

## Model Building Report

This document lists the results for the homology modelling project "PLEC-cds" submitted to SWISS-MODEL workspace on Nov. 16, 2023, 10:47 a.m.. The submitted primary amino acid sequence is given in Table T1.

If you use any results in your research, please cite the relevant publications:


- Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., Gumienny, R., Heer, F.T., de Beer, T.A.P., Rempfer, C., Bordoli, L., Lepore, R., Schwede, T. SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic Acids Res.* 46(W1), W296-W303 (2018). [M](#) [doi>](#)
- Bienert, S., Waterhouse, A., de Beer, T.A.P., Tauriello, G., Studer, G., Bordoli, L., Schwede, T. The SWISS-MODEL Repository - new features and functionality. *Nucleic Acids Res.* 45, D313-D319 (2017). [M](#) [doi>](#)
- Studer, G., Tauriello, G., Bienert, S., Biasini, M., Johner, N., Schwede, T. ProMod3 - A versatile homology modelling toolbox. *PLOS Comp. Biol.* 17(1), e1008667 (2021). [M](#) [doi>](#)
- Studer, G., Rempfer, C., Waterhouse, A.M., Gumienny, G., Haas, J., Schwede, T. QMEANDisCo - distance constraints applied on model quality estimation. *Bioinformatics* 36, 1765-1771 (2020). [M](#) [doi>](#)
- Bertoni, M., Kiefer, F., Biasini, M., Bordoli, L., Schwede, T. Modeling protein quaternary structure of homo- and hetero-oligomers beyond binary interactions by homology. *Scientific Reports* 7 (2017). [M](#) [doi>](#)

## Results

The SWISS-MODEL template library (SMTL version 2023-11-08, PDB release 2023-11-03) was searched with for evolutionary related structures matching the target sequence in Table T1. For details on the template search, see Materials and Methods. Overall 3124 templates were found (Table T2).

## Models

The following models were built (see Materials and Methods "Model Building"):

Model #01	File	Built with	Oligo-State	Ligands	GMQE
	PDB	ProMod3 3.3.0	monomer	None	0.22

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
H9F0F3.1.A	94.23	monomer	-	AFDB search	AlphaFold v2	-	0.59	1 - 1179	0.26	Plectin isoform 1c

The template contained no ligands.

Target MSGEDQEVRAVVEDGSNGSGSPSPGDTLPWNLEKTRSRGGGGPGNGSVLDPAAERAVIRIADERDRVQKKTFTKWVN  
H9F0F3.1. AMSGEDAEVRAVPEDVSNSSGSPSPGDTLPWNLGKTRSRSGGGAGSNGSVLDPAAERAVIRIADERDRVQKKTFTKWVN

Target KHLIKARHISDLIEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLRRHQVKLVNIRNDDIADGNPKLT  
H9F0F3.1. AKHLIKARHISDLIEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLRRHQVKLVNIRNDDIADGNPKLT

Target LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLLSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYRQ  
H9F0F3.1. ALGLIWTIILHFQISDIQVSGQSEDMTAKEKLLLSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYRQ

Target TNLENLDQAFSVAERDLGVTRLLDPEDVDVPQDEKSIITYVSSLYDAMPVPDQDGVKANELQLRWQEYRELVLVLLQ  
H9F0F3.1. ATNLENLDQAFSVAERDLGVTRLLDPEDVDVPQDEKSIITYVSSLYDAMPVPDQDGVKANELQLRWQEYRELVLVLLQ

Target WIRAHTAAFEERRFPSSFEIEILWCQFLKFKEKELPAKEADKNRSKGIYQSLEGAVQAGQLKVPYHPLDVEKEWGKL  
H9F0F3.1. AWIRHHTAAFEERRFPSSFEIEILWSQFLKFKEKELPAKEADKNRSKGIYQSLEGAVQAGQLKVPYHPLDVEKEWGKL

Target HVAILEREKQLRSEFERLERLRIVSKLQMEAGLCEEQLNQADALLQSDVRLAAGKAPQRAGEVERDLKADGMIRLLF  
H9F0F3.1. AHVAILEREKQLRSEFERLECLQRIVTKLQMEAGLCEEQLNQADTLLQSDVRLAAGKVPQRAGEVERDLKADSMIRLLF

Target NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNRLR-G-----T----PRHPELEDSTLRYLQDLLAWVE  
H9F0F3.1. ANDVQTLKDRHPQGEQMYRRVYRLHERLVAIRTEYNRLRKAGVAAPATQVTQVTLQSVQRRPELEDSTLRYLQDLLAWVE

Target ENQRRVDSAEWGVLPVSAEQLGSHRGLHQSVEEFRAKIERARTDEGLSPATRGAYRDCLGRDLQYAKLLNSSKARLR  
H9F0F3.1. AENQHRVDGAEWGVLPVSAEQLGSHRGLHQSIEEFRAKIERARSDEGLSPATRGAYRDCLGRDLQYAKLLNSSKARLR

Target SLESLHGFVAAATKELMWLSEKEEEEVGFWDWSEKNSNMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARPTV  
H9F0F3. 1. ASLESLHSFVAAATKELMWLNEKEEEEVGFWDSDRNTNMTAKKESYSALMRELELKEKKIKELQSAGDRLLREDHPARPTV

Target ESFQAALQTQWSWMLQLCCCEIAHLKENTAYFQFFSDVREAEQRLKQLQETLHRKYTCDRSITVTRLEDLLQDAQDEKDQ  
H9F0F3. 1. AESFQAALQTQWSWMLQLCCCEIAHLKENAAYFQFFSDVREAEQQLQKLQEALRRKYSCDRSATVTRLEDLLQDAQDEKEQ

Target LNEYRGHLSGLAKRAKAIIVQLTPRNPQTPTGRVPLLAVCDYKQVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPS  
H9F0F3. 1. ALNEYKGHLSGLAKRAKAIIVQLKPRHPAHPVRSRLPLLAVCDYKQVEVTVHKGDECQLVGPAQPSHWKVLSSSGSEAAVPS

Target VCFLVPPPNQEALEAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLELHY  
H9F0F3. 1. AVCFLVPPPNQEAQEAQVTRLEAQHQALVTLWHQLHVDMSLLAWQSLRRDVQLIRSWSLATFRTLKPEEQRQALHSLELHY

Target QAFLRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLQSLEQGEQESRCQRCISELKDIRLQLEACETRTRVHRLRPLDK  
H9F0F3. 1. AQAFLRDSQDAGGFGPEDRLMAEREYGSCSHHYQQLQSLEQGAQESRCQRCISELKDIRLQLEACETRTRVHRLRPLDK

Target EPARECAQRIAEQKKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLTISL  
H9F0F3. 1. AEPARECAQRIAEQKKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLTISL

Target VIRSTQGAEEALRAHEEQLEKAQAVPAALPELEATKAAMKKLRAQAEQPVFDALRDELRGAEVGERLQQRHGERDVE  
H9F0F3. 1. AVIHSTQGAEEVLRRAHEEQLEKAQAVPATLPELEATKASLKKLRSQAEQPVFDALRDELRGAEVGERLQQRHG-----

Target VERWREVRTQLLERWQAVLAQTDVVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEIQAVPLADSQAVREQLRQEKA  
H9F0F3. 1. A-----

Target LLEEIERHAEKVEECQRFQAKQYINAIKDYELQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQY  
H9F0F3. 1. A-----

Target IRFISETLRRMEEEERLAEQQRAEERERLAEVEAALEKQRQLAEAHAQAKAQAEREAQELQRRMQEEVARREEVAVDAQQ  
H9F0F3. 1. A-----

Target QKRSIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQALRARAEAEQKRQAQ  
H9F0F3. 1. A-----

Target EEAERLRRQVQEETQQRKQAEAEGLRVKAEAEAREKQRALQALEELRLQAEAEERRLRQAEAEERARQVQVALETAQRS  
H9F0F3. 1. A-----

Target AQAELQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQQAEARAREEAERELERWQLKANEALRLRLQAEVEAQ  
H9F0F3. 1. A-----

Target QKSLAQAEAEKQKEAAEREARRRGKAEQAVVRQRELAEQELERQRLAEGTAQQRLAAEQELIRLRAETEQGEQQRQLLE  
H9F0F3. 1. A-----

Target EELARLQSEAAAATQKRQLEAEALAKVRAEMEVLLASKARAEESRSSEKSKQRLAEAGRFRELAEEAARLRALAEAA  
H9F0F3. 1. A-----

Target KRQRQLAEEDAARQRAEAERVLSEKLAATSEATRLKTEAEIALKEKEAENERLRLRAEDEAFQRRRLEEQAQHKADIEE  
H9F0F3. 1. A-----

Target RLAQLRKASESELERQKGLVEDTLRQRQVVEEILALKASFEKAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQR  
H9F0F3. 1. A-----

Target QLAAEEERRRRREAEERVQKSLAAEEEAARQRKAALVEEERLAKAVEEARRLRERAEHESVRQLQLAQEAAQKRLQAEKA  
H9F0F3. 1. A-----

Target HAFVQKQEQELQQLTQQEQSVLEKLRSEAEAAARRAAEEAEERARAEREAQAQSRQVVEAERLKQAAEEQAQAQAQA  
H9F0F3. 1. A-----

Target AAELRKEAEQEAARRAQEAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLK  
H9F0F3. 1. A-----

Target AEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVAAQEAARL  
H9F0F3. 1. A-----

Target RQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQ  
H9F0F3. 1. A-----

Target RQLEMSAEERLRLRVAEMSRAQARAEEDAQFRKQAEIIGAKLHRTTELATQEKVTLVQTLETQRRQSDRDADRLREAIA  
H9F0F3. 1. A-----

Target ELEREKDKLKEAELLQLKSEEMQTVQQEQQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKLREE  
H9F0F3. 1. A-----

Target QQRQQQQMQQEQQLLASMEEARRRQHEAEEGVRRKQEEQLLLEQQRRQQEQQLAEENRRLRERLEHLEEEHRAALAHSE

H9F0F3. 1. A-----  
Target EITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGH  
H9F0F3. 1. A-----  
Target SSIAGLLLKPANEKLTIIYAALRRQLLSPGTALILLEAQAASGFLDPVRNRRLTVTEAVKEGVVGPELHHKLLSAERAVT  
H9F0F3. 1. A-----  
Target GYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDP SDDTKGFFD  
H9F0F3. 1. A-----  
Target PNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGGLVYTDSEARDVFEKATVSAPFGKFQGKTVTIWE LINSEYFTA  
H9F0F3. 1. A-----  
Target EQRRDLLRQFRTGKVTVEKIIKIVITVIEEHEQKGQLCFQGLRALVPAELLESGIIDWDLFRQLQLGERSVQEVAEVEG  
H9F0F3. 1. A-----  
Target VRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPATSARLTVDEAVRAGLVGPHEKL  
H9F0F3. 1. A-----  
Target LSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDQALSTGGTVDPKSHRLLPLDVACARGYLDEETSTALSAPR  
H9F0F3. 1. A-----  
Target DDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWE  
H9F0F3. 1. A-----  
Target LINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKD GK  
H9F0F3. 1. A-----  
Target TSVKDLSELSSLQTLQSGCLAGIYLESKEKVTIYEAMRGLLRPSTAILLLEAQAATGFLVDPVRNQRLYVHEAVKA  
H9F0F3. 1. A-----  
Target GVVGPHEKLLSAEKAVTGYKDPYSGTISLQFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACRQGYFD  
H9F0F3. 1. A-----  
Target EEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETRRAFEETQIDIP  
H9F0F3. 1. A-----  
Target GGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEKTEIVRQQNLASYDYVRRRLTAEDLYEA  
H9F0F3. 1. A-----  
Target RVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLLD  
H9F0F3. 1. A-----  
Target PVKGERLTVDEAVRKGLVGPHEHRLLSAERAVTGYRDPYTEQTISLQFQAMKKDLIPAEALRLDQALATGGIVDPRLG  
H9F0F3. 1. A-----  
Target FHLPLEVAYQRYLNKDTHTDQLSEPSEVRSYVDPSTDERLSYTLQLRRCRRDETSGFLPLSEARKLTFRGLRKQITVE  
H9F0F3. 1. A-----  
Target ELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEAQAATGY  
H9F0F3. 1. A-----  
Target VIDPIKGLKLTVEEAVRMGIVGPEFKLLSAERAVTGYKDPYSGKLISLQFQAMKKGLILKDHGIRLLEAQIATGGIIDP  
H9F0F3. 1. A-----  
Target EESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSKSS  
H9F0F3. 1. A-----  
Target VRKRRVVIDPETGKEMSVYEAYRKGLIDHQTYLELSECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLID  
H9F0F3. 1. A-----  
Target RSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTETLEKVSIT  
H9F0F3. 1. A-----  
Target EAMHRNLVDNITGQRLLEAQAQCTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALK  
H9F0F3. 1. A-----  
Target KGWLYYEAGQRFLVQYLTGGLIEPDTGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTCPKTKLISYKDALDRSMV  
H9F0F3. 1. A-----  
Target EEGTGLRLLEAAAQSSKGYSPYSVSGSGSTTGSRSGSRTGSRAGSRRGSFDATGSGFSMTFSSSSYSSSGYGRRYASGP  
H9F0F3. 1. A-----

Target TSSLGGPESAAA  
H9F0F3. 1. A-----

Model #06	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.48 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
1sjj.1.A	12.54	homo-dimer	0.00	HHblits	2DX	-	0.27	187 - 806	0.13	actinin

The template contained no ligands.

Target MSGEDQEVRAVEDGSNGGSGSPSPGDTLPWNLEKTQSRRRGGGGPGNGSVLDPAAERAVIRIADERDRVQKKTFTKWVN  
1sjj. 1. A -----

Target KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLHRHQVKLVNIRNDDIADGNPKLT  
1sjj. 1. A -----

Target LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMN--KVY  
1sjj. 1. A -----QRKTFTAWCNSHLRKA-GTQIENIEEDFRDGLKMLLLEVISGERLAKPERGKM

Target RQTNLENLDQAFSVAERDLGVT-RLDPEDVDVPQPEKSIITYVSSLYDAMPRVPDVQDGVKANELQLRWQEYRELVLL  
1sjj. 1. A RVHKISNVNKALDFIA-SKGVKLVSIGAEIIVDGNV--KMTLGMiWTIILRFAIQDISVE-----ETSAKEG

Target LLQWIRAHTAAFE---ERRFPSSFEEIEILWCQFLKFKETELP---AKEADKNRSKGIYQSLEGAVQAGQLKVPPGY--  
1sjj. 1. A LLLWYQRKTAPYKNVNIQNFHISWKDGLGFCALIHRHRPELIDYGKLRKDDPLTNLNTAFDVAEKYLDIPKMLDAEDIVG

Target -----HPLDVEKEWGLHVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRL--LA  
1sjj. 1. A TARPDEKAIMTYVSSFYHAFSGAQKAETAA-NRICKVLAVNQENEQLMEDYEKLASDLLEWIRRTIPWLENRAPENTMQA

Target AGKAPQRAGEVERDLKADG---MIRLLFNDV-QALKD-GRHPQGEQMYRRVYRLHERLVAIRT---EYNLRLRGTPRH  
1sjj. 1. A MQQKLEDFRDYRRLHKPPKVQEKQCLEINFNTLQTKLRLSNRPAFMPSEGMVSDINNAWGGLEAQEKGYEEWLLNEIRR

Target P---ELEDSTLRYLQDLLAWVEENQRRVDSAEWGV-DLPSVEAQLGSHRGLHQSVVEEFRAKIERARTDEGQLS---PAT  
1sjj. 1. A LERLDHLAEKFRKQASIHESWTDGKEAMLQKDYETATLSEIKALLKKHEAFESDLAAHQDRVEQIAAIAQELNELDYYD

Target RGAYRDCLGRDLQYAKLLNSSKARLSLES-----LHGFVAAATKELMWLSEKEEEEVGFDSERNNSNMAAKK  
1sjj. 1. A SPSVNARCQKICDQWDNLGALTQKRREALERTEKLETTIDQLYLEYAKRAAPFNWMEGAMEDLQDTFIVHTIEEIQGLT

Target EAYSALMRELELKEKKIKEI---QSTGDRLLREDH---PARPTVESFQAALQTQWSWMLQLCCCIEAHLKENTAY----  
1sjj. 1. A TAHEQFKATLPDADKERQAILGIHNEVSKIVQTYHVNMAGTNPYTTITPQEINGKWEHVRQLVPRRDQALMEEHARQQQN

Target ---FQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKQDQLENEYRGHLSGLAKRAKAIQVLTTPRNP  
1sjj. 1. A ERLRKQFGAQNIVIGPWIQTKMEEIGRISI---EMHGTLEDQLNHLRQYEKSIVNYKPKIDQLEGDHQIQIEAL-----

Target QPTRGRVPLLAVCDYKQVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCFLVPPPNQEALAEAVARLEAQHQALV  
1sjj. 1. A -----

Target TLWHQLHTDMKSLLAWSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLELHYQAFLRDSQDAGGFGPEDRLQAEREYGS  
1sjj. 1. A -----

Target CSRHYQQLLSLEQGEQEESRCQRCISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQKKAQAEVEGLGKGV  
1sjj. 1. A -----

Target ARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKTIISLVIRSTQGAEALRAHEEQKAEQAVPA  
1sjj. 1. A -----

Target ALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVERWRERVTLLEWQAVLAQTDVVRQR  
1sjj. 1. A -----

Target ELEQLGRQLRYYRESADPLGAWLQDARRRQEQIQAVPLADSQAVREQLRQEKALLEEIERHAEKVVEECQRFQKQYINAIK  
1sjj. 1. A -----

Target 1sjj. 1. A	DYELQLVTYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRF ISETLRRMEEEEERLAEQQRAEERE -----
Target 1sjj. 1. A	RLAEVEAALEKQRQLAEAHAQAKAQAEREAQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSSEAEIQAKARQV -----
Target 1sjj. 1. A	EAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQALRARAEAEQKRQAQEEAERLRRQVQEETQQRKQAEAEGLR -----
Target 1sjj. 1. A	VKAEAEAAAREKQRALQALEELRLQAEAEERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKTAQLERTLEEEH -----
Target 1sjj. 1. A	VTVVQLREEATRREQQQAEARAREEAERELERWQLKANEALRLRLQAE EVAQKSLAQAEAEKQKEAAEREARRRGKAE -----
Target 1sjj. 1. A	EQAVRQRELAEQEELERQRQLAEGTAQQRLAAEQELIRLRAETEQQGEQQRQLLEEELARLQSEAAAATQKRQELEAE LAKV -----
Target 1sjj. 1. A	RAEMEVLLASKARAEESRSSSEKSKRLEAEAGRFRELAEAAARLRALAEAKRQRQLAEEDAARQRAEAERVLSEKLA -----
Target 1sjj. 1. A	AISEATRLKTEAEIALKEKEAENERLRRLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQKGLVEDTLRQR -----
Target 1sjj. 1. A	RQVEEEILALKASFEKAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAEERVQKSLAAEEEA -----
Target 1sjj. 1. A	ARQRKAALEEVERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKRLQAEKKAHAFVQQKEQELQQT LQQEQSVLEKLR -----
Target 1sjj. 1. A	SEAEAAARRAAEEAEERARAEREAQSRQRVEEAERLKQAAEEQAQAQAQAAAEKLRKEAEQEAARRAQAEQAALRQK -----
Target 1sjj. 1. A	QAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSLDQELQRLKAEVTEAARQRSQVEEELFSVRVQMEEL -----
Target 1sjj. 1. A	GKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQ -----
Target 1sjj. 1. A	EATRLKAEAE LLQQKELAQEQARRLQEDKEQMAQQLAQETQG FQRTLETERQRQLEMSAEAEERLRLRVAEMSRAQARAE -----
Target 1sjj. 1. A	EDAQRFRKQAE EIGAKLHRTELATQEKVTLVQTLETQRQQSDRDADRLREAI AELEREKDKLKKEAELLQLKSEEMQTVQ -----
Target 1sjj. 1. A	QEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQQMQQE KQQLLASMEEARRRQH -----
Target 1sjj. 1. A	EAEEGVRRKQEELQLLEQQRQQQEQLLAENRRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNGQDAADGPAAEP -----
Target 1sjj. 1. A	EHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLKPANEKLT IYAALRRQLLS -----
Target 1sjj. 1. A	PGTALILLEAQAA SGFLDPVRNRRLTVTEAVKEGVVGPELHHKLLSAERAVTGKDPYTG EKISL FQAMKKDLIVREHG -----
Target 1sjj. 1. A	IRLLEAQIATGGVIDPVHSHRPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLL -----
Target 1sjj. 1. A	PLTDQAAKG GELVYTDSEARDVFEKATVSAPFGKFQKGTVTI WELINSEYFTAEQRRDLLRQFRTGKVTVEKIIKIVITV -----
Target 1sjj. 1. A	IEEHEQKGQLCFQGLRALVPAAELLES G I IDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYE -----
Target 1sjj. 1. A	ALKKELLQPEAAVALLEAQAGTGHVIDPATSARLTVDEAVRAGLVGP ELHEKLLSAEKAVTGKDPYSGQSVSLFQALKK -----
Target 1sjj. 1. A	GLIPREQGLRLLDAQLSTGGTVDPSPKSHRLPLDVACARGYLDEETSTALSAPRDDAKTY YDPRTWELATYSQLQQQCRPD -----
Target 1sjj. 1. A	PLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQELLRQFRTGKVTVE -----

Target  
1sjj. 1. A-----  
KIIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKGKTSVKDLSELSSLQTLQGGSGCLAGIYL

Target  
1sjj. 1. A-----  
EESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLYVHEAVKAGVVGPHEKLLSAEKAVTGYKDPYSG

Target  
1sjj. 1. A-----  
STISLFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLT

Target  
1sjj. 1. A-----  
YRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETTRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRA

Target  
1sjj. 1. A-----  
QLMADFQAGRVTKERMIIIIIEIIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESA

Target  
1sjj. 1. A-----  
WRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRKGLVGPELHDRLL

Target  
1sjj. 1. A-----  
SAERAVTGYRDPYTEQTISLFQAMKKDLIPAEALRLDDAQLATGGIVDPRLGFHLPLEVAYQRGYLNKDTHTDQLEPSE

Target  
1sjj. 1. A-----  
VRSYVDPSTDERLSYTLQLRRCCRDETSGFLPLPSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVS

Target  
1sjj. 1. A-----  
KNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEAQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKD

Target  
1sjj. 1. A-----  
KLLSAERAVTGYKDPYSGKLISLFQAMKKGLIKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTD

Target  
1sjj. 1. A-----  
PSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSKSSVRKRRVVIVDPETGKEMSVYEAYRKGL


Target  
1sjj. 1. A-----  
IDHQTYLELSEQECEWEEITISSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITEFADMLSGNAGG

Target  
1sjj. 1. A-----  
FRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTELEKVSITEAMHRNLVDNITGQRLLEAQAQCTGGII

Target  
1sjj. 1. A-----  
DPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYEAGQRFLEVQYLTGGLIEPDT

Target  
1sjj. 1. A-----  
PGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTCPKTKLKISYKDALDRSMVEEGTGLRLLLEAAQSSKGYSPYSVSG

Target  
1sjj. 1. A-----  
SGSTTGSRSRGTGSRAGSRRGSF DATGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA

Model #15	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.55 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
1hci.1.A	14.35	homo-dimer	0.00	HHblits	X-ray	2.80Å	0.28	302 - 734	0.09	ALPHA-ACTININ 2

The template contained no ligands.

Target  
1hci. 1. A-----  
MSGEDQEVRAVVEDGSNGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDP AERAVIRIADERDRVQKKTFTKWVN

Target  
1hci. 1. A-----  
KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYL RHRQVKLVNIRNDDIADGNPKLT

Target  
lhci. 1. A LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLLSQRMVEGYQGLRCDNFTSSWRDGRLFNAI IHRHKPMLIDMNKVYRQ-----

Target  
lhci. 1. A TNLENLDQAFSVAERDLGVTRLDPEDVDVPQPDEKSIITYVSSLYDAMPRPVDVQDGVKANELQLRWQEYRELVLVLLQ-----QENERLMEEYERLASELLE

Target  
lhci. 1. A WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAG---QLKVPPGYHPLDVEKEW  
WIRRTIPWLENRTPEKTMQAMQKLEDFRDYRRKHKPPKVQEKCLEINFNTLQTKLRISNRPAFMPSEGKMVSDIAGAW

Target  
lhci. 1. A GKLHVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDV----RLLAAGKAPQRAGEVERDLKAD  
QRLEQAEKGVEEWWLLNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILLQKDYESASLTEVRALLRKHEAFESDLAAHQ

Target  
lhci. 1. A GMIRLLFNDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNL---RLRGTPRHP-E---LEDSTLRYLQDLLAWVEEN  
DRVEQIAAIAQELNELDYHDAVNVDRCQKICDQWDRGLTQKRREALERMEKLETTIDQLHLEFAKRAAPFNWMEGA

Target  
lhci. 1. A QRRVDSAEWGVDLPSVEAQLGSHRGLHQSVVEEFAKI---ERARTDEGQ---LSP---ATRGAYRDCLGRDLQYAKLL  
MEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIMAIQNEVEKVIQSYNIRISSNPYSTVTMDLRTKWDKVK

Target  
lhci. 1. A NSSKARLSLESL-----HGFVAAATKELMWLSEKEEEEVGFDSERNSNMAAKKEAYSALMRELELKEKKIKE  
QLVPIRDQSLQEELARQHANERLRRQFAAQANAIGPWIQNMEEIARSSIQI-TGALEDQMNQLKQYEHNIINYKNNIDK

Target  
lhci. 1. A IQSTGDRLLREDHPARPTVESFQAALQTQWSWMLQLCCIEAHLKENTAYFQFFSDVREAEELRKLTQETLHRKYTCDRS  
LEGDHQLIQEALVFDNKHTNYTMEHIRVGWELLLTTIARTINEVETQIL-----

Target  
lhci. 1. A ITVTRLEDLLQDAQDEKDLNEYRGHLSGLAKRAKAIIVQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHKGDECQMLGPA-----

Target  
lhci. 1. A QPFHWKVLSSSGSEAAVPSVCFLVPPPNQEALAEAVARLEAQHQALVTLWHQLHTDMKSLLAWSLSRDVQLIRSWSLVTF-----

Target  
lhci. 1. A RTLKPEEQRQALRSLELHYQAFLRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLLSLEQGEQESRCQRCISELKD IRL-----

Target  
lhci. 1. A QLEACETRTRVHRLRLPLDKEPARECAQRIAEQQKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPT LRSELELTGKL-----

Target  
lhci. 1. A EQVRSLSAIYLEKLTISLVIRSTQGAEELRAHEEQLEKAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDEL R-----

Target  
lhci. 1. A GAQEVGERLQQRHGERDVEVERWRERV TQLLERWQAVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEIQ-----

Target  
lhci. 1. A AVPLADSQAVREQLRQEALLEEIERHAEKVEECQRFQKQYINAIKDYELQLV TYKAQLEPVASPAKKPKVQSGSESVIQ-----

Target  
lhci. 1. A EYVDLRTRYSELSTLTSQYIRFISETLRRMEEERLAEQQRAEERERLAEVEAALEKQRQLAEAHQAQAQAEERAEQELQ-----

Target  
lhci. 1. A RRMQEEVARREEVAVDAQQKRSIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETTERQRGGAEGE-----

Target  
lhci. 1. A LQALRARAEEAEQKRQAQEEAERLRRQVQEETQQRKRQAEELGLRVKAEAAAREKQALQALEELRLQAEEAERRLRQ-----

Target  
lhci. 1. A AEAERARQVQVALETAQRSAQAEQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQAEAEERAREEAERELERW-----

Target  
lhci. 1. A QLKANEALRLRLQAE EVAQKSLAQAEAEKQKEAAEREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQLAAEQE-----

Target  
lhci. 1. A LIRLRAETEQQEQRQLLEEELARLQSEAAAATQKRQELEAELAKVRAEMEVLLASKARAEESRSSEKSKQRLEAEAG-----

Target  
lhci. 1. A RFRELAEEAARLRALAEAAKRQRQLAEEDAARQRAEAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRLRAEDEA-----

Target  
lhci. 1. A FQRRRLEEQAQHKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEEILALKASFEKAAAGKAELELELGRIRGN-----

Target  
lhci. 1. A AEDTLRSKEQAEQEAARQRQLAAEEERRRREAEERVQKSLAAEEEAARQKAAL EEVERLKAKVEEARRLRERAEHESVR-----

Target  
lhci. 1. A QLQLAQEAAQKRLQAEKKAHAFVQKQELQQTLLQEQSVLEKLRSEAEAAARRAAEEAEARERAEREAAQSRQRVEEA-----

lhci. 1. A	-----
Target	ERLKQAAEEQAQAQAQAAAAEKLKEAEQEAAARRAQAEQAALRQKQAADAEMEKKHKKFAEQLTRQKAQVEQELTALRLK
lhci. 1. A	-----
Target	LEEDHQKSILDQELQRLKAEVTEAARQRSQVEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMK
lhci. 1. A	-----
Target	QVAEEAARLSVAAQEAAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMA
lhci. 1. A	-----
Target	QQLAQETQGFQRTLETERQRQLEMSAEAEERLRLRVAEMSRAQARAEEDAQRFKQAEIIGAKLHRTELATQEKVTLVQTL
lhci. 1. A	-----
Target	ETQRQQSDRDADRLREAIAELEREKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEKA
lhci. 1. A	-----
Target	KLERLFQDEVAKAQLREEQQRQQQMQUEKQQLLASMEEARRRQHEAEEGVRRKQEELQLEQQRQQEQLLAEENRRL
lhci. 1. A	-----
Target	RERLEHLEEEHRAALAHSEEITAAQAAATRALPNGQDAADGPAAPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGH
lhci. 1. A	-----
Target	TTVAELTQREDVRRYLQGHSSIAGLLLPANEKLTIIAALRRQLLSPGTALILLEAQAAASGFLDPVRNRRLTVTEAVKE
lhci. 1. A	-----
Target	GVVGPELHHKLLSAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFD
lhci. 1. A	-----
Target	EEMNRVLQDPSDDTKGFFDPNTHENLYLQLLERCVEDPETGLRLLPLTDQAAKGGLVYTDSEARDVFEEKATVSAPFGK
lhci. 1. A	-----
Target	FQGKTVTIWELINSEYFTAQRRDLLRQFRTGKVTVEKIIKIVITVIEEHEQKQQLCFQGLRALVPAELLESIGIIDWDL
lhci. 1. A	-----
Target	FRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARL
lhci. 1. A	-----
Target	TVDEAVRAGLVGPHELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDQALSTGGTVDPKSHRPLDV
lhci. 1. A	-----
Target	ACARGYLDEETSTALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQK
lhci. 1. A	-----
Target	ATVEVPVGSFQGRAVTIWELINSEYFTAQEQELLRQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGLRAPVPASE
lhci. 1. A	-----
Target	LLAAGILSSSQFEQLKDGKTSVKDLSELSSLQTLQSGGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLEAQAAATG
lhci. 1. A	-----
Target	FLVDPVRNQRLYVHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLQFQAMKKGLVREHGIRLLEAQIATGGIID
lhci. 1. A	-----
Target	PVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTR
lhci. 1. A	-----
Target	VYTEETTRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEKTEIVRQQN
lhci. 1. A	-----
Target	LASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLS
lhci. 1. A	-----
Target	AEVARLLLEAQAAATGFLDPVKGERLTVDEAVRKGVLGPELHDRLLSAERAVTGYRDPYTEQTISLQFQAMKKDLIPAEAA
lhci. 1. A	-----
Target	LRLDQALATGGIVDPRLGFHLPLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSYQQLRRRCRRDETSGFLFLP
lhci. 1. A	-----
Target	LSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKG
lhci. 1. A	-----
Target	IIRPGTAFELLEAQAAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLSLQFQAMKKGLILK
lhci. 1. A	-----



Target  
lhci. 1. A

DHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGL

Target  
lhci. 1. A

RLPLKEKKRERKTSSKSSVRKRRVIVDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIID

Target  
lhci. 1. A

RRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEE

Target  
lhci. 1. A

TGPVAGILDDETLEKVSITEAMHRNLVDNITGQRLLEAACTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAF

Target  
lhci. 1. A


CGFEDPRTKTKMSAAQALKGWLYYEAGQRFLEVQYLTTGGLIEPDTGPRVPLDEALQRGTVDARTAQKLRDVSAYSKYLT

Target  
lhci. 1. A

CPKTKLKISYKDALDRSMVEEGTGLRLLLEAAAQSSKGYSPYSVSGSGSTTGSRSRSTGSRAGSRRGSFDTATGSGFSMT

Target  
lhci. 1. A

FSSSSYSSSGYGRRYASGPTSSLGGPESAAA

Model #14	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.43 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
7ank.1.A	12.69	monomer	0.00	HHblits	X-ray	3.20Å	0.27	187 - 904	0.10	Alpha-actinin-2

The template contained no ligands.

