

## Model Building Report

This document lists the results for the homology modelling project "PLEC-CNV" submitted to SWISS-MODEL workspace on Nov. 16, 2023, 11:15 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:

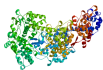
- Waterhouse, A., Bertoni, M., Bienert, S., Studer, G., Tauriello, G., Gumienny, R., Heer, F.T., de Beer, T.A.P., Rempfer, C., Bordoli, L., Lepore, R., Schwede, T. SWISS-MODEL: homology modelling of protein structures and complexes. *Nucleic Acids Res.* 46(W1), W296-W303 (2018). [doi>](#)
- Bienert, 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). [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). [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). [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). [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 1144 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    | 0.33 |

| Template   | Seq Identity | Oligo-state | QSQE | Found by    | Method       | Resolution | Seq Similarity | Range       | Coverage | Description        |
|------------|--------------|-------------|------|-------------|--------------|------------|----------------|-------------|----------|--------------------|
| H9FGT6.1.A | 90.19        | monomer     | -    | AFDB search | AlphaFold v2 | -          | 0.57           | 1058 - 2239 | 0.43     | Plectin isoform 1a |

The template contained no ligands.

Target RALAEAKRQRQLAEEDAARQRAEAERVLSEKLAATSEATRLKTEAEIALKEKEAENERLRLAEDEAFQRRRLLEEQAQ  
H9FGT6.1.A-----

Target HKADIEERLAQLRKASESELERQKGLVEDTLRQRQVEEEILALKASFEEAAGKAELELGRIRGNAEDTLRSKEQAE  
H9FGT6.1.A-----

Target QEAAQRQLAAEEERRRREAEEERVQKSLAEEEAARQKAALEEVEERLAKAVEEARLRERAEHESVRQLQLAQEAQKR  
H9FGT6.1.A-----

Target LQAEEKAHAFVQKQEQELQQTLLQEQSVLEKLRSSEAARRAAEEAEEARERAEREAQSRQRVEEAERLKQAEEQAQ  
H9FGT6.1.A-----

Target AQAQAQAAAEKLKAEQEAARRAQAEQAALRQKQAADAEMKHKFAEQTLRQKAQVEQELTALRLKLEETHQKSILD  
H9FGT6.1.A-----

Target QELQLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVA  
H9FGT6.1.A-----

Target AQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR  
H9FGT6.1.A-----

Target TLETERQRQLEMSAEERLRLRVAEMSRAQARAEDAQRFRKQAEIIGAKLHRTLATQEKVTLVQTLETQRQQSDRDA  
H9FGT6.1.A-----

Target RLREATAELEREKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAK  
H9FGT6. 1. A-----

Target AQLKREEQQRQQQMQQEQQLLASMEEARRRQHEAEQVRRKQEELQLEQQRQQEQQLAEENRRLRERLEHLEEHR  
H9FGT6. 1. A-----

Target AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGRLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDV  
H9FGT6. 1. A-----

Target RRYLQGHSSIAGLLLKPANEKLTIIAALRRQLSPGTALILLEAQAASGFLLDPVRNRRLTVTEAVKEGVVGPPELHHKLL  
H9FGT6. 1. A-----

Target SAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSD  
H9FGT6. 1. A-----

Target DTGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWEI  
H9FGT6. 1. A-----QLLERCVEDPETGLRLLPLTDKAAKGRELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWEI

Target NSEYFTAEQRDLLRQFRTGKVTVEKIIKIVITVIEEHEQKQQLCFQGLRALVPAEELLESGLIDWDLFRQLQLGERSVQ  
H9FGT6. 1. ANSEYFTAEQRDLLRQFRTGRITVEKIIKIIITVVEEQEQKQQLCFEGLRSLVPAEELLESVIDRELYHQLQQGERSVR

Target EVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVG  
H9FGT6. 1. AEVAEVDVARRALRGANVIAGVWLEEAGKLSYVDALKKDLLPSDVAVALLEAQAGTGHVIDPST SARLTVDEAVRAGLVG

Target PELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLLDAQLSTGGTVDPKSHRPLDVACARGYLDEETS  
H9FGT6. 1. APEFHEKLLSAEKAVTGYRDPYTQSVSLFQALKKGLIPREQGLRLLDAQLSTGGVDPKSHRVPDLVACARGFLDEETS

Target TALSAPRDDAKTYDPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQG  
H9FGT6. 1. ARALSAPRADAKAYCDPSTGEPVTYSELQQRCPDQLTGLSLLPLSEKAARARQEELYSELQARETFEKTVPDVPVGGFKG

Target RAVTIWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITVIEEETTRRERLSFSGLRAPVPASELLAAGILSSSQF  
H9FGT6. 1. ARTVTWELISSEYFTTEQRQELLRQFRTGKVTVEKVIKILITVIEEETLRQERLSFSGLRAPVPASELLASRVL SRAQF

Target EQLKDGKTSVKDLSELSSLQTLQSGGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLLEAQATGFLVDPVRNQRLY  
H9FGT6. 1. AEQLKDGKTTVKDLSELDSVRTLLQSGGCLAGIYLEDTKEKVTIYEAMRRGLLRPSTAILLLEAQATGFLVDPVRNQRLY

Target VHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLQFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVA  
H9FGT6. 1. AVHEAVKAGVVGPELHEQLLSAEKAVTGYRDPYSGSTISLQFQAMQKGLVLRQHGIRLLEAQIATGGVIDPVHSHRVPVDVA

Target CQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETTRAFF  
H9FGT6. 1. AYRRGYFDEEMNRVLADPSDDTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLKGAEKAEVVETTQVYTEEETTRAFF

Target ETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMI IIIIEIEIEKTEIVRQQNLASYDYVRRRLT  
H9FGT6. 1. AETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMI IIIIEIEIEKTEIIRQQGLASYDYVRRRLT

Target AEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLSAEVARLLLEAQA  
H9FGT6. 1. AAEDLYEARII SLETYNLLREGTRSLREALAESAWRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLSAEVARLLLEAQA

Target ATGFLLDPVKGERLTVDEAVRKGVLVGPPELHDLRLLSAERAVTGYRDPYTEQTISLQFQAMKKDLIPAEELRLLDAQLATGG  
H9FGT6. 1. AATGFLLDPVKGQRLTVDEAVRKGVLVGPPELHDLRLLSAERAVTGYRDPYTEQTISLQFQAMKKELIPTEEALRLLDAQLATGG

Target IVDPRLGFHLPLEVAYQRYGNKTDHDLQSEPSEVRSYVDPSTDERLSYTLQLLRCCRDETSGLFLLPLSEARKLTFRGL  
H9FGT6. 1. AIVDPRLGFHLPLEVAYQRYGNKTDHDLQSEPSEVRSYVDPSTDERLSYTLQLLRCCRDDGTGQLLPLSDARKLTFRGL

Target RKQITVEELVRSHVMDEATAQLRQEGLSIEEVSKNLQKFLEGTSSAGVLVDATKERLSVYQAMKKGIIRPGTAFELLE  
H9FGT6. 1. ARKQITVEELVRSQVMDEATALQREGLTSIEEVTKNLQKFLEGTSCAGVFVDATKERLSVYQAMKKGIIRPGTAFELLE

Target AQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLQFQAMKKGLILKDHGIRLLEAQIA  
H9FGT6. 1. AAQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLQFQAMKKGLILKDHGIRLLEAQI-

Target TGGIIDPEESHRLPVDVAYQRLGFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRER  
H9FGT6. 1. A-----


Target KTSSKSSVRKRRVIVDPETGKEMSVYAYRKGLIDHQTYLELSECEWEIEITISSDGVVKSMIIDRRSGRQYDIDEA  
H9FGT6. 1. A-----

Target IAKSLIDRSALDQYRAGTSLITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTET  
H9FGT6. 1. A-----

Target LEKVSITEAMHRNLVDNITGQRLLAEQACTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKM  
H9FGT6. 1. A-----

Target SAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTGPRVPLDEALQRGTVDARTAQKLRDVSAYSKYLTCPKTKLKISYKD

H9FGT6. 1. A-----  
Target ALDRSMVEEGTGLRLLEAAAQSSKGYSPYSVSGSGSTTGSRSRGSRTGSRAGSRRGSFDTGSGFSMTFSSSSYSSSGYG  
H9FGT6. 1. A-----  
Target RRYASGPTSSLGGPESAAA  
H9FGT6. 1. A-----

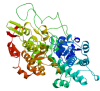
| Model #02                                                                         | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|-----------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.15 | 0.76 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range       | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|-------------|----------|-------------|
| 5dzz.1.A | 51.24        | monomer     | 0.00 | HHblits  | X-ray  | 2.60Å      | 0.45           | 1829 - 2314 | 0.18     | Desmoplakin |

The template contained no ligands.

Target RALAEAEKRQRQLAEEDAARQRAEAERVLSSEKLAATSEATRLKTEAEIALKEKEAENERLRRLAEDEAFQRRRLEEQAQ  
5dzz. 1. A-----  
Target HKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEELALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEAE  
5dzz. 1. A-----  
Target QEAAQRQLAAEEERRRREAEERVQKSLAAEEEAARQKAALVEERLKAKEVEARRLRERAEHESVRQLQLAQEAAQKR  
5dzz. 1. A-----  
Target LQAEEKAHAFVQKEQELQQTLLQEQSVLEKLRSSEAAARRAAEEAEARERAEAAQSRQRVEEAERLKQAEEEAQ  
5dzz. 1. A-----  
Target AQAQAQAAAEKLRKEAEQEAARRAQAEQAALRQKQAADAEMEKHKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILD  
5dzz. 1. A-----  
Target QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVA  
5dzz. 1. A-----  
Target AQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR  
5dzz. 1. A-----  
Target TLETERQRQLEMSAEERLRLRVAEMSRAQARAEDAQRFRKQAEIIGAKLHRTTELATQEKVTLVQTLETQRQQSDRDAD  
5dzz. 1. A-----  
Target RLREATAELEREKDKLKKEAELLQLKSEEMQTVQEQQLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAK  
5dzz. 1. A-----  
Target AQKLREEQQRQQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQEQQLAEENRRLRERLEHLEEEHR  
5dzz. 1. A-----  
Target AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDV  
5dzz. 1. A-----  
Target RRYLQGHSSIAGLLLKPANEKLTIIYAALRRQLSPGTALILLEAQAASGFLLDPVRNRRRLTVTEAVKEGVVGPETHHKL  
5dzz. 1. A-----  
Target SAERAVTGYKDPYTGEKISLQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRYGFDEEMNRVLQDPSD  
5dzz. 1. A-----  
Target DTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELI  
5dzz. 1. A-----  
Target NSEYFTAEQRDLLRQFRGTGKVTVEKIIKIVITVIEEHEQKGLCFQGLRALVPAAELLESGLIIDWDLFRQLQLGERSVQ  
5dzz. 1. A-----  
Target EVAEEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVDPATSARLTVDEAVRAGLVG

