVVODMAANVMTSGTHPRGSKHORTLSTDFSLRAKTAVIOAESKEHHSSEAEKTPET
TETKKKRKRNRKKKKGKGENVENSENAGDANHGAEEEEINIRLEDELEFPDLSGSKRVPSTAPAL
ENSTASNIKQLGLSNGVQETEDIPDPDLGSFEVENDSNDQILFKQAAETKSARKRRKRDRDQANK
AANDEMAEITIEQQMLQELGLKAKRDQGPKEAPIVNTPTPALKPPKTANGSGKNNRKSNOPIA
LDFAAMIDALEQKRDDAITTKNAPKKHVIKKKVKPELEPPRRPHNPLDSTCPKVKRGKEREFPK
PKKPSPLKKVILKEREEKRMRLLEEDPSGVSGSQVCVGVVNPESDLSQDEDKGKGSASAEELS
PVSQTSPPFMSPLSPSASPLQSGFNPIAKDSSNPALLKIHSRRYREYCTQMLEKDIDNCCLQF
LQNLVRYQDKQYHKDPKAKSKRRIVLGLREVTKHLKLQKIRCVIISPNEKIQSKGGLDDALN
NILNMCTEQEVPPYVFALGRRALGRACAKLVPVSVGVVFNFEQSERQFWRLIELTQKATDSYKEM
VSSVEKDLQENPNNRAGPSGVPNLFAHMGHSRTPSGCSAISFTSSILSEPISENYPYSEPETDS
KGYEVSKSPRSQVTGIQSSVINEQSSVYYETDAGNEADTEDYLEPVEPSKSPQPYFNHTGDSDE
DEDPDNIEDLPHIDSIHYGNFDLSVEILSQHSSRTIENSEAMSTHSSRTL RDGSPTMLLEKLNE
KHSSSSQQKIIDKDRIKSWVEATQGVGDDTRVDSGSAEEEAGQPVEGEEELCDITTAVDKEEVV
TAS

Monosiga brevicollis SBP2 - partial

TRPRVKRDEHAKRPPGRPGROPRAEDAPKTASAIKANRRRKKAALKLEGAKORAKERANLAASAA
LTPSPAAASHLSRLDASDTSASDDAEAPGPSTMLDFGLLIDOAORSKALEOSGKKTSSORGITG
GKKRPGANGNPANOOSPLGARVNOLDATAPTRRRGKERAVRKEKKPSOMROLMKEEQTARRRAH
DENVTGASSSGSIMPESRAQIPADPPSSPSPEGEGKSHSSEPSTVKGVDPEALSSSLTAAVSTS
LTLDESKSEPPQRKLTSPTSARTMPALESNFFPNRAPRLFSNNFRECVSALLCKRVC SHHGRCL
SCLRIALWFGFFSSLNPLQTRYCDHALDPEVDETVKQLLKDSMRFYNRAVEKNPMNAKARRRLV
LGANECHRKALALGKVKLLL VAPDQQRTNVP GALDDNLHQILQIASSETGTPVFFTL

Micromonas pusilla SBP2 (GenBank: EEH57887.1)

Monodelphis domestica SBP2 (Refseq: XP_001375702)

Monodelphis domestica SBP2L (Refseq: XP_001380472.1)

Nematostella vectensis SBP2

MVKKIMEKVGDDDESTKGATKOLNKPLIDOTDTKGI IKOVAGKKS PFLKRKDRPIVSKDAWARPO
GSKDNPRNADHSETRKNROYFENLKGVKESLNKTEERDNVDMKRWVKDR TASSVKDDKNHIKPN
SKOVPI SITVNNNRDAKKIWSKESNLSLSDITDIQPKTPVFVKEEFPDLSNTKQGENQSTLTSD
WLSGGTRMPILSYSAALKTKPQPRQLPDSREKPGRSSSQGSTEQENQSVKKKKKRKKKKKPTET
EGESSTTKQQPMPTKKTKPELQFDLGMLLSSVQGAFI IQWDNLDVFIQFQEVRTKDRKEKQVKK
AVVAGTLPTQIANSAAGLSKGV PQSAKPGPPVKVFHNMLDSTAPVIKRGKEREVPKKKKPSALK
RIILKEREKKKERENAEHEKTDDGDASGA EIASSNVEMADEEIKDQVEPPNTCTTQEEEQGKP
NDALSLSTPSDGEVKAKLHSRRFRDYCDQVLDKELNTVTLKLLSELVRFQDRVYFKDPEKAKAK
RRYVVG LREVT KHLK LKKIKCVILSPNIEQIKSAGGLDDALHNI ISLAHTNRIPVVFSLRRQIL
GRAVCKKVPVSAVGIFNYDGAQDLFKNLMELTENGRKVYAERWNAAQEALREELDNEHPVISCN
TEQGGPQEAQDSRACDGEHSDDGEADDGSESGESEGVTSEHPMTSCD TDKGGTQEDQASRES D
WVHPDDDFGESGKKC