Target  
7ank. 1. A

MSGEDQEVRAVVEDGSNGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN

Target  
7ank. 1. A

KHLIKQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLHRHQVKLVNIRNDDIADGNPKLT

Target  
7ank. 1. A

LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNK--VY  
-----QRKFTAWCNSHLRKA-GTQIENIEEDFRNGLKMLLLEVISGERLPKPD RGKM

Target  
7ank. 1. A

RQTNLENLDQAFSVAERDLGVT-RLDPEDVDVPQPEKSIITYVSSLYDAMPVPDVQDGVKANELQLRWQEYRELVL  
RFHKIANVNKALDYIA-SKGVLVSIGAEIIVDGNV--KMTLGMWTIILRFAIQDISVE-----ETSAKEG

Target  
7ank. 1. A

LLQWIRAHTAAFE---ERRFPSSFEEIEILWCQFLKFKETELPAKEAD---KNRSKGIYQSLEGAVQAGQLKVP  
PGYHP  
LLLWCQRKTAPYRNVNIQNFHTSWKDLGLCALIHRHPDLIDYSKLNKDDPIGNINLAMEIAEK----HLDIPKMLDA

Target  
7ank. 1. A

LDVEKEWGLHVAILEREQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLD  
EDIVNT-P-----KPDER--AIMTYVSCFYHAFAGAEQ-----AET---

Target  
7ank. 1. A

KADGMIRLLFNDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRV  
-A-----ANRICKVLAVNQENER-----LMEEYERLASELLEWIRRTIPWL

Target  
7ank. 1. A

DSAEWGVDLPSVEAQLGSHRGLHQSVEEFRAKIERARTDEGQLSPATRGAYRDCGLRDLQYAKLLNSSKARLSLES  
LH  
ENRTPEKTMQAMQKLEDFRDYRRKHKPP---KV-----QEKQLEINFNTLQTKLR-----

Target  
7ank. 1. A

GFVAAATKELMWLSEKEEEVGFWDSESRNSMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARP  
TVESFQAA  
-----I-----SNRPAFMPSEGMVSD

Target  
7ank. 1. A

LQTQWSWMLQLCCCEIAHLKE-----NTAYFQFFSDVREAEELRKLQETLHRKYTCDRSI-TVTRLEDLLQDAQDE  
IAGAWQRLEQAEKGYEELLNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILL---QKDYESASLTEVRALLRKHEAF

Target  
7ank. 1. A

KDQLNEYRGHLSGLAKRAKAIIVQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAA  
ESDLAAHQDRVEQIAAIAQELNELDY--H-----

Target VPSVCFLVPPPNQEALAEAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLE  
7ank. 1. A -----DAVNVNDRQCQKICDQWDRLGTLTQKRREALERM-----

Target LHYYAFLRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLLSLEQGEQEESSRCQRCISELKDIRLQLEACETRIVHRLRLP  
7ank. 1. A -----

Target LDKEPARECAQRIAEQQKAQAEVEGLGKGVARLSAEAEKVLAPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKT  
7ank. 1. A -----

Target ISLVIRSTQGAEELRAHEEQLEKAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGER  
7ank. 1. A -----

Target DVEVERWRERVLTLLERWQAVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEQIQAVPLADSQAVREQLRQ  
7ank. 1. A -----

Target EKALLEEIERHAEKVEECQRFQKQYINAIKDYELQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTYSELSTLT  
7ank. 1. A -----

Target SQYIRFISETLRRMEEERLAEQQRAEERERLAEVEAALEKQRQLAEAHAQAKAQAEAEQELQRRMQEEVARREEVAVD  
7ank. 1. A -----

Target AQQQKRSIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEIIRVVRLQLETTERRGGAEQELQALRAREEAEQKR  
7ank. 1. A -----

Target QAQEEAERLRRQVQEEQTKRQRAEELGLRVKAEAEAREKQRALQALEELRLQAEAEERRLQAEAEERARQVQVALETA  
7ank. 1. A -----

Target QRSQAELQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQAEERAREEAERELERWQLKANEALRLRLQAE  
7ank. 1. A -----

Target VAQQKSLAQAEAEKQKEAAEREARRRGKAEQAVRQRELAEQELERQRLAEGTAQQLAAEQELIRLRAETEQGEQQRQ  
7ank. 1. A -----

Target LLEEELARLQSEAAAATQKRQLEAEALAKVRAEMEVLLASKARAEESRSSEKSKRLEAEAGRFRELAEEAARLRALA  
7ank. 1. A -----

Target EEAKRQRLAEEDAARQRAEAERVLSEKLAATSEATRLKTEAEIALKEKEAENERLRLRAEDEAFQRRRLEEQAQHKAD  
7ank. 1. A -----

Target IEERLAQLRKASESELERQKGLVEDTLRQRQVVEEILALKASFEEKAAAGKAELELELGRIIGNAEDTLRSKEQAEQEA  
7ank. 1. A -----

Target RQRQLAAEEERRRREAEEERVQKSLAEEEAARQKAALVEVERLKAKVEEARRLRERAEHESVRQLLAQEAQKRLQAE  
7ank. 1. A -----

Target EKAHAFVQKEQELQQTQQEQSVLEKLRSAAEARRAAEEAEERARAEREAAQSRQVVEAERLKQAAEEQAQAAQ  
7ank. 1. A -----

Target AQAAAEKLRKEAEQEAARRAQAEQAALRQKQAADAEMEKKHFAEQTLRQKAQVEQELTALRLKLETDHQSILDQELQ  
7ank. 1. A -----

Target RLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVAAQEA  
7ank. 1. A -----

Target ARLRQLAEEDLAQQRALAEKMLKEQMVAQVQATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLET  
7ank. 1. A -----

Target ERQRQLEMSAEERLRLRVAEMSRAQARAEEDAQRFKQAEIIGAKLHRTLATQEKVTLVQTLETQRQQSDRDADRLRE  
7ank. 1. A -----

Target AIAELEREKDKLKEAELLQLKSEEMQTVQQEQQLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKL  
7ank. 1. A -----


Target REEQQRQQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQQEQLLAEENRRLRERLEHLEEEHRAALA  
7ank. 1. A -----

Target HSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYL  
7ank. 1. A -----

Target QGHSSIAGLLLKPANEKLTIIAALRRQLLSPGTALILLEAQAAASGFLDPVRNRRLTVTEAVKEGVVGPPELHHKLLSAER  
7ank. 1. A -----

Target AVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHGRGYFDEEMNRVLQDPSDDTKG  
7ank. 1. A -----

Target 7ank. 1. A	FFDPNTHENLTYLQLLERCVDPETGLRLLPLTDQAAKGGLVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEY -----
Target 7ank. 1. A	FTAEQRDDLRRQFRTGKVTVEKIIKIVITVIEEHEQKQLCFQGLRALVPAAELLESGLIDWDLFRQLQLGERSVQEVAE -----
Target 7ank. 1. A	VEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGPELH -----
Target 7ank. 1. A	EKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDDAQLSTGGTVDPKSHRLPLDVACARGYLDEETSTALS -----
Target 7ank. 1. A	APRDDAKTYDPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVT -----
Target 7ank. 1. A	IWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITVIEEVETRRERLSFSGLRAPVPASELLAAGILSSSQFEQLK -----
Target 7ank. 1. A	DGKTSVKDLSELSSLQTLQSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLYVHEA -----
Target 7ank. 1. A	VKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLFQAMKKGLVREHGIRLLEAQIATGGIDPVHSHRVPVDVACQRG -----
Target 7ank. 1. A	YFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVDPETGLRLLPLKGPEKAEVVETTRVYTEEETRRAFEETQI -----
Target 7ank. 1. A	DIPGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIEIEKTEIVRQQNLASYDYVRRRLTAEDL -----
Target 7ank. 1. A	YEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQAATGF -----
Target 7ank. 1. A	LLDPVKGERLTVDEAVRKGVLGPELHDLRLLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEELRLDDAQLATGGIVDP -----
Target 7ank. 1. A	RLGFHLPLEVAYQRYLNDTHDQLSEPSEVRSYVDPSTDERLSYQLLRRCRRDETSGLFLLPLSEARKLTFRGLRKQI -----
Target 7ank. 1. A	TVEELVRSHVMDEATAQRLQEGLTSSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEQAQA -----
Target 7ank. 1. A	TGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLIISLFQAMKKGLILKDHGIRLLEAQIATGGI -----
Target 7ank. 1. A	IDPEESHRLPVDVAYQRLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSS -----
Target 7ank. 1. A	KSSVRKRRVIVDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKS -----
Target 7ank. 1. A	LIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTLASWSDPTEETGPVAGILDTETLEKV -----
Target 7ank. 1. A	SITEAMHRNLVDNITGQRLLEAQAQCTGGIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQ -----
Target 7ank. 1. A	ALKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTCPKTKLKISYKDALDR -----
Target 7ank. 1. A	SMVEEGTGLRLLEAAAQSSKGYSPYSVSGSGSTTGSRSGSRTGSRAGSRRGSF DATGSGFSMTFSSSSYSSSGYGRRYA -----
Target 7ank. 1. A	SGPTSSLGGPESAAA -----

Model #02	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.53 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5dzz.1.A	45.12	monomer	0.00	BLAST	X-ray	2.60Å	0.40	3049 - 3553	0.10	Desmoplakin

The template contained no ligands.

Target 5dzz. 1. A	MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN -----
Target 5dzz. 1. A	KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLHRHQVKLVNIRNDDIADGNPKLT -----
Target 5dzz. 1. A	LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYRQ -----
Target 5dzz. 1. A	TNLENLDQAFSVAERDLGVTRLDPEDVDVPQPEKSIITYVSSLYDAMPRPVDVQDGVKANELQLRWQEYRELVLVLLQ -----
Target 5dzz. 1. A	WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAGQLKVPPGYHPLDVEKEWGKL -----
Target 5dzz. 1. A	HVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLKADGMIRLLF -----
Target 5dzz. 1. A	NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSAEGVDLP -----
Target 5dzz. 1. A	SVEAQLGSHRGLHQSVVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLESLSHGFWAAATKEL -----
Target 5dzz. 1. A	MWLSEKEEEEVGFWDWERNNSNMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARPTVESFQAALQTQWSWMLQ -----
Target 5dzz. 1. A	LCCIEAHLKENTAYFQFFSDVREAEEQLRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKQQLNEYRGHLSGLAKRAK -----
Target 5dzz. 1. A	AIVQLTPRNPTQPTRGRVPLLAVCDYKVEATVHKGDECQMLGPAQPFHVKVLSSSGSEAAVPSVCFLVPPPNQEALAV -----
Target 5dzz. 1. A	ARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLELHYQAFLRDSQDAGGFGPE -----
Target 5dzz. 1. A	DRLQAEREYGSCSRHYQQLLSLEQGEQEESRCRCISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQKA -----
Target 5dzz. 1. A	QAEVEGLGKGVARLSAAEAKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKTIISLVIRSTQGAEELRAHE -----
Target 5dzz. 1. A	EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELRGAEVGERLQQRHGERDVEVERWRERVTLQLLRWQ -----
Target 5dzz. 1. A	AVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEIQAVPLADSQAVREQLRQEKALLEEIERHAEKVEECQ -----
Target 5dzz. 1. A	RFAKQYINAIKDYEQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRFISETLRRMEEER -----
Target 5dzz. 1. A	LAEQQRAEERERLAEVEAALEKQRQLAEAHQAQAQAEAAQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSS -----
Target 5dzz. 1. A	EAEIQAKARQVEAAERSRLRIEEIIRVVRLQLETTERQRGGAEGELQALRARAEAEAAQKRQAQEEAERLRRQVQEETQR -----

Target 5dzz. 1. A KRQAEAEGLRVKAEAEAREKQRALQALEELRLQAEAEERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKT-----

Target 5dzz. 1. A AQLERTLEEEHVTVVQLREEATRREQQAEAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAA-----

Target 5dzz. 1. A EREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQLAAEQELIRLRAETEQQEQQRQLLEEELARLQSEAAAAATQK-----

Target 5dzz. 1. A RQELEAELAKVRAEMEVLLASKARAEESRSSEKSKQRLEAEAGRFRELAEEAARLRALAEAEAKRQRQLAEEDAARQRA-----

Target 5dzz. 1. A EAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRLRLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ-----

Target 5dzz. 1. A KGLVEDTLRQRRQVEEEILALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRRREAEEER-----

Target 5dzz. 1. A VQKSLAAEEEAARQRKAALAEVERLKAKVVEEARRLRERAEHESVRQLQLAQEAQKRLQAE EKAHAFVQQKEQELQQT-----

Target 5dzz. 1. A QQEQSVLEKL RSEAEAAARRAAEEAEARERAREEAQSRQRVEEAERLKQAAEEQAQAQAQAQAAAEKL RKEAEQEAARR-----

Target 5dzz. 1. A AQAEQAALRQKQAADAEMEKHKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKA EVTEAARQRSQVEEE-----

Target 5dzz. 1. A LFSVRVQMEELGK LKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAE-----

Target 5dzz. 1. A KMLKEKMQAVQEATRLKAEAE LLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEERLRLRV-----

Target 5dzz. 1. A AEMSRAQARAEEDAQRFRKQAEETGAKLHRTELATQEKVTLVQTLETQRQQSDRDADRLREAI AELEREKDKLKKEAE LL-----

Target 5dzz. 1. A QLKSEEMQTVQQEQ LLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKA QKLREEQQRQQQMQQEKQ LL-----

Target 5dzz. 1. A ASMEEARRRQHEAE EGVRRKQEELQLLEQQRQQQEQLLAENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG-----

Target 5dzz. 1. A QDAADGPAAEP EHA FEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLPANEKLT-----

Target 5dzz. 1. A IYAALRRQLLSPGTALILLEAQ AASGFLDPVRNRRLTVTEAVKEGVGP ELP HHLKLSAERAVTGYKDPYTGEKISLFQA-----

Target 5dzz. 1. A MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRYGFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC-----

Target 5dzz. 1. A VEDPETGLRLLPLTDQAAKG GELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTA EQRRDLLRQFRTGKVT-----

Target 5dzz. 1. A VEKIIKIVITVIEEHEQKGQLCFQGLRALVPAAELLESIGIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWL-----

Target 5dzz. 1. A EEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHV IDPATSARLTVDEAVRAGLVGP ELPHEKLLSAEKAVTGYKDPYSG-----VFDGLRKKV-----TAMQLYECQLIDKTTLDKLLKGKKSVEE-----VASEIQPFLRGAGSIAGASAPK-----

Target 5dzz. 1. A QSVSLFQALKKGLIPREQGLRL LDAQLSTGGTVDP SKSHRLPLDVACAR-----GYLDEETSTALS EKYSLV EAKRKKLISPESTVMLLEAQ AATGGIIDPHRNEKLTVD SAIARDLIDFDDRQIYAAEKAITGFDDPFSGKTVS-----

Target 5dzz. 1. A APRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARAR--QQELYSEVQAREAFQKATVEVPVGSFQGRAV VSEATIKKNLIDRETGMRLLEAQIASGGVDPVNSV-FLPKDVALARGLIDRDLYRSLNDPRDSQKNFVD-PVTKKKVSYV-----

Target 5dzz. 1. A TIWELINSEYFTA EQRQELLRQFRTGKVTVEKIIKIVITVIEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQL QLKERCRIEPTG-----LLLLSVQKRSM SFQGI RQPVTVTELVD SGILRPSTVNEL-----

Target 5dzz. 1. A KDGKTSVKDLSELSSLQTL LQGSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQ AATGFLVDPVRNQRLYVHE ESGQISYDEVERIKDFLQGSSCI--AGIYNETTKQLGIYEAMKIGLVRPGTALELLEAQ AATGFIVDPVSNLRLPVEE-----

Target 5dzz. 1. A AVKAGVVGPELPHEKLLSAEKAVTGYKDPYSGSTISLFQAMKGLV VREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQR AYKRGLVGIEFKEKLLSAERAVTGYNDPETGNIISLFQAMNKELIEKGHGIRLLEAQIATGGIIDPKESHRLPVDIAYKR-----

Target  
5dzz. 1. A

GYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETRRAFEETQ  
GYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLKERICKDEETGLCLLPLK-----

Target  
5dzz. 1. A

IDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEKTEIVRQQNLASYDYVRRRLTAED  
-----

Target  
5dzz. 1. A

LYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQATG  
-----

Target  
5dzz. 1. A

FLLDPVKGERLTVDEAVRKGLVGPELHDLRLLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEALRLDDAQLATGGIVD  
-----

Target  
5dzz. 1. A

PRLGFHLPLEVAYQRGYLNKDDHQLSEPSEVRSYVDPSTDERLSYTLQLRRCRRDETSGFLPLPLSEARKLTFRGLRKQ  
-----

Target  
5dzz. 1. A

ITVEELVRSHVMDEATAQRLQEGLTSSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKGGIIRPGTAFELLEAAQ  
-----

Target  
5dzz. 1. A

ATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQAMKKGLILKDHGIRLLEAQIATGG  
-----

Target  
5dzz. 1. A

IIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTS  
-----

Target  
5dzz. 1. A

SKSSVRKRRVVIVDPETGKEMSVYEAYRKGLIDHQTYLELSECEWEIEITISSDGVVKSMIIDRRSGRQYDIDEAIAK  
-----

Target  
5dzz. 1. A

SLIDRSALDQYRAGTSLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDDETLEK  
-----

Target  
5dzz. 1. A

VSITEAMHRNLVDNITGQRLLEAQAQTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAA  
-----

Target  
5dzz. 1. A

QALKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKL RDVSAYSKYLTCPKTKLKI SYKDALD  
-----

Target  
5dzz. 1. A

RSMVEEGTGLRLLEAAAQSSKGYSPYSVSGSGSTTGSRSRGTGSRAGSRGSDATGSGFSMTFSSSSYSSSGYGRRY  
-----

Target  
5dzz. 1. A

ASGPTSSLGGPESAAA  
-----

Model #18	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.44 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
4d1e.1.A	12.65	homo-dimer	0.00	HHblits	X-ray	3.50Å	0.26	627 - 1221	0.09	ALPHA-ACTININ-2

The template contained no ligands.

Target  
4d1e. 1. A

MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQSRRRGGGGPGNGSVLDP AERAVIRIADERDRVQKKTFTKWVN  
-----

Target  
4d1e. 1. A

KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYL RHRQVKLVNIRNDDIADGNPKLT  
-----

Target  
4d1e. 1. A

LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAI IHRHKPMLIDMNKVYRQ  
-----

Target  
4d1e. 1. A

TNLENLDQAFSVAERDLGVTRLLDPEDVDVPQPEKSIITYVSSLYDAMP RVPDVQDGVKANELQLRWQEYRELVL LLLQ  
-----

Target  
4dle. 1. A WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSGIYQSLEGAVQAGQLKVPPTYHPLDVEKEWGL  
-----

Target  
4dle. 1. A HVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLAAGKAPQRAGEVERDLKADGMIRLLF  
-----

Target  
4dle. 1. A NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSAEGWVDLP  
-----

Target  
4dle. 1. A SVEAQLGSHRGLHQSVVEEFAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLES LHGFVAAATKEL  
-----RLMEEYERLASELL

Target  
4dle. 1. A MWLSEKEEEVGFWDSESNMAAKKEAYSALMRELELKEKKIK-EIQST---GDRLL-REDHPARPTVESFQAALQTQ  
EWIRRTIPWLENRTPAATMQAMQKLEDFRDYRRKHKPKVQEKCLEINFNTLQTKLRISNRPAFMPSEGKMVSDIAGA

Target  
4dle. 1. A WSWMLQLCCIEAHLKE-----NTAYFFQFSDVREAEELRKLQETLHRKYTCDR-SITVTRLEDLLQDAQDEKDQL  
WQRLEQAQEGYEEWLLNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILLQ---KDYESASLTEVRALLRKHEAFESDL

Target  
4dle. 1. A NEYRGHLSGLAKRAKAIIVQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSV  
AAHQDRVEQIAAIAQELNELDY--H-D-----

Target  
4dle. 1. A CFLVPPPNQEALEAVARLEAQHQALVTLWHQLHTDMKSLLAW-----QSLSRDVQLIRSWSLVTFRTLKPEEQRQAL  
-----AVNVNDRCKKICDQWDRGLTLTQKRREALERMEKLETTIDQLHLEFAKRAAPFNNWME-----

Target  
4dle. 1. A RSLELHYQAFRLRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLLSLEQGEQESRCRCISELKDIRLQLEACETRIVHR  
-----GAMEDLQDM

Target  
4dle. 1. A LRLPLDKEPARECAQRIAEQQAQAEVEGLGKGVARLSAEAEKVLALPEP-----SPAAPT LRSELETLGKLEQVRSLS  
F---IV-HSIEEIQSLITAHEQFKATLPEADGERQSIMAIQNEVEKVIQSYNIRISSNPYSTVTMDELRTKWDKVKQLV

Target  
4dle. 1. A AIYLEKLKTI-----SLVIRSTQGAEALRAHEEQKEAQAVPAALPELEATKAAMKKLRAQAEQQPVFDALR  
PIRDQSLQEELARQHANERLRRQFAAQANAIGPWIQNKMEETAR--SSIQITGALEDQMNQLKQYEHNIINYKNNIDKLE

Target  
4dle. 1. A DELRGAQEVGERLQQRHGERDVEVERWRERVQTLLEWRQAVLAQTDVRQRELEQLGRQLRYYRESADPLGAWLQDARRRQ  
-----GDHQLIQEALV---FDNKHTNYTMEHIRVGWELLTTIARTINEVETQILTRD-----

Target  
4dle. 1. A EQIQAVPLADSQAVREQLRQEKALLEEIERHAEKVEECQRFQKQYINAIKDYELQLVITYKAQLEPVASPAKKPKVQSGSE  
-----

Target  
4dle. 1. A SVIQEYVDLTRYSELSTLTSQYIRFISETLRRMEEERLAEQQRAEERERLAEVEAALEKQRQLAEHAQAKAQAEAREA  
-----

Target  
4dle. 1. A QELQRRMQEEVARREEVAVDAQQQKRSIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETTERQGG  
-----

Target  
4dle. 1. A AEGELQALRARAEAEAQKRAQEEAERLRRQVQEETQKRQAEAEGLRVKAEAEAAAREKQALQALEELRLQAEAEER  
-----

Target  
4dle. 1. A RLRQAEAEARQVQVALETAQRSQAELQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQAEAEARAREEAERE  
-----

Target  
4dle. 1. A LERWQLKANEALRLRLQAE EVAQQSLAQAEAEKQKEAAEREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQRLA  
-----

Target  
4dle. 1. A AEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAATQKRQELEAEAKVRAEMEVLLASKARAEESRSSEKSKRLE  
-----

Target  
4dle. 1. A AEAGRFRELAEEAARLALAEAEAKRQRQLAEEDAARQRAEAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRLA  
-----

Target  
4dle. 1. A EDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEELALKASFEEKAAAGKAELELELGR  
-----

Target  
4dle. 1. A IRGNAEDTLRSKEAQEAARQRQLAAEEERRRREAEERVQKSLAAEEEAARQKAAL EEVERLKAKVEEARRLRERAEH  
-----

Target  
4dle. 1. A ESVRQLQLAQEAQKRLQAEKHAFAVQQKEQELQQTLLQEQSVLEKL RSEAEFAARRAAEEAEARERAEREAAQSRQR  
-----

Target  
4dle. 1. A VEEAERLKQAAEEQAQAQAQAAAAEKLRKEAEQEAARRAQEAALRQKQAADAEMEKKHKKFAEQTLRQKAQVEQELTA  
-----

Target  
LRLKLEETDHQKSILDQELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLRKARIEAENRALILRDKDNTQRLQEEA

4dle. 1. A -----  
Target EKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDK  
4dle. 1. A -----  
Target EQMAQQLAQETQGFQRTLETERQRQLEMSAEAEERLRLVAEMSRAQARAEDAQRFRKQAEIIGAKLHRTELATQEKVTL  
4dle. 1. A -----  
Target VQTLETQRQQSDRDADRLREAIAELEREKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIE  
4dle. 1. A -----  
Target EEKAKLERLFQDEVAKAKLREEQQRQQQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLEQQRQQQEQLLAAE  
4dle. 1. A -----  
Target NRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRL  
4dle. 1. A -----  
Target AQGHTTVAELTQREDVRRYLQGHSSIAGLLLPANEKLTIIYAALRRQLSPGTALILLEAQAASGFLLDPVRNRRLTVTE  
4dle. 1. A -----  
Target AVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISLQFQAMKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHR  
4dle. 1. A -----  
Target GYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSA  
4dle. 1. A -----  
Target PFGKFQGKTVTIWELINSEYFTAQRRLLRQFRTGKVTVEKIIKIVITVIEEHEQKGLCFQGLRALVPAAELLESII  
4dle. 1. A -----  
Target DWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT  
4dle. 1. A -----  
Target SARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLLDAQLSTGGTVDPSPKSHRL  
4dle. 1. A -----  
Target PLDVACARGYLDEETSTALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQARE  
4dle. 1. A -----  
Target AFQKATVEVPVGSFQGRAVTIWELINSEYFTAQRQELLRQFRTGKVTVEKIIKIVITVIEEVETTRRERLSFSGLRAPV  
4dle. 1. A -----  
Target PASELLAAGILSSSQFEQLKDGKTSVKDLSELSSLQTLQSGGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLLEAQ  
4dle. 1. A -----  
Target AATGFLVDPVRNQRLVHEAVKAGVGPPELHEKLLSAEKAVTGYKDPYSGSTISLQFQAMKGLVVREHGIRLLEAQIATG  
4dle. 1. A -----  
Target GIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEV  
4dle. 1. A -----  
Target ETTRYVTEETTRAFEETQIDIPGGSGHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEKTEIV  
4dle. 1. A -----  
Target RQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPITYQALKK  
4dle. 1. A -----  
Target GLLSAEVARLLLEAQATGFLDPVKGERLTVDEAVRKGLVGPPELHDRLLSAERAVTGYRDPYTEQTISLQFQAMKDLIP  
4dle. 1. A -----  
Target AEEALRLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSYTLRLRCRRDETSGL  
4dle. 1. A -----  
Target FLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQA  
4dle. 1. A -----  
Target MKKGIIRPGTAFELLEAQATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLIISLQFQAMKKG  
4dle. 1. A -----  
Target LILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDP  
4dle. 1. A -----  
Target QTGLRLLPLKEKKRERKTSKSSSVRKRVRVIVDPETGKEMSVYEAIRKGLIDHQTYLELSEQECEWEEITISSSDGVVKS  
4dle. 1. A -----



Target 4d1e. 1. A MIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSD

Target 4d1e. 1. A PTEETGPVAGILDTELEKVSITEAMHRNLVDNITGQRLLEAQAQCTGGIIDPNTGERFPVTDVAVNKGLVDKIMVDRINLA

Target 4d1e. 1. A QKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTGPRVPLDEALQRGTVDARTAQKL RDVSAYS

Target 4d1e. 1. A KYLTCPKTKLKISYKDALDRSMVEEGTGLRLLLEAAAQSSKGYSPYSVSGSGSTGSRSGSRTGSRAGSRRGSFDTGSG

Target 4d1e. 1. A FSMTPSSSSYSSSGYGRRYASGPTSSLGGPESAAA

Model #16	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.64 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
6s12.1.A	29.82	homo-dimer	0.00	HHblits	X-ray	3.10Å	0.36	62 - 448	0.08	Calponin homology domain protein putative

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
CA.1	Binding site not conserved.	CALCIUM ION
CA.4	Binding site not conserved.	CALCIUM ION
MG.2	Not in contact with model.	MAGNESIUM ION
MG.5	Not in contact with model.	MAGNESIUM ION
TRS.3	Not biologically relevant.	2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL
TRS.6	Not biologically relevant.	2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL

Target 6s12. 1. A MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN  
-----ELVAQWEKVQIKTFTKWVN

Target 6s12. 1. A KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPR-EKGRMRFHKLQNVQIALDYLRRHQVKLVNIRNDDIADGNPKL  
MHLAKKGRKINDVTDFKNGVELCALLEIIGETTICKVTNPKMRIQMTENLDKALRFIQSRDVKL TGIGPTDIVDGNVKL

Target 6s12. 1. A TLGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYR  
TLGLVWTLILRFATISELSAE----GLSAKQGLLLWCQKKCEPYP-VKVENFSESFKDGKVFCALIHRRHPDLLDWETVGE