5dzz. 1. A -----  
Target PELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDDAQLSTGGTVDPKSHRLPLDVACARGYLDEETS  
5dzz. 1. A -----  
Target TALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQG  
5dzz. 1. A -----  
Target RAVTIWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITIVIEEVETRRERLSFSGLRAPVPASELLAAGILSSSQF  
5dzz. 1. A -----  
Target EQLKDGTKSVKDLSELSSLQTLQSGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLY  
5dzz. 1. A -----  
Target VHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVA  
5dzz. 1. A -----  
Target CQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVDPETGLRLLPLKGPEKAEVVETTRVYTEEETTRAFF  
5dzz. 1. A -----  
Target ETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMI IIIIEIEKTEIVRQQNLASYDYVRRRLT  
5dzz. 1. A -----KLVFDGLRKKVT  
Target AEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLSAEVARLLLEAQA  
5dzz. 1. A AMQLYECQLIDKTTLDKLLKGKKSVEEVAS--ETQPFLRGAGSIAGAS-ASPKEKYSLEAKRKKLISPSTVMLLEAQA  
Target ATGFLDLPVKGERLTVDEAVRKLGLVPELHDLRLLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEALRLDDAQLATGG  
5dzz. 1. A ATGGIIDPHRNEKLTVDSAIARDLIDFDDRQIYAAEKAITGFDDPFSGKTVSVSEAIKKNLIDRETGMRLLEAQIASGG  
Target IVDPRLGFHLPLEVAYQRGYLNKDTHDQLSEPSE-VRSYVDPSTDERLSYTLQLRRCRRDETSGFLPLPLSEARKLTFRG  
5dzz. 1. A VVDPVNSVFLPKDVALARGLIDRLYRSLNDPRDSQKNFVDPVTKKKVSYVQLKERCRIEPHTGLLLLSVQKR-SMSFQG  
Target LRKQITVEELVRSHVMDEATAQRLQEG LTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELL  
5dzz. 1. A IRQPVTVTELVDSGILRPSTVNELESGQISYDEVGERIKDFLQGSSCIAGIYNETTKQLGIYEAMKIGLVRPGTALELL  
Target EAQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLSLQFQAMKKGLILKDHGIRLLEAQI  
5dzz. 1. A EAQAATGFIVDPVSNLRLPVEEAYKRGVLVIEFKDKLLSAERAVTGYNDPETGNIISLQFQAMNKELIEKHGIRLLEAQI  
Target ATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRE  
5dzz. 1. A ATGGIIDPKESHRLPVDIAYKRGYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLKERICKDEETGLCLLPLK-----  
Target RKTSSKSSVRKRRVIVDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDE  
5dzz. 1. A -----  
Target AIAKSLIDRSALDQYRAGTSLITEFADMLSGNAGGFRSRSSSVGSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTE  
5dzz. 1. A -----  
Target TLEKVSITEAMHRNLVDNITGQRLLEAQA CTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTK  
5dzz. 1. A -----  
Target MSAQAQKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKLRDVSAYS KYLTCPKTKLKISYK  
5dzz. 1. A -----  
Target DALDRSMVEEGTGLRLLEAAAQSSKGYSPYSVSGSGSTTGSRSRGTGSRAGSRRGSFDTGSGFSMTFSSSYSSSGY  
5dzz. 1. A -----  
Target GRRYASGPTSSLGGPESAAA  
5dzz. 1. A -----

| Model #03                                                                           | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|-------------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.12 | 0.68 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range       | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|-------------|----------|-------------|
| 5dzz.1.A | 54.32        | monomer     | 0.00 | HHblits  | X-ray  | 2.60Å      | 0.45           | 1160 - 1736 | 0.18     | Desmoplakin |

The template contained no ligands.

|                      |                                                                                                                                                                          |
|----------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Target<br>5dzz. 1. A | RALAEERKRQRLAEEDAARQRAEAERVLSEKLAATSEATRLKTEAEIALKEKEAENERLRRLAEDEAFQRRRLEEQAQ<br>-----                                                                                  |
| Target<br>5dzz. 1. A | HKADIEERLAQLRKASESELERQKGLVEDTLRQRQVEEELALKASFEEKAAAGKAELELELGRIRGNAEDTLRSKEQAE<br>-----                                                                                 |
| Target<br>5dzz. 1. A | QEAAQRQLAAEEERRRREAEEERVQKSLAAEEEAARQKAALVEERLKAKEVEARRLRERAEHESVRQLLAQEAQKR<br>-----                                                                                    |
| Target<br>5dzz. 1. A | LQAEEKAHAFVQKQEQELQQTQQEQSVLEKLRSEAEAAARRAAEEAEARERAEREAQSRQRVEEAERLKAABEEQAQ<br>-----                                                                                   |
| Target<br>5dzz. 1. A | AQAQAQAAAEKLRKEAEQEAARRAQAEQAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETHDQKSILD<br>-----                                                                                |
| Target<br>5dzz. 1. A | QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVA<br>-----                                                                                 |
| Target<br>5dzz. 1. A | AQEAARLRQLAEEDLAQQRALAEKMLKEKMAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR<br>-----                                                                                |
| Target<br>5dzz. 1. A | TLETERQRQLEMSAEERLRLRVAEMSRAQARAEDAQRFRKQABEIGAKLHRTTELATQEKVTLVQTLETQRQQSDRDAD<br>-----                                                                                 |
| Target<br>5dzz. 1. A | RLREAIAELEREKDKLKEAEELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAK<br>-----                                                                                |
| Target<br>5dzz. 1. A | AQKLREEQQRQQQMQQEQQLLASMEEARRRQHEAEEGVRRKQEEQLLEQQRQQEQQLAENRRRLRERLEHLEEEHR<br>-----                                                                                    |
| Target<br>5dzz. 1. A | AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDV<br>-----                                                                                |
| Target<br>5dzz. 1. A | RRYLQGHSSIAGLLKLANEKLTIYAALRRQLLSPGTALILLEAQAASGFLLDPVRNRRRLTVTEAVKEGVVGPPELHHKLL<br>-----                                                                               |
| Target<br>5dzz. 1. A | SAERAVTGYKDPYTGEKISLQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSD<br>-----                                                                                 |
| Target<br>5dzz. 1. A | DTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGGEVYTDSEARDVFEKATVSAPFGKFQGKTVTIWEI<br>-----                                                                                  |
| Target<br>5dzz. 1. A | NSEYFTAEQRDRLRQFRTGKVTVKEIKIKIVITVIEEHEQKGLCFQGLRALVPAAELLESGLIDWDLFRQLQLGERSVQ<br>-----DTSKLVFDGLRKKVTAMQLYECQLIDKTTLDKLLKGKKSVE                                        |
| Target<br>5dzz. 1. A | EVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVG<br>EVA--SEIQPFLRGAGSIAGAS--ASPKEKYSLVEAKRKKLISPESTVMLLEAQAAATGGIIDPHRNEKLTVD SAIARDLID |
| Target<br>5dzz. 1. A | PELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDLAQSTGGTVDPSPKSHRLPLDVACARGYLDEETS<br>FDDRQQIYAAEKAITGFDDPFSGKTVSYS EAIKKNLIDRETGMRLLEAQIASGGVDPVNSVFLPKDVALARGLIDRDLY     |
| Target<br>5dzz. 1. A | TALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQG<br>RSLNDPRDSQKNFVDPVTKKKVSYVQLKERCRIEPTGLLLLSVQKRS-----                                   |
| Target<br>5dzz. 1. A | RAVTIWELINSEYFTAEQRQELLRQFRTGKVTVKEIKIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQF<br>-----MSFQGI RQPVTVTVELVDSGILRPSTV                                                   |
| Target<br>5dzz. 1. A | EQLKDGTKSVKDLSELSSLQTLQGSGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLLEAQAAATGFLVDPVRNQRLY<br>NELESGQISYDEVGE--RIKDFLQGSSCIAGIYNETTKQLGIYEAMKIGLVRPGTALELLEAQAAATGFIVDPVSNLRPL     |
| Target<br>5dzz. 1. A | VHEAVKAGVGPPELHEKLLSAEKAVTGYKDPYSGSTISLQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVA<br>VEEAYKRGVLVGI EFKEKLLSAERAVTGYNDPETGNIISLQAMNKELIEKGHGIRLLEAQIATGGIIDPKESHRLPVDIA      |
| Target<br>5dzz. 1. A | CQRGYFDEEMNRVLEDPDSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEETTRAFE<br>YKRGYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLKERICDEETGLCCLPLK-----                         |

Target  
5dzz. 1. A

ETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMI I I I I E I I E K T E I V R Q Q N L A S Y D Y V R R R L T

Target  
5dzz. 1. A

AEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQA

Target  
5dzz. 1. A

ATGFLLDPVKGERLTVDEAVRKGLVGPETHDRLLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAAEALRLDDAQLATGG

Target  
5dzz. 1. A

IVDPRLGFHLPLEVAYQRGYLNKDTHTDQLSEPSEVRSYVDPSTDERLSYQLLRRCRRDETSGLFLLPLSEARKLTFRGL

Target  
5dzz. 1. A

RKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLE

Target  
5dzz. 1. A

AQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQAMKKGLILKDHGIRLLEAQIA

Target  
5dzz. 1. A

TGGIIDPEESHRLPVDVAYQRGLEDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRER

Target  
5dzz. 1. A

KTSSKSSVRKRRVIVDPETGKEMSVEAYRKGLIDHQTYLELSEQEWEETISSSDGVVKSMIIDRRSGRQYDIDEA

Target  
5dzz. 1. A

IAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTET

Target  
5dzz. 1. A

LEKVSITEAMHRNLVDNITGQRLLAQACTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKM

Target  
5dzz. 1. A

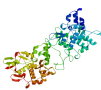
SAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKLRDVSAYSKYLTCPKTKLKISYKD

Target  
5dzz. 1. A

ALDRSMVEEGTGLRLLLEAAQSSKGYSPYSVSGSGSTTGSRSRTGSRAGSRSGFDTGSGFSMTFSSSSYSSSGYG

Target  
5dzz. 1. A

RRYASGPTSSLGGPESAAA

| Model #04                                                                           | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|-------------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.09 | 0.66 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range      | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|------------|----------|-------------|
| 5dzz.1.A | 47.22        | monomer     | 0.00 | HHblits  | X-ray  | 2.60Å      | 0.42           | 833 - 1405 | 0.18     | Desmoplakin |

The template contained no ligands.

