

10 20 30 40 50 60 70 80 90 100 110 120 130

B1 ---MFLQIFVAVILVQVVS---CCTYSWVYS---FDFPGQSKNEINSYINALDRNDVN-WADDALSNLGGVCCRPAPWNNVEQOVVYEDWTATLD-SDYTMAFCRVGYFLQGLYRSDTGWPRFKGY

B2 ---MLVQFLFAAFLVQVSS---CCTYSWVYS---FDFTPGQSKNEINSYINALDRNDVN-WADDPLSNLGGVCCQPAPWNNVEQOVVYEDWTATLD-SDYTMAFCRVGYFLQGLYRSDTGWPRFKGY

B3 ---MLIHIFVAVSLMQVVR---CCTYSNWGTS---FDKKGQSKNEINAYINGLDRNVSNWGDPLTFLEGGVCCQPPSPSNNVEQOVVYEDWTATLD-KDYSMAFCRVGYFLQGLYRSDTGWPHFKGY

B4 ---MLYQIVVVVLSMSVRS---CQSYSDWSLS---FDKPGQSMCDQINSYINALDRNHVD-WDDDPISHLGGVCCQPTSPWNNVEQOVVYEDWTATLD-RDNEMAFCPVGYFLQGLYRSDTGWPRYKGY

B5 ---MLLQIYGAVTLIHVYTS---CQAYTSWVYS---FDNPGQSKNQINYYINALDRFDVD-WNDPTLANLGGVCCCLLPPSPWNNVEQOVVYEDWTYYLD-NAFSMAFCPVGYFLQGLYRNRGAFSPYKGY

B6 ---MLYQIFVVVSLMPYVRS---CQSYSNWLLS---FDKPGQSKCDQINYYINALFRDYNV-RNYDPISSLGGVCCQPNSPWVSVEQOVVYEDWTITLD-RKNEWAFCPVGYFLQGLYISSS-----GY

B7 ---MLLQILVAVSVMLYVQS---CQSYSDWQYS---FNDPGQSKNEINDYIHALYRHDKY-SDDDNLSLGGVCCQLGDPWRNVQOVVYEDWTYYLD-YDNSMAFCHVGYFLQGLYRSDIWSPYKGY

B8 ---MVLVHAVVIVTVMSLAKS---CQNTNTSWAIS---FDRHGQSTRELQDKYINGLFRVGHLR-WDDPTINLGGVCCCSASQWPVKVERQVVYEDWTYYQLD-DNFRMAFCPVGYFLHGLYRSSASSP---GY

B9 ---MLKALLALLMLGKLSGVNA---ACYREDWSDS---FEREGSTIC---QHYTRKFOVNGDV--ANGRLGLLEGGVCCSAPPWISSKLOTVHANWDSFN-S-RGAVACPEGFFLRGLRRTGGSP---GY

B10 ---MVLQLIVFVFLVKT---HTACTKSWLTS---FDSAGQSMDEVYIIRGFERSAN--GDHSLNRLGGVCCSAPTFSWDMELVVYEDWTYYLD-TGNHWVFCPNGYFLQGLYRSDIWSPYKGY

B11 ---MMFVKVWVAMTLLGVADA---LCTYTSWMLS---FDSFGQSKNELNHYIYGLERSDVH--KDDQIFLLEGGVCCSAPSQWSNIELQVVYEDWTYKLD-RQNOWAHCPAGEFLQGLYRSDIWSPYKGY

B12 ---MFVLKFGVLLALIGKGS---LCAHTSWWDS---FNSPGQSKNEANFYINGLSRNEYK--KDDQITYLEGGVCCSAPSQWSNIELQVVYEDWTYKLD-RFDVWVNCPAGEFLHGLYRSDIWSPYKGY

B13 ---MLLLNVCVSLTILGLANA---LCAETSWWHS---FDSAGQSKDEANYYIKGLKRNLDL--NDDQIFLLEGGVCCSAPSQWSNIELQVVYEDWTYKLD-RSEBWAYCPAGEFLQGLYRSDIWSPYKGY

B14 ---MLLNLVCLVTLIGLTNA---VCAETSWWHS---FDSGQSKDEANYYIKGLKRNLDL--NDDQIFLLEGGVCCSAPSQWSNIELQVVYEDWTYKLD-RSEBWAYCPAGEFLQGLYRSDIWSPYKGY

B15 ---MKLFLFICVSVTLIKTAN---LCTYTSWLS---FDSTGLSVCKESQYIYHGFDRNTYM--DDDKLYLLEGGVCCSAPHQWSNSEIQVVYEDWTYKLD-RFDVWVNCPAGEFLHGLYRSDIWSPYKGY

B16 ---MLRFLFVFCVSVTLIKTAN---LCTNTSWWHS---FDSAGQSAKESKYYIYHGFDRNTYM--DDDKLYLLEGGVCCSAPHQWSNSEIQVVYEDWTYKLD-RFDVWVNCPAGEFLHGLYRSDIWSPYKGY