Target 6s12. 1. A QTNLENLDQAFSVAERDLGVTRLLDPEDVDV-PQPDEKSIITYVSSLYDAMPVPDVQDGVK-----ANELQLRWQE  
D-DRANLEKAFDVAEKELGIPKLLDVDDIVNMPRPDERSVMTYVAALYKVFSSNDQVEKAGKRAGNFLDLLRATEGMVHD

Target 6s12. 1. A YRELVLILLQWIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSGIYQSLEGAVQAG---QLKVPPG  
YEQRAQALKENIEAAINKMNGVEPSDEYHQVEQINETKNYRKGDKRAFIKEQGDLATLFGQINSKLGRMKRPVYVAPEG

Target 6s12. 1. A YHPLDVEKEWGKLVHAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVER  
LDPKSLEGYIANISEAERALRSKLN TAMR--NCLIALRKAFADPANATDAKINEYRTFVTD-----

Target 6s12. 1. A DLDKADGMIRLLFNDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQ  
-----

Target 6s12. 1. A RRVDSAEWGVDLPVSAQLGSHRGLHQSVVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLE  
-----

Target 6s12. 1. A SLHGFVAAATKELMWLSEKEEEEVGFWDSESNSMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARPTVESF  
-----

Target 6s12. 1. A QAALQTQWSWMLQLCCCEIAHLKENTAYFQFFSDVREAEQRLKQLQETLHRKYTCDRSITVTRLEDLLQDAQDEKDLNE  
-----

Target 6s12. 1. A	YRGHLSGLAKRAKAIVQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCF -----
Target 6s12. 1. A	LVPPPNQEALEAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFTLKPEEQRQALRSLELHYQAF -----
Target 6s12. 1. A	LRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLQSLEQGEQEESRCQRCISELKDIRLQLEACETRTRVHRLRLPLDKEPA -----
Target 6s12. 1. A	RECAQRIAEQKKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLTISLVIR -----
Target 6s12. 1. A	STQGAEELRAHEEQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVER -----
Target 6s12. 1. A	WRERTQLLERWQAVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEQIQAVPLADSQAVREQLRQEKALLE -----
Target 6s12. 1. A	EIERHAEKVEECQRFQAKQYINAIKDYELQLVTYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRF -----
Target 6s12. 1. A	ISETLRRMEEERLAEQQRAEERERLAEVEAALEKQRQLAEAHQAQAQAEAEQELQRRMQEEVARREEVAVDAQQQR -----
Target 6s12. 1. A	SIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEIIRVVRLQLETTERQRGGAEGELQALRARAEAEAKRQAQEEA -----
Target 6s12. 1. A	ERLRRQVQEETQRKRQAEELGLRVKAEAAAREKQRALQALEELRLQAEAAERRLRQAEARARQVQVALETAQRSQA -----
Target 6s12. 1. A	ELQSKHASFAEKTAQLERTLEEEHVTVVQLREEATREQQQAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKS -----
Target 6s12. 1. A	LAQAEAEKQKEAAEREARRRGKAEQAVRQRELAQEQLERQRQLAEGTAQQLAAEQELIRLRAETEQGEQQRQLLEEL -----
Target 6s12. 1. A	ARLQSEAAAAATQKRQELEAELAKVRAEMEVLLASKARAEESRSSEKSKRLEAEAGRFRELAEEAARLRALAEAAKRQ -----
Target 6s12. 1. A	RQLAEEDAARQRAEAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRLAEDEAFQRRRLEEQAQHKADIEERLA -----
Target 6s12. 1. A	QLRKASESELERQKGLVEDTLRQRRQVEEELALKASFKAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLA -----
Target 6s12. 1. A	AEERRRRREAEERVQKSLAEEEEARQRKAALEEVERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKRLQAEKHAHF -----
Target 6s12. 1. A	AVQQKEQELQQTLLQEQSVLEKLRSSEAAARRAAEEAEARERAEREAAQSRQRVEEAERLKQAAEEQAQAQAQAAAAE -----
Target 6s12. 1. A	KLRKEAEQEAARRAQAEQAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKAEV -----
Target 6s12. 1. A	TEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAQEAARLRQL -----
Target 6s12. 1. A	AEEDLAQQRALAEKMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQL -----
Target 6s12. 1. A	EMSAEAEERLRLVAEMSRAQARAEDAQRFRKQAEELGAKLHRTTELATQEKVTLVQTLETQRQQSDRDADRLREIAELE -----
Target 6s12. 1. A	REKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRRERFIEEEKAKLERLFQDEVAKAQLREEQQR -----
Target 6s12. 1. A	QQQQMQQEKQQLLASMEEAARRRQHEAEEGVRRKQEELQLLEQQRQQQEQLLAENRRRLRERLEHLEEEHRAALAHSEEIT -----
Target 6s12. 1. A	AAQAAATRALPNGQDAADGPAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSI -----
Target	AGLLKPAN EKLTIIYAALRRQLLSPGTALILLEAQ AASGFLDPVRNRRLTVTEAVKEGVGP ELP HHLKLSAERAVTGYK

6s12. 1. A -----

TargetDPYTGEKISLFFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNT

6s12. 1. A -----

TargetHENLTYLQLLERCVDPETGLRLLPLTDQAAKGGLVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTAQR

6s12. 1. A -----

TargetRDLLRQFRTGKVTVEKIIKIVITVIEEHEQKGLCFQGLRALVPAELLESGLIDWDLFRQLQLGERSVQVEAEVEGVRR

6s12. 1. A -----

TargetALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGPELHEKLLSA

6s12. 1. A -----

TargetEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLLDAQLSTGGTVDP SKSHRLPLDVACARGYLDEETSTALSAPRDDA

6s12. 1. A -----

TargetKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELIN

6s12. 1. A -----

TargetSEYFTAQRQELLRQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKDGTSTV

6s12. 1. A -----

TargetKDLSELSSLQTLQGGGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQAA TGFLVDPVRNQRLYVHEAVKAGV

6s12. 1. A -----

TargetGPHELHEKLLSAEKAVTGYKDPYSGSTISLFFQAMKKGLVVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEM

6s12. 1. A -----

TargetNRVLEDPDDTKGFFDPNTHENLTYRQLLERCVDPETGLRLLPLKGPEKA EVVETTRVYTEEETRRAFEETQIDIPGGG

6s12. 1. A -----

TargetSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVI

6s12. 1. A -----

TargetSRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQAA TGFLDPVK

6s12. 1. A -----

TargetGERLTVDEAVRKGLVGPELHRLLSAERAVTGYRDPYTEQTISLFFQAMKKDLIPAEALRLLDAQLATGGIVDPRLGFHL

6s12. 1. A -----

TargetPLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSYQLLRRCRRETSGLFLLPLSEARKLTFRGLRKQITVEELV

6s12. 1. A -----

TargetRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEAQAA TGVID

6s12. 1. A -----

TargetPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFFQAMKKGLILKDHGIRLLEAQIATGGIIDPEES

6s12. 1. A -----

TargetHRLPVDVAYQRLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSSKSSVRK

6s12. 1. A -----

TargetRRVIVDPETGKEMSVYEA YRKGLIDHQTYLELSEQECWEIEITISSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSA

6s12. 1. A -----

TargetLDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSYPISPA VSRTQLASWSDPTEETGPVAGILD TETLEKVSITEAM

6s12. 1. A -----

TargetHRNLVDNITGQRLLEAQACTGGIIDPNTGERFPVTD AVNKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGW

6s12. 1. A -----

TargetLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAKLRDVSAYS KYLTCPKTKLKISYKDALDRSMVEEG

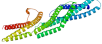
6s12. 1. A -----

TargetTGLRLLLEAAQSSKGYSPYSVSGSGSTGSRSGSRTGSRAGSRRGSF DATGSGFSMTFSSSSYSSSGYGRRYASGPTSS

6s12. 1. A -----

TargetLGGPESAAA

6s12. 1. A -----

Model #11	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.69 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5j1i.1.A	96.47	monomer	0.00	HHblits	X-ray	2.80Å	0.59	991 - 1351	0.08	Plectin

The template contained no ligands.

Target 5j1i.1.A MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQSRRRGGGPGNGSVLDPATERAVIRIADERDRVQKKTFTKWVN

Target 5j1i.1.A KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLHRHQVKLVNIRNDDIADGNPKLT

Target 5j1i.1.A LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYRQ

Target 5j1i.1.A TNLENLDQAFSVAERDLGVTRLLDPEDVDVPQDEKSIITYVSSLYDAMPRPVDVQDGVKANELQLRWQEYRELVLVLLQ

Target 5j1i.1.A WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAGQLKVPVPGYHPLDVEKEWGKL

Target 5j1i.1.A HVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLKADGMIRLLF

Target 5j1i.1.A NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSAEGVDDL

Target 5j1i.1.A SVEAQLGSHRGLHQSVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLES LHGFVAAATKEL

Target 5j1i.1.A MWLSEKEEEVGFWDWERNNSMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARPTVESFQAALQTQSWMLQ

Target 5j1i.1.A LCCCIEAHLKENTAYFQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKDQLNEYRGHLSGLAKRAK

Target 5j1i.1.A AIVQLTPRNPTQPTRGRVPLLAVCDYKVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCFLVPPPNQEALEAV

Target 5j1i.1.A ARLEAQHQALVTLWHQLHTDMKSLLAWSLRDVLIRWSLVTFRTLKPEEQRQALRSLELHYQAFRLDSQDAGGFGPE

Target 5j1i.1.A DRLQAEREYGSCSRHYQQLLSLEQGEQEESRCQRCISELKDIRLQLEACETRTRVHRLRLPLDKEPARECAQRIAEQQA  
-----QEESRCQRCISELKDIRLQLEACETRTRVHRLRLPLDKEPARECAQRIAEQQA

Target 5j1i.1.A QAEVEGLGKGVARLSAEAEKVLALPEPSAAPTTLRSELELTGKLEQVRSLSAIYLEKLKLTISLVIRSTQGAEELRAHE  
QAEVEGLGKGVARLSAEAEKVLALPEPSAAPTTLRSELELTGKLEQVRSLSAIYLEKLKLTISLVIRGTQGAEEVLRAHE

Target 5j1i.1.A EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVERWRRVTQLLERWQ  
EQLKEAQAVPATLPELEATKASLKKLRAQAEAAQPTFDALRDELGAQEVGERLQQRHGERDVEVERWRRVAQLLERWQ

Target 5j1i.1.A AVLAQTDVQRLEQLGRQLRYYRESADPLGAWLQDARRRQEIQAVPLADSQAVREQLRQEKALLEEIERHAEKVEECQ  
AVLAQTDVQRLEQLGRQLRYYRESADPLGAWLQDARRRQEIQAMPLADSQAVREQLRQEKALLEEIERHGEKVEECQ


Target 5j1i.1.A RFAKYINAIKDYLQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTYSELSTLTSQYIRFISSETLRRMEEER  
RFAKYINAIKDYLQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTYSELSTLTSQYIKFISSETLRRM-----

Target 5j1i.1.A LAEQQRAEERERLAEVEAALEKQRLAEAHQAQAQAEAAQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSS

Target 5j1i.1.A EAEIQAKARQVEAAERSRLRIEEIIRVVRLQLETTERQRGGAEGELQALRAREEAEAKRQAQEEAERLRRVQEETQR

Target 5jli.1.A	KRQAEAEGLRVKAEAEAREKQRALQALEELRLQAEAEERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKT -----
Target 5jli.1.A	AQLERTLEEEHVTVVQLREEATRREQQAEAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAA -----
Target 5jli.1.A	EREARRRGKAEEQAVRQRELAEQELERQRQLAEGTAQQRLAAEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAAATQK -----
Target 5jli.1.A	RQELEAELAKVRAEMEVLLASKARAEESRSSESKQRLEAEAGRFRELAEEAARLRALAEAAKRQRQLAEEDAARQRA -----
Target 5jli.1.A	EAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRLLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ -----
Target 5jli.1.A	KGLVEDTLRQRRQVEEELALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAEEER -----
Target 5jli.1.A	VQKSLAEEEEAARQRKAAL EEVERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKRLQAE EKAHAFVQQKEQELQQTL -----
Target 5jli.1.A	QQEQSVLEKL RSEAEAAARRAAEEAEARERAEERAAQSRQRVEEAERLKQAAEEQAQAQAQAAAAEKL RKEAEQEAARR -----
Target 5jli.1.A	AQAEQAALRQKQAADAEMEKHKFAEQTLRQKAQVEQELTALRLKLEETHQKSILDQELQRLKAEVTEAARQRSQVEEE -----
Target 5jli.1.A	LFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAE -----
Target 5jli.1.A	KMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEERLRLRV -----
Target 5jli.1.A	AEMSRAQARAEEDAQRFRKQAEETGAKLHRTELATQEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAELL -----
Target 5jli.1.A	QLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQLREEQQRQQQQMQQEKQQLL -----
Target 5jli.1.A	ASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQQEQLLAENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG -----
Target 5jli.1.A	QDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLKPANEKLT -----
Target 5jli.1.A	IYAALRRQLLSPGTALILLEAQAASGFLDPVRNRRLTVTEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISL FQA -----
Target 5jli.1.A	MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC -----
Target 5jli.1.A	VEDPETGLRLLPLTDQAAKGGEVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTA EQRRDLLRQFRTGKVT -----
Target 5jli.1.A	VEKIIKIVITVIEEHEQKQLCFQGLRALVPAAELLESGLIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWL -----
Target 5jli.1.A	EEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVDPATSARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSG -----
Target 5jli.1.A	QSVSLFQALKKGLIPREQGLRLDLAQLSTGGTVDPKSHRPLDVCARGYLDEETSTALSAPRDDAKTYYPDPTWELAT -----
Target 5jli.1.A	YSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTA EQRQELL -----
Target 5jli.1.A	RQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKD GKTSVKDLSELSSLQTLL -----
Target 5jli.1.A	QGGGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLEAQAAATGFLVDPVRNQRLYVHEAVKAGVVGPPELHEKLLSAEK -----
Target	AVTGYKDPYSGSTISL FQAMKKGLVVREHGIRLLEAQIATGGIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKG -----

5jli.1.A -----  
Target FFDPNTHENLTyrQLLERCVEDPETGLRLLPLKGPEKAEEVETTRVYTEEETRRAFEETQIDIPGGGSHGGSTMSLWEVM  
5jli.1.A -----  
Target QSDLIPEEQRAQLMADFQAGRVTKERMI I I I I E I IEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTR  
5jli.1.A -----  
Target SLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRK  
5jli.1.A -----  
Target LVGPELHDRLLSAERAVTGYRDPYTEQTISL FQAMKKDLIPAEELRLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNK  
5jli.1.A -----  
Target DTHDQLSEPSEVRSYVDPSTDERLSYTQLLRRCRRDETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRL  
5jli.1.A -----  
Target QEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKGIIRPGTAFELLEAQAATGYVIDPIKGLKLTVEEAV  
5jli.1.A -----  
Target RMGIVGPEFKDLLSAERAVTGYKDPYSGKLISL FQAMKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRL  
5jli.1.A -----  
Target FDEEMNEILTDP SDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSSKSSVRKRRVIVDPETGKE  
5jli.1.A -----  
Target MSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITE  
5jli.1.A -----  
Target FADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILD TETLEKVSITEAMHRNLVDNITGQRL  
5jli.1.A -----  
Target LEAQA CTGGIIDPNTGERFPVTD AVNKGLVDKIMVDRINLAQKAF CGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQ  
5jli.1.A -----  
Target YLTGGLIEPDT PGRVPLDEALQRGTVDARTAKLRDVSAYS KYLTC PKTKL KISYKDALDRSMVEEGTGLRLLEAAQSS  
5jli.1.A -----  
Target KGYSPYSVSGSGSTTGSRSRTGSRAGSRRGSF DATGSGFSMTFSSSSYSSSGYGRRYASGPTSSLG GPESAAA  
5jli.1.A -----

Model #04	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.65 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5dzz.1.A	54.12	monomer	0.00	HHblits	X-ray	2.60Å	0.45	2977 - 3553	0.11	Desmoplakin

The template contained no ligands.

Target MSGEDQEVRAVEDGSNGSGSPSGDTLPWNLEKTQRSRRGGGGPGNGSVLDP AERAVIRIADERDRVQKKTFTKWVN  
5dzz.1.A -----  
Target KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLRHRQVKLVNIRNDDIADGNPKLT  
5dzz.1.A -----  
Target LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAI IHRHKPMLIDMNKVYRQ  
5dzz.1.A -----  
Target TNLENLDQAFSVAERDLGVTRLLDPEDVDVPQ PDEKSIITYVSSLYDAMP RVPDVQDGVKANELQLRWQEYREL VLLLLQ  
5dzz.1.A -----  
Target WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAGQLKVP PGYHPLDVEKEWGKL

5dzz. 1. A -----  
Target HVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLKADGMIRLLF  
5dzz. 1. A -----  
Target NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSAEWGVDLP  
5dzz. 1. A -----  
Target SVEAQLGSHRGLHQSVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLESLHGFVAAATKEL  
5dzz. 1. A -----  
Target MWLSEKEEEEVGFWDWSEKSNMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPPARPTVESFQAALQTQWSWMLQ  
5dzz. 1. A -----  
Target LCCCIEAHLKENTAYFQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKQQLNEYRGHLSGLAKRAK  
5dzz. 1. A -----  
Target AIVQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHKGDECQMLGPAQPPHVKVLSSSGSEAAVPSVCFLVPPPNQEALEAV  
5dzz. 1. A -----  
Target ARLEAQHQALVTLWHQLHTDMKSLLAWSLSRDVQLIRWSLVTFRTLKPEEQRQALRSLELHYQAFLRDSQDAGGFGPE  
5dzz. 1. A -----  
Target DRLQAEREYGSCSRHYQQLLSLEQGEQEESRCQRCISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQQKA  
5dzz. 1. A -----  
Target QAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKTIISLVIRSTQGAEELRAHE  
5dzz. 1. A -----  
Target EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVERWRERVTLLELRWQ  
5dzz. 1. A -----  
Target AVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEIQAVPLADSQAVREQLRQEKALLEIERHAEKVEECQ  
5dzz. 1. A -----  
Target RFAKQYINAIKDYLQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRFISETLRRMEEEER  
5dzz. 1. A -----  
Target LAEQQRAEERERLAEVEAALEKQRQLAEHAQAKAQAEAEQELQRRMQEEVARREEVAVDAQQQKRSIQEELQQLRQSS  
5dzz. 1. A -----  
Target EAEIQAQARQVEAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQALRAREEAEAKRQAQEEAERLRRQVQEETQR  
5dzz. 1. A -----  
Target KRQAEELGLRVKAEAEAREKQRALQALEELRLQAEAAERRLRQAEAEARARQVQVALETAQRSAQELQSKHASFAEKT  
5dzz. 1. A -----  
Target AQLERTLEEEHVTVVQLREEATRREQQAEEAERAREEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAA  
5dzz. 1. A -----  
Target EREARRRGKAEQAVRQRELAEQELERQRLAEGTAQQLAAEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAAATQK  
5dzz. 1. A -----  
Target RQELEAELAKVRAEMEVLLASKARAEESRSSEKSKRLEAEAGRFRELAEEAARLRALAEAAKRQRQLAEEDAARQRA  
5dzz. 1. A -----  
Target EAERVLSEKLA AIS EATRLKTEAEIALKEKEAENERLRLRAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ  
5dzz. 1. A -----  
Target KGLVEDTLRQRRQVEEELALKASFEEKAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAER  
5dzz. 1. A -----  
Target VQKSLAEEEEAARQRKAAL EEVERLKAKVEEARRLRERAEHESVRQLQLAQEAQKRLQAEKHAFAVQQKEQELQOTL  
5dzz. 1. A -----  
Target QQEQSVLEKLRSEAEAAARRAAEEAEERARAEREAQSRQRVEEAERLKQAAEEQAQAQAQAAAEKLRKEAEQEAARR  
5dzz. 1. A -----  
Target AQAEQAALRQKQAADAEMEKHKFAEQTLRQKAQVEQELTALRLKEETDHQKSILDQELQRLKAEVTEAARQRSQVEEE  
5dzz. 1. A -----  
Target LFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAQAQAARLRQLAEEDLAQQRALAE  
5dzz. 1. A -----

Target 5dzz. 1. A KMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEAERLRLRV-----

Target 5dzz. 1. A AEMSRAQARAEEDAQRFKQAEIEGAKLHRTTELATQEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAEELL-----

Target 5dzz. 1. A QLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQQMQQEKQQL-----

Target 5dzz. 1. A ASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQQEQLLAEENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG-----

Target 5dzz. 1. A QDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLPANEKLT-----

Target 5dzz. 1. A IYAALRRQLLSPGTALILLEAQAASGFLDPVRNRRLTVTEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISLFAQ-----

Target 5dzz. 1. A MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC-----

Target 5dzz. 1. A VEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTAEQRRDLLRQFRTGKVT-----

Target 5dzz. 1. A VEKIIKIVITVIEEHEQKQGLCFQGLRALVPAAEELLESGLIDWDLFRQLQLGERSVQEVAEVEGVRRALRSGSVIAGVWL-----DTSKLVFDGLRKKVTAMQLYECQLIDKTTLDKLLKGKKSVEEVA--SEIQPFLRGAGSIAGAS--

Target 5dzz. 1. A EEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSGASPKEYSLVEAKRKKLISPES TVMLLEAQAATGGI IDPHRNEKLTVD SA IARDLIDFDDRQQIYAAEKAITGFD DPFSG

Target 5dzz. 1. A QSVSLFQALKKGLIPREQGLRLDAQLSTGGTVDP SKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYYPDRTWELATKTVSVSEAIKKNLIDRETGMRLLEAQIASGGVVDPVNSVFLPKDVALARGLIDRDLYRSLNDPRDSQKNFVDPVTKKKVS

Target 5dzz. 1. A YSQLQQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQELLYVQLKERCRIEPTGLLLSVQKRS-----

Target 5dzz. 1. A RQFRTGKVTVEKIIKIVITIVIEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKD GKTSVKDLSELSSLQTLL-----MSFQGIRQPVTVTELVD SGILRPSTVNELESQQISYDEVG--ERIKDFL

Target 5dzz. 1. A QGSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLYVHEAVKAGVVGPPELHEKLLSAEKQGSSCIAGIYNETTKQLGIYEA MKIGLVRPGTALELLEAQAATGFIVDPVSNLRLPVEEAYKRGVGI EFKEKLLSAER

Target 5dzz. 1. A AVTGYKDPYSGSTISLFAQMKKGLVVREHGIRLLEAQIATGGI IDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGAVTGYNDPETGNIISLFAQMNKELIEKGHGIRLLEAQIATGGI IDPKESHRLPVDIAYKRGYFNEELSEILSDPSDDTKG

Target 5dzz. 1. A FFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETTRA FEETQIDIPGGGSHGGSTMSLWEVMFFDPNTEENLTYLQLKERICKDEETGLCLLPLK-----

Target 5dzz. 1. A QSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTR-----

Target 5dzz. 1. A SLREVLEAESAWRYLYGTGCVAGVYLP GSRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRKG-----

Target 5dzz. 1. A LVGPPELHDLRLLSAERAVTGYRDPYTEQTISLFAQMKKDLIPAEALRLLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNK-----

Target 5dzz. 1. A DTHDQLSEPSEVRSYVDPSTDERLSY TQLLRRCRRETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRL-----

Target 5dzz. 1. A QEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIIRPGTAFELLEAQAATGYVIDPIKGLKLTVEEAV-----

Target 5dzz. 1. A RMGIVGPEFKDLLSAERAVTGYKDPYSGKLISLFAQMKKGLILKDHGIRLLEAQIATGGI IDPEESHRLPVDVAYQRGL-----

Target 5dzz. 1. A FDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSSKSSVRKRRVVIVDPETGKE-----

Target 5dzz. 1. A MSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITE-----

Target 5dzz. 1. A FADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILD TETLEKVSITEAMHRNLVDNITGQRL-----



Target  
5dzz. 1. A

LEAQA

CTGGI

IDPNT

GERFP

VTDA

VNKGL

VDKIM

VDRIN

LAQKA

FCGF

EDPRT

KTMSA

AAQAL

KKGW

LYYE

AQGR

FLEV

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Target  
5dzz. 1. A

YLTG

GLIE

PDTP

GRVPL

DEAL

QRGT

VDART

AQKL

RDVS

SAYSK

YLTCP

KTCLK

ISYK

DALDR

SMVE

EETGL

RLL

EEAA

QSS

Target  
5dzz. 1. A

KGY

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
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Model #12	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.75 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
4z6g.1.A	66.86	monomer	0.00	HHblits	X-ray	2.65Å	0.51	65 - 412	0.08	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
PO4.1	Not biologically relevant.	PHOSPHATE ION
PO4.2	Not biologically relevant.	PHOSPHATE ION

Target  
4z6g. 1. A

MSGED

QEVRA

VVEDG

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
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Target 4z6g. 1. A	QAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKTKTISLVIRSTQGAEELRAHE
Target 4z6g. 1. A	EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELRGAEVGERLQQRHGERDVEVERWRERVTLQLLRWQ
Target 4z6g. 1. A	AVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEQIQAVPLADSQAVREQLRQEKALLEEIERHAEKVEECQ
Target 4z6g. 1. A	RFAKQYINAIKDYEQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRFISETLRRMEEEER
Target 4z6g. 1. A	LAEQQRAEERERLAEVEAALEKQRQLAEAHQAQAQAEREAEQELQRRMQEEVARREEVAVDAQQQKRSIQEELQQLRQSS
Target 4z6g. 1. A	EAEIQAKARQVEAAERSRLRIEEEIRVVRLQLLETTERQRGGAEGELQALRARAEAEAKRQAQEEAERLRRQVQEETQR
Target 4z6g. 1. A	KRQAEAEGLRVKAEAEAAAREKQRALQALEELRLQAEAAERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKT
Target 4z6g. 1. A	AQLERTLEEEHVTVVQLREEATRREQQQAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAA
Target 4z6g. 1. A	EREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQRLAAEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAAATQK
Target 4z6g. 1. A	RQELEAELAKVRAEMEVLLASKARAEESRSSEKSKRLEAEAGRFRELAEEAARLRALAEAAKRQRQLAEEDAARQRA
Target 4z6g. 1. A	EAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRRLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ
Target 4z6g. 1. A	KGLVEDTLRQRRQVEEEILALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRRREAEER
Target 4z6g. 1. A	VQKSLAAEEEAARQRKAAL EEVERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKRLQAE EKAHAFVQQKEQELQQTL
Target 4z6g. 1. A	QQEQSVLEKL RSEAEAAARRAAEEAEARERAEREAQSRQRVEEAERLKQA AEEQAQAQAQAAAEKLKEAEQEAAARR
Target 4z6g. 1. A	AQAEQAALRQKQAADAEMEKHKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKA EVTEAARQRSQVEEE
Target 4z6g. 1. A	LFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAAQEAAARLRQLAEEDLAQQRALAE
Target 4z6g. 1. A	KMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEAEERLRLRV
Target 4z6g. 1. A	AEMSRAQARAEDAQRFRKQAE EIGAKLHRTLATQEKVTLVQTLETQRQQSDRDA DRLREATAELEREKDKLKKEAELL
Target 4z6g. 1. A	QLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQQMQQEKQQLL
Target 4z6g. 1. A	ASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQQEQLLA EENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG
Target 4z6g. 1. A	QDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLKPANEKLT
Target 4z6g. 1. A	IYAALRRQLLSPGTALILLEAQ AASGFLDPVRNRRLTVTEAVKEGVVGP ELPHHKLLSAERAVTGYKDPYTGEKISLFAQA
Target 4z6g. 1. A	MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRYGFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC
Target 4z6g. 1. A	VEDPETGLRLLPLTDQAAKG GELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTA EQRRDLLRQFRTGKVT
Target	VEKIIKIVITVIEEHEQKQQLCFQGLRALVPAAELLES GII DWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWL

4z6g. 1. A -----  
Target EEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPATSARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSG  
4z6g. 1. A -----  
Target QSVSLFQALKKGLIPREQGLRLDLAQLSTGGTVDPSPKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYYPDRTWELAT  
4z6g. 1. A -----  
Target YSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAERQRELL  
4z6g. 1. A -----  
Target RQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKDGTSTVKDLSELSSLQTLL  
4z6g. 1. A -----  
Target QGSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLEAQATGFLVDPVRNQRLVHEAVKAGVVGPELHEKLLSAEK  
4z6g. 1. A -----  
Target AVTGYKDPYSGSTISLFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSSDDTKG  
4z6g. 1. A -----  
Target FFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETTRAFETQIDIPGGGSHGGSTMSLWEVM  
4z6g. 1. A -----  
Target QSDLIPEEQRAQLMADFQAGRVTKERMI III IEI IEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTR  
4z6g. 1. A -----  
Target SLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLEAQATGFLDPVKGERLTVDEAVRKG  
4z6g. 1. A -----  
Target LVGPPELHDLRLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEELRLDLAQLATGGIVDPRLGFHLPLEVAYQRGYLNK  
4z6g. 1. A -----  
Target DTHDQLSEPSEVRSYVDPSTDERLSYTQLLRRCRRDETSGFLPLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRL  
4z6g. 1. A -----  
Target QEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEAQATGYVIDPIKGLKLTVEEAV  
4z6g. 1. A -----  
Target RMGIVGPEFKDLLSAERAVTGYKDPYSGKLISLFQAMKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGL  
4z6g. 1. A -----  
Target FDEEMNEILTDPSSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSSKSSVRKRRVVIVDPETGKE  
4z6g. 1. A -----  
Target MSVYEAYRKGLIDHQTYLELSEQEWEIEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTSLITE  
4z6g. 1. A -----  
Target FADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDDETLEKVSITEAMHRNLVDNITGQRL  
4z6g. 1. A -----  
Target LEAQAQTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQ  
4z6g. 1. A -----  
Target YLTGGLIEPDTGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTCPKTKLKISYKDALDRSMVEEGTGLRLLEAAQSS  
4z6g. 1. A -----  
Target KGYYPSPYSVSGSGSTGSRSGSRTGSRAGSRRGSFDTGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA  
4z6g. 1. A -----

Model #05	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.73 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5dzz.1.A	51.14	monomer	0.00	HHblits	X-ray	2.60Å	0.45	3645 - 4131	0.11	Desmoplakin

The template contained no ligands.