Ostreococcus lucimarinus SBP2 (Refseq: XP_001417625.1)

Ostreococcus tauri SBP2 (GenBank: CAL51930.1)

Phaeodactylum tricornutum SBP2 (Refseq: XP_002176757.1)

Plasmodium vivax SBP2 (Refseq: XP_001351170.1)

Rattus norvegicus SBP2 (NP_076492.1)

Rattus norvegicus SBP2L (XP_001077702.1)

Saccoglossus kowalevskii SBP2L

MLICQVVRSDSYECLYIQYTKHVTKCFSYINNWKAKTLSAEVEPFV PNR LGDGT TGDKSLPQQH
YSDSSLPSALNNASKDQNSNVNIGELPSYMINCYPFVQDSCITDVRWQQGAQHHPHQPYGNPH
SEFY PQQQPPLPYPGYYPGYPINPYVTGYQPHQLPPPYPQGYPHKGGYRSNRQGGNKQNKNNRR
RNKGGSADTKSVGVQKTSSGEKVIIIPSKDIKRKIKTVIYVDACQQTDFPDDL ANLSLLERPSSF
RKAKAKNRRKTQSQQTRRTNISSTDSEFEEAQVDSDSGYSSPKHCRNLSVGSSTQGI VTDAA T
GTPSSNTPASNTRVPSTSNVNTTTPSNTQATMASMAGPPVMSYAGAVAKAKVPVASVVT PSAID
RTHVAQQAMKTQWNKSKVINSTNRNLQSEPHDRKEVPADTINSTVSGTTATELVAQPIKKKKRQ
RKRKNSRDSGRSANSSINSLARSDLLTTPVPSAE EFGALKFEDDTEYQDLPSVVPNRSEDRPTV
MSYSAVVQQRTTTPPTMTVHGSYVDKSDNYEDTEVKMKMLPEELMSPEVAVSTVKEGKNARKRR
KKALIATQAAAEYSEITEEQKQLQENLKKPNKRTKMPIEFDLGDM LAALETPI TNPLDSSAPV
KRGKEREQPAKKKPSALKRVILREREEKRLRILGECTLSDDDTNKVMFQEVDEEIEQGVQLSQ
ESSEWTTGQSAVANEYEPTLTWF AAKFWTTKSSCWFSYTVPN AALPKIHSRRFREYCNQMLDKE
VDGCCTTLLQTLCRFQDKQYHKDPTRAKSRRRIVMGLREVT KHLRLRKVKCLLISP NLERIQSK
GGLDEALDVIISLAQE QDVPFIFALGRKALGRAVNKLVPVSVVGIFNYDGAENTFRELLDLSAK
ARAVYNDMVV TYQQEIESQNAARIAKHRQHMGHNRNLSGCSGISFSSVISEPISENYPDPEPEF
DEFGREIEQGNAYSQDHGNITSTR LERTDEEVEKTITTEVLNSYDNDGDVNVECLRTRSRSSSQ

NVKEDGEGDDDDVDDDDDEEEEEEEEEEDDDDLSEEDDNCEITLENDKVCDSFVVDKDRIECWV
AEAQSCISSLKIEDIENVPCHEAAGNSHPPDIPENVRPGSSSQEVDTSSEKNCHSDSRYPNSS

Strongylocentrotus purpuratus SBP2L (XP_001188118.1)*
italicized region was appended to the Refseq entry based on EST data from
Paracentrotus lividus and the *S. purpuratus* genome