B17 ---MHFLKACAIMDLEITNA---YCTYESWGT---FDSFGQSTCQEVNYYIYGLLNRDLK--IDDQINLLEGGVCCSAPSQWSNIEEQVVYEDWTYKLD-RSEBWAYCPAGEFLQGLYRSDIWSPYKGY

B18 ---MMFFKVCITMTLFEIANA---VCRSTSWTRR---FDSAGQSKDSVDFEMRGLQRSQDL--WYDEISQLGGVCCSASPQWSKSEPVYIYADWSDLDW-GYNVWVDCPAGEFLQGLYRSDIWSPYKGY

B19 ---MMLFSKLWALVTLIGLVDA---LCTESLWSNR---INYHGQSTCKEPTYIYNGLQRDLH--QNDGLHLLEGGVCCSAPSQWSNIEEQVVYEDWTYKLD-RSEBWAYCPAGEFLHGLYRSDIWSPYKGY

B20 ---MLFSKLCVMTVTLIGLVDA---LCTVSWSQRTRTVNFGLSSQNEYNFYFMNGLRDLH--QNDGLHLLEGGVCCSAPSQWSNIEEQVVYEDWTYKLD-RSEBWAYCPAGEFLHGLYRSDIWSPYKGY

B21 ---MMLFSKLCVMTVTLIGLVDA---ECVKTSWVQN---VNYEGQLKKEYDFYINGLERNSTE--NFDGLHLLEGGVCCSAPPRLYLDSDTIVYIYENWGWKFEQ--NRRWAYCPAGEFLHGLYRSDIWSPYKGY

B22 ---MLFLKFCFIMTLIGLVDA---KCHNFPWSGNFKVAGQSICHRGSIGNSEFKGLIRNSLK-SKSEGLDVIYAAVCCCTFDEEYLSGDDVVVYANWQKTFK--DQSWRSCPSGYFLQGLYRSDIWSPYKGY

B23 ---MMLLKLKLVMTVTLIGLVVNG---MTVWFSKNSRSDHQVLCKD---YDYSVYVGGFLN---HTDALTNLGGVCCSEKMQRGNSS-ALVVEYEDWTYKLD-RSEBWAYCPAGEFLHGLYRSDIWSPYKGY

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SIGNAL PEPTIDE

SMALL LOBE

Domain 1

140 150 160 170 180 190 200 210 220 230 240 250 260

B1 LFNLEEARCTKPAHPLNYGTQDDIDVSSCMGRKQCS-CPGGYFLTGLYRADGDDLYFLKRIKCCCTPAAKPLEMDEKSKIQTRIMDTLNNMANLAHYMGYGWCYGCHGLAVGEDFTRNGFTWAADTRT

B2 LFNLEEARCTKPAHPLNYGTQDDIDVSSCMGRKQCS-CPGGYFLTGLYRADGDDLYFLKRIKCCCTPAAKPLEMDEKSKIQTRIMDTLNNMANLAHYMGYGWCYGCHGLAVGEDFTRNGFTWAADTRT

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B8 LFNLEEARCTKPAHPLNYGTQDDIDVSSCMGRKQCS-CPGGYFLTGLYRADGDDLYFLKRIKCCCTPAAKPLEMDEKSKIQTRIMDTLNNMANLAHYMGYGWCYGCHGLAVGEDFTRNGFTWAADTRT

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B21 LFNLEEARCTKPAHPLNYGTQDDIDVSSCMGRKQCS-CPGGYFLTGLYRADGDDLYFLKRIKCCCTPAAKPLEMDEKSKIQTRIMDTLNNMANLAHYMGYGWCYGCHGLAVGEDFTRNGFTWAADTRT

B22 LFNLEEARCTKPAHPLNYGTQDDIDVSSCMGRKQCS-CPGGYFLTGLYRADGDDLYFLKRIKCCCTPAAKPLEMDEKSKIQTRIMDTLNNMANLAHYMGYGWCYGCHGLAVGEDFTRNGFTWAADTRT