Target  
5dzz. 1. A

RALAEAKRQRQLAEEDAARQRAEAERVLSEKLA AIS EATRLKTEAEIALKEKEAENERLRRLAED EAFQRRRLEEQA AQ

Target  
5dzz. 1. A

HKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEEILALKASFEEKAAAGKAELELELGRIRGNAEDTLRSKEQAE

Target  
5dzz. 1. A

QEAAQRQLAAEEERRRREAEEERVQKSLAEEEEAARQRKAAL EEVERLKAKVEEARRLRERAEHESVRQLQLAQEA AQKR

Target  
5dzz. 1. A

LQAEEKAHAFVQQKEQELQQTLQQEQSVLEKL RSEAEAAARRAAEEAEERERAEREAAQSRQRVEEAERLQQAEEEAQ

Target  
5dzz. 1. A

AQAQAQAAAEKL RKEAEQEAARRAQAEQAALRQKQAADAEMEKKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILD

|                      |                                                                                                                                                                        |
|----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Target<br>5dzz. 1. A | QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQLQEEAEKMKQVAEEAARLSVA<br>-----                                                                             |
| Target<br>5dzz. 1. A | AQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR<br>-----                                                                             |
| Target<br>5dzz. 1. A | TLETERQRQLEMSAEERLRLRVAEMSRAQARAEEDAQFRFKQAEIIGAKLHRTELATQEKVTLVQTLETQRQQSDRDAD<br>-----                                                                               |
| Target<br>5dzz. 1. A | RLREATAELEREKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAK<br>-----                                                                              |
| Target<br>5dzz. 1. A | AQKLREEQQRQQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLEQQRQQQEQLLAENRRLRERLEHLEEHR<br>-----                                                                                  |
| Target<br>5dzz. 1. A | AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDV<br>-----TSKLVPDGLRKKVTAMQLYECQLIDKTTLDKLLKGKKSVEEVA--SEI                              |
| Target<br>5dzz. 1. A | RRYLQGHSSIAGLLLKPANEKLTIIYAALRRQLSPGTALILLEAQAAAGFLLDPVRNRRLTVTEAVKEGVVGPPELHHKLL<br>QPFLRGAGSIAGAS-ASPKEYSLVEAKRKKLISPESTVMLLEAQAAATGGIIDPHRNEKLTVDSAIARDLIDFDDRQQIY  |
| Target<br>5dzz. 1. A | SAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSD<br>AAEKAITGFDDPPFSGKTIVSVSEAIKKNLIDRETGMRLLEAQIASGGVDPVNSVFLPKDVALARGLIDRDLYRSLNDPRD |
| Target<br>5dzz. 1. A | DTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELI<br>SQKNFVDPVTKKKVSIVQLKERCRIEPTGLLLLSVQKRS-----                                        |
| Target<br>5dzz. 1. A | NSEYFTAQRDRLRQFRTGKVTVKEIIKIVITVIEEHEQKGLCFQGLRALVPAAELLESGLIDWDLFRQLQLGERSVQ<br>-----MSFQGIQPVTVTELVDSGILRPSTVNELESQGISYD                                             |
| Target<br>5dzz. 1. A | EVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPATSARLTVDEAVRAGLVG<br>EVGE--RIKDFLQGSSCIAGIYNETTKKGLIYEAMKIGLVRPGTALELLEAQAAATGFIVDPVSNLRLPVEEAYKRGLVG   |
| Target<br>5dzz. 1. A | PELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDLAQLSSTGGTVDPKSHRPLDVACARGYLDEETS<br>IEFKEKLLSAERAVTGYNDPETGNIISLQFQAMKELIEKGHGIRLLEAQIATGGIIDPKESHRLPVDIAYKRGYFNEELS    |
| Target<br>5dzz. 1. A | TALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQG<br>EILSDPSDDTKGFFDPNTEENLTYLQLKERICKDEETGLCLLPLK-----                                   |
| Target<br>5dzz. 1. A | RAVTIWELINSEYFTAQRQELLRQFRTGKVTVKEIIKIVITIVIEEVETRRERLSFSGLRAPVPASELLAAGILSSSQF<br>-----                                                                               |
| Target<br>5dzz. 1. A | EQLKDGTKSVKDLSELSSLQTLQSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEAQAAATGFLVDPVRNQRLY<br>-----                                                                                |
| Target<br>5dzz. 1. A | VHEAVKAGVGPPELHEKLLSAEKAVTGYKDPYSGSTISLQFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVA<br>-----                                                                              |
| Target<br>5dzz. 1. A | CQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETRAFE<br>-----                                                                               |
| Target<br>5dzz. 1. A | ETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIIEKTEIVRQQNLASYDYVRRRLT<br>-----                                                                            |
| Target<br>5dzz. 1. A | AEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEAQA<br>-----                                                                              |
| Target<br>5dzz. 1. A | ATGFLLDPVKGERLTVDEAVRKGVLVGPPELHDLRLLSAERAVTGYRDPYTEQTISLQFQAMKKDLIPAAEALRLDLAQLATGG<br>-----                                                                          |
| Target<br>5dzz. 1. A | IVDPRLGFHLPLEVAYQRGYLNKDTHTDQLSEPSEVRSYVDPSTDERLSYTQLLRRCRRDETSGFLPLPLSEARKLTFRGL<br>-----                                                                             |
| Target<br>5dzz. 1. A | RKQITVEELVRSHVMDEATAQRLQEGLTISIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLE<br>-----                                                                             |
| Target<br>5dzz. 1. A | AQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLIISLQFQAMKKGLILKDHGIRLLEAQIA<br>-----                                                                            |
| Target<br>5dzz. 1. A | TGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRER<br>-----                                                                              |
| Target<br>5dzz. 1. A | KTSSKSSVRKRRVIVDPETGKEMSVYEAIRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEA<br>-----                                                                               |


Target IAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTET  
5dzz. 1. A -----

Target LEKVSITEAMHRNLVDNITGQRLLEAQAQCTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKM  
5dzz. 1. A -----

Target SAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKLRDVSAYSKYLTCPKTKLKISYKD  
5dzz. 1. A -----

Target ALDRSMVEEGTGLRLLLEAAAQSSKGYSPYSVSGSGSTTGSRSRGTGSRAGSRSGSFATGSGFSMTFSSSSYSSSGYG  
5dzz. 1. A -----

Target RRYASGPTSSLGGPESAAA  
5dzz. 1. A -----

| Model #06                                                                         | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|-----------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.04 | 0.69 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range       | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|-------------|----------|-------------|
| 5dzz.1.A | 45.93        | monomer     | 0.00 | BLAST    | X-ray  | 2.60Å      | 0.41           | 1163 - 1462 | 0.10     | Desmoplakin |

The template contained no ligands.

Target RALAEAEKRQRQLAEEDAARQRAEAERVLSKLAATSEATRLKTEAEIALKEKEAENERLRRLAEDEAFQRRRLEEQAQ  
5dzz. 1. A -----

Target HKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEELALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAE  
5dzz. 1. A -----

Target QEAAQRQLAAEEERRRREAEEERVQKSLAAEEEAARQKAALVEERLKAKEVEARRLRERAEHESVRQLQLAQEAQKR  
5dzz. 1. A -----

Target LQAEEKAHAFVQKEQELQQTLLQEEQSVLEKLRLSEAEAAARRAAEEEAERERAEAAQSRQRVEEAERLKQAEEEAQ  
5dzz. 1. A -----

Target AQAQAQAAAEKLRKEAEQEAAARRAQAEQAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILD  
5dzz. 1. A -----

Target QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVA  
5dzz. 1. A -----

Target AQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR  
5dzz. 1. A -----

Target TLETERQRQLEMSAEERLRLRVAEMSRAQARAEEAQRFRKQAEIIGAKLHRTTELATQEKVTLVQTLETQRQQSDRDAD  
5dzz. 1. A -----

Target RLREAIAELEREKDKLKEAEELLQKSEEMQTVQEEQLLQETQALQQSFLSEKDSLLQRRERFIEEEKAKLERLFQDEVAK  
5dzz. 1. A -----

Target AQKLREEQQRQQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLEQQRQQQEQLLAEENRRLRERLEHLEEEHR  
5dzz. 1. A -----

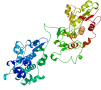
Target AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHHTVAELTQREDV  
5dzz. 1. A -----

Target RRYLQGHSSIAGLLLKPANEKLTIIYAALRRQLLSPGTALILLEAQAASGFLLDPVRNRRLTVTEAVKEGVVGPPELHHKLL  
5dzz. 1. A -----

Target SAERAVTGYKDPYTGEKISLFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRYGFDEEMNRVLQDPSD  
5dzz. 1. A -----



|                      |                                                                                                                                                                        |
|----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Target<br>5dzz. 1. A | DTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWEI<br>-----                                                                                |
| Target<br>5dzz. 1. A | NSEYFTAEQRDLLRQFRTGKVTVEKIIKIVITVIEEHEQKGLCFQGLRALVPAAELLESGLIDWDLFRQLQLGERSVQ<br>-----KLVFDGLRKKVTAMQLYECQLIDKTTLDKLLKGKKSVE                                          |
| Target<br>5dzz. 1. A | EVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVG<br>EVAS--EIQPFLRGAGSIAGAS-ASPKEKYSLVEAKRKKLISPES TVMLLEAQATGGIIDPHRNEKLTVD SAIARDLID |
| Target<br>5dzz. 1. A | PELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLLDAQLSTGGTVDPSPKSHRLPLDVACARGYLDEETS<br>FDDRQIYAAEKAITGFDDPFSGKTVSVSEAIKKNLIDRETGMRLLEAQIASGGVDPVNSVFLPKDVALARGLIDRDLY    |
| Target<br>5dzz. 1. A | TALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQG<br>RSLNDPRDSQKNFVDPVTKKKVSYVQLKERCRIEPTGLLLL-----SVQKRSM-----SFQG                       |
| Target<br>5dzz. 1. A | --RAVTIWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGLRAPVPASELLAAGILSSS<br>IRQPVTVTELVD SGILRPSTVNEL-----                                                     |
| Target<br>5dzz. 1. A | QFEQLKDGKTSVKDLSELSSLQTLLQSGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLEAQATGFLVDPVRNQR<br>-----                                                                                 |
| Target<br>5dzz. 1. A | LYVHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLFQAMKGLVVREHGIRLLEAQIATGGIIDPVHSHRPVD<br>-----                                                                                |
| Target<br>5dzz. 1. A | VACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETRA<br>-----                                                                               |
| Target<br>5dzz. 1. A | FEETQIDIPGGSGHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEKTEIVRQQLASYDYVRRR<br>-----                                                                              |
| Target<br>5dzz. 1. A | LTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQALKKGLLSAEVARLLLEA<br>-----                                                                              |
| Target<br>5dzz. 1. A | QAATGFLDPVKGERLTVDEAVRKGLVGPELHRLLSAERAVTGYRDPYTEQTISLFQAMKKDLIPAEELRLDDAQLAT<br>-----                                                                                 |
| Target<br>5dzz. 1. A | GGIVDPRLGFHLPLEVAYQRYLNKDTHDQLSEPSEVRSYVDPSTDERLSYTLRLRCRRDETSGLFLLPLSEARKLTFR<br>-----                                                                                |
| Target<br>5dzz. 1. A | GLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIIRPGTAFEL<br>-----                                                                             |
| Target<br>5dzz. 1. A | LEAQATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQAMKGLILKDHGIRLLEAQ<br>-----                                                                                |
| Target<br>5dzz. 1. A | IATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKR<br>-----                                                                              |
| Target<br>5dzz. 1. A | ERKTSSKSSVRKRRVVIVDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSDGVVKSMIIDRRSGRQYDID<br>-----                                                                               |
| Target<br>5dzz. 1. A | EATAKSLIDRSALDQYRAGTSLITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDT<br>-----                                                                              |
| Target<br>5dzz. 1. A | ETLEKVSITEAMHRNLVDNITGQRLLEAQACTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKT<br>-----                                                                              |
| Target<br>5dzz. 1. A | KMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDARTAQKLRDVSAYS KYLTCPKTKLKISY<br>-----                                                                             |
| Target<br>5dzz. 1. A | KDALDRSMVEEGTGLRLLLEAAQSSKGYSPYSVSGSGSTGSRSGSRTGSRAGSRRGSFDTGSGFSMTFSSSSYSSSG<br>-----                                                                                 |
| Target<br>5dzz. 1. A | YGRRYASGPTSSLGGPESAAA<br>-----                                                                                                                                         |

| Model #05                                                                         | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|-----------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.03 | 0.59 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range       | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|-------------|----------|-------------|
| 5dzz.1.A | 38.27        | monomer     | 0.00 | HHblits  | X-ray  | 2.60Å      | 0.38           | 2071 - 2659 | 0.18     | Desmoplakin |

The template contained no ligands.