Target 5dzz. 1. A	MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQSRRRGGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN
Target 5dzz. 1. A	KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLRRHQVKLVNIRNDDIADGNPKLT
Target 5dzz. 1. A	LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYRQ
Target 5dzz. 1. A	TNLENLDQAFSVAERDLGVTRLLDPEDVDVPQPDEKSIITYVSSLYDAMPRPVDVQDGVKANELQLRWQEYRELVLVLLQ
Target 5dzz. 1. A	WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAGQLKVPPGYHPLDVEKEWGKL
Target 5dzz. 1. A	HVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLKADGMIRLLF
Target 5dzz. 1. A	NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSAEGVDLP
Target 5dzz. 1. A	SVEAQLGSHRGLHQSVVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLES LHGFVAAATKEL
Target 5dzz. 1. A	MWLSEKEEEEVGFWDWERNNSMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPPARPTVESFQAALQTQWSWMLQ
Target 5dzz. 1. A	LCCIEAHLKENTAYFQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKDLNEYRGHLSGLAKRAK
Target 5dzz. 1. A	AIVQLTPRNPTQPTRGRVPLLAVCDYKQEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCFLVPPPNQEALAV
Target 5dzz. 1. A	ARLEAQHQALVTLWHQLHTDMKSLLAWSLSRDVQLIRWSLVTFRTLKPEEQRQALRSLELHYQAFLRDSQDAGGFGPE
Target 5dzz. 1. A	DRLQAEREYGSCSRHYQQLQSLEQGEQEESRCRCISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQQA
Target 5dzz. 1. A	QAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKLTISLVIRSTQGAEELRAHE
Target 5dzz. 1. A	EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVERWRERVTLLERWQ
Target 5dzz. 1. A	AVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEIQAVPLADSQAVREQLRQEKALLEETERHAEKVEECQ
Target 5dzz. 1. A	RFAKQYINAIKDYLQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRFISETLRRMEEER
Target 5dzz. 1. A	LAEQQRAEERERLAEVEAALEKQRQLAEAHQAQAQAEAEQELQRRMQEEVARREEVAVDAQQQKRSIQEELQQLRQSS
Target 5dzz. 1. A	EAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQALRARAEAEQAQKQAQEEAERLRRQVQEETQR
Target 5dzz. 1. A	KRQAEELGLRVKAEAEAREKQRALQALEELRLQAEAAERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKT
Target 5dzz. 1. A	AQLERTLEEEHVTVVQLREEATRREQQAEAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAA
Target 5dzz. 1. A	EREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQLAAEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAAATQK

Target 5dzz. 1. A RQELEAELAKVRAEMEVLLASKARAEESRSSEKSKRLEAEAGRFRELAEEAARLRALAEAAKRQRQLAEEDAARQRA-----

Target 5dzz. 1. A EAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRRRLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ-----

Target 5dzz. 1. A KGLVEDTLRQRRQVEEEILALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAAARQRQLAAEEERRRREAEEER-----

Target 5dzz. 1. A VQKSLAAEEEAARQRKAAL EEVERLKAKVVEARRLRERAEHESVRQLQLAQEAAQKRLQAEKKAHAFVQQKEQELQQT-----

Target 5dzz. 1. A QQEQSVLEKLRSEAEAAARRAAEEAEARERAEERAAQSRQRVEEAERLKQAAEEQAQAQAQAAAEKLRKEAEQEAAARR-----

Target 5dzz. 1. A AQAEQAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETHQKSILDQELQRLKAEVTEAARQRSQVEEE-----

Target 5dzz. 1. A LFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAAQEAAARLRQLAEEDLAQQRALAE-----

Target 5dzz. 1. A KMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEERLRLRV-----

Target 5dzz. 1. A AEMSRAQARAEDAQRFRKQAEIIGAKLHRTLATQEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAELL-----

Target 5dzz. 1. A QLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQMQQEKQQL-----

Target 5dzz. 1. A ASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQEQQLAEENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG-----

Target 5dzz. 1. A QDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLKPAN EKLT-----

Target 5dzz. 1. A IYAALRRQLSPGTALILLEAQASGFLDPVRNRRLTVTEAVKEGVGPPELHHKLLSAERAVTGYKDPYTGEKISL FQA-----

Target 5dzz. 1. A MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRYGFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC-----

Target 5dzz. 1. A VEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTAQRRLDLRQFRTGKVT-----

Target 5dzz. 1. A VEKIIKIVITVIEEHEQKGQLCFQGLRALVPAAEELLESIGIIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWL-----

Target 5dzz. 1. A EEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSG-----

Target 5dzz. 1. A QSVSLFQALKKGLIPREQGLRLD AQLSTGGTVDP SKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYDPTWELAT-----

Target 5dzz. 1. A YSQLQQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAQRQELL-----

Target 5dzz. 1. A RQFRTGKVTVEKIIKIVITIVIEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKDGKTSVKDLSLSSLQTL-----

Target 5dzz. 1. A QGSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLEAQAA TGFLVDPVRNQRLYVHEAVKAGVVGPELHEKLLSAEK-----

Target 5dzz. 1. A AVTGYKDPYSGSTISL FQAMKGLV VREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDP SDDTKG-----

Target 5dzz. 1. A FFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETTRAFEETQIDIPGGGSHGGSTMSLWEVM-----

Target 5dzz. 1. A QSDLIPEEQRAQLMADFQAGRVTKERMI I I I IEI IEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTR-----SKLVFDGLRKKVTAMQLYECQLIDKTTLDKLLKGKK

Target 5dzz. 1. A SLREVLEAESAWRYLYGTGCVAGVYLP GSRQTLPIYQALKKGLLSAEVARL LLEAQAA TGFLDPVKGERLTVDEAVRKG-----SVEEVAS--ETQPFLRGAGSIAGAS--ASPKEKYSLEVAKRKKLISPESTM LLEAQAA TGGIIDPHRNEKLTVD SAIARD

Target LVGPELHDRLLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEELRLLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNK  
5dzz. 1. A LIDFDDRQQIYAAEKAITGFDDPFSGKTVSVSEAIKKNLIDRETGMRLLEAQIASGGVDPVNSVFLPKDVALARGLIDR

Target DTHDQLSEPSE-VRSYVDPSTDERLSYTHLRRRCDSTGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQR  
5dzz. 1. A DLYRSLNDRDSQKNFVDPVTKKKVSYVQLKERCRIEPTGLLLSVQKR-SMSFQGIQPVTVTELVDGILRSTVNE

Target LQEGLTISIEVSKNLQKFLEGTSSIAAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEQAATGYVIDPIKGLKLTVEEA  
5dzz. 1. A LESGQISYDEVERIKDFLQGSSCIAGIYNETTKQLGIYEAMKIGLVRPGTALELLEQAATGFIVDPVSNRLRPVEEA

Target VRMGIVGPEFKDLLSAERAVTGKDPYSGKLISLFQAMKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRG  
5dzz. 1. A YKRGVLGIEFKEKLLSAERAVTGNDPETGNIISLFQAMNKELIEKGHGIRLLEAQIATGGIIDPKESHRLPVDIAYKRG

Target LFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSKSSVRKRRVIVDPETGK  
5dzz. 1. A YFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLKERICDEETGLCCLPLK-----


Target EMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSIT  
5dzz. 1. A -----

Target EFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTETLEKVSITEAMHRNLVDNITGQR  
5dzz. 1. A -----

Target LLEAQAQTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEV  
5dzz. 1. A -----

Target QYLTGGLIEPDTGPRVPLDEALQRGTVDARTAQKLRDVSAYS KYLTCPKTKLKISYKDALDRSMVEEGTGLRLLEAAQAS  
5dzz. 1. A -----

Target SKGYSPYSVSGSGSTTGSRSRGTGSRAGSRGSGFDTATGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA  
5dzz. 1. A -----

Model #20	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.50 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
8iah.1.2	15.20	monomer	0.00	HHblits	EM	-	0.28	186 - 630	0.22	Spectrin beta chain

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
ADP.1	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.2	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.3	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.4	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.5	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.6	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.7	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.8	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.9	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.10	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.11	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.12	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE

Target MSGEDQEVRAVVEDGSNGSGSPSPGDTLPWNLEKTQSRRRGGGGPGNGSVLDP AERAVIRIADERDRVQKKTF TKWVN  
8iah. 1. 2 -----


Target KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLRHRQVKLVNIRNDDIADGNPKLT  
8iah. 1. 2 -----

Target 8iah. 1. 2	LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLLSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNK--VY -----VQKKTFTKWVNSHLARV-SCRITDLYKDLRDGRMLIKLLEVLSGEMLPKPTKGKM
Target 8iah. 1. 2	RQTNLENLDQAFSVAERDLGVTRL-LDPEDVDVPQPEKSIITYVSSLYDAMPRVPDVQDGVKANELQLRWQEYRELVL RIHCLENVDKALQFLK-EQRVHLENMGSHDIVDGNH--RLVLGLIWTIILRFQIQDIVVQTQEG-----RETRSAKDA
Target 8iah. 1. 2	LLQWIRAHTAAF---EERRFPSSFEEIEILWCQFLKFKETELPAK-EAD---KNRSKGIYQSLEGAVQAGQLKVPPGYHP LLLWCQMKTAGYPNVNFTNTSSWKDGLAFNALIHKHRPDLIDFDKLKDSNARHNLEHAFDVAERQ-----LGTIQLLDP
Target 8iah. 1. 2	LDVE-----KEWGKLVHAIL--EREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRL-- EDVFTENPDEKSIITYVVAFYHYFSKMKVLAVEGKRVGKVIDHAIETEKMIKYSGLASDLLTWIEQTITVLNSRKFANS
Target 8iah. 1. 2	-LAAGKAPQRAGEVERDLK--A--DGMIRLLFNDVQA-LKDGR---HPQGEQMYRRVYRLHERLVAIRTEYNLRLRGT LAGVQQQLQAFSTYRTVEKPPKFQEKGNLEVLLFTIQSRMRANNQKVYTPHDGKLVSDINRAWESLEEAEYRRELALRSE
Target 8iah. 1. 2	PRH----PELEDSTLRYLQDLLAWVEENQRRVDSAEGWVDLPVSVEAQLGSHRGLHQSVVEEFAKIERARTDEGQLS---P LIRQEKLEQLARRFRKAAMRETWLNENQRLVAQDNFGYDLAAVEAAKKKHEAIEDTAAAYEERVRALEDLARELELENY
Target 8iah. 1. 2	ATRGAYRDCLGRDLQYAKLLNSSKARLSLE---SLHGFVAAATKELMWLSEKEEEEVGFWDWSEKSNMAAKKEAYSAL HDQKRITARKDNILRLWNYLQELLQSRQRLETTLALQQLFQDMLHSIDWMDIKAHLLSAEFGKHLEAEDLLQKHKLM
Target 8iah. 1. 2	MRELELKEKKIKEIQSTGDRLLREDH---PARPTVESFQAALQTQWSWMLQLCCIEAHLKENTAYFQFFSDVREAEQQL EADIAIQGDKVKAITAATLQFTEETGYQPCDPQVIRDRVSHLEQCFAELSNTAAGRKAQLEQSKRLWKLFWEMDEAKSWI
Target 8iah. 1. 2	RKLQETLHRKYTCDSITVTRLEDLLQDAQDEKDLNEYRGHLSGLAKRAKAI VQLTPRNPTQPTRGRVPLLAVCDYKQV KEKEQIYS--SLGYGKDLT SVLILQRKHKA FEDELRRLDPHLDQIFQEAEDMVALKQFG--YP-----K--NEAW---
Target 8iah. 1. 2	EATVHKGDECMQLGPAQPFHWKVLSSSGSEAAVPSVCFLVPPPNQEALEAVARLEAQHQALVTLWHQLHTDMKSLLAWS -----V-----KEVSAQWDQLKEVPAQWNQLKELAASRKKNLQDTENFFQ
Target 8iah. 1. 2	LSRDVQLIRSWSLVTFRTLKPEEQ---RQALRSLELHYQAFLRDSQDAGGF-----GPEDRLQAEREYGSCS FQGDVDDLKAWLQDAHKLLSGEDVGQDEGATRALGKKHKDFLEELEESRGVMEHLEQQAQDFPERFRDSPDVNRLQVLR
Target 8iah. 1. 2	RHYQQLQSLSEQGEQ---ESRCQRCISELKDIRLQLEACETRTRVHRLRLPLDKEPARECAQRIAEQKKAQAEVEGLGKG DLYQQVVAQADLRRQRLQDALDLYTVFGETDACELWMGEKEKWLAQ-MDIPD---TLEDLEVQHRFDILDQEMKTLIAQ
Target 8iah. 1. 2	VARLSAEAEKVLALPEPSPAAPT LRSELELTGKLEQVRSLSAIYLEKLKTISL---VIRSTQGAEALRAHEEQLEAQ IDGVNVAANSLVESN--HPRSTEVKQYQDHLNTRWREFQTMVLARREAVDSALRVHNYCVDCEETSKWIIDTKKVVESTK
Target 8iah. 1. 2	AVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVERWRERVTLLERWQAVLAQTD DLGQDLAGVMAIQRKLSGLERDVAAIQVRVGALEQ-----ESHRLMES---HREQEKDIGERQAYVEELWQGLQALK
Target 8iah. 1. 2	VRQRELEQLGRQLRYYRESADPLGAWLQDARRRQEIQIYAVPLADSQAVREQLRQEKALLEEIERHAEKVEECQRFQAKQYI GQEALLGKS-SQLQAFQLDADFPAWLSAQKEVASK--DMPESLPEAEQLLQQAALKDDIDRHQENYQHVKASGEKVI
Target 8iah. 1. 2	NAIKDYELQLVTYKAQLEPVASPAKKPKVQSGSESVIQEYVDLTRYSELSTLTSQYIRFISETLRRMEEEERLAEQRA HG-----
Target 8iah. 1. 2	EERERLAEVEAALEKQRQLAEAHAKAKAQAEREAEQLQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSSEAEIQA -----
Target 8iah. 1. 2	ARQVEAAERSRLRIEEIIRVVRLQLETTERQRGGAEGELQALRARAEAEAKRQAQEEAERLRRQVQEETQRKRQAEAE -----
Target 8iah. 1. 2	LGLRVKAEAEAREKQALQALEELRLQAEAEERRLQAEAEERARQVQVALETAQRSQAELQSKHASFAEKTAQLERTL -----
Target 8iah. 1. 2	EEHVTVVQLREEATRREQQAEAEARAREEAERELERWQLKANEALRLRLQAEVAQQKSLAQAEAEKQKEAAEREARR -----
Target 8iah. 1. 2	GKAEQAVRQRELAEQELERQRLAEGTAQRLAAEQELIRLRAETEQQEQQLLEEELARLQSEAAAATQKRQELEAE -----
Target 8iah. 1. 2	LAKVRAEMEVLLASKARAEESRSSEKSKRLEAEAGRFRLEAEEARLRALAEAAKRQRLAEEDAARQRAEAEVLS -----
Target 8iah. 1. 2	EKLAAISEATRLKTEAEIALKEKEAENERLRLRAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQKGLVEDT -----
Target 8iah. 1. 2	LRQRRQVEEIEILALKASFEKAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRLAAEEERRRREAEERVQKSLAA -----
Target	EEEAARQRKAAL EEVERLKAKVEEARRLRERAEHESVRQLQLAQEAQAQKRLQAEKKAHAFVQQKEQELQQLQQEQSVL

8iah. 1. 2 -----  
Target EKL RSEAE AARRAAEEAEERERAEREAAQSRQRVEEAERLKQAAEEQAQAQAQAAAAEKL RKEAEQE AARRAQAEQAA  
8iah. 1. 2 -----  
Target LRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKAEVTEAARQRSQVEEELFSVRVQ  
8iah. 1. 2 -----  
Target MEELGKLKARIEAENRALILRDKDNTQRL LQEEAEKMKQVAEEAARLSVAAQE AARLRQLAEEDLAQQRALAEKMLKEKM  
8iah. 1. 2 -----  
Target QAVQEATRLKAE AELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGGFQRTLETERQRQLEMSAE AERLRLRVAEMSRAQ  
8iah. 1. 2 -----  
Target ARAEEDAQRFRKQAE EIGAKLHRTELATQEKVTLVQTLETQRQQSDRDADRLREAI AE LEREKDKLKKEAELLQLKSEEM  
8iah. 1. 2 -----  
Target QTVQEQELLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQM QQEKQQLLASMEEAR  
8iah. 1. 2 -----  
Target RRQHEAE EGVRRKQEELQLLEQQRQQEQQLLAEENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNGQDAADGP  
8iah. 1. 2 -----  
Target AAEP EHA FEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLKPANEKLTIIYAALRR  
8iah. 1. 2 -----  
Target QLLSPGTALILLEAQAASGFLLDPVRNRRLTVTEAVKEGVVGP ELHHKLLSAERAVTGYKDPYTGEKISL FQAMKKDLIV  
8iah. 1. 2 -----  
Target REHGIRLLEAQIATGGVIDPVHSHRPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERCVEDPETG  
8iah. 1. 2 -----  
Target LRLPLTDQAAKG GELVYTDSEARDVF EKATVSAPFGKFQGKTVTIWELINSEYFTAEQR RDLLRQFRTGKVTVEKIIKI  
8iah. 1. 2 -----  
Target VITVIEEHEQKGQLCFQGLRALVPAELLES GII DWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKL  
8iah. 1. 2 -----  
Target SIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGP ELHEKLLSAEKAVTGYKDPYSGQSVSLFQ  
8iah. 1. 2 -----  
Target ALKKGLIPREQGLRL LDAQLSTGGTVDP SKSHRLPLDVACARGYLDEETSTALSAPRDDAKTY YDPRTWELATYSQLQQQ  
8iah. 1. 2 -----  
Target CRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQELLRQFRTGK  
8iah. 1. 2 -----  
Target VTVEKIIKIVITIVEEVETRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKD GKTSVKDLSELSSLQTL LQSGGCLA  
8iah. 1. 2 -----  
Target GIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLYVHEAVKAGVVGP ELHEKLLSAEKAVTGYKD  
8iah. 1. 2 -----  
Target PYSGSTISL FQAMKKGLV VREHGIRLLEAQIATGGIIDPVHSHRPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTH  
8iah. 1. 2 -----  
Target ENLTYRQLLERCVEDPETGLRLPLKGPEKAEVVETTRVYTEETRRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPE  
8iah. 1. 2 -----  
Target EQRAQLMADFQAGRVTKERMI IIIIE IIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLE  
8iah. 1. 2 -----  
Target AESAWRYLYGTGCVAGVYLP GSRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRKGVLGP ELH  
8iah. 1. 2 -----  
Target DRLLSAERAVTGYRDPYTEQTISL FQAMKKDLIPAE EALRL LDAQLATGGIVDPRLGFHLPLEVAYQRGYLNKDTHDQLS  
8iah. 1. 2 -----  
Target EPSEVRSYVDPSTDERLSY TQLLRRCRRDETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSI  
8iah. 1. 2 -----  
Target EEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEAQAATGYVIDPIKGLKLTVEEAVRMGIVGP  
8iah. 1. 2 -----



Target 8iah. 1. 2	EFKDKLLSAERAVTGYKDPYSGKLI SLFQAMKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGLFDEEMNE
Target 8iah. 1. 2	ILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSKSSVRKRRVVIVDPETGKEMSVYEAY
Target 8iah. 1. 2	RKGLIDHQTYLELSECEWEIEITISSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITEFADMLSG
Target 8iah. 1. 2	NAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTELEKVSITEAMHRNLVDNITGQRLEAACT
Target 8iah. 1. 2	GGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYLTGGLI
Target 8iah. 1. 2	EPDTPGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTCPKTKLISYKDALDRSMVEEGTGRLLEAAAQSSKGYSPY
Target 8iah. 1. 2	SVSGSGSTTGSRSGRTGSRAGSRRGSFDTGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA

Model #17	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.65 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
6s13.1.A	29.82	homo-dimer	0.00	HHblits	X-ray	3.10Å	0.36	62 - 448	0.08	Calponin homology domain protein putative

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
CA.1	Binding site not conserved.	CALCIUM ION
CA.2	Binding site not conserved.	CALCIUM ION

Target 6s13. 1. A	MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQSRRRGGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWWN -----ELVAQWEKVQIKTFTKWWN
Target 6s13. 1. A	KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPR-EKGRMRFHKLQNVQIALDYLRRHQVKLVNIRNDDIADGNPKL MHLAKKGRKINDVTDFKNGVELCALLEIIGETTICKVTNPKMRIQMTENLDKALRFIQSRDVKLGTIGPTDIVDGNVKL
Target 6s13. 1. A	TLGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAI IHRHKPMLIDMNKVYR TLGLVWTLILRFAISELSAE---GLSAKQGLLLWCQKKCEPYP-VKVENFSESFKDGKVFCAL IHRHRPDLLDWETVGE
Target 6s13. 1. A	QTNLENLDQAFSVAERLDGVTRLLDPEDVDV-PQPDEKSIITYVSSLYDAMPRPVDPVDQGVK-----ANELQLRWQE D-DRANLEKAFDVAEKELGIPKLLDVDDIVNMPRPDERSVMTYVAALYKVFSSNDQVEKAGKRAGNFLDLLRATEGMVHD
Target 6s13. 1. A	YRELVLLLLQWIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSGIYQSLEGAVQAG---QLKVPPG YEQRAQALKENIEAAINKMNGVEPSDEYHQVKEQINETKNYRKGDKRAFIKEQGDLATLFGQINSKLRGMKRPVYVAPEG
Target 6s13. 1. A	YHPLDVEKEWGKLVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVER LDPKSLEGYIANISEAERALRSKLN TAMR--NCLIALRKAFADPANATDAKINEYRTFVTD-----
Target 6s13. 1. A	DLDKADGMIRLLFNDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQ -----
Target 6s13. 1. A	RRVDSAEWGVDLPSVEAQLGSHRGLHQSVVEEFAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLE -----
Target 6s13. 1. A	SLHGFVAAATKELMWLSEKEEEEVGFDSERNSNMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARPTVESF -----
Target	QAALQTQWSWMLQLCCIEAHLKENTAYFQFFSDVREAEELRKQLQETLHRKYTCDRSITVTRLEDLLQDAQDEKDLNE

6s13. 1. A -----

Target YRGHLSGLAKRAKAIVQLTPRNPTQPTRGRVPLLAVCDYKQEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCF

6s13. 1. A -----

Target LVPPPNQEALEAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLELHYQAF

6s13. 1. A -----

Target LRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLLSLEQGEQESRCQRCISELKDIRLQLEACETRTRVHRLRLPLDKEPA

6s13. 1. A -----

Target RECAQRIAEQKKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLTISLVIR

6s13. 1. A -----

Target STQGAEELRAHEEQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVER

6s13. 1. A -----

Target WRERVTQLLERWQAVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEQIQAVPLADSQAVREQLRQEKALLE

6s13. 1. A -----

Target EIERHAEKVEECQRFQAKYINAIKDYELQLVTYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRF

6s13. 1. A -----

Target ISETLRRMEEEERLAEQQRAEERERLAEVEAALEKQRQLAEHAQAKAQAEREAEQLQRRMQEEVARREEVAVDAQQQKR

6s13. 1. A -----

Target SIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQALRARAEAEAKRQAQEEA

6s13. 1. A -----

Target ERLRRQVQEETQRKRQAEELGLRVKAEAAAREKQRALQALEELRLQAEAAERRLRQAEARARQVQVALETAQRSQAQ

6s13. 1. A -----

Target ELQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKS

6s13. 1. A -----

Target LAQAEAEKQKEAAEREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQLAAEQELIRLRAETEQGEQQRQLLEEEL

6s13. 1. A -----

Target ARLQSEAAAAATQKRQELEAELAKVRAEMEVLLASKARAEESRSSSEKSKRLEAEAGRFRELAEEAARLRALAEAAKRQ

6s13. 1. A -----

Target RQLAEEDAARQRAEAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRLAEDEAFQRRRLEEQAQHKADIEERLA

6s13. 1. A -----

Target QLRKASESELERQKGLVEDTLRQRRQVEEEILALKASFEEAAAGKAELELELGRI RNAEDTLRSKEQAEQEAARQQLA

6s13. 1. A -----

Target AEEERRRREAEEERVQKSLAEEEAARQKAALEEVEERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKRLQAEKHAHF

6s13. 1. A -----

Target AVQQKEQELQQTLLQEQSVLEKLRSEAEAAARRAAEEAEARERAEREAAQSRQRVEEAERLKQAAEEQAQAQAQAAAE

6s13. 1. A -----

Target KLRKEAEQEAAARRAQAEQAALRQKQAADAEMEKKKF AEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKAEV

6s13. 1. A -----

Target TEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVAAQEAARLRQL

6s13. 1. A -----

Target AEEDLAQQRALAEKMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQL

6s13. 1. A -----

Target EMSAEERLRLRVAEMSRAQARAEDAQRFRKQAEIIGAKLHRTELATQEKVTLVQTLETQRQQSDRDADRLREAI AELE

6s13. 1. A -----

Target REKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAKLREEQQR

6s13. 1. A -----

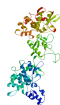
Target QQQQMMEQEKQLLASMEEAARRRQHEAEEGVRRKQEELQLLEQQRQQEQQLLAEENRRLRERLEHLEEHRAALAHSEEIT

6s13. 1. A -----

Target AAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSI

6s13. 1. A -----

Target 6s13. 1. A	AGLLKPAN EKLTIIYAALRRQLSPGTALILLEAQAASGFLDPVRNRRLTVTEAVKEGVVGP ELHHKLLSAERAVTGYK -----
Target 6s13. 1. A	DPYTGEKISL FQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNT -----
Target 6s13. 1. A	HENLTYLQLLERCVEDPETGLRLLPLTDQAAKG GELVYTDSEARDVFEKATVSAPFGKFQGKTVTI WELINSEYFTA EQR -----
Target 6s13. 1. A	RDLLRQFR TGKVTVEKIIKIVITVIEEHEQKGQLCFQGLRALVPAAE LLESGIIDWDLFRQLQLGERSVQEVAEVEGVRR -----
Target 6s13. 1. A	ALRSGSVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGP ELHEKLLSA -----
Target 6s13. 1. A	EKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLLDAQ LSTGGTVDP SKSHRLPLDVACARGYLDEETSTALSAPRDDA -----
Target 6s13. 1. A	KTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELIN -----
Target 6s13. 1. A	SEYFTA EQRQELLRQFR TGKVTVEKIIKIVITVIEEVETTRRERLSFSGLRAPVPA SELLAAGILSSSQFEQLKDGKTSV -----
Target 6s13. 1. A	KDLSLSSLQTL LQGSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQATGFLVDPVRNQRLYVHEAVKAGV -----
Target 6s13. 1. A	GPELHEKLLSAEKAVTGYKDPYSGSTISL FQAMKKGLVVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEM -----
Target 6s13. 1. A	NRVLEDP SDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETTRAFEETQIDIPGGG -----
Target 6s13. 1. A	SHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVI -----
Target 6s13. 1. A	SRESYSLLREGTRSLREVLEASAWRYLYGTGCVAGVYLP GSRQTLPIYQALKKGLLSAEVARLLLEAQATGFLDPVK -----
Target 6s13. 1. A	GERLTVDEAVRKGLVGP ELHDRLLSAERAVTGYRDPYTEQTISL FQAMKKDLIPAEALRLLDAQ LATGGIVDPRLGFHL -----
Target 6s13. 1. A	PLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSY TQLLRRCRRDETSGLFLLPLSEARKLTFRGLRKQITVEELV -----
Target 6s13. 1. A	RSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKGIIRPGTAFELLEAQATGYVID -----
Target 6s13. 1. A	PIKGLKLTVEEA VRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISL FQAMKKGLILKDHGIRLLEAQIATGGIIDPEES -----
Target 6s13. 1. A	HRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSKSSVRK -----
Target 6s13. 1. A	RRVVIDPETGKEMS VYEAYRKGLIDHQTYLELSEQECWE EITISSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSA -----
Target 6s13. 1. A	LDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISP AVSRTQLASWSDPTEETGPVAGILDTETLEKVSITEAM -----
Target 6s13. 1. A	HRNLVDNITGQRLLEAQA CTGGIIDPNTGERFPVTD AVNKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKW -----
Target 6s13. 1. A	LYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQR GTVDARTAQKL RDVSAYSKYLTCPKTKLKISYKDALDRSMVEEG -----
Target 6s13. 1. A	TGLRLL EAAAQSSKGYSPYSVSGSGSTTGSRS GSRTGSRAGSRRGSF DATGSGFSMTFSSSSYSSSGYGRRYASGPTSS -----
Target 6s13. 1. A	LGGPESAAA -----

Model #08	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.63 ± 0.05

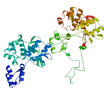
Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5dzz.1.A	47.12	monomer	0.00	HHblits	X-ray	2.60Å	0.42	2649 - 3222	0.11	Desmoplakin

The template contained no ligands.