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SMALL LOBE

LARGE LOBE

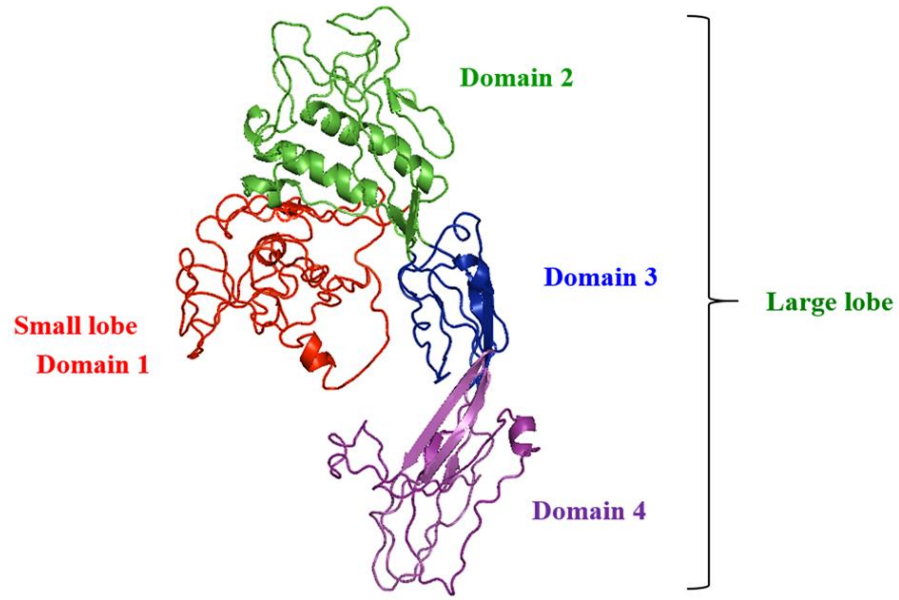
Domain 1

Domain 2


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B2  QFTLTGKLEKVEGTSVNVKWEKMKL-----NRRDVSNGNDEPGRNITTYLAASGPADKPAV-----VEYPKVNLNNKEPFKPIEIPVTEVKV--
B3  QFTLTGKLEKVEGTSINVKWQKVKL-----NRRDVSNDKVSARNITTYIAKSGPADKPAV-----VEYPKVNLNNQESFKPVQIPVTEVKVSR
B4  QFTLTGKLEKVEGTHVDVXWEKIPL-----SRRDVSSEVPASNITTYIATSGPADKPAV-----VEYPKVELLNKEPFEPPIRIPVSNIKV--
B5  QFTLTGKLEKVEGTHIYIKWEKMPQ-----GRRDVSREDEEPASNITTYIAAPGPADKPAV-----VEYPKVLDLNKVPFEPFQIPITSV--
B6  QFSLTGKLEKVEGTHIYIWEKISQ-----GRRDVSLEAPASNITTYIAAPGPADKPAI-----VEYPKVELLNKEPFEPPIQIPVSNIKV--
B7  QFTLTGKLEKVEGTYINVEWEKIPL-----NRRNVNRDEAPASNITTYIATSGPADKPAV-----VEYPKVELLNKEPFEPPIQIPVRNVKV--
B8  EFALNGRLEFVFGTDASVVWEKVNLI-----TKRDVLVNDTTKSTHPYVAKSGPLDKPAE-----VQYPPVQISNKEPVPVVSVIPVN-----
B9  QFTLNGEFEDTMGTSVDVVWGPVTK---RKRELSPLKFSN---PIFRENRITAEIGPHDLPVH-----VDKPNIEFLDTAKICEFDVVPVNISYLV--
B10 EFTLSGTHEHVGKRIDVWLNVKISM---TKREAHFGSRSRQCNIIGKTHYARPGNDAPAI-----VKYPPVTLVNSEPYREGPHYVENKSA--
B11 EITLNGKLEHVSGTKIDIKWETRELNKNFNRRSETDDSKANTPOLNNGTFEATVGPNDKPVV-----VKYPPVELVNAEPPFELDILPANQESS--
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B13 QFTLNGKLEHVAGTKIDVIWENARL---NRRSVPDESEPTPYFDNSPFFAKVGPNDKPVV-----VKYPPVVLVNAEPPFILETFPVKPESN--
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B15 EFTLNGKLEHVAGTKIDVIWENARL---NRRSIRDKIKSSTPQLDNSTFEATVGLNDKPVV-----VKYPPVVLVNSEPFFQFESIPFDPDSN--
B16 EFTLNGKLEHVAGTKIDVIWENARL---NRRSIRDKIKSSTPQFDNSTFEARVGPDKKPVV-----VKYPPVVLVNSEPFFQLESIPVDPNSI--
B17 EFTLSGKLEHVAGTKIDVIWENARL---NRRSVDPKRKSNISHLAYSSEFATVGPDKKPVV-----VKYPPVELANAELFKQESILLNPNTT--
B18 EFTLNGKLEHVAGRNVVVIWVKTRL---NRRSVVDTINSTHHTHIGNITFIARVGPNDKPVV-----VKYPPVLDNAEPPFKLETIPLNPDFN--
B19 QFTLNGRLEQVYVYKSVHSLVDLTKL---RSPSVRRKRQTETFYVND--TFIAKAGPDDKPVV-----VNYPEISLQEI SPIELEPILNDPDS--
B20 QLKLRGRKEEYVYVIGKSLHTLVFKAA---ND---RRKRETEYFYFNG--TFIAKAGPDDKPVV-----VNYPEISSKGNRIQLEPIFNDFVSS--
B21 KFTLNGKLEHVAGAKFDSMLTLMKL---NSFSGLEENQTEYQYVND--ILIAKEGPKDKPVDRKIPEYVLKYPKVDLDDANPLKLEPILKDLDYSS--
B22 TFTVSGKLERVWGSKIDVWWEKGRN---IR-SVPNEVKFENICPDR--VFIVDAGPMDTPI-----VEYPKVNLINEDWDEIEQIPITTDGT--
B23 AFTLSGKLEHLAGSKIDVWWEKVRLL---HRRSTYDELGAGNSCPNR--TYIAKIGPSDKPAK-----VNYPKINIPKAKPSEIK--PTLAD---
Cons eeeeeeeeeee eeeeeeee e eeeee e e eeee e e eeee eeee

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Biomphalysin 1