|                      |                                                                                            |
|----------------------|--------------------------------------------------------------------------------------------|
| Target<br>5dzz. 1. A | RALAEAAKRQRLAEEDAARQRAEAERVLSEKLAATSEATRLKTEAEIALKEKEAENERLRRLAEDAEFQRRRLEEQAQ<br>-----    |
| Target<br>5dzz. 1. A | HKADIEERLAQLRKASESELERQKGLVEDTLRQRQVEEELALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAE<br>-----    |
| Target<br>5dzz. 1. A | QEAARQRQLAAEEERRRREAEEERVQKSLAAEEEAARQRKAALAEVERLKAKVEEARLRERAEHESVRQLQLAQEAAQKR<br>-----  |
| Target<br>5dzz. 1. A | LQAEEKAHAFVQKQEQELQQTQQEQSVLEKLRSEAEAAARRAAEEAEARERAEREAQSRQRVEEAERLKQAABEEQAQ<br>-----    |
| Target<br>5dzz. 1. A | AQAQAQAAAEKLRKEAEQEAARRAQEAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILD<br>-----    |
| Target<br>5dzz. 1. A | QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVA<br>-----   |
| Target<br>5dzz. 1. A | AQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR<br>-----   |
| Target<br>5dzz. 1. A | TLETERQRQLEMSAEERLRLRVAEMSRAQARAEDAQRFRKQABEIGAKLHRTELATQEKVTLVQTLETQRQQSDRDAD<br>-----    |
| Target<br>5dzz. 1. A | RLREAIAELEREKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAK<br>-----  |
| Target<br>5dzz. 1. A | AQKLREEQQRQQQMQQEQQLLASMEEAARRQHEAEEGVRRKQEELQLLEQQRQQEQQLAEENRRLRERLEHLEEEHR<br>-----     |
| Target<br>5dzz. 1. A | AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAAQLQEAGILSTEELQRLAQGHTTVAELTQREDV<br>-----  |
| Target<br>5dzz. 1. A | RRYLQGHSSIAGLLLPANEKLTIIYAALRRQLLSPGTALILLEAQAAASGFLLDPVRNRRLTVTEAVKEGVVGPELHHKLL<br>----- |
| Target<br>5dzz. 1. A | SAERAVTGYKDPYTGKISLQAMKKDLIVREHGIRLEAQIATGGVIDPVHSHRVPVDVAYHRYGFDEEMNRVLQDPSD<br>-----     |
| Target<br>5dzz. 1. A | DTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELI<br>-----   |
| Target<br>5dzz. 1. A | NSEYFTAEQRDLLRQFRTGKVTVKEIIKIVITVIEEHEQKGLCFGLRALVPAAELLESGLIIDWDLFRQLQLGERSVQ<br>-----    |
| Target<br>5dzz. 1. A | EVAEEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVG<br>-----  |
| Target<br>5dzz. 1. A | PELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLLDAQLSTGGTVDPKSHRPLDVACARGYLDEETS<br>-----    |
| Target<br>5dzz. 1. A | TALSAPRDDAKTYYPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQG<br>-----    |
| Target<br>5dzz. 1. A | RAVTIWELINSEYFTAEQRQELLRQFRTGKVTVKEIIKIVITVIEEVETTRRERLSFSGLRAPVPASELLAAGILSSSQF<br>-----  |

Target 5dzz. 1. A EQLKDGKTSVKDLSELSSLQTLQGSGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFLVDPVRNQRLY-----

Target 5dzz. 1. A VHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLFAQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVA-----

Target 5dzz. 1. A CQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTyrQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETRRAFE-----

Target 5dzz. 1. A ETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEKTEIVRQQNLASYDYVRRRLT-----

Target 5dzz. 1. A AEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLSAEVARLLLEAQA-----

Target 5dzz. 1. A ATGFLLDPVKGERLTVDEAVRKGLVGPELHDLRLLSAERAVTGYRDPYTEQTISLFAQAMKKDLIPAEELRLDLAQLATGG-----

Target 5dzz. 1. A IVDPRLGFHLPLEVAYQRGYLNKDTHTDQLSEPSEVRSYVDPSTDERLSYTLQLLRRCRRDETSGLFLLPLSEARKLTFRGL-----DTSKLVFDGL

Target 5dzz. 1. A RKQITVEELVRSHVMDEATAQRLQEGLTSEEVSKNLQKFLEGTSSiAGVLVDATKERLSVYQAMKKGIIRPGTAFELLE  
RKKVTAMQLYECQLIDKTLTKLLKGGKSVVEEVAIEQPFLRGAGSIAGAS-ASPKEKYSLEAKRKKLISPESTMVLL

Target 5dzz. 1. A AQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLTISLFAQAMKKGLILKDHGIRLLEAQIA  
AQAATGGIIDPHRNEKLTVDIAIARDLIDFDDRQIYAIEKAITGFDDPFSGKTVSVSEAIKKNLIDRETGMRLLEAQIA

Target 5dzz. 1. A TGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRER  
SGGVDPVNSVFLPKDVALARGLIDRDLRSLNDPRDSQKNFVDPVTKKVSIVYQLKERCRIEPHTGLLLSVQKRSM--

Target 5dzz. 1. A KTSSKSSVRKRRVIVDPETGKEMSVEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRRSGRQYDIDEA  
-----SFQGIHQPVTVTELVDGILRPS-----

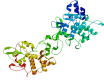
Target 5dzz. 1. A IAKSLIDRSALDQYRAGTSLITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETGPVAGILDTET  
-----TVNELESGQISYDEVGE-----RIKDFLQGSSCIAGIYNETT

Target 5dzz. 1. A LEKVSITEAMHRNLVDNITGQRLLEAACTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKM  
KQKLGIEYAMKIGLVRPGTALELLEAAATGFIVDPVSNLRLPVEEAYKRGLVIGIEFKELLSAERAVTGYNDPETGNII

Target 5dzz. 1. A SAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTGPRVPLDEALQRTVDARTAQKLKRDVSAYSKYLTCPKTKLKISYKD  
SLFAQMNKELIEKHGIRLLEAQIATGGIIDPKESHRLPVDIAYKRGYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQ

Target 5dzz. 1. A ALDRSMVEETGLRLLEAAQSSKGYSPYSVSGSGSTGSRSGSRTGSRAGSRRGSFDTGSGFSMTFSSSSYSSSGYG  
LKERICDEETGLCLLPLK-----

Target 5dzz. 1. A RRYASGPTSSLGGPESAAA-----

| Model #08                                                                           | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|-------------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.01 | 0.56 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range      | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|------------|----------|-------------|
| 5dzz.1.A | 37.12        | monomer     | 0.00 | BLAST    | X-ray  | 2.60Å      | 0.38           | 837 - 1326 | 0.17     | Desmoplakin |

The template contained no ligands.

Target 5dzz. 1. A RALAEAEKRQRQLAEEDAARQRAEAERVLSEKLAATSEATRLKTEAEIALKEKEAENERLRLRAEDEAFQRRRLEEQAQ-----

Target 5dzz. 1. A HKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEELALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAE-----

|                      |                                                                                                                                                                       |
|----------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Target<br>5dzz. 1. A | QEAARQRQLAAEEERRRREAEEERVQKSLAAEEEAARQRKAALEEVERLKAKVVEEARRLRERAHEHESVRQLQLAQEAAQKR<br>-----                                                                          |
| Target<br>5dzz. 1. A | LQAEKHAHAFVQKQEQELQQTQQEQSVLEKLRSSEAEARRAAEEAEARERAEREAAQSRQRVVEEAERLKQAEEQAQ<br>-----                                                                                |
| Target<br>5dzz. 1. A | AQAQAQAAAEKLKEAEQEAARRAQAEQAALRQKQAADAEMEKHKKF AEQTLRQKAQVEQELTALRLKLEETHQKSILD<br>-----                                                                              |
| Target<br>5dzz. 1. A | QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQLQEEAEKMKQVAEEAARLSVA<br>-----                                                                            |
| Target<br>5dzz. 1. A | AQEAARLRQLAEEDLAQQRALAEKMLKEKMAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR<br>-----                                                                               |
| Target<br>5dzz. 1. A | TLETERQRQLEMSAEERLRLRVAEMSRAQARAEDAQRFRKQAEIIGAKLHRTELATQEKVTLVQTLETQRQQSDRDAD<br>-----                                                                               |
| Target<br>5dzz. 1. A | RLREATAELEREKDKLKKEALLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAK<br>-----                                                                              |
| Target<br>5dzz. 1. A | AQKLREEQQRQQMQQEQKQLLASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQEQQLLAENRRLRERLEHLEEHR<br>-----                                                                                 |
| Target<br>5dzz. 1. A | AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDV<br>-----VFDGLRKKVTAMQLYECQLIDKTTLDKLLGKKSVEEVAS--EI                                  |
| Target<br>5dzz. 1. A | RRYLQGHSSIAGLLLKPANEKLTIIAALRRQLSPGTALILLEAQAASGFLLDPVRNRRLTVTEAVKEGVGPPELHHKLL<br>QPFLRGAGSIAGASASP--KEKYSLVEAKRKKLISPESTMVLLLEAQAATGGIIDPHRNEKLTVDSAIARDLIDFDDRQQIY |
| Target<br>5dzz. 1. A | SAERAVTGYKDPYTGEKISLQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSD<br>AAEKAITGFDDPFSGKTVSVSEAIKKNLIDRETGMRLLEAQIASGGVDPVNSVFLPKDVALARGLIDRDLYRSLNDPRD    |
| Target<br>5dzz. 1. A | DTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGGEVLYTDSEARDVFEKATVSAPFGKFQG--KTVTIWE<br>SQKNFVDPVTKKKVSIVQLKERCRIEPTGLLLLSV-----QKRMS-----FQGIRQPVTVTE                    |
| Target<br>5dzz. 1. A | LINSEYFTAEQRDL-----LRQFRTGKVTVEKIIKIVITVIEEHEQKGQLCFQGLRALVPAAEELLESQ---<br>LVDSGILRPSTVNELESQISYDEVGERIKDFLQGSSCIAGIYNETTKQKLGIEAMKI---GLVRPGTALELLEAQAAT            |
| Target<br>5dzz. 1. A | --IIDWDLFRQLQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVI<br>GFIVDPVSNLRLPVEEAYKRLVGIEFKEKLLSAERAVTGYNDPETGNIISLQAMNKELIEKGHGIRLLEAQIATGGII    |
| Target<br>5dzz. 1. A | DPATSARLTVDEAVRAGLVGPPELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDAQLSTGGTVDPSPK<br>DPKESHRLPVDIAYKRGYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLKERICDEETGLCLL-----           |
| Target<br>5dzz. 1. A | SHRLPLDVACARGYLDEETSTALSAPRDDAKTYYPRTWELATYSQLQQQCRPDPLTGLSLLPLSEEAAARARQQELYSEV<br>-----                                                                             |
| Target<br>5dzz. 1. A | QAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGL<br>-----                                                                             |
| Target<br>5dzz. 1. A | RAPVPASELLAAGILSSSQFEQLKDGTSVKDLSELSSLQTLLQSGCLAGIYLESKEKVTIYAMRRGLLRPSTAILL<br>-----                                                                                 |
| Target<br>5dzz. 1. A | LEAQAATGFLVDPVRNQRLYVHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLQAMKKGLVVREHGIRLLEAQ<br>-----                                                                              |
| Target<br>5dzz. 1. A | IATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEK<br>-----                                                                             |
| Target<br>5dzz. 1. A | AEVVETTRYVTEETTRAFEETQIDIPGGSGHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEK<br>-----                                                                             |
| Target<br>5dzz. 1. A | TEIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQ<br>-----                                                                             |
| Target<br>5dzz. 1. A | ALKKGLLSAEVARLLLEAQAATGFLDPVKGERLTVDEAVRKGLVGPELHDRLLSAERAVTGYRDPYTEQTISLQAMKK<br>-----                                                                               |
| Target<br>5dzz. 1. A | DLIPAEALRLLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSYTLRRCCRDE<br>-----                                                                                |
| Target<br>5dzz. 1. A | TSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSEEVSKNLQKFLEGTSSIAGVLVDATKERLS<br>-----                                                                              |

Target  
5dzz. 1. A    VYQAMKGGIIRPGTAFELLEQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQA  
-----

Target  
5dzz. 1. A    MKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERC  
-----

Target  
5dzz. 1. A    VTDPQTGLRLLPLKEKKRERKTSKSSVRKRRVVIVDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDG  
-----

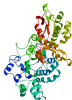
Target  
5dzz. 1. A    VVKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRQTQA  
-----

Target  
5dzz. 1. A    SWSDPTEETGPVAGILDTELEKVSITEAMHRNLVDNITGQRLLEAQAQTGGIIDPNTGERFPVTDVANKGLVDKIMVDR  
-----

Target  
5dzz. 1. A    INLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTGPRVPLDEALQRGTVDARTAQKLRDV  
-----

Target  
5dzz. 1. A    SAYSKYLTCPKTKLKISYKDALDRSMVEEGTGLRLLLEAAAQSSKGYSPYSVSGSGSTTGSRSRGTGSRAGSRRGSFDA  
-----

Target  
5dzz. 1. A    TGSGFSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA  
-----

| Model #07                                                                          | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|------------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.01 | 0.55 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range       | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|-------------|----------|-------------|
| 5dzz.1.A | 45.24        | monomer     | 0.00 | BLAST    | X-ray  | 2.60Å      | 0.40           | 1232 - 1736 | 0.17     | Desmoplakin |

The template contained no ligands.