APRLSAEVDPPFVPGSTPPSYPPSSMTAMYYNAPSHQHQQQOHHHAPQPLHHPHQHQHHHQQTIP
GMVPQPSQVVSQVSGMLSEATAAMPGLKPPPPSQPQGGGGGGGMQOYQTSASAVATMNGKKVP
LTELPRYITTCYPFVQDSSTGAAPATETWMGYPNSSQQPNQPHQPQQHQHPPLPLPPTSQHPL
SHQPPQTTTPMYAPPPPPPPGHQPPSAHLTQQQNQEYFPVHPGYNQVPHQTPPPAAASPGGPLY
QQGAYQQHGGTYQPHLTGTAPHHPTHHHHTQSPTPMPLASQSSMPAGGVPVSHTPFAPPPMMTP
PSQSPSPYPFVPPPPHGAATPGGYDAALPGTQPTLPSYGQYGYGAYPGPQVKVRGQRP MNKDHR
YPGGYQNKGREHYQAYVPPPTDLPKPKTKTVVFAEACAQTDFFPEAIANKPLSDKTSNLTSRSKA
KTRKKSQGNQGTGRDASSSSDSEVENTPHDSDSGYYSPLHAQQHNSTGLVSTYSTQTGKPTYSNV
AMNKSPPHQSRTVEQNTFTQNPQLVVPQGPPLGQLGAPVVIQGRFTPVQPGIPSRFPVMP
MSYANMLTKPRAANPPPPPLANVGYPPQRPNNVFPTQPPPTYRNMVAVSPAPMLYQQQQQQQQRRM
QSPVPAPQKPPVTPEDTPRKRKQKRTKGKKDGEVELEKPKMVNAATYAKPPQIQDKEEYPGLPL
GSPAGNKFQGMSTGGRPISYSSALQQRAPVQLVNESSEEEEEESGGDPSSIIKPEELLSPANVM
STIKEGKNARKRRKKAIMATQAAAKEYSEITEEQRLHENMKKQKRTKMPIEFDLGDMLAAL
KQQQEIRAKQQQQQQLIQRGVPASRNQVFAPNVATMDPYSSQSRPVKDVPRGHNPLDMTAPVKR
GKERELPAKKKPSALKRVILKEREKKRLRTLEESRLSDDSGLSPPATGMGRSNPTQVATKIHS
RRFREYCNQVLDKIDIDGCCTTLLQTLVKFQDRQYHKDPAKGLSQGLSQGLSQGFSQGFSGYGF
SHGFSQGLSQDAPSDRGSFPGFNASQSDLSPLSQMSPLSMSPLSPGSPSSGLSSPATGMGRSNPT
QVATKIHSRRFREYCNQVLDKIDIDGCCTTLLQTLVKFQDRQYHKDPAKAKMKRRLVMGLREVTK
HLKLKKIKCVVVSPNLERIQSKGGLDEAMDRISSLASEQNVPLIFALGRKALGRAVNKVVPVSV
VGIFNYDGAEDTYKQLLDLSTRARNAYADMVRKFQOELEAANAASAARMAKHRHMHGHNRLSG
CSAISFSSVISEPISENYPNPEPEVDSQGREIEPDPTTPTTYSPPQGGGCSSDAGQQHPSAPMRS
LSFTGTGSGVISNSTDDTIHKEEKDGGGSSVGKDYVMSETSSRTLTAGEGDQDLEEGSKEDVGRV
ELEEELEAGLVDQDHDEEEDEEEDEDEDAEVIKANILLPEDGAPEKRVADWVAEAQQCIESL
TVDDESGDDGDAKKKGVGKKDEKPSDANISPEQVGKMLTSLEV

Tetrahymena thermophila SBP2 (Refseq: XP_001011959.2)

Tetraodon nigroviridis SBP2

MDFTSQDQVMGKNPLNAQRKGFRGARSAPHSAGRSKPLKSDFVPFEVRINDFPELAGSKSATC
HENWRSTSLSTSPPKQPTVSLKFQIMHFSVKALCEFTSWASIASQLPKKPVPSSQSEIDGKHLQ
TQDDCEQQEEVTPGKKKRRKKKNAKSKDVDAESEEPASYQEPPKIEDEEEFPDLFLSLTVNDR
MMPSSNAGYEEIRKEGVHLPDSSKENLNVPKGQSKDVALNGQKTEKSSSKKSKAPVQLDIGNVL
ANFEKKQQSHRSRQDAKSVILSVGGGLPIVQKQPRQKKSARQQDKIAHNPLDSTSPLVKKKGKQ
REVPKAKKPTPLKKVILKEREERKQRRLLLEERGLLPEQESWPAEEAAAEQHNTTDEVGSPPEE
LCELLALNAANQVAKGHDEEPEKDKTVEQQTATPSASYPTSRLKIHSRKFRDYCTQMLSKDVD
ECVTTLKELVRFQDRLYQKDPMKARMKRLVMGLREVQKHLKLRKLCVIIISPNCERIQSKGG
LDEALHTIIDTCREQEVFPVFALSRLKALGRCVNVKAVPVSLSVGIFNYDGAQDFYHKMIELSSEAR