Target 5dzz. 1. A	MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQSRRRGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN -----
Target 5dzz. 1. A	KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLHRHQVKLVNIRNDDIADGNPKLT -----
Target 5dzz. 1. A	LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYRQ -----
Target 5dzz. 1. A	TNLENLDQAFSVAERDLGVTRLDPEDVDVPQDEKSIITYVSSLYDAMPRPVDVQDGVKANELQLRWQEYRELVLVLLQ -----
Target 5dzz. 1. A	WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAGQLKVPPGYHPLDVEKEWGKL -----
Target 5dzz. 1. A	HVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLKADGMIRLLF -----
Target 5dzz. 1. A	NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSAEGVDDL -----
Target 5dzz. 1. A	SVEAQLGSHRGLHQSVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLES LHGFVAAATKEL -----
Target 5dzz. 1. A	MWLSEKEEEVGFWDWERNNSMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARPTVESFQAALQTQSWMLQ -----
Target 5dzz. 1. A	LCCIEAHLKENTAYFQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKQQLNEYRGHLSGLAKRAK -----
Target 5dzz. 1. A	AIVQLTPRNPTQPTRGRVPLLAVCDYKVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCFLVPPPNQEALAV -----
Target 5dzz. 1. A	ARLEAQHQALVTLWHQLHTDMKSLAWQSLSRDVQLIRWSLVTFRTLKPEEQRQALRSLELHYQAFLRDSQDAGGFGPE -----
Target 5dzz. 1. A	DRLQAEREYGSCSRHYQQLLSLEQGEQEESRCRCISELKDIRLQLEACETRTVHRLRLPLDKEPARECAQRIAEQKKA -----
Target 5dzz. 1. A	QAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKTIISLVIRSTQGAEELRAHE -----
Target 5dzz. 1. A	EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVERWRERVTLLELRWQ -----
Target 5dzz. 1. A	AVLAQTDVRQRELEQLGRQLRYYRESADPLGAWLQDARRRQEQIQAVPLADSQAVREQLRQEKALLEEIERHAEKVEECQ -----
Target 5dzz. 1. A	RFAKQYINAIKDYLQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRFISETLRRMEEEER -----
Target 5dzz. 1. A	LAEQQRAEERERLAEVEAALEKQRQLAEAHAQAKAQAEAAQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSS -----
Target 5dzz. 1. A	EAEIQAKARQVEAAERSRLRIEEIIRVVRLQLETTERQRGGAEGELQALRARAEAEAKRQAQEEAERLRRQVQEETQR -----

Target 5dzz. 1. A	KRQAEAEGLRVKAEAEAREKQRALQALEELRLQAEAEERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKT -----
Target 5dzz. 1. A	AQLERTLEEEHVTVVQLREEATRREQQAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAA -----
Target 5dzz. 1. A	EREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQRLAAEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAAATQK -----
Target 5dzz. 1. A	RQELEAELAKVRAEMEVLLASKARAEESRSSESKQRLEAEAGRFRELAEEAARLRALAEAAKRQRQLAEEDAARQRA -----
Target 5dzz. 1. A	EAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRLLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ -----
Target 5dzz. 1. A	KGLVEDTLRQRRQVEEEILALKASFEEAAAGKAELELELGRI RNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAEEER -----
Target 5dzz. 1. A	VQKSLAE EEEAARQRKAAL EEVERLKAKV EEARRLRERAEHESVRQLQLAQEAAQKRLQAE EKAHAFVQQKEQELQQTL -----
Target 5dzz. 1. A	QQEQSVLEKL RSEAEAAARRAAEEAEERARAEREAQSRQRVEEAERLKQAE EEAQAQAQAQAAAEKL RKEAEQEAAARR -----
Target 5dzz. 1. A	AQAEQAALRQKQAADAEMEKHKFAEQTLRQKAQVEQELTALRLKLEETHQKSIDLQELQRLKAEVTEAARQRSQVEEE -----
Target 5dzz. 1. A	LFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAE -----
Target 5dzz. 1. A	KMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEERLRLRV -----
Target 5dzz. 1. A	AEMSRAQARAEDAQRFRRQAEETGAKLHRTELATQEKVTLVQTLETQRQQSDRDADRLREAI AELEREKDKLKKEAELL -----
Target 5dzz. 1. A	QLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQQMQQEKQQLL -----
Target 5dzz. 1. A	ASMEEARRRQHEAE EGVRRKQEELQLLEQQRQQQEQLLA EENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG -----
Target 5dzz. 1. A	QDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLPANEKLT -----DTSKLVFDGLRKKVTAMQLYECQLIDKTTLDKLLKGKKSVEEVA--SEIQPFLRGAGSIAGAS--ASPKEYS
Target 5dzz. 1. A	IYAALRRQLLSPGTALILLEAQAASGFLDPVRNRLTVTEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISL FQA LVEAKRKKLISP ESTVM LLEAQAATGGIIDPHRNEKLTVDSAIARDLIDFDDRQQIYAAEKAITGFDDPFSGKT VSVSEA
Target 5dzz. 1. A	MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC IKKNLIDRETGMRLLEAQIASGGVDPVNSVFLPKDVALARGLIDRDLYRSLNDPRDSQKNFVDPVTKKKVS YVQLKERC
Target 5dzz. 1. A	VEDPETGLRLLPLTDQAAKGGE LVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTA EQRRDLLRQFRTGKVT RIEPTHG LLLLSVQKR-----
Target 5dzz. 1. A	VEKIIKIVITVIEEHEQGQLCFQGLRALVPAAELLESGLIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWL -----SMSFQGIRQPVVTTELVDSGILRPSTVNELESGQISYDEVGE--RIKDFLQGSSCIAGIYN
Target 5dzz. 1. A	EEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSG ETTKQKLG IYEAMKIGLVRPGTALELLEAQAATGFIVDPVSNLRLPV EEA YKRG LVGIEFKEKLLSAERAVTGYNDPETG
Target 5dzz. 1. A	QSVSLFQALKKGLIPREQGLRL LDAQLSTGGTVDP SKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYYPDRTWELAT NIISL FQAMNKELIEKGHGIRLLEAQIATGGIIDPKESHRLPVDIAYKRGYFNEELSEILSDPSDDTKGFFDPNTEENLT
Target 5dzz. 1. A	YSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTA EQRQELL YLQLKERICKDEETGLCLPLK-----
Target 5dzz. 1. A	RQFRTGKVTVEKIIKIVITVIEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKD GKTSVKDLSELSSLQTLL -----
Target 5dzz. 1. A	QGGGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLEAQAATGFLVDPVRNQRLYVHEAVKAGVVGPPELHEKLLSAEK -----
Target	AVTGYKDPYSGSTISL FQAMKGLVVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKG

5dzz. 1. A -----  
Target FFDPNTHENLTyrQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETRRAFEETQIDIPGGGSHGGSTMSLWEVM  
5dzz. 1. A -----  
Target QSDLIPeeQRAQLMADFQAGrvTKermIIIIIEIIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTR  
5dzz. 1. A -----  
Target SLREVLEAESAWRYLYGTGCVAGVYLPgsRqTLPIYQALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRKg  
5dzz. 1. A -----  
Target LVGPelHdRLLSAERAVTGYRDPYtEQTISLfqAMKkDLIPAEeALRLlDAQLATGGIVDPRLGFHLPLEVAYQRGYLNk  
5dzz. 1. A -----  
Target DTHDQLSEPSEvRSYVDPSTDERLSYtQLLRRCRRDETSGFLlPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRL  
5dzz. 1. A -----  
Target QEGLTSIEEVSKNLQKFLEGTSSiAGVLVDATKERLSVYqAMKGIIRPGTAFELLEAQAATGYVIDPIKGLKLTVEEAV  
5dzz. 1. A -----  
Target RMGIvGPEfKdKLLSAERAVTGYKDPYSGKLISLfqAMKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGL  
5dzz. 1. A -----  
Target FDEEMNEILTDPSDDTKGFFDPNTEENLYLqLMERCvTDPQTGLRLLPLKEKKRERKTSskSSVRKRRVIVDPETGKE  
5dzz. 1. A -----  
Target MSVYEAYRKGLIDHQTYLELSEQeCEWEEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTlSITE  
5dzz. 1. A -----  
Target FADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDtETLEKVSITEAMHRNLVDNITGQRL  
5dzz. 1. A -----  
Target LEAQACTGGIIDPNTGERFPVTDaVNKGLVDKIMVDRINLAQKAfCGFEDPRTKTKMSAAQALKKGWLYYEAGQRfLEVQ  
5dzz. 1. A -----  
Target YLTGGLIEPDTPGRVPLDEALQRGTVDARTaQKLrdVSAYSkyLTCPKTKLKISYKDAlDRSMVEEGTGLRLLEAAaQSS  
5dzz. 1. A -----  
Target KGYSPYSVSGSGSTTGSrSGSRTGSrAGSRRGSFDATGSGfSMTfSSSSYSSSGYGRRYASGPTSSLGpESAAa  
5dzz. 1. A -----

Model #10	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.59 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5dzz.1.A	38.07	monomer	0.00	HHblits	X-ray	2.60Å	0.38	3888 - 4476	0.11	Desmoplakin

The template contained no ligands.

Target MSGEDQEVRAVVEDGSNGGSGSPSGDTLPWNLEKTQRSRRGGGGPGNGSVLDPaERAVIRIADERDRVQKKTfTKWVN  
5dzz. 1. A -----  
Target KHLIKAQRHISDLyEDLRdGHNLISLLEVLSGDSLPREKGRMRfHKLQNVQIAlDYLRHRQVKLVNIrNDIDIADGNPKLT  
5dzz. 1. A -----  
Target LGLIWtIILHFQISDIQVSGQSEDMtAKEKLLWSQRMVEGYQGLRCdNFTSSWRDGRlFNaiIHRHKPMLIDMNkVYRQ  
5dzz. 1. A -----  
Target TNLENLDQAFSVAERDLGVTRLLDPEDVDVPQpDEKSIITyVSSLYDAMPRVpDVQDGvKANELQLRWQeYRELvLLLLQ  
5dzz. 1. A -----  
Target WIRAHTAAFEERRFPSSFEeIEILWCfLKFkETELPAKEADKNRSKGIYQSLegAVQAGQLKvPPGYHPLDVEKEWgKL

5dzz. 1. A -----  
Target HVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLKADGMIRLLF  
5dzz. 1. A -----  
Target NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSAEWGVDLP  
5dzz. 1. A -----  
Target SVEAQLGSHRGLHQSVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLESLHGFVAAATKEL  
5dzz. 1. A -----  
Target MWLSEKEEEEVGFWDWSEKSNMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPPARPTVESFQAALQTQWSWMLQ  
5dzz. 1. A -----  
Target LCCCIEAHLKENTAYFQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKQQLNEYRGHLSGLAKRAK  
5dzz. 1. A -----  
Target AIVQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHKGDECQMLGPAQPPHVKVLSSSGSEAAVPSVCFLVPPPNQEALEAV  
5dzz. 1. A -----  
Target ARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLELHYQAFLRDSQDAGGFGPE  
5dzz. 1. A -----  
Target DRLQAEREYGSCSRHYQQLLSLEQGEQEESRCQRCISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQQKA  
5dzz. 1. A -----  
Target QAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKTIISLVIRSTQGAEELRAHE  
5dzz. 1. A -----  
Target EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVERWRERVTLLELRWQ  
5dzz. 1. A -----  
Target AVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEIQAVPLADSQAVREQLRQEKALLEIERHAEKVEECQ  
5dzz. 1. A -----  
Target RFAKQYINAIKDYLQLVTYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRFISETLRRMEEEER  
5dzz. 1. A -----  
Target LAEQQRAEERERLAEVEAALEKQRQLAEHAQAKAQAEAEQELQRRMQEEVARREEVAVDAQQQKRSIQEELQQLRQSS  
5dzz. 1. A -----  
Target EAEIQAQARQVEAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQALRAREEAEQKRQAQEEAERLRRQVQEETQR  
5dzz. 1. A -----  
Target KRQAEELGLRVKAEAEAREKQRALQALEELRLQAEAAERRLRQAEAEERARQVQVALETAQRSAQELQSKHASFAEKT  
5dzz. 1. A -----  
Target AQLERTLEEEHVTVVQLREEATRREQQAEAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAA  
5dzz. 1. A -----  
Target EREARRRGKAEQAVRQRELAEQELERQRLAEGTAQQLAAEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAAATQK  
5dzz. 1. A -----  
Target RQELEAELAKVRAEMEVLLASKARAEESRSSEKSKRLEAEAGRFRELAEEAARLRALAEAAKRQRQLAEEDAARQRA  
5dzz. 1. A -----  
Target EAERVLSEKLA AIS EATRLKTEAEIALKEKEAENERLRLRAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ  
5dzz. 1. A -----  
Target KGLVEDTLRQRRQVEEELALKASFEEKAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAER  
5dzz. 1. A -----  
Target VQKSLAEEEEAARQRKAAL EEVERLKAKVEEARRLRERAEHESVRQLQLAQEAQKRLQAEKHAFAVQQKEQELQOTL  
5dzz. 1. A -----  
Target QQEQSVLEKL RSEAEAAARRAAEEAEERARAEREAQSRQRVEEAERLQAAEEQAQAQAQAAAEKL RKEAEQEAAARR  
5dzz. 1. A -----  
Target AQAEQAALRQKQAADAEMEKHKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKA EVTEAARQRSQVEEE  
5dzz. 1. A -----  
Target LFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVA AQEAARLRQLAEEDLAQQRALAE  
5dzz. 1. A -----

Target 5dzz. 1. A KMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEAEERLRLRV-----

Target 5dzz. 1. A AEMSRAQARAEDAQRFRKQAEIEGAKLHRTTELATQEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAEELL-----

Target 5dzz. 1. A QLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQQMQQEKQQL-----

Target 5dzz. 1. A ASMEEARRRQHEAEEGVRRKQEELQLEEQRRQQEQLLAEENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG-----

Target 5dzz. 1. A QDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLPANEKLT-----

Target 5dzz. 1. A IYAALRRQLSPGTALILLEAQAAASGFLDPVRNRRLTVTEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISLFAQ-----

Target 5dzz. 1. A MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC-----

Target 5dzz. 1. A VEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTAEQRRDLLRQFRTGKVT-----

Target 5dzz. 1. A VEKIIKIVITVIEEHEQKGQLCFQGLRALVPAELLESGIIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWL-----

Target 5dzz. 1. A EEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSG-----

Target 5dzz. 1. A QSVSLFQALKKGLIPREQGLRLDAQLSTGGTVDPSPKSHRPLDVCARGYLDEETSTALSAPRDDAKTYYPDRTWELAT-----

Target 5dzz. 1. A YSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQELL-----

Target 5dzz. 1. A RQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKD GKTSVKDLSELSSLQTL-----

Target 5dzz. 1. A QGSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQATGFLVDPVRNQRLYVHEAVKAGVVGPELHEKLLSAEK-----

Target 5dzz. 1. A AVTGYKDPYSGSTISLFQAMKKGLVVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKG-----

Target 5dzz. 1. A FFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETTRA FEETQIDIPGGGSHGGSTMSLWEVM-----

Target 5dzz. 1. A QSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTR-----

Target 5dzz. 1. A SLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQATGFLDPVKGERLTVDEAVRKG-----

Target 5dzz. 1. A LVGPPELHDLRLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEALRLLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNK-----

Target 5dzz. 1. A DTHDQLSEPSEVRSYVDPSTDERLSYTLQLLRCRRDETSGFLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRL-----DTSKLVFDGLRKKVTAMQLYECQLIDKTTLDKL

Target 5dzz. 1. A QEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEAQATGYVIDPIKGLKLTVEEAVLKGKKSVEEVASEIQPFRLRGAGSIAGAS-ASPKEKYSLVAEKRKKLISPESTVMLEAQATGGIIDPHRNEKLTVDSAI

Target 5dzz. 1. A RMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQAMKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGLARDLIDFDDRQQIYAAEKAITGFDDPFSGKTVSVSEATKKNLIDRETGMRLLEAQIASGGVVDPVNSVFLPKDVALARGL

Target 5dzz. 1. A FDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSKSSSVRKRVRVIDVPETGKEIDRDLYRSLNDPRDSQKNFVDPVTKKVSYVQLKERCRIEPTGLLLLSVQKRSM-----SFQG----

Target 5dzz. 1. A MSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITE-----IRQPVTVTELVDSGILRPSTVNELESGQISYDE

Target 5dzz. 1. A FADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTLASWSDPTEETGPVAGILDDETLEKVSITEAMHRNLVDNITGQRLVGER-----IKDFLQGSSCIAGIYNETTKQKLGIYEAMKIGLVRPGTALEL



Target LEAQAQTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQ  
5dzz. 1. A LEAQAATGFIVDPVSNLRLPVVEAYKRGLVGIEFKEKLLSAERAVTGYNDPETGNIISLFQAMNKELIEKGHGIRLLEAQ

Target YLTGGLIEPDTGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTCPKTKLKISYKDALDRSMVEEGTGLRLLEAAAQSS  
5dzz. 1. A IATGGIIDPKESHRLPVDIAYKRGYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLKERICKDEETGLCLLPLK----

Target KGYSPSPYSVSGSGSTTGSRSRGTGSRAGSRRGSFDTGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA  
5dzz. 1. A -----

Model #13	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.62 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
6s17.1.A	27.80	homo-dimer	0.00	HHblits	X-ray	3.30Å	0.35	63 - 480	0.09	Calponin homology domain protein putative

The template contained no ligands.

Target MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN  
6s17. 1. A -----LVAQWEKVQIKTFTKWVN

Target KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPR-EKGRMRFHKLQNVQIALDYLRHRQVKLVNIRNDDIADGNPKL  
6s17. 1. A MHLAKKGRKINDVTTDFKNGVELCALLEIIGETTICKVTNPKMRIQMTENLDKALRFIQSRDVKLTGIGPTDIVDGNVKL

Target TLGLIWTIILHFQISDIQVSGQSEDMTAKELLLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYR  
6s17. 1. A TLGLVWTLILRFAISELSAE----GLSAKQGLLLWCQKKCEPYP-VKVENFSESFKDGKVFICALIHRHRPDLLDWETVGE

Target QTNLENLDQAFSVAERDLGVTRLLDPEDVDV-PQPDEKSIITYVSSLYDAMPRPVDVQDGVK-----ANELQLRWQE  
6s17. 1. A -DDRANLEKAFDVAEKELGIPKLLDVDDIVNMPRPDERSVMTYVAALYKVFSSNDQVEKAGKRAGNFLDLLRATEGMVHD

Target YRELVLLLLQWIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSGIYQSLEGAVQAG---QLKVPPG  
6s17. 1. A YEQRAQALKENIEAAINKMNGVEPSDEYHQVEQINETKNYRKGDKRAFIKEQGDLATLFGQINSKLRGMKRPVYVAPEG

Target YHPLDVEKEWGKLVHAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVER  
6s17. 1. A LDPKSLEGYIANISEAERALRSKLNTAMR--NCLIALRKAFADPANATDAKINEYRTFVTDETSEAPLEEQVATLKAKLE

Target DLDKADGMIRLLFNDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQ  
6s17. 1. A ELKQVEAQLPPIE-----

Target RRVDSAEWGVDLPSVEAQLGSHRGLHQSVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLE  
6s17. 1. A -----

Target SLHGFVAAATKELMWLSEKEEEEVGFWDSESNMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARPTVESF  
6s17. 1. A -----

Target QAALQTQWSWMLQLCCCIEAHLKENTAYFQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKDQLNE  
6s17. 1. A -----

Target YRGHLSGLAKRAKAIVQLTPRNPTQPTRGRVPLLAVCDYKQEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCF  
6s17. 1. A -----

Target LVPPPNQEALEAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLELHYQAF  
6s17. 1. A -----


Target LRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLLSLEQGEQEESRCQRCISELKDIRLQLEACETRTRVHRLRLPLDKEPA  
6s17. 1. A -----

Target RECAQRIAEQQAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKTIISLVIR  
6s17. 1. A -----

Target STQGAEELRAHEEQLEAQAVPAALPELEATKAAMKKLRAQAEQQPVFDALRDELRGAEVGERLQQRHGERDVEVER  
6s17. 1. A -----

Target 6s17.1.A	WRERVTLLERWQAVLAQTDVRQRELEQLGRQLRYYRESADPLGAWLQDARRRQEQIQAVPLADSQAVREQLRQEKALLE -----
Target 6s17.1.A	EIERHAEKVEECQRFQAKQYINAIKDYLQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRF -----
Target 6s17.1.A	ISETLRRMEEEEERLAEQQRAEERERLAEVEAALEKQRQLAEHAQAKAQAEREAQELQRRMQEEVARREEVAVDAQQQKR -----
Target 6s17.1.A	SIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEEEIRVVRLQLETTERQRGGAEGELQALRARAEAEAKRQAQEEA -----
Target 6s17.1.A	ERLRRQVQEETQRKRQAEAEGLRVKAEAAAREKQRALQALEELRLQAEAAERRLRQAEAEERARQVQVALETAQRSQAQ -----
Target 6s17.1.A	ELQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQAEAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKS -----
Target 6s17.1.A	LAQAEAEKQKEAAEREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQRLAAEQELIRLRAETEQGEQQRQLLEEL -----
Target 6s17.1.A	ARLQSEAAAAATQKRQELEAEALAKVRAEMEVLLASKARAEESRSSEKSKRLEAEAGRFRELAEEAARLRALAEAAKRQ -----
Target 6s17.1.A	RQLAEEDAARQRAEAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRRLAEDEAFQRRRLEEQAQHKADIEERLA -----
Target 6s17.1.A	QLRKASESELERQKGLVEDTLRQRRQVEEEILALKASFEEAAAGKAELELELGRI RNAEDTLRSKEQAEQEAARQRQLA -----
Target 6s17.1.A	AEEERRRREAEEERVQKSLAAEEEAARQRKAALEEVEERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKRLQAEKHAHF -----
Target 6s17.1.A	AVQQKEQELQQTLLQEQSVLEKLRSEAEAAARRAAEEAEARERAEREAAQSRQRVEEAERLKQAAEEQAQAQAQAAAAE -----
Target 6s17.1.A	KLRKEAEQEAAARRAQAEQAALRQKQAADAEMEKHKKF AEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKAEV -----
Target 6s17.1.A	TEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVAQEAARLRQL -----
Target 6s17.1.A	AEEDLAQQRALAEKMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQL -----
Target 6s17.1.A	EMSAEERLRLRVAEMSRAQARAEDAQRFRKQAEIIGAKLHRTLATQEKVTLVQTLETQRQQSDRDADRLREIAELE -----
Target 6s17.1.A	REKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAKLREEQQR -----
Target 6s17.1.A	QQQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQQEQLLAEENRRLRERLEHLEEHRAALAHSEIIT -----
Target 6s17.1.A	AAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSI -----
Target 6s17.1.A	AGLLLPANEKLTIIYAALRRQLLSPGTALILLEAQAAASGFLDPVRNRRLTVTEAVKEGVVGPPELHHKLLSAERAVTGYK -----
Target 6s17.1.A	DPYTGEKISLFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNT -----
Target 6s17.1.A	HENLTYLQLLERCVDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTAQR -----
Target 6s17.1.A	RDLLRQFRTGKVTVEKIIKIVITVIEEHEQKGQLCFQGLRALVPAELLESGLIDWDLFRQLQLGERSVQEVAEVEGVRR -----
Target 6s17.1.A	ALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVGPPELHEKLLSA -----
Target	EKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDDAQLSTGGTVDPKSHRPLDVCARGYLDEETSTALSAPRDDA

6s17. 1. A -----  
Target KTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELIN  
6s17. 1. A -----  
Target SEYFTAERQELLRQFRTGKVTVEKIIKIVITIVEEVETRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKDGKTSV  
6s17. 1. A -----  
Target KDLSELSSLQTLQSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLYVHEAVKAGV  
6s17. 1. A -----  
Target GPHELHEKLLSAEKAVTGYKDPYSGSTISLFQAMKKGLVVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEM  
6s17. 1. A -----  
Target NRVLEDPDDTKGFFDPNTHENLTYRQLLERCVDPETGLRLLPLKGPEKAEVVETTRVYTEETTRAFFETQIDIPGGG  
6s17. 1. A -----  
Target SHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVI  
6s17. 1. A -----  
Target SRESYSLLREGTRSLREVLEASAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLDPVK  
6s17. 1. A -----  
Target GERLTVDEAVRKGLVGPETHDRLLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEALRLDAQLATGGIVDPRLGFHL  
6s17. 1. A -----  
Target PLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSYQQLRRCRDETSGLFLLPLSEARKLTFRGLRKQITVEELV  
6s17. 1. A -----  
Target RSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEAQAATGYVID  
6s17. 1. A -----  
Target PIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQAMKKGLIKDHGIRLLEAQIATGGIIDPEES  
6s17. 1. A -----  
Target HRLPVDVAYQRLGFDEEMNEILTDPDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSKSSVRK  
6s17. 1. A -----  
Target RRVVIDPETGKEMSVEYAYRKGLIDHQTYLELSEQECWEIEITISSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSA  
6s17. 1. A -----  
Target LDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTETLEKVSITEAM  
6s17. 1. A -----  
Target HRNLVDNITGQRLLEAQAQCTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGW  
6s17. 1. A -----  
Target LYYEAGQRFLEVQYLTGGLIEPDTGRVPLDEALQRGTVDARTAKLRDVSAYSKYLTCPKTKLKISYKDALDRSMVEEG  
6s17. 1. A -----  
Target TGLRLLLEAAAQSSKGYSPYSVSGSGSTGSRSGSRTGSRAGSRRGSFDATGSGFSMTFSSSSYSSSGYGRRYASGPTSS  
6s17. 1. A -----  
Target LGGPESAAA  
6s17. 1. A -----

Model #19	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.72 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
3pe0.1.A	88.53	monomer	0.00	HHblits	X-ray	2.95Å	0.58	626 - 899	0.06	Plectin

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
CA.1	Not in contact with model.	CALCIUM ION

Target 3pe0. 1. A	MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN
Target 3pe0. 1. A	KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLRHRQVKLVNIRNDDIADGNPKLT
Target 3pe0. 1. A	LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLLSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYRQ
Target 3pe0. 1. A	TNLENLDQAFSVAERDLGVTRLLDPEDVDVPQPDEKSIITYVSSLYDAMPRPVDVQDGVKANELQLRWQEYRELVLALLQ
Target 3pe0. 1. A	WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAGQLKVPPTYHPLDVEKEWGKL
Target 3pe0. 1. A	HVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLKADGMIRLLF
Target 3pe0. 1. A	NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSAEGVLDLP
Target 3pe0. 1. A	SVEAQLGSHRGLHQSVVEEFAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLESLSHGFAAATKEL -----RSLESLSHSFAAATKEL
Target 3pe0. 1. A	MWLSEKEEEEVGFWDSESNMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHDPARTVESFQAALQTQWSWMLQ MWLNEKEEEEVGFWDSDRNTNMTAKKESYSALMRELELKEKKIKELQNAGDRLLREDHDPARTVESFQAALQTQWSWMLQ
Target 3pe0. 1. A	LCCCEIAHLKENTAYFQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKDQLNEYRGHLSGLAKRAK LCCCEIAHLKENAAYFQFFSDVREAEGLQLQLQALRRKYSCDRSATVTRLEDLLQDAQDEKEQLNEYKGHLSGLAKRAK
Target 3pe0. 1. A	AIVQLTPRNPTQPTRGRVPLLAVCYDKQVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCFLVPPPNQEALEAV AVVQLKPRHPAHPMRGRPLLAVCYDKQVEVTVHKGDECQLVGPAQPSHWKVLSSSGSEAAVPSVCFLVPPPNQEAQEA
Target 3pe0. 1. A	ARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLELHYQAFRLDSQDAGGFGPE TRLEAQHQALVTLWHQLHVDKM-----
Target 3pe0. 1. A	DRLQAEREYGSCSRHYQQLLSLEQGEQEESRCQRCISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQQKA
Target 3pe0. 1. A	QAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLKLTISLVIRSTQGAEELRAHE
Target 3pe0. 1. A	EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELRGAEVGERLQQRHGERDVEVERWRERVQTLLERWQ
Target 3pe0. 1. A	AVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEIQIQAIVPLADSQAVREQLRQEKALLEEIERHAEKVEECQ
Target 3pe0. 1. A	RFAKQYINAIKDYLQLVITYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTYSELSTLTSQYIRFISETLRRMEEER
Target 3pe0. 1. A	LAEQQRAEERERLAEVEAALEKQRQLAEAHAQAKAQAEAEQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSS
Target 3pe0. 1. A	EAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETTERQGGAEQELQALRARAEAEAKRQAQEEAERLRRQVQEETQR
Target 3pe0. 1. A	KRQAEAEGLRVKAEAEAREKQRALQALEELRLQAEAEERRLRQAEAEERARQVQVALETAQRSAAELQSKHASFAEKT
Target 3pe0. 1. A	AQLERTLEEEHVTVVQLREEATRREQQAEAEERAREEAERELERWQLKANEALRLRLQAEVAQQKSLAQAEAEKQKEAA
Target 3pe0. 1. A	EREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQLAAEQELIRLRAETEQQEQQRQLLEEELARLQSEAAAAATQK
Target 3pe0. 1. A	RQELEAEELAKVRAEMEVLASKARAEESRSSEKSKQRLAEAGRFRELAEEAARLRALAEAAKRQRQLAEEDAARQRA

Target  
3pe0. 1. A EAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRRLAEDAEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ  
-----

Target  
3pe0. 1. A KGLVEDTLRQRRQVEEEILALKASFKEAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRRREAEEER  
-----

Target  
3pe0. 1. A VQKSLAEEEEAARQRKAAL EEVERLKAKVVEARRLRERAHEHESVRQLQLAQEAAQKRLQAEKKAHAFVQQKEQLQQTL  
-----

Target  
3pe0. 1. A QQEQSVLEKLRSEAEARRAAEEAEERARAEREAAQSRQRVEEAERLKQAAEEQAQAQAQAAAEKLRKEAEQEAARR  
-----

Target  
3pe0. 1. A AQAEQAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKAEVTEAARQRSQVEEE  
-----

Target  
3pe0. 1. A LFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAE  
-----

Target  
3pe0. 1. A KMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEAERLRLRV  
-----

Target  
3pe0. 1. A AEMSRAQARAEEDAQRFRKQAEETGAKLHRTELATQEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAELL  
-----

Target  
3pe0. 1. A QLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQLREEQQRQQQMQQEKQQLL  
-----

Target  
3pe0. 1. A ASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQQEQLLAENRRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG  
-----

Target  
3pe0. 1. A QDAADGPAAPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLKPANEKLT  
-----

Target  
3pe0. 1. A IYAALRRQLLSPGTALILLEAQAASGFLDPVRNRRLTVTEAVKEGVGPPELHHKLLSAERAVTGYKDPYTGEKISLFAQ  
-----

Target  
3pe0. 1. A MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC  
-----

Target  
3pe0. 1. A VEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELINSEYFTAQRRDLLRQFRTGKVT  
-----

Target  
3pe0. 1. A VEKIIKIVITVIEEHEQKGQLCFQGLRALVPAELLESGIIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWL  
-----

Target  
3pe0. 1. A EEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPATSARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSG  
-----

Target  
3pe0. 1. A QSVSLFQALKKGLIPREQGLRLDDAQLSTGGTVDPKSHRPLDVACARGYLDEETSTALSAPRDDAKTYYPRTWELAT  
-----

Target  
3pe0. 1. A YSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAQRRQELL  
-----

Target  
3pe0. 1. A RQFRTGKVTVEKIIKIVITVIEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKDGTSVKDLSELSSLQTL  
-----

Target  
3pe0. 1. A QGSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLYVHEAVKAGVGPPELHEKLLSAEK  
-----

Target  
3pe0. 1. A AVTGYKDPYSGSTISLFAQMKGVLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKG  
-----

Target  
3pe0. 1. A FFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETTRAFEETQIDIPGGGSHGGSTMSLWEVM  
-----

Target  
3pe0. 1. A QSDLIPEEQRAQLMADFQAGRVTKERMIIIIEIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTR  
-----

Target  
3pe0. 1. A SLREVLEASAWRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRKG  
-----

Target  
3pe0. 1. A LVGPPELHDLRLSAERAVTGYRDPYTEQTIISLFAQMKGDLIPAEELRLLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNK  
-----

Target  
3pe0. 1. A

DTHDQLSEPSEVRSYVDPSTDERLSYTLQLLRRCRRDETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRL

Target  
3pe0. 1. A

QEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKGIIRPGTAFELLEQAATGYVIDPIKGLKLTVEEAV

Target  
3pe0. 1. A

RMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQAMKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGL

Target  
3pe0. 1. A

FDEEMNEILTDPSDDTKGFFDPNTEENLYLQLMERCVTDPQTGLRLLPLKEKKRERKTSSKSSVRKRRVIVDPETGKE

Target  
3pe0. 1. A

MSVYEAYRKGLIDHQTYLELSEQECWEIEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITE

Target  
3pe0. 1. A

FADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTLASWSDPTEETGPVAGILDDETLEKVSITEAMHRNLVDNITGQRL

Target  
3pe0. 1. A

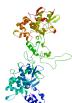
LEAQAQTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQ

Target  
3pe0. 1. A

YLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKL RDVSAYSKYLTCPKTKLKISYKDALDRSMVEEGTGLRLLEAAAQSS

Target  
3pe0. 1. A

KGYYSPPYSVSGSGSTTGSRSRGTGSRAGSRRGSFDTGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA

Model #09	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.60 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
5dzz.1.A	48.75	monomer	0.00	BLAST	X-ray	2.60Å	0.43	2654 - 3223	0.11	Desmoplakin

The template contained no ligands.