Target  
5dzz. 1. A    RALAEAAKRQRQLAEEDAARQRAEAERVLSEKLAATSEATRLKTEAEIALKEKEAENERLRRLADEAFQRRRLEEQAQ  
-----

Target  
5dzz. 1. A    HKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEILALKASFEEAAAGKAELELELGRIRGNAEDTLRSKEQAE  
-----

Target  
5dzz. 1. A    QEAAQRQLAAEEERRRREAEEERVQKSLAAEEEAARQKAALEEVERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKR  
-----

Target  
5dzz. 1. A    LQAEEKAHAFVQKQEQELQQTQQEQSVLEKLRSEAAARRAAEEAEARERAEREAQSRQRVEEAERLKQAEEEAQ  
-----

Target  
5dzz. 1. A    AQAQAQAAAEKLRKEAEQAARRAQEAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETDHQKSILD  
-----

Target  
5dzz. 1. A    QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVA  
-----

Target  
5dzz. 1. A    AQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR  
-----

Target  
5dzz. 1. A    TLETERQRQLEMSAEERLRLRVAEMSRAQARAEEAQRFRKQAEETGAKLHRTTELATQEKVTLVQTLETQRQQSDRDAD  
-----

Target  
5dzz. 1. A    RLREATAELEREKDKLKEAEELLQLKSEEMQTVQQEQQLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAK  
-----

Target  
5dzz. 1. A    AQLREEQQRQQQMQQEQQLLASMEEARRRQHEAEEGVRRKQEELQLEQQRQQEQQLAEENRRLRERLEHLEEEHR  
-----

Target AALAHSEETAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDV  
5dzz. 1. A -----

Target RRYLQGHSSIAGLLLPANEKLTIIAALRRQLLSPGTALILLEAQAAASGFLLDPVRNRRLTVTEAVKEGVVGPELHHKLL  
5dzz. 1. A -----

Target SAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSD  
5dzz. 1. A -----

Target DTGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWEI  
5dzz. 1. A -----

Target NSEYFTAEQRDRLRQFRTGKVTVEKIIKIVITVIEEHEQKQCLCFQGLRALVPAAELLESGLIDWDLFRQLQLGERSVQ  
5dzz. 1. A -----

Target EVAEVEGVRRLRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTVDEAVRAGLVG  
5dzz. 1. A -----VFDGLRKKV-----TAMQLYECQLIDKTTLDKLLKGKKSVEE-----VA

Target PELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLDLAQSTGGTVDPSSKSHRLPLDVACARGYLDEETS  
5dzz. 1. A SEIQPFLRGAGSIAGASAPK--EKYSLVEAKRKKLISPESTVMLLEAQIATGGIIDPHRNEKLTVD SAIARDLIDFDDR

Target TALSAPRDDAKTYDPRTWELATYSQLQQCRPDPLTGLSLP-----LSEEAARAR--QQELYSEVQ  
5dzz. 1. A QQIYAAEKAITGFDDPFSGKTVSVSEAIKKNLIDRETGMRLLEAQIASGGVDPVNSVFLPKDVALARGLIDRDLYRSLN

Target AREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITIVEEVETTRRERLSFSGLR  
5dzz. 1. A DPRDSQKNFVD--PVTKKKVSIVQLKERCRIEPTG-----LLLLSVQKRSM SFQGIR

Target APVPASELLAAGILSSSQFEQLKDGT SVKDLSELSSLQTLLQGSGLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLL  
5dzz. 1. A QPVTVTELVD SGILRPSTVNELESGQISYDEVGERIKDFLQGSSCI--AGIYNETTKQKLG IYEAMKIGLVRPGTALELL

Target EAQAATGFLVDPVRNQRLVHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLQFQAMKKGLVREHGIRLLEAQI  
5dzz. 1. A EAQAATGFI VDPVSNLRLPV EEA YKRG LVGIEFKEKLLSAERAVTGYNDPETGNIISLQFQAMNKELIEKGHGIRLLEAQI

Target ATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKA  
5dzz. 1. A ATGGIIDPKESHRLPVDIAYKRGYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLKERICKEETGLCLLPLK-----

Target EVVETTRVYTEEETRRAFEETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEKT  
5dzz. 1. A -----

Target EIVRQQNLASYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGSRQTLPIYQA  
5dzz. 1. A -----

Target LKKGLLSAEVARLLLEAQIATGFLDPVKGERLTVDEAVRKG LVGPELHDLRLSAERAVTGYRDPYTEQTISLQFQAMKKD  
5dzz. 1. A -----

Target LIPAEELRLDLAQIATGGIVDPRLGFHLPLEVAYQRGYLNKDTHDQLSEPSEVRSYVDPSTDERLSYTLRLRCRRDET  
5dzz. 1. A -----

Target SGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLT SIEEVSKNLQKFLEGTSSIAGVLVDATKERLSV  
5dzz. 1. A -----

Target YQAMKKGIIIRPGTAFELLEAQIATGYVIDPIKGLKLTVEEA VRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLQFQAM  
5dzz. 1. A -----

Target KKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRG LFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERC V  
5dzz. 1. A -----

Target TDPQTGLRLLPLKEKKRERKTSKSSVRKRRVVIDPETGKEMSVYEAYRKGLIDHQTYLELSECEWEWEITISSSDGV  
5dzz. 1. A -----

Target VKSMIIDRRSGRQYDIDEAIAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISP AVSRTQLAS  
5dzz. 1. A -----

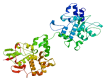
Target WSDPTEETGPVAGILDTETLEKVSITEAMHRNLVDNITGQRLLEAQACTGGIIDPNTGERFPVTD AVNKGLVDKIMVDRI  
5dzz. 1. A -----

Target NLAQKAFCGFEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTPGRVPLDEALQRGTVDART AQKLRDVS  
5dzz. 1. A -----

Target AYSKYLTCPKTKLKISYKDALDRSMVEEGTGLRLLEAAAQSSKGYSPYSVSGSGSTTGSRS GSRTGSRAGSRRG SFDAT  
5dzz. 1. A -----

Target GSGFSMTFSSSSYSSSGYGRRYASGPTSSSLGGPESAAA

5dzz. 1. A -----


| Model #09                                                                         | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|-----------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.01 | 0.55 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range      | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|------------|----------|-------------|
| 5dzz.1.A | 41.31        | monomer     | 0.00 | BLAST    | X-ray  | 2.60Å      | 0.39           | 904 - 1406 | 0.17     | Desmoplakin |

The template contained no ligands.

|                      |                                                                                                                                                                        |
|----------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Target<br>5dzz. 1. A | RALAEAAKRQRLAEEDAAARQRAEAERVLSKLA AIS EATRLKTEAEIALKEKEAENERLRR LAEDEAFQRRRL EEQAAQ<br>-----                                                                           |
| Target<br>5dzz. 1. A | HKADIEERLAQLRKASESELERQKGLVEDTLRQRQVEEEILALKASF EKAAAGKAELELELGRIRGNAEDTLRSKEQAE<br>-----                                                                              |
| Target<br>5dzz. 1. A | QEAA RQRLAAEEERRRREAEEERVQKSLAEEEEAA RQKAALEEVERLKAKVEEARRLRERAEHESVRQLQLAQEAAQKR<br>-----                                                                             |
| Target<br>5dzz. 1. A | LQAE EKAHAFVQQKEQELQQT LQQEQSVLEKL RSEAEAAARRAAEEAEARERAEREA AQSRQRVEEAERLKQA AEEQAQ<br>-----                                                                          |
| Target<br>5dzz. 1. A | AQAQAQAAAEKLRKEAEQEAAARRAQEAALRQKQAADAEMEKHKKF AEQTLRQKAQVEQELTALRLKLEETDHQKSILD<br>-----                                                                              |
| Target<br>5dzz. 1. A | QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVA<br>-----                                                                              |
| Target<br>5dzz. 1. A | AQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEAE LLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR<br>-----                                                                             |
| Target<br>5dzz. 1. A | TLETERQRQLEMSAEERLRLRVAEMSRAQARA EEDAQRFRKQAE EIGAKLHRTELATQEKVTLVQTLETQRQQSDRDAD<br>-----                                                                             |
| Target<br>5dzz. 1. A | RLREATAELEREKDKLKKEAELLQLKSEEMQTVQQEQLLQETQALQQSFLSEKDSLLQRERFIEEEKAKLERLFQDEVAK<br>-----                                                                              |
| Target<br>5dzz. 1. A | AQKLREEQQRQQQMQQEQQLLASMEEARRRQHEAEEGVRRKQEELQLLEQQRQQEQQLLA EENRRLRERLEHLEEEHR<br>-----                                                                               |
| Target<br>5dzz. 1. A | AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQ LQEAGILSTEELQRLAQGHTTV AELTQREDV<br>-----                                                                            |
| Target<br>5dzz. 1. A | RRYLQGHSSIAGLLLKPANEKLTIIYAALRRQLSPGTALILLEAQ AASGFLDPVRNRRLTVTEAVKEGVVGP ELHHKLL<br>-----VFDGLRKKV-----TAMQLYECQLIDKTTLDKLLKGKKSVEE-----VASEIQPF LR                   |
| Target<br>5dzz. 1. A | SAERAVTGYKDPYTGEKISL FQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSD<br>GAGSIAGASAPK--EKYSLVEAKRKKLISP ESTVMLLEAQATGGIIDPHRNEKLTVD SAIARDLIDFDDRQQIYAAEK  |
| Target<br>5dzz. 1. A | DTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQA AKGGELVYTDSEARDVFEKATVSAPFGKFQGKTVTI WELI<br>AITGFDDPFGSKTVSVSEAIKKNLIDRETGMRLLEA--QIASGGVDPVNS----VFLPKDVALARG-----LI        |
| Target<br>5dzz. 1. A | NSE-YFTAEQRDLLRQFRTGKVTEKIIKIVITVIEEHE-----QKGQLCFQGLRALVPAAELLES GII DWDLFR<br>DRDLYRSLNDPRDSQKNFVDPVTKKKVS YVQLKERCRIEPTG LLLLLSVQKRSM SFQGIRQPVTVTELVD SGILRPSTVN   |
| Target<br>5dzz. 1. A | QLQLGERSVQEVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPAT SARLTV<br>ELESQQISYDEVGE--RIKDFLQGSSCIAGIYNETTKQLGIYEAMKIGLV RPGTALELLEAQATGFI VDPVSNLRLPV  |
| Target<br>5dzz. 1. A | DEAVRAGLVGP ELHEKLLSAEKAVTGYKDPYSQSVSLFQALKKGLIPREQGLRLD AQLSTGGTVDP SKSHRLPLDVAC<br>EEAYKRGLVGIEFKEKLLSAERAVTGYNDPETGNIISL FQAMNKELIEKGHGIRLLEAQIATGGIIDPKESHRLPVDIAY |
| Target               | ARGYLDEETSTALSAPRDDAKTYYPDRTWELATYSQLQQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKAT                                                                                       |