IAYEVMLSNLEQTSAAEEEPQTCTLAEKINTSSEDAQPPEPEYMKIWNKILEKDNSNKLLNLEEQ
LSILHLESECPESTNDEES

Tetraodon nigroviridis SBP2L (GenBank: CAF99852.1)

Thalassiosira pseudoanna SBP2

NK SIGTPATKKGRQLAPRKKKLTTLKKRVLEERLRVWKERNDGSSVDDESAQLGGEGPLKRAK
IDGANDSLSGEVVTPTTTTLLIENFVRPDEDDLTDDEYDELLSNVISLAESVGRVVSFVPRP
SSTANTSEDGGGDTEEEAKYVGSAFVKYAFSKDANAGNNILDGVIVGGQPIRTFLLLGVDDFSG
SCTGEGNGMPPSAEEERKWNLAVMRMTSERQSPMRDPSELTDGNGSSMSVDHSPSNTIVFHKI
LCDDDYEDEGALQESLDDIKSLAIQYGQVTDARAATTGRDKGDVYISYKAQVSAEKAVQQLNGV
IVGGSNILVSTQLES PHYKQPSGAVEIILSNVLNESDFEDED CMNESIEDISNMARKYGLIGKV
YAQTSGEQGRGNVRVEYLEGEEAARRAAQQLNGLTIGGVVISATAVSSSINANDADEKQANSRDS
QPEKEAPPPMYSGDKIIPERFAACKRVPKIPNAGIPRSYASKINDERATPLLVEMLGELMRLQE
RSKDDKNARARRRLVMGLREVARGIRAHKVKMVMANNLDEYGAIDSKLQEILDMARAEDLPIL
YELNKRRLGKAIGKSIKVS SVVGIQNADGAHEPFKKLKRMLGMA

Toxoplasma gondii SBP2 (GenBank: EEE23583.1)*
deleted residues 692-721 based on EST data

Trichinella spiralis SBP2 (translated EST GenBank: ES273228.1)

Trichoplax adhaerens SBP2

MDATKSEDEDKREPSKVQVLSAGAVPFVPSYFLNKQEDNLVADKLTSSSKHAQLQNKKNIHRRN
KASGYAANYYPNMPSPVRTNNSLPLPGMPGSSNNLTPCDQYLPIDYCPFIPIPYQYPPNTISDN
YLMNHRGYYPPIPGNYNQKKKPFQRHSNPDVKHDTHEKDTKVQSNEKEVSQVNNDTNTVDTTSNR
NNNNANQNEKKITPLAGNSADLLQETKKS KRKKKKKKNTPANDKVLSTATASDNSHQEIPIISNDK
NQQTQDAISVQTPSSILDVVSMTLNPSSLEQSEIEDFPQLKINSESNVNTSTVKSYSQVLQMP
PSKQSDTKTIPQDNDNDINRKDLNSSSTSNDNDHKDDSNQDQETKSKKKKKKKKKKANQGAKAID
RKTTFNIGEIIISQSQQRQTTSNNKEKVKN TKKGITISIGISNPGIYVHKKNEDSQRSLLP SQSD
KKVKPLNPLDSSASTIMHGKQRETPKKKKPSLLKRVLKERNDKKKSKDIRAHSPLNLYQDNNL
IEIADETHQCLSLSTQHHPKVGTLFLT VTKYGSIDGLTEQSTKSDIHSRKFREYCDHVLSKEIN
NYIWDLRLRELVRFQDRQYQKDPIKAKIRRRYVLGLREIQKYLRLKKLKCVVISPNLEKITYEGG
IDHTLQRIIETCHFQNPVVFGLNRHSLGRAVKRHVPVSIVGVVNYDGVHEKYHELMKLVKTAR
EDYKNLKVKKLLENITN

Xenopus tropicalis SBP2 (Refseq: NP_001090731.1)

Xenopus tropicalis SBP2L (GenBank: AAI67330.1)