Target  
5dzz. 1. A

MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDP AERAVIRIADERDRVQKKTFTKWVN

Target  
5dzz. 1. A

KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLHRHQVKLVNIRNDDIADGNPKLT

Target  
5dzz. 1. A

LGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAIIHRHKPMLIDMNKVYRQ

Target  
5dzz. 1. A

TNLENLDQAFSVAERDLGVTRLLDPEDVDVPQDEKSIITYVSSLYDAMPRPVDVQDGVKANELQLRWQEYRELVL LLLQ

Target  
5dzz. 1. A

WIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAGQLKVPPGYHPLDVEKEWGKL

Target  
5dzz. 1. A

HVAILEREKQLRSEFERLERLRIVSKLQMEAGLCEEQLNQADALLQSDVRLLAAGKAPQRAGEVERDLKADGMIRLLF

Target  
5dzz. 1. A

NDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQDLLAWVEENQRRVDSA EWGVDLP

Target  
5dzz. 1. A

SVEAQLGSHRGLHQSVVEEFRAKIERARTDEGQLSPATRGAYRDCLGRDLQYAKLLNSSKARLSLES LHGFVAAATKEL

Target  
5dzz. 1. A

MWLSEKEEEEVGFWDSESNSMAAKKEAYSALMRELELKEKKIKEIQSTGDRLLREDHPARPTVESFQAALQTQWSWMLQ

Target 5dzz. 1. A	LCCCIEAHLKENTAYFQFFSDVREAEELRKLQETLHRKYTCDRSITVTRLEDLLQDAQDEKDQLNEYRGHLSGLAKRAK
Target 5dzz. 1. A	AIVQLTPRNPTQPTRGRVPLLAUCDYKQVEATVHKGDECQMLGPAQPFHWKVLSSSGSEAAVPSVCFLVPPPNQEALEAV
Target 5dzz. 1. A	ARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTLKPPEEQRQALRSLELHYQAFLRDSQDAGGFGPE
Target 5dzz. 1. A	DRLQAEREYGSCSRHYQQLLSLEQGEQESRCQRCISELKDIRLQLEACETRTRVHRLRLPLDKEPARECAQRIAEQQKA
Target 5dzz. 1. A	QAEVEGLGKGVARLSAAEAKVLALPEPSPAAPTLRSELELTGKLEQVRSLSAIYLEKLTISLVIRSTQGAEELRAHE
Target 5dzz. 1. A	EQLKEAQAVPAALPELEATKAAMKKLRAQAEAAQPVFDALRDELGAQEVGERLQQRHGERDVEVERWRERVQTLLERWQ
Target 5dzz. 1. A	AVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQDARRRQEQIQAVPLADSQAVREQLRQEKALLEIERHAEKVEECQ
Target 5dzz. 1. A	RFAKQYINAIKDYLQLVTYKAQLEPVASPAKKPKVQSGSESVIQEYVDLRTRYSELSTLTSQYIRFISETLRRMEEEER
Target 5dzz. 1. A	LAEQQRAEERERLAEVEAALEKQRQLAEAHQAQAQAEREAEQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSS
Target 5dzz. 1. A	EAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQALRARAEAEAKRQAQEEAERLRRQVQEEETQR
Target 5dzz. 1. A	KRQAEAEGLRVKAEAEAAAREKQRALQALEELRLQAEAEERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKT
Target 5dzz. 1. A	AQLERTLEEEHVTVVQLREEATRREQQQAEAEERAREEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAA
Target 5dzz. 1. A	EREARRRGKAEQAVRQRELAEQELERQRQLAEGTAQQLAAEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAAATQK
Target 5dzz. 1. A	RQELEAEALAKVRAEMEVLASKARAEESRSSEKSKRLEAEAGRFRELAEEAARLRALAEAAKRQRQLAEEDAARQRA
Target 5dzz. 1. A	EAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRRLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQ
Target 5dzz. 1. A	KGLVEDTLRQRRQVEEELALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAEER
Target 5dzz. 1. A	VQKSLAAEEEAARQRKAAL EEVERLKAKEVEARRLRERAEHESVRQLQLAQEAAQKRLQAEKKAHAFVQQKEQELQQT
Target 5dzz. 1. A	QQEQSVLEKLRS EAEARRAAEEAEARERAEERAAQSRQRVEEAERLKQAEEQAAQAAQAAAEKLRKEAEQEAARR
Target 5dzz. 1. A	AQAEQAALRQKQAADAEMEKKHFAEQTLRQKAQVEQELTALRLKLEETDHQKSILDQELQRLKAEVTEAARQRSQVEEE
Target 5dzz. 1. A	LFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAE
Target 5dzz. 1. A	KMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEERLRLRV
Target 5dzz. 1. A	AEMSRAQARAEDAQRFRKQAEETGAKLHRTLATQEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAELL
Target 5dzz. 1. A	QLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQQMQQEKQQLL
Target 5dzz. 1. A	ASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQEQQLAEENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNG
Target	QDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLPANEKLT

5dzz. 1. A -----VFDGLRKKVTAMQLYECQLIDKTTLDKLLKGKKSVEEVAS--EIQPFLRGAGSIAGASASP-KEKYS

Target IYAALRRQLLSPGTALILLEAQAASGFLLDPVRNRRLTVTEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISLFAQ  
5dzz. 1. A LVEAKRKKLISPESTVMLLEAQAATGGIIDPHRNEKLTVDSAIARDLIDFDDRQQIYAAEKAITGFDDPFSGKTVSVSEA

Target MKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERC  
5dzz. 1. A IKKNLIDRETGMRLLEAQIASGGVVDPVNSVFLPKDVALARGLIDRDLYRSLNDPRDSQKNFVDPVTKKKVSYVQLKERC

Target VEDPETGLRLLPLTDQAAKGGEVYTDSEARDVFEKATVSAPFGKFQG--KTVTIWELINSEYFTAEQRRDLLRQRTGK  
5dzz. 1. A RIEPHTGLLLSV-----QKRMS-----FQGIRQPVTVELVDSGILRPSTVNEL-----

Target VTVEKIIKIVITVIEEHEQKGQLCFQGLRALVPAELLESGLIIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGV  
5dzz. 1. A -----ESGQISYD-----EVGER-----IKDFLQGSSCIAGI

Target WLEEARQKLSIYEALKKELLQPEAAVALLEAQAAGTGHVIDPATSARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPY  
5dzz. 1. A YNETTKQLGIYEAMKIGLVRPGTALELLEAQAATGFIVDPVSNLRLPVEEAYKRGLVGIEFKEKLLSAERAVTGYNDPE

Target SGQSVSLFQALKKGLIPREQGLRLDDAQLSTGGTVDPSPKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYDPRTWEL  
5dzz. 1. A TGNIIISLFQAMNKELIEKHGIRLLEAQIATGGIIDPKESHRLPVDIAYKRGYFNEELSEILSDPSDDTKGFFDPNTEEN

Target ATYSQLQQQCRPDPLTGLSLLPLSEEAAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQE  
5dzz. 1. A LTYLQLKERICKDEETGLCLLPLKE-----

Target LLRQFRTGKVTVEKIIKIVITIVEEVETRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKDGTKSVKDLSELSSLQT  
5dzz. 1. A -----

Target LLQSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLEAQAATGFLVDPVRNQRLYVHEAVKAGVVGPPELHEKLLSA  
5dzz. 1. A -----

Target EKAVTGYKDPYSGSTISLFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDT  
5dzz. 1. A -----

Target KGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETTRAFEETQIDIPGGGSHGGSTMSLWE  
5dzz. 1. A -----

Target VMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREG  
5dzz. 1. A -----

Target TRSLREVLEAESAWRYLYGTGCVAGVYLPGRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLLDPVKGERLTVDEAVR  
5dzz. 1. A -----

Target KGLVGPPELHDRLLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEELRLDDAQLATGGIVDPRLGFHLPLEVAYQRGYL  
5dzz. 1. A -----

Target NKDTHDQLSEPSEVRSYVDPSTDERLSYTLRRRCRRDETSGFLPLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQ  
5dzz. 1. A -----

Target RLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEAQAATGYVIDPIKGLKLTVEE  
5dzz. 1. A -----

Target AVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQAMKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQR  
5dzz. 1. A -----

Target GLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRERKTSSKSSVRKRRVVIDPETG  
5dzz. 1. A -----

Target KEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSI  
5dzz. 1. A -----


Target TEFADMLSGNAGGFRRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTELEKVSITEAMHRNLVDNITGQ  
5dzz. 1. A -----

Target RLLEAQAQCTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLE  
5dzz. 1. A -----

Target VQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKLRDVSAYS KYLTCPKTKLKS YKDALDRSMVEEGTGLRLLLEAAAQ  
5dzz. 1. A -----

Target SSKGYSPYSVSGSGSTTGSRSGRSRTGSRAGSRRGSFDTGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA  
5dzz. 1. A -----



Model #21	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.59 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
4d1e.1.A	25.11	homo-dimer	0.00	HHblits	X-ray	3.50Å	0.33	65 - 738	0.15	ALPHA-ACTININ-2

The template contained no ligands.

Target 4d1e. 1. A MSGEDQEVRAVVEDGSNGSGSPSPGDTLPWNLEKTQSRRRGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN  
-----LLDPAWEKQQRKTFTAWCN

Target 4d1e. 1. A KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPR-EKGRMRFHKLQNVQIALDYLHRHQVKLVNIRNDDIADGNPKL  
SHLRKAGTQIENIEEDFRNGLKMLLLEVISGERLPKPDRCGMRFHKIANVKNALDYIASKGVKLVSIGAEIIVDGNVKM

Target 4d1e. 1. A TLGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAI IHRHKPMLIDMNKVYR  
TLGMIWTIILRFAIQDISVE----ETSAKEGLLLWCQRKTAPYRNVNIQNFHTSWKDGLGLCALIHRHRPDLIDYSKLNK

Target 4d1e. 1. A QTNLENLDQAFSVAERDLGVTRLLDPEDV-DVPQPDEKSIITYVSSLYDAMPVPDVQDGVK-----ANELQLRWQE  
DDPIGNINLAMEIAEKHLDIPKMLDAEDIVNTPKPDERAIMTYVSCFYHAFAGAEQAETAANRICKVLAVNGENERLMEE

Target 4d1e. 1. A YRELVLLLLQWIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSKGIYQSLEGAVQAG---QLKVPPG  
YERLASELLEWIRRTIPWLENRTPAATMQAMQKKLEDFRDYRRKHKPPKVQEKQCLEINFNTLQTKLRISNRPAPMPSEG

Target 4d1e. 1. A YHPLDVEKEWGKLVHAILEREKQLRSEFERLERLRIVSKLQMEAGLCEEQLNQADALLQSDV----RLLAAGKAPQKQAG  
KMVSDIAGAWQRLQAEKGYEELLNEIRRLERLEHLAEKFRQKASTHETWAYGKEQILLQKDYESASLTEVRALLRKHE

Target 4d1e. 1. A EVERDLKADGMIRLLFNDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNL---RLRGTPRHP---ELEDSTLRYL  
AFESDLAAHQDRVEQIAAIAQELNELDYHDAVNVNDRCKIKCDQWDLGTLTQKRREALERMEKLLTIDQLHLEFAKRA

Target 4d1e. 1. A QDLLAWVEENQRRVDSAEGVDLPVSVEAQLGSHRGLHQSVVEEFAKIERARTDEGQL-----S---PATRGAYRDCLG  
APFNNWMEGAMEDLQDMFIVHSIEEIQSLITAHEQFKATLPEADGERQSIMAIQNEVEKVIQSYNIRISSNPYSTVTMD

Target 4d1e. 1. A RLDLQYAKLLNSSKARLSLES---L-----HGFVAAATKELMWLSEKEEEEVGFWDWERNNSMAAKKEAYSALMRE  
ELRTKWVKVQLVPIRDQSLQEELARQHANERLRRQFAAQANAIGPWIQNKMEETARSSIQ-ITGALEDQMNQLKQYEHN

Target 4d1e. 1. A LELKEKKIKEIQSTGDRLLREDHPARPTVESFQAALQTQWSWMLQLCCIEAHLKENTAYFFQFSDVREAEQRLKLQET  
IINYKKNIDKLEGDHQLIQEALVFDNKHTNYTMEHIRVGVWELLLTTIARTINEVETQILTRDA-----

Target 4d1e. 1. A LHRKYTCDRSITVTRLEDLLQDAQDEKDQLNEYRGHLSGLAKRAKAIIVQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHK  
-----

Target 4d1e. 1. A GDECQMLGPAQPFHWKVLSSSGSEAAVPSVCFVPPPNQEALAEAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQ  
-----

Target 4d1e. 1. A LIRSWSLVTFRTLKPEEQRQALRSLELHYQAFRLRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLQSLEQGEQESRCQR  
-----

Target 4d1e. 1. A CISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQQKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLR  
-----

Target 4d1e. 1. A SELETLGKLEQVRSLSAIYLEKLKTIISLVIRSTQGAEALRAHEEQLEKAQAVPAALPELEATKAAMKKLRAQAEAAQP  
-----

Target 4d1e. 1. A VFDALRDELRGAEVGERLQQRHGERDVEVERWRERVTLQLERWQAVLAQTDVQRQRELEQLGRQLRYRESADPLGAWLQ  
-----

Target 4d1e. 1. A DARRRQEQIQAVPLADSQAVREQLRQEKALLEEIERHAEKVEECQRFQAKYINAIKDYELQLVITYKAQLEPVASPAKKPK  
-----

Target 4d1e. 1. A VQSGSESVIQEYVDLRTRYSELSTLSQYIRFISETLRRMEEEERLAEQQRAEERERLAEVEAALEKQRLAEAHAQAKA  
-----

Target 4d1e. 1. A QAEREAQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETT  
-----

Target 4dle. 1. A	ERQRGGAEGELQALRARAEAEAKRQAQEEAERLRRQVQEETQKRQAEAEELGLRVKAEAEAAAREKQRALQALEELRLQ
Target 4dle. 1. A	AEEAERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQQAERAR
Target 4dle. 1. A	EAEERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAAEREARRRGKAEQAVRQRELAEQELERQRQLAEGT
Target 4dle. 1. A	AQQRLAAEQELIRLRAETEQGEQQRLLEEELARLQSEAAAATQKRQLEAEELAKVRAEMEVLLASKARAEESRSSEK
Target 4dle. 1. A	SKQRLEAEAGRFRELAEEAARLRALAEAEKRQRQLAEEDAARQRAEAERVLSEKLAAISEATRLKTEAEIALKEKEAENE
Target 4dle. 1. A	RLRRLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEELALKASFEEKAAAGKAE
Target 4dle. 1. A	ELELGRI RNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAEEERVQKSLAAEEEAARQRKAAL EEVERLKAKVEEARRL
Target 4dle. 1. A	RERAEHESVRQLQLAQEAAQKRLQAEKKAHAFVQQKEQELQQTLLQQEQSVLEKL RSEAEAAARRAAEEAEERARAEREA
Target 4dle. 1. A	AQSRQRVEEAERLKQAEEQAQAQAQAQAAAEKLRKEAEQEAARRAQAEQAALRQKQAADAEMEKHKKFAEQTLRQKAQV
Target 4dle. 1. A	EQELTALRLKLEETHQKSILDQELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQR
Target 4dle. 1. A	LLQEEAEKMKQVAEEAARLSVAQAQAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQAR
Target 4dle. 1. A	RLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEERLRLVAEMSRAQARAEEDAQFRKQAEIIGAKLHRTLAT
Target 4dle. 1. A	QEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAEELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQ
Target 4dle. 1. A	RERFIEEEKAKLERLFQDEVAKAQLREEQQRQQQMQQEKQQLASMEEARRRQHEAEEGVRRKQEELQLEQQRQQQE
Target 4dle. 1. A	QLLAENRRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILST
Target 4dle. 1. A	EELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLKPANEKLTIIYAALRRQLLSPGTALILLEAQASGFLDPVRNR
Target 4dle. 1. A	RLTVTEAVKEGVGPPELHHKLLSAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPV
Target 4dle. 1. A	DVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFE
Target 4dle. 1. A	KATVSAPFGKFQGKVTVTIWELINSEYFTAQRRDLLRQFRTGKVTVEKIIKIVITVIEEHEQKQLCFQGLRALVPAEL
Target 4dle. 1. A	LESGIIDWDLFRQLQLGERSVQEVAEEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGH
Target 4dle. 1. A	VIDPAT SARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDDAQLSTGGTVDP
Target 4dle. 1. A	SKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELY
Target 4dle. 1. A	EVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAQRRQELLRQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFS
Target 4dle. 1. A	GLRAPVPASELLAAGILSSSQFEQLKDGKTSVKDLSSELSSLQTLQSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAI
Target	LLLEAQATGFLVDPVRNQRLYVHEAVKAGVGPPELHEKLLSAEKAVTGYKDPYSGSTISLQFQAMKKGLVREHGIRLLE

4dle. 1. A

-----

Target

AQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGP

4dle. 1. A

-----

Target

EKAENVETTRVYTEETRRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEII

4dle. 1. A

-----

Target

EKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPI

4dle. 1. A

-----

Target

YQALKKGLLSAEVARLLLEAQAATGFLLDPVKGERLTVDEAVRKGLVGPELHDLRLLSAERAVTGYRDPYTEQTISLFAQM

4dle. 1. A

-----

Target

KKDLIPAEELRLDAQLATGGIVDPRLGPHLPLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSYTQLLRRCRR

4dle. 1. A

-----

Target

DETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKER

4dle. 1. A

-----

Target

LSVYQAMKKGIIIRPGTAFELLEQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLF

4dle. 1. A

-----

Target

QAMKKGILKDHGIRLLEAQAATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQIME

4dle. 1. A

-----

Target

RCVTDPQTGLRLLPLKEKKRERKTSSKSSVRKRRVIVDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISS

4dle. 1. A

-----

Target

DGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTSLITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQ

4dle. 1. A

-----

Target

LASWSDPTEETGPVAGILDTETLEKVSITEAMHRNLVDNITGQRLLEAQAQCTGGIIDPNTGERFPVTDVANKGLVDKIMV

4dle. 1. A

-----

Target

DRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTGPRVPLDEALQRGTVDARTAQKLK

4dle. 1. A

-----

Target

DVSAYSKYLCPTKTKLISYKDALDRSMVEEGTGLRLEAAAQSSKGYSPYSVSGSGSTTGSRSGSRTGSRAGSRRGSF

4dle. 1. A

-----

Target

DATSGGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA

4dle. 1. A

-----

Model #23	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.57 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
1sjj.1.B	26.16	homo-dimer	0.00	HHblits	2DX	-	0.33	64 - 737	0.15	actinin

The template contained no ligands.

Target

MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDPAAERAVIRIADERDRVQKKTFTKWVN

1sjj. 1. B

-----DPAWEKQQRKTFTAWCN

Target

KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPR-EKGRMRFHKLQNVQIALDYLRRHQVKLVNIRNDDIADGNPKL

1sjj. 1. B

SHLRKAGTQIENIEEDFRDGLKMLLLEVISGERLAKPERGKMRVHKISNVNKALDFIASKGVKLVSIGAEIIVDGNVKM

Target

TLGLIWTIILHFQISDIQVSGQSEDMTAKEKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAI IHRHKPMLIDMNKVYR

1sjj. 1. B

TLGMIWTIILRFQIDISVE---ETSAKEGLLLWYQRKTAPYKNVNIQNFHISWKDGLGFCAL IHRHPELIDYGKLRK

Target

QTNLENLDQAFSVAERDLGVTRLLDPEDVD-VPQPDEKSIITYVSSLYDAMPVPDVQDGV-----KANELQLRWQE

1sjj. 1. B DDPLTNLNTAFDVAEKYLDIPKMLDAEDIVGTARPDEKAIMTYVSSFYHAFSGAQAETAANRICKVLAVNQENEQLMED

Target YRELVLALLQWIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSGIYQSLEGAVQAG---QLKVPPG  
1sjj. 1. B YEKLASDLLEWIRRTIPWLENRAPENTMQAMQKLEDFRDYRRLHKPPKVQEKQLEINFNTLQTKLRLSNRPAFMPSEG

Target YHPLDVEKEWGKLVAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDV---RLLAAGKAPQQRAG  
1sjj. 1. B KMVSDINNAWGGLEQAEGGYEELLNEIRRLERLDHLAEKFRQKASIHESWTDGKEAMLQQKDYETATLSEIKALLKKHE

Target EVERDLDKADGMIRLLFNDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNL---RLRGTPRHP---ELEDSTLRYL  
1sjj. 1. B AFESDLAAHQDRVEQIAAIAQELNELDYDPSVSNARCQKICDQWDNLGALTQKRREALERTEKLLTIDQLYLEYAKRA

Target QDLLAWVEENQRRVDSAEWGVLDPSVEAQLGSHRGLHQSVEEFRAKIERARTDE-----GQLS---PATRGAYRDCLG  
1sjj. 1. B APFNNWMEGAMEDLQDTFIVHTIEEIQGLTTAHEQFKATLPDADKERQAILGIHNEVSKIVQTYHVNMAGTNPYTTITPQ

Target RLDLQYAKLLNSSKARLSLES-----LH-GFVAAATKELMWLSEKEEEEVGFDSERNSNMAAKKEAYSALMRE  
1sjj. 1. B EINGKWEHVRQLVPRRDQALMEEHARQQQNERLRKQFGAQANVIGPWIQTKMEEIGRISIEMH-GTLEDQLNHLRQYEKS

Target LELKEKKIKEIQSTGDRLLREDHPARPTVESFQAALQTQWSWMLQLCCIEAHLKENTAYFQFFSDVREAAEQRLKLQET  
1sjj. 1. B IVNYKPKIDQLEGDHQIQEALIFDNKHTNYTMEHIRVGEWQLLTTIARTINEVENQILTRD-----

Target LHRKYTCDRSITVTRLEDLLQDAQDEKDLNEYRGHLSGLAKRAKAIIVQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHK  
1sjj. 1. B -----

Target GDECQMLGPAQPFHWKVLSSSGSEAAVPSVCFVPPPNQEALAEAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQ  
1sjj. 1. B -----

Target LIRSWSLVTFRTLKPEEQRQALRSELHYQAFLRDSQDAGFGPEDRLQAEREYGCSCRHYQQLLSLEQGEQEESRCQR  
1sjj. 1. B -----

Target CISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQQKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPT LR  
1sjj. 1. B -----

Target SELETLGKLEQVRSLSAIYLEKLTISLVIRSTQGAEALRAHEEQLEKAQAVPAALPELEATKAAMKKLRAQAEAQQP  
1sjj. 1. B -----

Target VFDALRDELGAQEVGERLQQRHGERDVEVERWRERV TQLLERWQAVLAQTDVRQRELEQLGRQLRYRESADPLGAWLQ  
1sjj. 1. B -----

Target DARRRQEIQAVPLADSQAVREQLRQE KALLEEIERHAEKVEECQRFQKQYINAIKDYLQLV TYKAQLEPVASPAKKPK  
1sjj. 1. B -----

Target VQSGSESVIQEYVDLRTRYSELSTLTSQYIRF ISETLRMEEERLAEQQRAEERERLAEVEAALEKQRQLAEHAQAKA  
1sjj. 1. B -----

Target QAEREAQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSSEAEIQAKARQVEAERSRLRIEEEIRVVRLQLETT  
1sjj. 1. B -----

Target ERQRGGAEGELQALRARAEEAEQKRQAQEEAERLRQVQEETQRKRQAEAEGLRVKAEAEAREKQRALQALEELRLQ  
1sjj. 1. B -----

Target AEEAERRLRQAEAEERARQVQVALETAQRSQAELQSKHASFAEKTAQLERTLEEHTVVVQLREEATRREQQAEAEERAR  
1sjj. 1. B -----

Target EEAERELERWQLKANEALRLRLQAE EVAQQKSLAQAEAEKQKEAAEREARRRGKAEQAVRQRELAEQELEQRQLAEGT  
1sjj. 1. B -----

Target AQQRLAAEQELIRLRAETE QGEQQRQLLEEELARLQSEAAAATQKRQLEAE LAKVRAEMEVLLASKARAEESRSSEK  
1sjj. 1. B -----

Target SKQRLEAEAGRFRELAEEAARLRALAE EAKRQRQLAEEDAARQRAEAERVLSEKLAAI SEATRLKTEAEIALKEKEAENE  
1sjj. 1. B -----

Target RLRRLAEDEAFQRRRLLEEQAQHKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEEILALKASFEKAAAGKAEL  
1sjj. 1. B -----

Target ELELGRIIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAEERVQKSLAAEEEAARQKAALEEVEERLKA KVEEARRL  
1sjj. 1. B -----

Target RERAEHESVRQLQLAQEAAQKRLQAE EKAHAFVQQKEQELQQTLQQEQSVLEKLRSEAEAAARRAAEEAEERAEAREA  
1sjj. 1. B -----

Target AQSQRVVEEAERLKQAAEEQAQAQAQAAAEKLRKEAEQEAARRAQAEQAALRQKQAADAEMEKKH KFAEQTLRQKAQV  
1sjj. 1. B -----

Target 1sjj. 1. B	EQELTALRLKLEETHQKSILDQELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKNTQR -----
Target 1sjj. 1. B	LLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQAR -----
Target 1sjj. 1. B	RLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEAEERLRLVAEMSRAQARAEEDAQRFKQAEIIGAKLHRTELAT -----
Target 1sjj. 1. B	QEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQ -----
Target 1sjj. 1. B	RERFIEEEKAKLERLFQDEVAKAQLREEQQRQQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQQE -----
Target 1sjj. 1. B	QLLAENRRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILST -----
Target 1sjj. 1. B	EELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLKPANEKLTIIYAALRRQLLSPGTALILLEAQAASGFLDPVRNR -----
Target 1sjj. 1. B	RLTVTEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPV -----
Target 1sjj. 1. B	DVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGGLVYTDSEARDVFE -----
Target 1sjj. 1. B	KATVSAPFGKFQGKTVTIWELINSEYFTAQRRDLLRQFRTGKVTVEKIIKIVITVIEEHEQKQLCFQGLRALVPAEL -----
Target 1sjj. 1. B	LESGIIDWDLFRQLQLGERSVQVEAVEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGH -----
Target 1sjj. 1. B	VIDPAT SARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDDAQLSTGGTVDP -----
Target 1sjj. 1. B	SKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYDPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYS -----
Target 1sjj. 1. B	EVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAQRRQELLRQFRTGKVTVEKIIKIVITVIEEVETRRERLSFS -----
Target 1sjj. 1. B	GLRAPVPASELLAAGILSSSQFEQLKDGTKSVKDLSELSSLQTLQSGCLAGIYLESKEKVTIYEAMRRGLRPSTAI -----
Target 1sjj. 1. B	LLLEAQAATGFLVDPVRNQRLYVHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLQFQAMKKGLVREHGIRLLE -----
Target 1sjj. 1. B	AQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGP -----
Target 1sjj. 1. B	EKAEVVETTRYVTEETTRAFEETQIDIPGGSGHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEII -----
Target 1sjj. 1. B	EKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGRQTLPI -----
Target 1sjj. 1. B	YQALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRKGLVGPELHDLRLSAERAVTGYRDPYTEQTISLQFQAM -----
Target 1sjj. 1. B	KKDLIPAEELRLDDAQLATGGIVDPRLGFHLPLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSYTLRRCR -----
Target 1sjj. 1. B	DETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKER -----
Target 1sjj. 1. B	LSVYQAMKGGIIRPGTAFELLEAQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLF -----
Target 1sjj. 1. B	QAMKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQME -----
Target 1sjj. 1. B	RCVTDPTGLRLLPLKEKKRERKTSKSSVRKR RVIVDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISS -----

Target 1sjj. 1. B DGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQ-----

Target 1sjj. 1. B LASWSDPTEETGPVAGILDTETLEKVSITEAMHRNLVDNITGQRLLEAQAQCTGGIIDPNTGERFPVTDVANKGLVDKIMV-----

Target 1sjj. 1. B DRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKLR-----

Target 1sjj. 1. B DVSAYSKYLTCPKTKLKISYKDALDRSMVEEGTGLRLLEAAQSSKGYSPYSVSGSGSTTGSRSGSRTGSRAGSRRGSF-----

Target 1sjj. 1. B DATGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA-----

Model #03	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer	None	0.00	0.55 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
8iah.1.2	38.97	monomer	0.00	BLAST	EM	-	0.38	57 - 526	0.12	Spectrin beta chain

Excluded ligands

Ligand Name.Number	Reason for Exclusion	Description
ADP.1	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.2	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.3	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.4	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.5	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.6	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.7	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.8	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.9	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.10	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.11	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE
ADP.12	Binding site not conserved.	ADENOSINE-5'-DIPHOSPHATE

Target 8iah. 1. 2 MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQSRRRGGGGPGNGSVLDP AERAVIR--IADERDRVQKKTFTKWV-----ERSRIKALADEREVVQKKTFTKWV

Target 8iah. 1. 2 NKHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPR-EKGRMRFHKLQNVQIALDYLRHRQVKLVNIRNDDIADGNPKNSHLARVSCRITDLYKDLRDGRMLIKLLEVLSGEMLPKPTKGKMRIHCLENVDKALQFLKEQRVHLENMGSHDIVDGNHR

Target 8iah. 1. 2 LTLGLIWTIILHFQISDIQVSGQS--EDMTAKEKLLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAI IHRHKPMLIDMNKLVLGLIWTIILRFQIQDIVVQTQEGRETRSAKDALLWCQMKTAGYPNVNVTNFTSSWKDGLAFNALIHKHRPDLIDFDK

Target 8iah. 1. 2 VYRQTNLLENLDQAFSVAERDLGVTRLLDPEDVDVPQPDEKSIIITYVSSLYDAMP-----RVPDVQDGVKANELQLLKDSNARHNLEHAFDVAERQLGIITQLLDPEDVFTENPDEKSIIITYVAFYHYFSKMVLAVEGKRVGKVIDHAITEKMI