5dzz. 1. A KRGYFNEELSEILSDPSDDTKGFFDPNTEENLTYLQLKERICKDEETGLCLLPLKE-----  
Target VEPVGSFQGRAVTIWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITIVEEVETRRERLSFSGLRAPVPASELL  
5dzz. 1. A -----  
Target AAGILSSSQFEQLDKGKTSVKDLSELSSLQTLQSGSCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLLEAQAATGFL  
5dzz. 1. A -----  
Target VDPVRNQRLYVHEAVKAGVVGPELHEKLLSAEKAVTGYKDPYSGSTISLQAMKKGLVREHGIRLLEAQIATGGIIDPV  
5dzz. 1. A -----  
Target HSHRPVDVACQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVDPETGLRLLPLKGPEKAEVVETTRVY  
5dzz. 1. A -----  
Target TEEETRAFEETQIDIPGGSGHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIIIIEIEIEKTEIVRQQNLA  
5dzz. 1. A -----  
Target SYDYVRRRLTAEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLSAE  
5dzz. 1. A -----  
Target VARLLLEAQAATGFLDPVKGERLTVDEAVRKGLVGPPELHDRLLSAERAVTGYRDPYTEQTISLQAMKKDLIPAEALR  
5dzz. 1. A -----  
Target LLDAQLATGGIVDPRLGFHLPLEVAYQRGYLNKDHQDQLSEPSEVRSYVDPSTDERLSYTLQLLRRCRRDETSGLFLLPLS  
5dzz. 1. A -----  
Target EARKLTFRGLRKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGII  
5dzz. 1. A -----  
Target RPGTAFELLEAQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLQAMKKGLILKDH  
5dzz. 1. A -----  
Target GIRLLEAQIATGGIIDPEESHRLPVDVAYQRGLFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRL  
5dzz. 1. A -----  
Target LPLKEKKRERKTSKSSVRKRRVVIDPETGKEMSVYEAYRKGLIDHQTYLELSEQECEWEEITISSSDGVVKSMIIDRR  
5dzz. 1. A -----  
Target SGRQYDIDEAIAKSLIDRSALDQYRAGTSLITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRTQLASWSDPTEETG  
5dzz. 1. A -----  
Target PVAGILDTETLEKVSITEAMHRNLVDNITGQRLLAEQACTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFGC  
5dzz. 1. A -----  
Target FEDPRTKTKMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDTGRVPLDEALQRGTVDARTAQKL RDVSAYS KYLTC P  
5dzz. 1. A -----  
Target KTKLKISYKDALDRSMVEEGTGLRLLLEAAAQSSKGYSPYSVSGSGSTTGSRSRTGSRAGSRRGSFDTGSGFSMTFS  
5dzz. 1. A -----  
Target SSSYSSSGYGRRYASGPTSSLGGPESAAA  
5dzz. 1. A -----

| Model #10                                                                           | File | Built with    | Oligo-State | Ligands | GMQE | QMEANDisCo Global |
|-------------------------------------------------------------------------------------|------|---------------|-------------|---------|------|-------------------|
|  | PDB  | ProMod3 3.3.0 | monomer     | None    | 0.00 | 0.37 ± 0.05       |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Range       | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|-------------|----------|-------------|
| 5dzz.1.A | 35.94        | monomer     | 0.00 | BLAST    | X-ray  | 2.60Å      | 0.37           | 2386 - 2660 | 0.08     | Desmoplakin |

The template contained no ligands.



|                      |                                                                                    |
|----------------------|------------------------------------------------------------------------------------|
| Target<br>5dzz. 1. A | RALAEAEKRQRQLAEEDAAQRRAEAERVLSKLAATSEATRLKTEAEIALKEKEAENERLRRLAEDEAFQRRRLEEQAQ     |
| Target<br>5dzz. 1. A | HKADIEERLAQLRKASESELERQKGLVEDTLRQRRQVEEEILALKASFEKAAAGKAELELELGRIRGNAEDTLRSKEAQE   |
| Target<br>5dzz. 1. A | QEAAQRQLAAEEERRRREAEEERVQKSLAAEEEAARQRKAALEEVERLKAKVEEARRLRERAHEHSVRQLQLAQEAAQKR   |
| Target<br>5dzz. 1. A | LQAEKKAHAFVQKKEQELQQTLLQEQSVLEKLRSEAEARRAAEEEAERERAEREAQSRQRVEEAERLKQAABEEQAQ      |
| Target<br>5dzz. 1. A | AQAQAQAAAEKLRKEAEQEARRAQAEQAALRQKQAADAEMEKHKKFAEQTLRQKAQVEQELTALRLKLEETHQKSILD     |
| Target<br>5dzz. 1. A | QELQRLKAEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLLQEEAEKMKQVAEEAARLSVA   |
| Target<br>5dzz. 1. A | AQEAARLRQLAEEDLAQQRALAEKMLKEKMQAVQEATRLKAEALLQQQKELAQEQARRLQEDKEQMAQQLAQETQGFQR    |
| Target<br>5dzz. 1. A | TLETERQRQLEMSAEERLRLRVAEMSRAQARAEEDAQRFRKQAEIIGAKLHRTTELATQEKVTLVQTLETQRQQSDRDAD   |
| Target<br>5dzz. 1. A | RLREATAELEREKDKLKKEAELLQLKSEEMQTVQEQQLQETQALQQSFLSEKDSLLQRRERFIEEEKAKLERLFQDEVAK   |
| Target<br>5dzz. 1. A | AQKLREEQQRQQMQQEKQQLLASMEEARRRQHEAEEGVRRKQEELQLEQQRQQEQQLAEENRRLRERLEHLEEEHR       |
| Target<br>5dzz. 1. A | AALAHSEEITAAQAAATRALPNGQDAADGPAAEPEHAFEGLRQKVPAQQLQEAGILSTEELQRLAQGHTTVAELTQREDV   |
| Target<br>5dzz. 1. A | RRYLQGHSSIAGLLLKPANEKLTIIYAALRRQLLSPGTALILLEAQAASGFLLDPVRNRRLTVTEAVKEGVVGPETHHKL   |
| Target<br>5dzz. 1. A | SAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEAQIATGGVIDPVHSHRVPVDVAYHRYGFDEEMNRVLQDPSD  |
| Target<br>5dzz. 1. A | DTKGFFDPNTHENLTYLQLLERCVEDPETGLRLLPLTDQAAKGELVYTDSEARDVFEKATVSAPFGKFQGKTVTIWELI    |
| Target<br>5dzz. 1. A | NSEYFTAEQRDDLRLQFRTGKVTVEKIIKIVITVIEEHEQKGLCFQGLRALVPAAELLESGLIDWDLFRQLQLGERSVQ    |
| Target<br>5dzz. 1. A | EVAEVEGVRRALRGSGVIAGVWLEEARQKLSIYEALKKELLQPEAAVALLEAQAGTGHVIDPATSARLTVDEAVRAGLVG   |
| Target<br>5dzz. 1. A | PELHEKLLSAEKAVTGYKDPYSGQSVSLFQALKKGLIPREQGLRLLDAQLSTGGTVDPKSHRPLDVACARGYLDEETS     |
| Target<br>5dzz. 1. A | TALSAPRDDAKTYDPRTWELATYSQLQQCRPDPLTGLSLLPLSEEAARARQQELYSEVQAREAFQKATVEVPVGSFQG     |
| Target<br>5dzz. 1. A | RAVTIWELINSEYFTAEQRQELLRLQFRTGKVTVEKIIKIVITVIEEVETRRERLSFSGLRAPVPASELLAAGILSSSQF   |
| Target<br>5dzz. 1. A | EQLKDGTKSVKDLSELSSLQTLQGGSGCLAGIYLESKEKVTIYEAMRRGLLRPSTAILLLEQAATGFLVDPVRNQRLY     |
| Target<br>5dzz. 1. A | VHEAVKAGVVGPETHKLLSAEKAVTGYKDPYSGSTISLQFQAMKKGLVREHGIRLLEAQIATGGIIDPVHSHRVPVDVA    |
| Target<br>5dzz. 1. A | CQRGYFDEEMNRVLEDPSDDTKGFFDPNTHENLTYRQLLERCVEDPETGLRLLPLKGPEKAEVVETTRVYTEEETTRAPE   |
| Target<br>5dzz. 1. A | ETQIDIPGGGSHGGSTMSLWEVMQSDLIPEEQRAQLMADFQAGRVTKERMIIEIEIEKTEIVRQQNLASYDYVRRRLT     |
| Target<br>5dzz. 1. A | AEDLYEARVISRESYSLLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPQSRQTLPIYQALKKGLLSAEVARLLLEAQA   |
| Target<br>5dzz. 1. A | ATGFLLDVPVKGERLTVDEAVRKGLVGPETHDRLLSAERAVTGYRDPYTEQTISLQFQAMKKDLIPAAEALRLLDAQLATGG |

|            |                                                                                   |
|------------|-----------------------------------------------------------------------------------|
| Target     | IVDPRLGFHLPLEVAYQRGYLNKDHQDLSEPSEVRSYVDPSTDERLSYQQLLRRCRRDETSGLFLLPLSEARKLTFRGL   |
| 5dzz. 1. A | -----                                                                             |
| Target     | RKQITVEELVRSHVMDEATAQRLQEGLTSIEEVSKNLQKFLEGTSSIAGVLVDATKERLSVYQAMKKGIIIRPGTAFELLE |
| 5dzz. 1. A | -----                                                                             |
| Target     | AQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKDKLLSAERAVTGYKDPYSGKLISLFQAMKKGLILKDHGIRLLEAQIA  |
| 5dzz. 1. A | -----                                                                             |
| Target     | TGGIIDPEESHRLPVDVAYQRLGFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQLMERCVTDPQTGLRLLPLKEKKRER  |
| 5dzz. 1. A | -----IIDPHRNEKLTVDSA                                                              |
| Target     | IAKSLIDRSALDQYRAGTLSITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRQLASWSDPTEETGPVAGILDTET   |
| 5dzz. 1. A | IARDLIDFDDRQIYAAEKAITGFDDPFSGKT-----                                              |
| Target     | LEKVSITEAMHRNLVDNITGQRLLAQACTGGIIDPNTGERFPVTDVANKGLVDKIMVDRINLAQKAFCGFEDPRTKTKM   |
| 5dzz. 1. A | ---VSVSEAIKKNLIDRETGMRLLEAQIASGGVVDPVNSVFLPKDVALARGLIDRDLYRSLNDPRDSQKNFVDPVTKKKV  |
| Target     | SAAQALKKGWLYYEAGQRFLVQ-----YLTGGLIEPDT-----PGRVPLDEALQRGTVDARTAKLR                |
| 5dzz. 1. A | SYVQLKERCRIEPHTGLLLSVQKRSMFQGIQPVTVTELVDGILRPSTVNELESQQISYDE-----VGERIKDFLQ       |
| Target     | DVSAYSKYLTCPKTKLKISYKDALDRSMVEEGTGLRLLAAQSSKGYSPYSVSGSGSTTGSRSGSRTGSRAGSRRGSF     |
| 5dzz. 1. A | GSSCIAGIYN-ETTKQLGIYEAMKIGLVRPGTALELLEAQA-----                                    |
| Target     | DATGSFGSMTFSSSSYSSSGYGRRYASGPTSSLGGPESAAA                                         |
| 5dzz. 1. A | -----                                                                             |

## 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>](#)
- **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>](#)

Table T1:

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

RALAEAAKRRQRLAEEDAAARQRAEAERVLSEKLAAISEATRLKTEAEIALKEKEAENERLRLRLAEDEAFQRRRLLEEQAQHKADIEERLAQLRKASESEL  
ERQKGLVEDTLRQRRQVEEIIALKASFEEKAAAGKAELELELGRIRGNAEDTLRSKEQAEQEAARQRLAAEEERRRREAEEERVQKSLAAEEEAARQRKA  
ALEEVERLAKVVEEARLRERAEHESVRQLQLAQEAQKRLQAEKKAHAFVQQKEQLQQLTQQEQSVLEKLRSEAAARRAAEEEAERERAEERAAQ  
SRQRVEEAERLKQAAEEQAQAQAQAQAAAEKLKEAEQEAARRAQEAQALRQKQAADAEMEKKHKAFAEQTLRQKAQVEQELTALRLKLEETDHQKSILD  
QELQRLKAIEVTEAARQRSQVEEELFSVRVQMEELGKLKARIEAENRALILRDKDNTQRLQEEAEKMKQVAEEAARLSVAQEAARLRQLAEEDLAQQR  
LAEKMLKEKMQAVQEATRLKAEAEELLQQQKELAQEQARRLQEDKEQMAQQQLAQETQGFQRTLETERQRQLEMSAEERLRLRVAEMSRAQARAEEEDAQR  
RKQAEETGAKLHRTTELATQEKVTLVQTLETQRQQSDRDADRLREATAELEREKDKLKEAEELLQLKSEEMQTVQQEQQLQETQALQQSFLSEKDSLLQRE  
RFIEEEKAKLERLFQDEVAKAQKLREEQQRQQQQMQQEQQLLASMEEARRRQHEAEEGVRRKQEEQLQLEQQRQQEQQLLAEENRRLRERLEHLEEEHR  
AALAHSEIITAQAATRALPNEGDAADGPAEPEHAFEGFLRQKVPAAQQLQEQAGILSTEELQRLAQGHHTVAELTQREDVRRYLQGHSSIAGLLLKPA  
KLTIIYAALRRQLLSPGTALILLEAQAASGFLDLPVRNRLTVTEAVKEGVGPELHHKLLSAERAVTGYKDPYTGEKISLQFQAMKKDLIVREHGIRLLEA  
QIATGGVIDPVHSHRVPVDVAYHRGYFDEEMNRVLQDPSDDTKGFFDPNTHENLTYLQLLERCVEDEPETGLRLLPLTDQAAKGGLVYTDSEARDVFEKA  
TVSAPFGKFGQKTVTIWELINSEYFTAEQRDLRLRQFRTGKVTVEKIIKIVITVIEEHEQKQQLCFQGLRALVPAEELLESIGIIDWDLFRQLQLGERSVQ  
EVAEVEGVRRLRGSGVIAGVWLEEARQKLSIYEALKKELQPEAAVALLEAQAGTGHVIDPAT SARLTVD EAVRAGLVGPPELHEKLLSAEKAVTGYKDP  
YSGQSVSLFQALKKGLIPREQGLRLLDAQLSTGGTVDPKSHRLPLDVCARGYLDEETSTALSAPRDDAKTYDPRTWELATYSQLQQQCRPDPLTGLS  
LLPLSSEAAARQQLYSEVQAREAFQKATVEVPVGSFQGRAVTIWELINSEYFTAEQRQELLRQFRTGKVTVEKIIKIVITVIEEVETTRRERLSFSG  
RAPVPASELLAAGILSSSQFEQLKDGKTSVKDLSELSSQLTLLQSGGCLAGIYLEESKEKVTIYEAMRRGLLRPSTAILLEAQAAATGFLVDPVRNQR  
VHEAVKAGVGPPELHEKLLSAEKAVTGYKDPYSGSTISLQFQAMKKGLVVRHGHIRLLEAQIATGGIIDPVHSHRVPVDVACQRGYFDEEMNRVLEDP  
TKGFFDPNTHENLTYRQLLERCVEDEPETGLRLLPLKGPKEAEVVETTRVYTEEETRAFEETQIDIPGGGSHGGSTMSLWEVMSDLIPPEQRAQLMA  
QAGRVTKERMIIIIIEIEKTEIVRQQLNASYDYVRRRLTAEDLYEARVISRESYSLREGTRSLREVLEAESAWRYLYGTGCVAGVYLPGRSQTLP  
ALKKGLLSAEVARLLLEAQAAATGFLDLPVKGERLTVDEAVRKGVLGPPELHDLRLLSAERAVTGYRDPYTEQTIISLQFQAMKKDLIPAEALRL  
LDAQLATGGI  
IVDPRGLFHLPLEVAYQRYGLNKDTHDQLEPSEVRSYVDPSTDERLSYTLQLRRCRDETSGLFLLPLSEARKLTFRGLRKQITVEELVRSHVMD  
EATA  
QRLQEGTSLIEEVSKNLFLEGTSSIAGVLVDATKERLSVYQAMKKGIIRPGTAFELLEQAATGYVIDPIKGLKLTVEEAVRMGIVGPEFKLLS  
AE  
RAVTGYKDPYSGKLSLQFQAMKKGLILKDHGIRLLEAQIATGGIIDPEESHRLPVDVAYQRLGFDEEMNEILTDPSDDTKGFFDPNTEENLTYLQ  
LMERC  
VTDPQTGLRLLPLKEKKRERKTSKSSSVRKRVRVIVDPETGKEMSVYAYRKGILDHQTYLLELSEQCEWEEITISSSDGVVKSMTIDRRSGRQYD  
IDEA  
IAKSLIDRSALDQYRAGTSLITEFADMLSGNAGGFRSRSSSVGSSSSYPISPAVSRQTQLASWSDPTEETGPVAGILDTELEKVSITEAMHRN  
LVDNITG  
QRLLEAQACTGGIIDPNTEGRFPVTDVANKGLVDKIMVDRINLAQKAFCEFDPRTKTMSAAQALKKGWLYYEAGQRFLEVQYLTGGLIEPDT  
PGRVPL  
DEALQRTGTDARTAQKLRDVSAYSKYLTCPKTKLKSISKDALDRSMVEEGTGLRLLLEAAQSSKGYSPYVSVSGSTTSGRSRSGTSGRAGS  
RGSFDA  
TGSGFSMTFSSSSSYSSSGYGRYASGPTSSSLGGPESAAA

Table T2:

| Template   | Seq Identity | Oligo-state | QSQE | Found by    | Method       | Resolution | Seq Similarity | Coverage | Description                                             |
|------------|--------------|-------------|------|-------------|--------------|------------|----------------|----------|---------------------------------------------------------|
| H9FGT6.1.A | 90.19        | monomer     | -    | AFDB search | AlphaFold v2 | NA         | 0.57           | 0.43     | Plectin isoform 1a                                      |
| 5dzz.1.A   | 51.24        | monomer     | -    | HHblits     | X-ray        | 2.60Å      | 0.45           | 0.18     | Desmoplakin                                             |
| 5dzz.1.A   | 54.32        | monomer     | -    | HHblits     | X-ray        | 2.60Å      | 0.45           | 0.18     | Desmoplakin                                             |
| 5dzz.1.A   | 51.48        | monomer     | -    | BLAST       | X-ray        | 2.60Å      | 0.45           | 0.17     | Desmoplakin                                             |
| 5dzz.1.A   | 47.22        | monomer     | -    | HHblits     | X-ray        | 2.60Å      | 0.42           | 0.18     | Desmoplakin                                             |
| 5dzz.1.A   | 38.27        | monomer     | -    | HHblits     | X-ray        | 2.60Å      | 0.38           | 0.18     | Desmoplakin                                             |
| 1lm7.1.A   | 63.75        | homo-dimer  | 0.08 | HHblits     | X-ray        | 3.00Å      | 0.48           | 0.09     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm7.1.A   | 65.56        | homo-dimer  | 0.09 | HHblits     | X-ray        | 3.00Å      | 0.50           | 0.09     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 2n03.1.A   | 99.02        | monomer     | -    | BLAST       | NMR          | NA         | 0.61           | 0.07     | Plectin                                                 |
| 2n03.1.A   | 99.01        | monomer     | -    | HHblits     | NMR          | NA         | 0.61           | 0.07     | Plectin                                                 |
| 1lm7.1.A   | 64.66        | homo-dimer  | 0.09 | BLAST       | X-ray        | 3.00Å      | 0.50           | 0.08     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm7.1.A   | 62.34        | homo-dimer  | 0.07 | BLAST       | X-ray        | 3.00Å      | 0.47           | 0.09     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 5dzz.1.A   | 61.34        | monomer     | -    | BLAST       | X-ray        | 2.60Å      | 0.47           | 0.09     | Desmoplakin                                             |
| 5dzz.1.A   | 47.54        | monomer     | -    | BLAST       | X-ray        | 2.60Å      | 0.43           | 0.09     | Desmoplakin                                             |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Coverage | Description                                             |
|----------|--------------|-------------|------|----------|--------|------------|----------------|----------|---------------------------------------------------------|
| 1lm7.1.A | 60.58        | homo-dimer  | 0.07 | BLAST    | X-ray  | 3.00Å      | 0.47           | 0.09     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 5dzz.1.A | 44.92        | monomer     | -    | BLAST    | X-ray  | 2.60Å      | 0.42           | 0.09     | Desmoplakin                                             |
| 1lm5.1.B | 62.74        | homo-dimer  | 0.08 | HHblits  | X-ray  | 1.80Å      | 0.49           | 0.08     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm7.1.A | 47.93        | homo-dimer  | -    | BLAST    | X-ray  | 3.00Å      | 0.43           | 0.09     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm7.1.A | 51.87        | homo-dimer  | -    | HHblits  | X-ray  | 3.00Å      | 0.44           | 0.09     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 5dzz.1.A | 45.93        | monomer     | -    | BLAST    | X-ray  | 2.60Å      | 0.41           | 0.10     | Desmoplakin                                             |
| 1lm5.1.A | 62.74        | homo-dimer  | 0.08 | HHblits  | X-ray  | 1.80Å      | 0.49           | 0.08     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm5.1.B | 62.81        | homo-dimer  | 0.09 | BLAST    | X-ray  | 1.80Å      | 0.49           | 0.07     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm7.1.A | 52.08        | homo-dimer  | -    | BLAST    | X-ray  | 3.00Å      | 0.44           | 0.09     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm5.1.A | 62.81        | homo-dimer  | 0.09 | BLAST    | X-ray  | 1.80Å      | 0.49           | 0.07     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 5dzz.1.A | 45.24        | monomer     | -    | BLAST    | X-ray  | 2.60Å      | 0.40           | 0.17     | Desmoplakin                                             |
| 4qmd.1.A | 38.62        | monomer     | -    | HHblits  | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 5dzz.1.A | 42.68        | monomer     | -    | BLAST    | X-ray  | 2.60Å      | 0.40           | 0.09     | Desmoplakin                                             |
| 5dzz.1.A | 37.12        | monomer     | -    | BLAST    | X-ray  | 2.60Å      | 0.38           | 0.17     | Desmoplakin                                             |
| 4qmd.1.A | 39.46        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.39           | 0.07     | Envoplakin                                              |
| 4qmd.2.A | 38.62        | monomer     | -    | HHblits  | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 4qmd.1.A | 47.09        | monomer     | -    | HHblits  | X-ray  | 1.60Å      | 0.42           | 0.07     | Envoplakin                                              |
| 4qmd.1.A | 37.30        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 4qmd.1.A | 37.37        | monomer     | -    | HHblits  | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 4qmd.2.A | 39.46        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.39           | 0.07     | Envoplakin                                              |
| 4qmd.1.A | 46.63        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.42           | 0.07     | Envoplakin                                              |
| 4qmd.1.A | 37.63        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 5dzz.1.A | 41.31        | monomer     | -    | BLAST    | X-ray  | 2.60Å      | 0.39           | 0.17     | Desmoplakin                                             |
| 4qmd.2.A | 47.09        | monomer     | -    | HHblits  | X-ray  | 1.60Å      | 0.42           | 0.07     | Envoplakin                                              |
| 4qmd.2.A | 46.63        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.42           | 0.07     | Envoplakin                                              |
| 4qmd.1.A | 37.10        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 4qmd.2.A | 37.37        | monomer     | -    | HHblits  | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 4qmd.2.A | 37.63        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 4qmd.2.A | 37.10        | monomer     | -    | BLAST    | X-ray  | 1.60Å      | 0.38           | 0.07     | Envoplakin                                              |
| 1lm5.1.A | 29.95        | homo-dimer  | -    | HHblits  | X-ray  | 1.80Å      | 0.35           | 0.07     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm5.1.B | 29.95        | homo-dimer  | -    | HHblits  | X-ray  | 1.80Å      | 0.35           | 0.07     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm5.1.B | 27.84        | homo-dimer  | -    | BLAST    | X-ray  | 1.80Å      | 0.36           | 0.07     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 2n03.1.A | 35.53        | monomer     | -    | HHblits  | NMR    | NA         | 0.36           | 0.07     | Plectin                                                 |
| 1lm5.1.A | 27.84        | homo-dimer  | -    | BLAST    | X-ray  | 1.80Å      | 0.36           | 0.07     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |
| 1lm7.1.A | 32.07        | homo-dimer  | -    | HHblits  | X-ray  | 3.00Å      | 0.35           | 0.09     | subdomain of Desmoplakin Carboxy-Terminal domain (DPCT) |