Target 8iah. 1. 2 RWQEYRELVLILLQWIRAHTAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSGKIYQSLEGAVQAGQLKV--EYSGGLASDLLTWIEQITITVLNSRKFANSLAGVQQQLQAFSTYRTVEKPPKFQEGKNLEVLLFTIQSRMRANNQKVYT

Target 8iah. 1. 2 -PPGYHPLDVEKEWGKLVHAILEREKQLRSEFERLERLRQIVSKLQMEAGLCEEQLNQADALLQSD---VRLLAAGKAPQPHDGKLVSDINRAWESLEEA EYRRELALRSELIRQEKEQLARRFDRKAAMRETWLNENQRLVAQDNFGYDLAAVEAAKK

Target 8iah. 1. 2 RAGEVERDLKADGMIRLLFNDVQALK-DGRHPQGEQMYRR--VYRLHERLVAIRTEYNLRLRGTPRHPELEDSTLRYLQKHEA IETDTAA YEERVRALEDLARELELENYHDQKRITARKDNILRLWNYLQELLQSRQRLETTLALQQL-----FQ

Target 8iah. 1. 2 DLLA---WVEENQRRVDSA EWGVDLPSVEAQLGSHRGLHQSVEEFRAKIERAR-----TDEGQLSPATRGAYRDCLGRL  
DMLHSIDWMDEIKAHLLSAEFGKHLLEAEDLLQKHKLMEADIAIQGDKVKAITAATLQFTEETGYQPCDPQVIRDRVSHL

Target 8iah. 1. 2 DLQYAKLLNSSKARLSLES LHGFVAAATKELMWLSEKEEEEVGFWDWSE RNSNMAAKKEAYSALMRELELKEKKIKEIQS  
EQCFAELSNTAAGRKAQLE-----

Target 8iah. 1. 2 TGDRLLR EDHPARPTVESFQAALQTQWSWMLQLCCCIEAHLKENTAYFQFFSDVREAE EQRLKLQETLHRKYTCDRSITV  
-----

Target 8iah. 1. 2 TRLEDLLQDAQDEKDLNEYRGHLSGLAKRAKAI VQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHKGDECQMLGPAQPF  
-----

Target 8iah. 1. 2 HWKVLSSSGSEAAVPSVCFLVPPPNQEAL EAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQLIRSWSLVTFRTL  
-----

Target 8iah. 1. 2 KP EEQRQALRSLELHYQAF LRDSQDAGGFGPEDRLQAEREY GSCSRHYQQLQSLEQGEQ EESRCQRCISELKDIRLQLE  
-----

Target 8iah. 1. 2 ACETRTVHRLRLPLDKEPARECAQR IAEQQKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPTLRSELELT LGKLEQV  
-----

Target 8iah. 1. 2 RLSIAIYLEKLKTISLVIRSTQGAE EALRAHEEQLEQAQVPAALPELEATKAAMKKLRAQAE AQPVFDALRDEL RGAQ  
-----

Target 8iah. 1. 2 EVGERLQQRHGERDVEVERWRERV TQLLERWQAVLAQTDVRQRELEQLGRQLRYYRESADPLGAWLQDARRRQE QIQAVP  
-----

Target 8iah. 1. 2 LADSQAVREQLRQE KALLEEIERHAEKVEECQRFAKQYINAIKDYELQLV TYKAQLEPVASPAKKPKVQSGSESVIQEYV  
-----

Target 8iah. 1. 2 DLRTYSELSTLTSQYIRF ISETLRRMEEEERLAEQQR AEERERLAEVEAALEKQRQLAEAHAQAKAQAERE AQELQRRM  
-----

Target 8iah. 1. 2 QEEVARREEVAVDAQQKKRSIQEELQQLRQSSEAEIQA KARQVEAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQA  
-----

Target 8iah. 1. 2 LRARAEAEAKRQAQEEAERLRRQVQEETQRKRQAEAE LGLRVKAEAEAAAREKQRALQALEELRLQAE EAERRLRQAEA  
-----

Target 8iah. 1. 2 ERARQVQVALETAQRSAQAE LQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQQAEARAREEAERELERWQLK  
-----

Target 8iah. 1. 2 ANEALRLRLQAE EVAQQKSLAQAEAEKQKEAAEREARRRGKAE EQAVRQRELAEQELERQRQLAEGTAQQRLAAEQELIR  
-----

Target 8iah. 1. 2 LRAETE QGEQQRQLLEEELARLQSEAAAATQKRQELAEALAKVRAEMEVLLASKARAE EESRSSEKSKRLEAEAGRFR  
-----

Target 8iah. 1. 2 ELAE EAARLRALAE EAKRQRQLAEEDAA RQRAEAERV LSEKLAAI SEATRLKTEAEIALKEKEAENERLRR LAEDEAFQR  
-----

Target 8iah. 1. 2 RRLEEQA AQHKADIEERLAQLRKASESELERQKGLVEDTLRQRQVEEEILALKASF EKAAAGKAELELELGRIRGNAED  
-----

Target 8iah. 1. 2 TLR SKEAQEQEAARQRQLAAEEERRRREAEERVQKSLAAEEEAARQRKAAL EEVERLKAKVEEARRLRERAEHESVRQLQ  
-----

Target 8iah. 1. 2 LAQEA AQKRLQAE EKAHAFVQQKEQELQQT LQQEQSVLEKL RSEAEAAARRAAEEAEERARAEREAAQSRQRVEEAERL  
-----

Target 8iah. 1. 2 KQAAEEQAQAQAQAAAAEKL RKEAEQEAARRAQAEQAALRQKQAADAEME KHKKFAEQTLRQKAQVEQEL TALRLKLEE  
-----

Target 8iah. 1. 2 TDHQKSILDQELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVA  
-----

Target 8iah. 1. 2 EE AARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAE LLQQQKELAQEQARRLQEDKEQMAQQ L  
-----

Target 8iah. 1. 2 AQETQGFQRTLETERQRQLEMSAE AERLRLRVAEMSRAQARA EEDAQRFRKQAE EIGAKLHRTELATQEKVTLVQTLETQ  
-----

Target 8iah. 1. 2 RQQSDRDADRLREATAELEREKDKLKKEAE LLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLE  
-----

8iah. 1. 2 -----  
Target RL FQDEVAKAQKLREEQRRQQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQEQQLAEENRRLRER  
8iah. 1. 2 -----  
Target LEHLEEEHRAALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTV  
8iah. 1. 2 -----  
Target AELTQREDVRRYLQGHSSIAGLLKPANeklTIYAALRRQLSPGTALILLEAQASGFLLDPVRNRRLTVTEAVKEGVV  
8iah. 1. 2 -----  
Target GPelHHKLLSAERAVTGYKDPYTGEKISL FQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEM  
8iah. 1. 2 -----  
Target NRVLQDPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGGE LVYTDSEARDVFEKATVSAPFGKFQG  
8iah. 1. 2 -----  
Target KTVTIIWELINSEYFTAEQRDRLRQFRTGKV TVEKIIKIVITVIEEHEQKGQLCFQGLRALVPAAELLESGLIIDWDLFRQ  
8iah. 1. 2 -----  
Target LQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTV D  
8iah. 1. 2 -----  
Target EAVRAGLVGPelHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLLDAQLSTGGTVDP SKSHRLPLDVACA  
8iah. 1. 2 -----  
Target RGYLDEETSTALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATV  
8iah. 1. 2 -----  
Target EVPVGSFQGRAVTIWELINSEYFTAEQRQELLRQFRTGKV TVEKIIKIVITIVIEEVETRRERLSFSGLRAPVPASELLA  
8iah. 1. 2 -----  
Target AGILSSSQFEQLKDGKTSVKDLSELSSLQTL LQSGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLLEAQATGFLV  
8iah. 1. 2 -----  
Target DPVRNQRLYVHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISL FQAMKKGLVREHGIRLLEAQIATGGIIDPVH  
8iah. 1. 2 -----  
Target SHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYT  
8iah. 1. 2 -----  
Target EEETRRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEKTEIVRQQNLAS  
8iah. 1. 2 -----  
Target YDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEV  
8iah. 1. 2 -----  
Target ARLLLEAQATGFLLDPVKGERLTVDEAVRKGLVGPELHDRLLSAERAVTGYRDPYTEQTISL FQAMKKDLIPAEELRL  
8iah. 1. 2 -----  
Target LDAQLATGGIVDPRLGFHLPLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSY TQLLRRCRRDETSGLFLLPLSE  
8iah. 1. 2 -----  
Target ARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIR  
8iah. 1. 2 -----  
Target PGTA FELLEAQATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDLLSAERAVTGYKDPYSGKLISL FQAMKKGLILKDHG  
8iah. 1. 2 -----  
Target IRLLEAQIATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLL  
8iah. 1. 2 -----  
Target PLKEKKRERKTSSKSSVRKRRVIVDPETGEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSDGVVKSMIIDRRS  
8iah. 1. 2 -----  
Target GRQYDIDEAIAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGP  
8iah. 1. 2 -----  
Target VAGILDTETLEKVSITEAMHRNLVDNITGQRLLEAQACTGGIIDPNTGERFPVTD AVNKGVLVDKIMVDRINLAQKAFCGF  
8iah. 1. 2 -----  
Target EDPRTKTMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTCPK  
8iah. 1. 2 -----



Target8iah. 1. 2TKLKISYKDALDRSMVEEGTGLRLLEAAQSSKGYSPYSVSGSGSTTGSRS GSRTGSRAGSRRGSF DATGSGFSMTFSS-----

Target8iah. 1. 2SSYSSSGYGRRYASGPTSSLGGPESAAA-----

Model #22	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.57 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
1sjj.1.A	26.16	homo-dimer	0.00	HHblits	2DX	-	0.33	64 - 737	0.15	actinin

The template contained no ligands.

Target1sjj. 1. AMSGEDQEVRAVEDGSNGGSGSPSPGDTLPWNLEKTQRSRRGGGGPGNGSVLDP AERAVIRIADERDRVQKKTFTKWVN-----DPAWEKQQRKTTTAWCN

Target1sjj. 1. AKHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPR-EKGRMRFHKLQNVQIALDYL RHRQVKLVNIRNDDIADGNPKLSHLRKAGTQIENIEEDFRDGLKMLLLEVISGERLAKPERGKMRVHKISNVNKALDFIASKGVKLVSIGAEEIVDGNV KM

Target1sjj. 1. ATLGLIWTIILHFQISDIQVSGQSEDMTAKEKLLLSQRMVEGYQGLRCDNFTSSWRDGR LFNAIIHRHKPMLIDMNKVYRTLGM IWTIILRF AIQDISVE-----ETSAKEG LLLWYQRKTAPYKNVNIQNFHISWKDGLGFCAL IHRHRPELIDY GKL RK

Target1sjj. 1. AQTNLENLDQAFSVAERDLGVTRLLDPEDVD-VPQPDEKSIITYVSSLYDAMP RVPDVQDGV-----KANELQLRWQEDDPLTNLNTAFDVAEKYLDIPKMLDAEDIVGTARPDEKAIMTYVSSFYHAFSGAQKAETAANRICKVLAVNQENEQLMED

Target1sjj. 1. AYRELVLLLLQWIRAHATAAFEERRFPSSFEEIEILWCQFLKFKETELPAKEADKNRSGIYQSLEGAVQAG---QLKVPPGYEKLASDLLEWIRRTIPWLENRAPENTMQAMQKLEDFRDYRRLHKPPKVQEKQLEINFNTLQTKLRLSNRP AFMPSEG

Target1sjj. 1. AYHPLDVEKEWGKLVHAILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDV---RLLAAGKAPQRAGKMVSDINNAWGGLEQAEGYEEWLLNEIRRLERLDHLAEKFRQKASIHESWTDGKEAMLQKQDYETATLSEIKALLKKHE

Target1sjj. 1. AEVERDLDKADGMIRLLFNDVQALKDGRHPQGEQMYRRVYRLHERLVAIRTEYNL---RLRGTPRHP----ELEDSTLRYLAFESDLAAHQDRVEQIAAIAQELNELDYDPSV NARCQKICDQWDNLGALTQKRREALERTEK LLETIDQLYLEYAKRA

Target1sjj. 1. AQDLLAWVEENQRRVDSAEWGV DLP SVEAQLGSHRGLHQSVEEFRAKIERARTDE-----GQLS---PATRGAYRDCLGAPFNWMEGAMEDLQD TFI VHTIEEIQGLTTAHEQFKATLPDADKERQAILGIHNEVSKIVQTYHVN MAGTPYTTITPQ

Target1sjj. 1. ARLDLQYAKLLNSSKARLSLES-----LH-GFVAAATKELMWLSEKEEEEVGF DWSERN SNMAAKKEAYSALMREIENGKWEHVRQLVPRRDQALMEEHARQQQNERLRKQFGA QANVIGPW IQTKMEEIGRISIEMH-GTLEDQLNHLRQY EKS

Target1sjj. 1. ALELKEKKIKEIQSTGDRLLREDHPARPTVESFQAALQTQWSWMLQLCCCIEAHLKENTAYFQFFSDVREAE EQLRKLQETIVNYKPKIDQLEGDHQQIQEALIFDNKHTNYTMEHIRVGWEQLLTTIARTINEVENQILTRD-----

Target1sjj. 1. ALHRKYTCDRSITVTRLEDLLQDAQDEK DQLNEYRGHLSGLAKRAKAI VQLTPRNPTQPTRGRVPLLAVCDYKQVEATVHK-----

Target1sjj. 1. AGDECQMLGPAQPFWKVLSSSGSEAAVPSVCFLVPPPNQEAL EAVARLEAQHQALVTLWHQLHTDMKSLLAWQSLSRDVQ-----

Target1sjj. 1. ALIRSWSLVTFR TLKPEEQRQALRSLELHYQAF LRDSQDAGGFGPEDRLQAEREYGSCSRHYQQLLSLEQGEQEESRCRQ-----

Target1sjj. 1. ACISELKDIRLQLEACETRIVHRLRLPLDKEPARECAQRIAEQQKAQAEVEGLGKGVARLSAEAEKVLALPEPSPAAPT LR-----

Target1sjj. 1. ASELETLGKLEQVRSLSAIYLEKLK TISLVIRSTQGAEALRAHEEQ LKEAQAVPAALPELEATKAAMKKLRAQAE AQQP-----

Target1sjj. 1. AVFDALRDEL RGAQEVGERLQQRHGERDVEVERWRERV TQLLERWQAVLAQTDVRQRELEQLGRQLRYYRESADPLGAWLQ-----

Target 1sjj. 1. A	DARRRQEQIQAVPLADSQAVREQLRQEKALLEEIERHAEKVEECQRFQAKQYINAIKDYELQLVTYKAQLEPVASPAKKPK -----
Target 1sjj. 1. A	VQSGSESVIQEYVDLRTRYSELSTLTSQYIRFISETLRRMEEEEERLAEQQRAEERERLAEVEAALEKQRQLAEAHAQAKA -----
Target 1sjj. 1. A	QAEREAQELQRRMQEEVARREEVAVDAAQQKRSIQEELQQLRQSSEAEIQAKARQVEAAERSRLRIEEEIRVVRLQLETT -----
Target 1sjj. 1. A	ERQRGGAEGELQALRARAEAEAKRQAQEEAERLRRQVQEETQRKRQAEAEELGLRVKAEAEAAAREKQRALQALEELRLQ -----
Target 1sjj. 1. A	AEEAERRLRQAEARARQVQVALETAQRSQAELQSKHASFAEKTAQLERTLEEEHVTVVQLREEATRREQQQAERAR -----
Target 1sjj. 1. A	EEAERELERWQLKANEALRLRLQAEVAQQKSLAQAEAEKQKEAAEREARRRGKAEQAVRQRELAEQELERQRQLAEGT -----
Target 1sjj. 1. A	AQQLAAEQELIRLRAETEQGEQQRQLLEEELARLQSEAAAATQKRQLEAEELAKVRAEMEVLLASKARAEESRSSEK -----
Target 1sjj. 1. A	SKQRLEAEAGRFRELAEEAARLRALAEAKRQRQLAEEDAARQRAEAERVLSEKLAAISEATRLKTEAEIALKEKEAENE -----
Target 1sjj. 1. A	RLRRLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEELALKASFEEAAAAGKAEL -----
Target 1sjj. 1. A	ELELGRI RNAEDTLRSKEAQEQEAARQRQLAAEEERRRREAEEERVQKSLAAEEEAARQRKAAL EEVERLKAKVEEARRL -----
Target 1sjj. 1. A	RERAEHESVRQLQLAQEAAQKRLQAEKKAHAFVQQKEQELQQTLLQQEQSVLEKL RSEAEAAARRAAEEAEARERAEREA -----
Target 1sjj. 1. A	AQSRQRVEEAERLKQAAEEQAQAQAQAAAEKLRKEAEQEAARRAQAEQAALRQKQAADAEMEKHKKFAEQTLRQKAQV -----
Target 1sjj. 1. A	EQELTALRLKLEETHQKSILDQELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKNQTR -----
Target 1sjj. 1. A	LLQEEAEKMKQVAEEAARLSVAAQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQAR -----
Target 1sjj. 1. A	RLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEERLRLRVAEMSRAQARAEEDAQFRKQAEETGAKLHRTELAT -----
Target 1sjj. 1. A	QEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKKEAEELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQ -----
Target 1sjj. 1. A	RERFIEEEKAKLERLFQDEVAKAQLREEQQRQQQMQQEKQQLASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQQE -----
Target 1sjj. 1. A	QLLAEEENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILST -----
Target 1sjj. 1. A	EELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLKPANEKLTIIYAALRRQLLSPGTALILLEAQAASGFLDPVRNR -----
Target 1sjj. 1. A	RLTVTEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPV -----
Target 1sjj. 1. A	DVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFE -----
Target 1sjj. 1. A	KATVSAPFGKFQGKTVTIWE LINSEYFTAQRRDLLRQFRTGKVTVEKIIKIVITVIEEHEQKQQLCFQGLRALVPAEL -----
Target 1sjj. 1. A	LESGIIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGH -----
Target 1sjj. 1. A	VIDPAT SARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDDAQLSTGGTVDP -----
Target 1sjj. 1. A	SKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYYPRTWELATYSQLQQQCRPDPLTGLSLLPLSEEAARARQQELYS -----

Target  
1s.jj. 1. A

EVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFS

Target  
1s.jj. 1. A

GLRAPVPASELLAAGILSSSQFEQLKDGTKSVKDLSELSSLQTLQGGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAI

Target  
1s.jj. 1. A

LLLEAQAATGFLVDPVRNQRLYVHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLFAQMKKGLVVRHGIRLLE

Target  
1s.jj. 1. A

AQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGP

Target  
1s.jj. 1. A

EKAEVVETTRVYTEETTRRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEII

Target  
1s.jj. 1. A

EKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLP

Target  
1s.jj. 1. A

YQALKKGLLSAEVARLLLEAQAATGFLLDPVKGERLTVDEAVRKGVLVGPETHDRLLSAERAVTGYRDPYTEQTISLFAQM

Target  
1s.jj. 1. A

KKDLIPAEELRLDAQLATGGIVDPRLGFHLPLEVAYQRYLKNKDTHTDQLSEPSEVRSYVDPSTDERLSYQLLRRCRR

Target  
1s.jj. 1. A

DETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKER

Target  
1s.jj. 1. A

LSVYQAMKGIIRPGTAFELLEAQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDLLSAERAVTGYKDPYSGKLISLF

Target  
1s.jj. 1. A

QAMKKGILKDHGIRLLEAQAATGGIIDPEESHRLPVDVAYQRLGFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQME

Target  
1s.jj. 1. A

RCVTDPQTGLRLLPLKEKKRERKTSSKSSVRKRRVIVDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISS

Target  
1s.jj. 1. A

DGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTSLITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQ

Target  
1s.jj. 1. A

LASWSDPTEETGPVAGILDTETLEKVSITEAMHRNLVDNITGQRLLEAQAQCTGGIIDPNTGERFPVTDVANKGLVDKIMV

Target  
1s.jj. 1. A

DRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTGPRVPLDEALQRGTVDARTAKLR

Target  
1s.jj. 1. A

DVSAYSKYLCPTKTKLISYKDALDRSMVEEGTGLRLEAAAQSSKGYSPYSVSGSGSTTGSRSRSTGSRAGSRRRGSF

Target  
1s.jj. 1. A

DATGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA

Model #07	File	Built with	Oligo-State	Ligands	GMQE	QMEANDisCo Global
	PDB	ProMod3 3.3.0	monomer (matching prediction)	None	0.00	0.47 ± 0.05

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Range	Coverage	Description
1s.jj.1.B	12.54	homo-dimer	0.00	HHblits	2DX	-	0.27	187 - 806	0.13	actinin

The template contained no ligands.

Target  
1s.jj. 1. B

MSGEDQEVRAVVEDGSNGGSGSPSPGDTLPWNLEKTQSRRRGGGPGNGSVLDPAERAVIRIADERDRVQKKTFTKWVN

Target 1sjj. 1. B KHLIKAQRHISDLYEDLRDGHNLISLLEVLSGDSLPREKGRMRFHKLQNVQIALDYLRHRQVKLVNIRNDDIADGNPKLT-----

Target 1sjj. 1. B LGLIWTIILHFQISDIQVSGQSEDMTAKKLLWSQRMVEGYQGLRCDNFTSSWRDGRLFNAI IHRHKPMLIDMN--KVY-----QRKTF TAWCNSHLRKA--GTQIENIEEDFRDGLKMLLLEVISGERLAKPERGKM

Target 1sjj. 1. B RQTNLENLDQAFSVAERDLGVT--RLDPEDVDVPQPEKSIITYVSSLYDAMPVPDVQDGVKANELQLRWQEYRELVL RVHKISNVNKALDFIA--SKGVKLVSIGAEEIVDGNV--KMTLGMTWTIILRFATQDISVE-----ETSAKEG

Target 1sjj. 1. B LLQWIRAHTAAFE---ERRFPSSFEEIEILWCQFLKFKETELP----AKEADKNRSKGIYQSLEGAVQAGQLKVP PGY-- LLLWYQRKTAPYKNVNIQNFHISWKDGLGFCAL IHRHRPELIDYGKLRKDDPLTNLNTAFDVAEKYLDIPKMLDAEDIVG

Target 1sjj. 1. B -----HPLDVEKEWGLHVAIILEREKQLRSEFERLERLQRIVSKLQMEAGLCEEQLNQADALLQSDVRL---LA TARPDEKAIMTYVSSFYHAFSGAQAETAA--NRICKVLAVNQENEQLMEDYEKLASDLLEWIRRTIPWLENRAPENTMQA

Target 1sjj. 1. B AGKAPQRAGEVERDLKADG---MIRLLFNDV--QALKD--GRHPQGEQMYRRVYRLHERLVAIRT---EYNLRLRGTPRH MQQKLEDFRDYRRLHKPKVKVEKQCLEINFNTLQTKLRLSNRPAFMPSEGMVSDINNAWGGLEQAEKG YEEWLLNEIRR

Target 1sjj. 1. B P---ELEDSTLRYLQDLLAWVEENQRRVDSA EWGV--DLPSVEAQLGSHRGLHQSV EEFRAKIERARTDEGQLS---PAT LERLDHLAEKFRKASIHESWTDGKEAMLQKQDYETATLSEIKALLKKHEAFESDLAAHQDRVEQIAATAQELNELDYDD

Target 1sjj. 1. B RGAYRDCLGRDLQYAKLLNSSKARLSLES-----LHGFVAAATKELMWLSEKEEEEVGFDSERNNSNMAAKK SPSVNARCQKICDQWNLGALTQKRREALERTEKLETTIDQLYLEYAKRAAPFNWMEGAMEDLQDTFIVHTIEEIQGLT

Target 1sjj. 1. B EAYSALMRELELKEKKIKEI---QSTGDRLLREDH---PARPTVESFQAALQTQWSWMLQLCCIEAHLKENTAY---- TAHEQFKATLPDADKERQAILGIHNEVSKIVQTYHVMAGTNPYTTITPQEINGKWEHVRQLVPRRDQALMEEHARQQQN

Target 1sjj. 1. B ---FQFFSDVREAEELRKLQETLHRKYTCDSRITVTRLEDLLQDAQDEKDLNEYRGHLSGLAKRAKAI VQLTPRNPT ERLRKQFGA QANVIGPWIQTKMEEIGRISI----EMHGTLEDQLNHLRQYEKSIVNYKPKIDQLEGDHQIQEAL-----

Target 1sjj. 1. B QPTRGRVPLAVCDYKQVEATVHKGDECQMLGPAQPFHWKLVSSSGSEAAVPSVCFLVPPPNQEAL EAVARLEAQHQALV-----

Target 1sjj. 1. B TLWHQLHTDMKSL LAWQSLSRDVQLIRSWSLVTFRTLKPEEQRQALRSLELHYQAFLRDSQDAGGFGPEDRLQAEREYGS-----

Target 1sjj. 1. B CSRHYQQLLSLEQGEQEESRCQRCISELKD IRLQLEACETRTRVHRLRLPLDKEPARECAQRIAEQQKAQAEVEGLGKGV-----

Target 1sjj. 1. B ARLSAEAEKVLALPEPSAAPT LRSELELTGKLEQVRSLSAIYLEKTKTISLVIRSTQGAEELRAHEEQ LKEAQAVPA-----

Target 1sjj. 1. B ALPELEATKAAMKKLRAQAEAAQPVFDALRDELRGAEVGERLQQRHGERDVEVERWRERV TQLLERWQAVLAQTDVRQR-----

Target 1sjj. 1. B ELEQLGRQLRYYRESADPLGAWLQDARRRQEIQAVPLADSQAVREQLRQE KALLEEIERHAEKVEECQRF AKQYINAIK-----

Target 1sjj. 1. B DYELQLV TYKAQLEPVASPAKKPKVQSGSESVIQEYVDLTRYSELSTLTSQYIRFIS ETLRRMEEEERLAEQQRAEERE-----

Target 1sjj. 1. B RLAEVEAALEKQRQLAEAHAQAKAQAEREAQELQRRMQEEVARREEVAVDAQQKRSIQEELQQLRQSSEAEIQA KARQV-----

Target 1sjj. 1. B EAAERSRLRIEEEIRVVRLQLETTERQRGGAEGELQALRARAEAEAQKRAQEAEERLRRQVQEETQRKRQAE AELGLR-----

Target 1sjj. 1. B VKAEAEAAAREKQALQALEELRLQAEAEERRLRQAEARARQVQVALETAQRSQAELQSKHASFAEKTAQLERTLEEEH-----

Target 1sjj. 1. B VTVVQLREEATRREQQQAEERAREEAERELRWQLKANEALRLRLQAE EVAQKSLAQAEAEKQKEAAEREARRRGKAE-----

Target 1sjj. 1. B EQAVRQRELAEQELERQRQLAEGTAQQRLAAEQELIRLRAETEQQGEQQRQLLEEEELARLQSEAAAATQKRQELEAE LAKV-----

Target 1sjj. 1. B RAEMEVLLASKARAEESRSSEKSKQRLAEAFAGRFRELAEEAARLRALAEAKRQRQLAEEDAARQRAEAERV LSEKLA-----

Target 1sjj. 1. B AISEATRLKTEAEIALKEKEAENERLRLAEDEAFQRRRLEEQAQHKADIEERLAQLRKASESELERQKGLVEDTLRQR-----

Target 1sjj. 1. B RQVEEELALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRQLAAEEERRRREAEERVQKSLAAEEEA-----

1sjj. 1. B	-----
Target	ARQRKAAL EEVERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKRLQAEKKAHAFVQQKEQELQQTLLQQEQSVLEKLR
1sjj. 1. B	-----
Target	SEAEAAARRAAEEAEERERAEREAAQSRQRVEEAERLKQAAEEQAQAQAQAAAAEKLKEAEQEAARRAQEAALRQK
1sjj. 1. B	-----
Target	QAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETHQKSILDQELQRLKAEVTEAARQRSQVEEELFSVRVQMEEL
1sjj. 1. B	-----
Target	GKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVAAQEAAARLRQLAEEDLAQQRALAEKMLKEKMQAVQ
1sjj. 1. B	-----
Target	EATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQRTLETERQRQLEMSAEERLRLRVAEMSRAQARAE
1sjj. 1. B	-----
Target	EDAQRFRKQAEIEGAKLHRTTELATQEKVTLVQTLETQRQQSDRDADRLREAIAELEREKDKLKEAELLQLKSEEMQTVQ
1sjj. 1. B	-----
Target	QEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQMKEKQQLLASMEEARRRQH
1sjj. 1. B	-----
Target	EAEEGVRRKQEELQLLEQQRQQEQQLLAENRRLRERLEHLEEEHRAALAHSEEITAAQAAATRALPNGDAADGPAAP
1sjj. 1. B	-----
Target	EHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDVRRYLQGHSSIAGLLLKPANEKLTIIYAALRRQLLS
1sjj. 1. B	-----
Target	PGTALILLEAQAASGFLDPVRNRRLTVTEAVKEGVVGPPELHHKLLSAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHG
1sjj. 1. B	-----
Target	IRLLEAQIATGGVIDPVHSHRPVDVAYHRGYFDEEMNRVLQDPSSDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLL
1sjj. 1. B	-----
Target	PLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQKTVTIWELINSEYFTAQRRDLLRQFRTGKVTVEKIIKIVITV
1sjj. 1. B	-----
Target	IEEHEQKGQLCFQGLRALVPAEELLESGLIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYE
1sjj. 1. B	-----
Target	ALKKELLQPEAAVALLEAQAGTGHVIDPATSARLTVDEAVRAGLVGPELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKK
1sjj. 1. B	-----
Target	GLIPREQGLRLDLAQLSTGGTVDPSPKSHRLPLDVACARGYLDEETSTALSAPRDDAKTYDPRTWELATYSQLQQCRPD
1sjj. 1. B	-----
Target	PLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAQEQELLRQFRTGKVTVE
1sjj. 1. B	-----
Target	KIIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQFEQLKDGTSVKDLSELSSLQTLQSGGCLAGIYL
1sjj. 1. B	-----
Target	EESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLYVHEAVKAGVVGPPELHEKLLSAEKAVTGYKDPYSG
1sjj. 1. B	-----
Target	STISLQFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLT
1sjj. 1. B	-----
Target	YRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETTRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRA
1sjj. 1. B	-----
Target	QLMADFQAGRVTKERMIIIIIEIEIEKTEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEESA
1sjj. 1. B	-----
Target	WRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRKGLVGPPELHDLRL
1sjj. 1. B	-----
Target	SAERAVTGYRDPYTEQTISLQFQAMKKDLIPAEALRLDLAQLATGGIVDPRLGFHLPLEVAYQRGYLNKDHQDQLEPSE
1sjj. 1. B	-----
Target	VRSYVDPSTDERLSYTLRLRRCRDETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVS
1sjj. 1. B	-----

Target 1s.jj. 1. B	KNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKD
Target 1s.jj. 1. B	KLLSAERAVTGYKDPYSGKLISLFQAMKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTD
Target 1s.jj. 1. B	PSDDTKGFFDPNTEENLTYQLMERCVTDPQTGLRLLPLKEKKRERKTSSKSSVRKRRVVIVDPETGKEMSVYEAYRKGL
Target 1s.jj. 1. B	IDHQTYLELSECEWEIEITISSSDGVVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTSLSITEFADMLSGNAGG
Target 1s.jj. 1. B	FRSRSSSVGSSSYPIPAVSRTQLASWSDPTEETGPVAGILDTETLEKVSITEAMHRNLVDNITGQRLLEAQAQTGGII
Target 1s.jj. 1. B	DPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYL TGGLIEPDT
Target 1s.jj. 1. B	PGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTCPKTKLKISYKDALDRSMVEEGTGLRLLEAAAQSSKGYSPYSVSG
Target 1s.jj. 1. B	SGSTTGSRSRGTGSRAGSRRGSFDTATSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA

## Materials and Methods

### Template Search

Template search with has been performed against the SWISS-MODEL template library (SMTL, last update: 2023-11-08, last included PDB release: 2023-11-03).

### Template Selection

For each identified template, the template's quality has been predicted from features of the target-template alignment. The templates with the highest quality have then been selected for model building.

### Model Building

Models are built based on the target-template alignment using ProMod3 (Studer et al.). Coordinates which are conserved between the target and the template are copied from the template to the model. Insertions and deletions are remodelled using a fragment library. Side chains are then rebuilt. Finally, the geometry of the resulting model is regularized by using a force field.

### Model Quality Estimation

The global and per-residue model quality has been assessed using the QMEAN scoring function (Studer et al.).

### Ligand Modelling

Ligands present in the template structure are transferred by homology to the model when the following criteria are met: (a) The ligands are annotated as biologically relevant in the template library, (b) the ligand is in contact with the model, (c) the ligand is not clashing with the protein, (d) the residues in contact with the ligand are conserved between the target and the template. If any of these four criteria is not satisfied, a certain ligand will not be included in the model. The model summary includes information on why and which ligand has not been included.

### Oligomeric State Conservation

The quaternary structure annotation of the template is used to model the target sequence in its oligomeric form. The method (Bertoni et al.) is based on a supervised machine learning algorithm, Support Vector Machines (SVM), which combines interface conservation, structural clustering, and other template features to provide a quaternary structure quality estimate (QSQE). The QSQE score is a number between 0 and 1, reflecting the expected accuracy of the interchain contacts for a model built based a given alignment and template. Higher numbers indicate higher reliability. This complements the GMQE score which estimates the accuracy of the tertiary structure of the resulting model.

## References

- **BLAST**  
Camacho, C., Coulouris, G., Avagyan, V., Ma, N., Papadopoulos, J., Bealer, K., Madden, T.L. BLAST+: architecture and applications. BMC Bioinformatics 10, 421-430 (2009).  [doi>](https://doi.org/10.1186/1471-2108-10-421)

- **HHblits**

Steinegger, M., Meier, M., Mirdita, M., Vöhringer, H., Haunsberger, S. J., Söding, J. HH-suite3 for fast remote homology detection and deep protein annotation. *BMC Bioinformatics* 20, 473 (2019).  [doi.org/10.1186/s12922-019-0561-1](https://doi.org/10.1186/s12922-019-0561-1)

### Table T1:

Primary amino acid sequence for which templates were searched and models were built.

[illegible]

### Table T2:

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Coverage	Description
H9F0F3.1.A	94.23	monomer	-	AFDB search	AlphaFold v2	NA	0.59	0.26	Plectin isoform 1c
5dzz.1.A	45.12	monomer	-	BLAST	X-ray	2.60Å	0.40	0.10	Desmoplakin
8iah.1.2	38.97	monomer	-	BLAST	EM	NA	0.38	0.12	Spectrin beta chain
8iah.1.3	38.97	monomer	-	BLAST	EM	NA	0.38	0.12	Spectrin beta chain
5dzz.1.A	54.12	monomer	-	HHblits	X-ray	2.60Å	0.45	0.11	Desmoplakin
5dzz.1.A	51.14	monomer	-	HHblits	X-ray	2.60Å	0.45	0.11	Desmoplakin
1sjj.1.A	12.54	homo-dimer	-	HHblits	2DX	NA	0.27	0.13	actinin
1sjj.1.B	12.54	homo-dimer	-	HHblits	2DX	NA	0.27	0.13	actinin
5dzz.1.A	51.48	monomer	-	BLAST	X-ray	2.60Å	0.45	0.10	Desmoplakin
5dzz.1.A	47.12	monomer	-	HHblits	X-ray	2.60Å	0.42	0.11	Desmoplakin
5dzz.1.A	48.75	monomer	-	BLAST	X-ray	2.60Å	0.43	0.11	Desmoplakin
5dzz.1.A	38.07	monomer	-	HHblits	X-ray	2.60Å	0.38	0.11	Desmoplakin
5j1i.1.A	96.47	monomer	-	HHblits	X-ray	2.80Å	0.59	0.08	Plectin

Template	Seq Identity	Oligo-state	QSQE	Found by	Method	Resolution	Seq Similarity	Coverage	Description
8iah.1.1	38.97	monomer	-	BLAST	EM	NA	0.38	0.12	Spectrin beta chain
5ji1.1.A	96.37	monomer	-	BLAST	X-ray	2.80Å	0.59	0.08	Plectin
4z6g.1.A	66.86	monomer	-	HHblits	X-ray	2.65Å	0.51	0.08	Microtubule-actin cross-linking factor 1, isoforms 1/2/3/5
6sl7.1.A	27.80	homo-dimer	-	HHblits	X-ray	3.30Å	0.35	0.09	Calponin homology domain protein putative
3f7p.1.A	96.93	monomer	-	HHblits	X-ray	2.75Å	0.60	0.06	Plectin-1
7ank.1.A	12.69	monomer	-	HHblits	X-ray	3.20Å	0.27	0.10	Alpha-actinin-2
1hci.1.A	14.35	homo-dimer	-	HHblits	X-ray	2.80Å	0.28	0.09	ALPHA-ACTININ 2
7a8u.1.A	14.35	homo-dimer	-	HHblits	X-ray	3.80Å	0.28	0.09	Alpha-actinin-2
7a8t.1.A	14.35	homo-dimer	-	HHblits	X-ray	2.69Å	0.28	0.09	Alpha-actinin-2
6sl2.1.A	29.82	homo-dimer	-	HHblits	X-ray	3.10Å	0.36	0.08	Calponin homology domain protein putative
6sl3.1.A	29.82	homo-dimer	-	HHblits	X-ray	3.10Å	0.36	0.08	Calponin homology domain protein putative
4d1e.1.A	12.65	homo-dimer	-	HHblits	X-ray	3.50Å	0.26	0.09	ALPHA-ACTININ-2
3pe0.1.A	88.53	monomer	-	HHblits	X-ray	2.95Å	0.58	0.06	Plectin
8iah.1.Z	15.20	monomer	-	HHblits	EM	NA	0.28	0.22	Spectrin beta chain
8iah.1.Y	23.78	monomer	-	HHblits	EM	NA	0.32	0.25	Spectrin beta chain
8iah.1.X	23.78	monomer	-	HHblits	EM	NA	0.32	0.25	Spectrin beta chain
8iah.1.W	23.78	monomer	-	HHblits	EM	NA	0.32	0.25	Spectrin beta chain
8iah.1.Z	23.78	monomer	-	HHblits	EM	NA	0.32	0.25	Spectrin beta chain
8iah.1.0	23.78	monomer	-	HHblits	EM	NA	0.32	0.25	Spectrin beta chain
8iah.1.1	23.78	monomer	-	HHblits	EM	NA	0.32	0.25	Spectrin beta chain
8iah.1.2	23.78	monomer	-	HHblits	EM	NA	0.32	0.25	Spectrin beta chain
8iah.1.3	23.78	monomer	-	HHblits	EM	NA	0.32	0.25	Spectrin beta chain
8iah.1.Y	15.20	monomer	-	HHblits	EM	NA	0.28	0.22	Spectrin beta chain
8iah.1.X	15.20	monomer	-	HHblits	EM	NA	0.28	0.22	Spectrin beta chain
8iah.1.W	15.20	monomer	-	HHblits	EM	NA	0.28	0.22	Spectrin beta chain
8iah.1.0	38.97	monomer	-	BLAST	EM	NA	0.38	0.12	Spectrin beta chain
8iah.1.0	15.20	monomer	-	HHblits	EM	NA	0.28	0.22	Spectrin beta chain
8iah.1.1	15.20	monomer	-	HHblits	EM	NA	0.28	0.22	Spectrin beta chain
8iah.1.2	15.20	monomer	-	HHblits	EM	NA	0.28	0.22	Spectrin beta chain
8iah.1.3	15.20	monomer	-	HHblits	EM	NA	0.28	0.22	Spectrin beta chain
4d1e.1.A	25.11	homo-dimer	-	HHblits	X-ray	3.50Å	0.33	0.15	ALPHA-ACTININ-2
1sjj.1.A	26.16	homo-dimer	-	HHblits	2DX	NA	0.33	0.15	actinin
1sjj.1.B	26.16	homo-dimer	-	HHblits	2DX	NA	0.33	0.15	actinin
8iah.1.Y	38.97	monomer	-	BLAST	EM	NA	0.38	0.12	Spectrin beta chain
8iah.1.X	38.97	monomer	-	BLAST	EM	NA	0.38	0.12	Spectrin beta chain
8iah.1.W	38.97	monomer	-	BLAST	EM	NA	0.38	0.12	Spectrin beta chain
8iah.1.Z	38.97	monomer	-	BLAST	EM	NA	0.38	0.12	Spectrin beta chain

The table above shows the top 50 filtered templates. A further 1,277 templates were found which were considered to be less suitable for modelling than the filtered list.

1aa2.1.A, 1aj3.1.A, 1aoa.1.A, 1aww.1.A, 1awx.1.A, 1b07.1.A, 1bhd.1.A, 1bhd.2.A, 1bkr.1.A, 1c1g.1.A, 1c1g.1.B, 1c1g.2.A, 1c1g.2.B, 1csk.1.A, 1csk.2.A, 1cun.1.A, 1cun.1.B, 1d7m.1.A, 1d7m.1.B, 1dxx.1.A, 1fmk.1.A, 1g83.1.A, 1g83.2.A, 1g8x.1.A, 1g8x.1.B, 1gl5.1.A, 1gri.1.A, 1gri.1.B, 1h67.1.A, 1hci.1.A, 1k9a.1.A, 1k9a.2.A, 1k9a.3.A, 1k9a.5.A, 1k9a.6.A, 1ksw.1.A, 1lck.1.A, 1lm5.1.A, 1lm5.1.B, 1lm7.1.A, 1m3a.1.A, 1m3b.1.A, 1mb8.1.A, 1mv3.1.A, 1ng2.1.A, 1opk.1.A, 1opl.1.A, 1owa.1.A, 1p2x.1.A, 1p5s.1.A, 1pa7.1.A, 1pxy.1.A, 1pxy.2.A, 1qag.1.A, 1qag.2.A, 1qcf.1.A, 1qly.1.A, 1quu.1.A, 1rt8.1.A, 1s1n.1.A, 1s35.1.A, 1sh5.1.A, 1sh5.1.B, 1sh6.1.A, 1sjj.1.A, 1sjj.1.B, 1tjt.1.A, 1u4q.1.A, 1u4q.2.A, 1u5p.1.A, 1uec.1.A, 1ueg.1.A, 1ujo.1.A, 1v5k.1.A, 1vka.1.A, 1wfw.1.A, 1wjo.1.A, 1wku.1.A, 1wix.1.A, 1wxt.1.A, 1wyl.1.A, 1wym.1.A, 1wyn.1.A, 1woy.1.A, 1wyp.1.A, 1wyq.1.A, 1wyr.1.A, 1x6g.1.A, 1x79.1.B, 1x79.1.C, 1y57.1.A, 1ywo.1.A, 1ywp.1.A, 2abl.1.A, 2b9c.1.A, 2b9c.1.B,



2coi.1.A, 2co0i.1.A, 2co0o.2.A, 2c0ut.2.A, 2d3e.1.A, 2d3e.1.B, 2d85.1.A, 2d86.1.A, 2d87.1.A, 2d88.1.A, 2d89.1.A, 2dfs.1.A, 2dfs.1.H, 2dk9.1.A, 2dx1.1.A, 2dyb.1.A, 2dyb.2.A, 2e7s.1.A, 2e7s.1.B, 2e7s.10.A, 2e7s.10.B, 2e7s.2.A, 2e7s.2.B, 2e7s.3.A, 2e7s.3.B, 2e7s.4.A, 2e7s.4.B, 2e7s.5.A, 2e7s.5.B, 2e7s.6.A, 2e7s.6.B, 2e7s.7.A, 2e7s.7.B, 2e7s.8.A, 2e7s.8.B, 2e7s.9.A, 2e7s.9.B, 2e9k.1.A, 2ee7.1.A, 2efr.1.A, 2efr.1.B, 2efs.1.A, 2efs.1.B, 2egc.1.A, 2ege.1.A, 2elb.1.A, 2epd.1.A, 2eqb.1.B, 2eqb.1.C, 2eyi.1.A, 2eyn.1.A, 2eyw.1.A, 2eyz.1.A, 2fo0.1.A, 2fxm.1.A, 2fxm.1.B, 2fxo.1.A, 2fxo.1.B, 2fxo.2.A, 2fxo.2.B, 2h8h.1.A, 2i1j.1.A, 2i1k.1.A, 2iak.1.A, 2j6k.1.A, 2j7i.1.A, 2jv9.1.A, 2k2r.1.A, 2k3s.1.A, 2k79.1.A, 2k7a.1.A, 2kr3.1.A, 2kym.1.A, 2l3g.1.A, 2l3s.1.A, 2lmj.1.A, 2lqn.1.A, 2lqw.1.A, 2lx7.1.A, 2n03.1.A, 2ocy.1.A, 2ocy.1.B, 2odu.1.A, 2odv.1.A, 2oto.1.A, 2oto.1.B, 2oto.2.A, 2oto.2.B, 2ptk.1.A, 2pz1.1.A, 2q13.1.A, 2qjz.1.A, 2qjz.2.A, 2r0o.1.A, 2r0o.2.A, 2r8u.1.A, 2rn8.1.A, 2rna.1.A, 2rqr.1.A, 2rqv.1.A, 2rqw.1.A, 2rr8.1.A, 2spc.1.A, 2spc.1.B, 2src.1.A, 2v66.1.A, 2v66.1.B, 2v66.1.C, 2v66.1.D, 2v71.1.A, 2v71.1.B, 2vzc.1.A, 2vzd.1.A, 2vzd.2.A, 2vzg.1.B, 2w4u.1.K, 2w4u.1.L, 2w4u.1.M, 2wa5.1.A, 2wa6.1.A, 2wa7.1.A, 2wfn.1.A, 2y3a.1.B, 2yrn.1.A, 2z0o.1.A, 3a98.1.A, 3a98.2.A, 3byh.1.B, 3co1.1.A, 3dtp.1.A, 3dtp.1.B, 3edu.1.A, 3edv.1.A, 3edv.1.B, 3f31.1.A, 3f31.1.B, 3f57.1.A, 3f7p.1.A, 3fb2.1.A, 3fb2.2.A, 3fer.1.A, 3fer.2.A, 3fer.4.A, 3hoc.1.A, 3hop.1.A, 3l6x.1.A, 3jak.1.C, 3jax.1.A, 3jax.1.B, 3jbh.1.A, 3jbh.1.B, 3jv3.1.A, 3kbt.1.A, 3kbt.2.A, 3kbu.1.A, 3kbu.2.A, 3ky9.1.A, 3l3x.1.A, 3l3x.1.B, 3lue.1.K, 3nhn.1.A, 3o0z.1.A, 3o0z.1.B, 3o0z.2.A, 3o0z.2.B, 3oja.1.B, 3pdy.1.A, 3pdy.2.A, 3pe0.1.A, 3plt.1.A, 3plt.1.B, 3plt.2.A, 3r6n.1.A, 3r6n.2.A, 3s84.1.A, 3s84.1.B, 3tnu.1.B, 3u1c.1.A, 3u1c.2.A, 3u59.1.A, 3u59.1.B, 3u59.2.A, 3u59.3.A, 3uf4.1.A, 3uul.1.A, 3uum.1.A, 3uum.2.A, 3uun.1.A, 3uun.2.A, 3vkg.1.A, 3vkg.1.B, 3vkh.1.A, 3vkh.2.A, 3vry.2.A, 3vs3.2.A, 3vs7.1.A, 3vs7.2.A, 3wuq.1.A, 4a7f.1.B, 4a7f.1.H, 4b7l.1.A, 4b7l.2.A, 4d1e.1.A, 4d8k.1.A, 4edl.1.A, 4edl.2.A, 4edl.3.A, 4edl.4.A, 4edl.5.A, 4edm.1.A, 4edm.2.A, 4edn.1.A, 4edn.2.A, 4edn.5.A, 4gkw.1.A, 4gkw.1.B, 4h5y.1.A, 4h8s.1.A, 4h8s.1.B, 4h8s.2.A, 4h8s.2.B, 4hpg.1.C, 4jio.1.A, 4jio.2.A, 4l3i.1.A, 4l3i.1.B, 4l6y.1.A, 4l6y.1.B, 4lin.1.A, 4lin.1.B, 4lin.1.C, 4lin.2.A, 4lin.2.B, 4lin.2.C, 4lin.3.A, 4lin.3.B, 4lin.3.C, 4lin.4.A, 4lin.4.B, 4lin.4.C, 4l18.1.B, 4l18.1.C, 4mh6.1.A, 4mt6.1.A, 4p1w.1.C, 4p1w.1.F, 4pd3.1.A, 4pd3.2.A, 4q28.1.A, 4q57.1.B, 4q58.1.A, 4q58.2.A, 4q59.1.A, 4q59.2.A, 4qmd.1.A, 4qmd.2.A, 4rfx.1.A, 4rfx.1.B, 4rfx.2.A, 4rfx.2.B, 4rfx.3.A, 4rh7.1.A, 4rm8.1.A, 4rm8.2.A, 4tql.1.A, 4txi.1.A, 4txk.1.A, 4u5w.1.B, 4u5w.1.D, 4uer.1.a, 4uxv.1.A, 4xa1.1.A, 4xa1.1.B, 4xa1.2.A, 4xa1.2.B, 4xa3.1.A, 4xa3.1.B, 4xa6.1.A, 4xa6.1.B, 4xa6.2.A, 4xa6.2.B, 4xi2.1.A, 4zdg.1.A, 4zdw.1.B, 4zdw.1.C, 4zry.1.A, 5a36.1.A, 5a37.1.A, 5a38.1.A, 5a4b.1.A, 5a5t.1.A, 5ayh.1.A, 5bvr.1.A, 5c5b.1.B, 5cj0.1.A, 5cj0.1.B, 5cj1.1.A, 5cj1.1.B, 5cj1.2.A, 5cj1.2.B, 5cj1.3.A, 5cj1.3.B, 5cj1.4.A, 5cj1.4.B, 5dzz.1.A, 5gox.1.A, 5gox.1.B, 5h0g.1.A, 5i4e.1.A, 5ih2.1.A, 5ih2.2.A, 5ijn.1.F, 5ijn.1.G, 5ijn.1.H, 5ijn.1.L, 5ijn.1.R, 5j1f.1.A, 5j1f.2.A, 5j1g.1.A, 5j1h.1.A, 5j1h.2.A, 5j1i.1.A, 5j4o.1.A, 5jhf.1.C, 5jhf.3.C, 5l0o.1.A, 5l23.1.A, 5m6s.1.A, 5mo4.1.A, 5nl6.1.A, 5nl6.1.B, 5nl7.1.A, 5nl7.2.A, 5nug.1.A, 5tby.1.A, 5tby.1.B, 5to5.1.A, 5to5.1.B, 5to6.1.A, 5to6.1.B, 5to6.1.C, 5to6.1.D, 5to7.1.A, 5to7.1.B, 5to7.1.C, 5to7.1.D, 5tvb.1.A, 5tvb.1.B, 5ul6.1.A, 5wjb.1.A, 5wjb.1.B, 5wlq.1.A, 5wlz.1.A, 5wlz.1.B, 5wlz.1.C, 5wlz.1.D, 5xg2.1.A, 6amv.1.A, 6amw.1.A, 6anu.1.G, 6atv.1.A, 6b25.1.A, 6b26.1.A, 6b27.1.A, 6b27.2.A, 6b27.5.A, 6b28.1.A, 6d8c.1.A, 6djl.1.B, 6djl.2.A, 6djl.3.A, 6djl.4.A, 6ek8.1.A, 6el1.1.T, 6f1t.1.U, 6f1t.1.h, 6f3f.1.A, 6fec.1.A, 6fsa.1.A, 6fyy.1.g, 6gao.1.A, 6gao.1.B, 6gao.1.C, 6gap.1.A, 6gap.1.B, 6gap.1.C, 6gy6.1.B, 6gy7.1.A, 6gy7.2.A, 6gy7.3.A, 6gy7.4.A, 6h2x.1.A, 6ian.1.A, 6ian.1.B, 6ian.2.A, 6ian.2.B, 6ici.1.A, 6ign.1.A, 6ixv.1.A, 6ixv.2.A, 6ixv.3.A, 6ixv.4.A, 6jlb.1.A, 6jlb.1.B, 6jlb.1.C, 6jlb.1.D, 6kn7.1.P, 6kn7.1.Q, 6kn8.1.P, 6kn8.1.Q, 6l5h.1.A, 6l5h.1.B, 6l5j.1.A, 6l5j.1.B, 6l5j.2.A, 6l5j.2.B, 6m3p.1.B, 6m3q.1.B, 6m3r.1.B, 6m5g.1.F, 6mi3.1.A, 6mi3.1.B, 6mi4.1.A, 6mi4.1.B, 6mib.1.B, 6nf1.1.A, 6o31.1.A, 6oa6.1.A, 6pf2.1.A, 6pf2.1.B, 6pfp.1.A, 6pfp.1.B, 6pfp.2.A, 6pfp.2.B, 6rlb.1.A, 6rlb.1.B, 6sc2.1.A, 6sc2.1.B, 6sdf.1.A, 6sdf.2.A, 6sl2.1.A, 6sl3.1.A, 6sl7.1.A, 6snz.1.A, 6snz.1.B, 6snz.2.A, 6snz.2.B, 6swt.1.A, 6u42.439.A, 6u42.440.A, 6u42.441.A, 6u42.442.A, 6up6.1.A, 6upn.1.A, 6uui.1.B, 6uy7.1.A, 6uy8.1.A, 6uy8.2.A, 6uy9.1.A, 6vec.1.L, 6vzf.1.A, 6w2s.1.9, 6w2t.1.d, 6wg3.1.A, 6x5z.1.B, 6x5z.1.D, 6xe9.1.A, 6xe9.1.D, 6xf1.1.A, 6xf1.2.A, 6xf2.1.A, 6xf2.2.A, 6yam.1.g, 6ybd.1.C, 6yjd.1.A, 6yrl.1.A, 6yrl.1.B, 6yrl.1.C, 6yrl.1.D, 6yrn.1.A, 6yrn.1.B, 6yrn.1.C, 6yrn.1.D, 6yrn.2.A, 6yrn.2.B, 6yrn.2.C, 6yrn.2.D, 6ys4.1.A, 6ys4.2.A, 6ys4.2.B, 6ys4.2.C, 6ys4.3.A, 6ys4.3.B, 6ysy.1.A, 6yuf.1.C, 6yvud.1.C, 6yvu.1.A, 6yvv.1.A, 6

8glv.603.A, 8glv.756.A, 8glv.844.A, 8glv.854.A, 8glv.855.A, 8glv.856.A, 8glv.891.A, 8glv.892.A, 8glv.902.A, 8glv.913.A, 8glv.951.A, 8glv.952.A, 8glv.953.A, 8glv.959.A, 8glv.960.A, 8glv.962.A, 8glv.963.A, 8glv.966.A, 8glv.974.A, 8gmb.1.A, 8i7o.1.A, 8i7o.11.A, 8i7o.18.A, 8i7o.19.A, 8i7o.20.A, 8i7o.27.A, 8i7o.28.A, 8i7o.31.A, 8i7o.47.A, 8i7o.48.A, 8i7o.49.A, 8i7o.56.A, 8i7o.57.A, 8i7o.59.A, 8i7o.91.A, 8i7o.92.A, 8i7r.107.A, 8i7r.108.A, 8i7r.109.A, 8i7r.110.A, 8i7r.111.A, 8i7r.112.A, 8i7r.113.A, 8i7r.114.A, 8i7r.115.A, 8i7r.128.A, 8i7r.130.A, 8i7r.132.A, 8i7r.133.A, 8i7r.134.A, 8i7r.135.A, 8i7r.136.A, 8i7r.137.A, 8i7r.138.A, 8i7r.139.A, 8i7r.140.A, 8i7r.19.A, 8i7r.2.A, 8i7r.20.A, 8i7r.21.A, 8i7r.213.A, 8i7r.214.A, 8i7r.215.A, 8i7r.216.A, 8i7r.22.A, 8i7r.24.A, 8i7r.25.A, 8i7r.26.A, 8i7r.27.A, 8i7r.398.A, 8i7r.4.A, 8i7r.411.A, 8i7r.42.A, 8i7r.43.A, 8i7r.44.A, 8i7r.45.A, 8i7r.46.A, 8i7r.47.A, 8i7r.48.A, 8i7r.49.A, 8i7r.5.A, 8i7r.62.A, 8i7r.63.A, 8i7r.64.A, 8i7r.65.A, 8i7r.69.A, 8i7r.70.A, 8i7r.71.A, 8i7r.73.A, 8i7r.74.A, 8i7r.75.A, 8iah.1.2, 8iah.1.4, 8iah.1.5, 8iah.1.6, 8iah.1.7, 8iai.1.1, 8iai.1.2, 8iai.1.T, 8iai.1.U, 8iai.1.W, 8iai.1.X, 8iyj.11.A, 8iyj.12.A, 8iyj.13.A, 8iyj.14.A, 8iyj.15.A, 8iyj.16.A, 8iyj.35.A, 8iyj.357.A, 8iyj.358.A, 8iyj.359.A, 8iyj.36.A, 8iyj.360.A, 8iyj.361.A, 8iyj.37.A, 8iyj.378.A, 8iyj.379.A, 8iyj.38.A, 8iyj.380.A, 8iyj.381.A, 8iyj.382.A, 8iyj.383.A, 8iyj.384.A, 8iyj.385.A, 8iyj.386.A, 8iyj.387.A, 8iyj.39.A, 8iyj.404.A, 8iyj.405.A, 8iyj.406.A, 8iyj.407.A, 8iyj.408.A, 8iyj.424.A, 8iyj.425.A, 8iyj.426.A, 8iyj.427.A, 8iyj.428.A, 8iyj.429.A, 8iyj.430.A, 8iyj.431.A, 8iyj.432.A, 8iyj.433.A, 8iyj.450.A, 8iyj.451.A, 8iyj.452.A, 8iyj.453.A, 8iyj.454.A, 8iyj.455.A, 8iyj.456.A, 8iyj.457.A, 8iyj.458.A, 8iyj.459.A, 8iyj.476.A, 8iyj.477.A, 8iyj.478.A, 8iyj.479.A, 8iyj.480.A, 8iyj.481.A, 8iyj.543.A, 8iyj.544.A, 8iyj.545.A, 8iyj.546.A, 8iyj.547.A, 8iyj.548.A, 8iyj.549.A, 8iyj.56.A, 8iyj.57.A, 8iyj.58.A, 8iyj.59.A, 8iyj.60.A, 8iyj.61.A, 8iyj.81.A, 8iyj.82.A, 8iyj.83.A, 8iyj.84.A, 8j07.1.A, 8j07.149.A, 8j07.152.A, 8j07.153.A, 8j07.156.A, 8j07.163.A, 8j07.2.A, 8j07.3.A, 8j07.31.A, 8j07.78.A, 8j07.844.A, 8j07.848.A, 8j07.849.A, 8j07.851.A, 8j07.852.A, 8j07.853.A, 8j07.854.A, 8j07.856.A, 8j07.857.A, 8j07.859.A, 8j07.860.A, 8j07.861.A, 8j07.862.A, 8j07.863.A, 8j07.864.A, 8j07.866.A, 8j07.867.A, 8j07.868.A, 8j07.869.A, 8j07.876.A, 8j07.877.A, 8j07.894.A, 8j07.896.A, 8j07.899.A, 8j07.908.A, 8j07.915.A, 8j07.916.A, 8j07.935.A, 8j07.937.A, 8j07.954.A, 8j07.956.A, 8j07.963.A, 8j07.965.A, 8p0s.1.A, 8p0s.1.B, 8p4y.1.A, 8ppl.1.L, 8q4g.1.G, 8q4g.1.H, 8q6t.1.A, 8q6t.1.B, 8q6t.1.H, 8q6t.1.N, 8q6t.1.O, 8q6t.1.Q, 8snb.124.A, 8snb.125.A, 8snb.126.A, 8snb.127.A, 8snb.128.A, 8snb.129.A, 8snb.130.A, 8snb.133.A, 8snb.135.A, 8snb.63.A, 8snb.64.A, 8srq.1.H, 8ssn.1.A, 8ssn.2.A, 8tek.1.A, 8tek.1.B, 8tek.1.D, 8tek.1.F, 8tek.1.I, 8th8.1.A, 8th8.1.D, 8th8.1.E, 8th8.1.J, 8th8.1.K, 8th8.1.P, 8th8.1.R, 8tid.1.1, 8tid.1.2, 8tid.1.3, 8tid.1.A, 8tid.1.B, 8tid.1.D, 8tid.1.E, 8tid.1.J, 8tid.1.K, 8tid.1.N, 8tid.1.P, 8tid.1.S, 8tid.1.T, 8tj5.1.U, 8tj5.1.V, 8tj5.1.W, 8tj5.1.Y, 8tj5.1.b, 8tj5.1.c, 8tj5.1.d, 8to0.18.A, 8to0.23.A, 8to0.397.A, 8to0.398.A, 8to0.400.A, 8to0.409.A, 8to0.410.A, 8to0.415.A, 8to0.439.A, 8to0.460.A, 8to0.462.A, 8to0.72.A, 8tvl.1.A, 8u95.1.A, 8u95.1.B