| Template | Seq Identity | Oligo-state | QSQE | Found by | Method | Resolution | Seq Similarity | Coverage | Description |
|----------|--------------|-------------|------|----------|--------|------------|----------------|----------|-------------|
| 5dzz.1.A | 35.94        | monomer     | -    | BLAST    | X-ray  | 2.60Å      | 0.37           | 0.08     | Desmoplakin |

The table above shows the top 50 filtered templates. A further 544 templates were found which were considered to be less suitable for modelling than the filtered list.

1d7m.1.A, 1d7m.1.B, 1lm5.1.A, 1lm5.1.B, 1lm7.1.A, 2b9c.1.A, 2b9c.1.B, 2d3e.1.A, 2d3e.1.B, 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, 2efr.1.A, 2efr.1.B, 2efs.1.A, 2efs.1.B, 2fxm.1.A, 2fxm.1.B, 2fxo.1.A, 2fxo.1.B, 2fxo.2.A, 2fxo.2.B, 2i1k.1.A, 2n03.1.A, 2ocy.1.A, 2ocy.1.B, 2oto.1.A, 2oto.1.B, 2oto.2.A, 2oto.2.B, 2v66.1.A, 2v66.1.B, 2v66.1.C, 2v66.1.D, 2w4u.1.K, 2w4u.1.L, 3cl3.1.C, 3cl3.1.D, 3dtp.1.A, 3dtp.1.B, 3jax.1.A, 3jax.1.B, 3o0z.1.A, 3o0z.1.B, 3o0z.2.A, 3o0z.2.B, 3oja.1.B, 3vkg.1.A, 3vkg.1.B, 3vkh.1.A, 3vkh.2.A, 4a7f.1.B, 4a7f.1.H, 4gkw.1.A, 4gkw.1.B, 4ll8.1.B, 4ll8.1.C, 4mh6.1.A, 4q28.1.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, 4whe.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, 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, 5ijn.1.F, 5ijn.1.G, 5ijn.1.H, 5ijn.1.L, 5ijn.1.R, 5nen.1.A, 5nen.1.B, 5nug.1.A, 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, 5wjb.1.A, 5wjb.1.B, 5wlq.1.A, 5wlz.1.A, 5wlz.1.B, 5wlz.1.C, 5wlz.1.D, 5y05.1.A, 6f1t.1.U, 6f1t.1.h, 6h2x.1.A, 6ian.1.A, 6ian.1.B, 6ian.2.A, 6ian.2.B, 6ixv.1.A, 6ixv.2.A, 6ixv.3.A, 6ixv.4.A, 6jlb.1.A, 6jlb.1.B, 6jlb.1.C, 6jlb.1.D, 6l5j.1.A, 6l5j.1.B, 6l5j.2.A, 6l5j.2.B, 6mi3.1.A, 6mi3.1.B, 6mi4.1.A, 6mi4.1.B, 6pf2.1.A, 6pf2.1.B, 6pfp.1.A, 6pfp.1.B, 6pfp.2.A, 6pfp.2.B, 6snz.1.A, 6snz.1.B, 6snz.2.A, 6snz.2.B, 6u42.439.A, 6u42.440.A, 6vzf.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, 6ys4.1.B, 6ys4.2.A, 6ys4.2.B, 6ys4.3.A, 6ys4.3.B, 6z26.1.A, 6z26.1.B, 6z26.2.A, 6z26.2.B, 6z6f.1.C, 6z6f.1.D, 6z6h.1.C, 6z6h.1.D, 6z6o.1.C, 6z6o.1.D, 6z6p.1.C, 6z6p.1.D, 6z9l.1.A, 6zbc.1.A, 6zbe.1.A, 6znm.1.H, 6znm.1.J, 6zpm.1.A, 6zpm.1.B, 6zyw.1.B, 6zyw.1.C, 7abk.1.A, 7d9n.1.A, 7d9n.1.B, 7dl2.1.A, 7dl2.1.D, 7ju4.1.A, 7ju4.1.E, 7ju4.1.J, 7ju4.1.K, 7k58.1.A, 7k58.1.B, 7k58.1.D, 7k5b.1.A, 7k5b.1.B, 7k5b.1.C, 7kek.1.A, 7kek.1.D, 7ko4.1.P, 7ko4.1.Q, 7ko5.1.P, 7ko5.1.Q, 7kog.1.A, 7kog.1.B, 7kzm.1.6, 7kzm.1.O, 7kzm.1.Q, 7moq.1.C, 7moq.1.X, 7moq.1.Z, 7n85.1.E, 7n85.1.H, 7n85.1.K, 7n85.1.N, 7n9f.1.4, 7n9f.1.5, 7n9f.1.8, 7n9f.1.9, 7n9f.1.E, 7n9f.1.H, 7n9f.1.K, 7n9f.1.N, 7nyw.1.B, 7nyx.1.A, 7nyx.1.B, 7nyy.1.A, 7nyy.1.B, 7nyz.1.B, 7nz0.1.A, 7nz0.1.B, 7nz3.1.A, 7o3w.1.A, 7o3w.1.B, 7o3w.1.C, 7o3w.1.D, 7o3w.1.E, 7o3w.1.F, 7o3x.1.A, 7o3x.1.B, 7o3x.1.C, 7o3x.1.D, 7o3x.1.E, 7o3x.1.F, 7o3y.1.A, 7o3y.1.B, 7o3y.1.C, 7o3y.1.E, 7o3y.1.F, 7o3z.1.A, 7o3z.1.B, 7o3z.1.C, 7o3z.1.D, 7o3z.1.E, 7o3z.1.F, 7o40.1.A, 7o40.1.B, 7o40.1.C, 7o40.1.D, 7o40.1.E, 7o40.1.F, 7ogt.1.B, 7per.1.G, 7per.1.J, 7qcd.1.A, 7qcd.1.B, 7r5k.43.A, 7r5k.49.A, 7r5k.53.A, 7r5k.54.A, 7r5k.94.A, 7r5k.95.A, 7rro.121.A, 7rro.122.A, 7rro.123.A, 7rro.153.A, 7rro.154.A, 7rro.156.A, 7rro.157.A, 7rro.158.A, 7rro.56.A, 7rro.57.A, 7rro.58.A, 7rro.61.A, 7rro.62.A, 7rro.63.A, 7tbi.50.A, 7tbi.51.A, 7tdz.1.3, 7tdz.1.5, 7tve.1.D, 7ung.57.A, 7ung.58.A, 7ung.59.A, 7uti.1.Q, 7uti.1.R, 7uti.1.S, 7uti.1.T, 7uw5.1.A, 7ux1.1.A, 7vf2.1.C, 7vf2.1.D, 7vf5.1.B, 7vf5.1.C, 7vop.1.0, 7vop.1.2, 7vop.1.4, 7vop.1.5, 7wkk.1.G, 7wkk.1.I, 7wkk.1.J, 7wkk.1.L, 7wkk.1.U, 7wkk.1.X, 7woo.1.H, 7wot.1.W, 7yg4.1.B, 7yg4.1.C, 7z8f.1.0, 7z8f.1.7, 7z8f.1.8, 7z8f.1.Z, 7zr1.1.C, 7zr1.1.D, 8aud.1.A, 8bd7.1.G, 8bwy.1.B, 8bwy.1.C, 8bx8.1.A, 8bx8.1.B, 8dd0.1.G, 8dd0.1.H, 8dzz.1.A, 8g4l.100.A, 8g4l.101.A, 8g4l.102.A, 8g4l.104.A, 8g4l.118.A, 8g4l.17.A, 8g4l.18.A, 8g4l.19.A, 8g4l.20.A, 8g4l.21.A, 8g4l.22.A, 8g4l.35.A, 8g4l.36.A, 8g4l.58.A, 8g4l.59.A, 8g4l.60.A, 8g4l.61.A, 8g4l.62.A, 8g4l.63.A, 8g4l.76.A, 8g4l.77.A, 8g4l.99.A, 8glv.195.A, 8glv.215.A, 8glv.216.A, 8glv.217.A, 8glv.218.A, 8glv.346.A, 8glv.347.A, 8glv.357.A, 8glv.358.A, 8glv.359.A, 8glv.360.A, 8glv.420.A, 8glv.421.A, 8glv.455.A, 8glv.456.A, 8glv.492.A, 8glv.498.A, 8glv.530.A, 8glv.531.A, 8glv.542.A, 8glv.554.A, 8glv.602.A, 8glv.603.A, 8glv.756.A, 8glv.844.A, 8glv.854.A, 8glv.891.A, 8glv.902.A, 8glv.913.A, 8glv.953.A, 8glv.959.A, 8glv.960.A, 8glv.962.A, 8glv.966.A, 8i7o.47.A, 8i7o.48.A, 8i7o.49.A, 8i7o.56.A, 8i7o.57.A, 8i7o.59.A, 8i7r.107.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.129.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, 8iah.1.5, 8iah.1.6, 8iah.1.7, 8iai.1.2, 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, 8j07.1.A, 8j07.163.A, 8j07.2.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, 8j07.859.A, 8j07.860.A, 8j07.861.A, 8j07.863.A, 8j07.864.A, 8j07.868.A, 8j07.876.A, 8j07.877.A, 8j07.894.A, 8j07.896.A, 8j07.899.A, 8j07.908.A, 8j07.916.A, 8j07.935.A, 8j07.937.A, 8j07.954.A, 8j07.956.A, 8j07.963.A, 8j07.965.A, 8p4y.1.A, 8q4g.1.G, 8q4g.1.H, 8q6t.1.A, 8q6t.1.B, 8q6t.1.H, 8q6t.1.N, 8q6t.1.O, 8q6t.1.Q, 8srq.1.H, 8tek.1.D, 8tek.1.F, 8tek.1.H, 8th8.1.A, 8th8.1.D, 8th8.1.E, 8th8.1.K, 8th8.1.P, 8th8.1.R, 8tid.1.2, 8tid.1.3, 8tid.1.A, 8tid.1.D, 8tid.1.E, 8tid.1.K, 8tid.1.N, 8tid.1.P, 8tid.1.S, 8tj5.1.U, 8tj5.1.b, 8to0.397.A, 8to0.398.A, 8to0.400.A, 8to0.409.A, 8to0.410.A, 8to0.412.A, 8to0.415.A, 8tv1.1.A, 8u95.1.A, 8u95.1.B