

# Phyre2.2

Email katiecmorrison@gmail.com

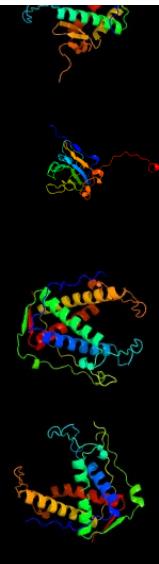
Description 5GKY\_1\_Chains\_A\_C\_E\_G\_Ryanodine\_receptor\_1\_Oryctolagus\_cuniculus\_9986\_

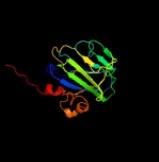
Date Tue Oct 21 22:34:15 BST 2025

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Detailed template information

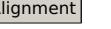
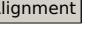
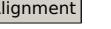
| #  | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information  |
|----|----------|--------------------|----------|------------|--------|---|
| 1  | c8vjkA_  |                    |          | 100.0      | 98     | PDB header: membrane protein<br>Chain: A: PDB Molecule: Ryanodine receptor 1<br>PDBTitle: structure of mouse ryr1 (high-ca2+/cff/atp dataset)<br>PDB Entry: PDBe RCSB PDBJ  |
| 2  | c8vjkH_  |                    |          | 100.0      | 98     | PDB header: membrane protein<br>Chain: H: PDB Molecule: Ryanodine receptor 1<br>PDBTitle: structure of mouse ryr1 (high-ca2+/cff/atp dataset)<br>PDB Entry: PDBe RCSB PDBJ  |
| 3  | c9c1eB_  |                    |          | 100.0      | 72     | PDB header: membrane protein<br>Chain: B: PDB Molecule: Ryanodine receptor 3<br>PDBTitle: mink ryr3 in closed conformation<br>PDB Entry: PDBe RCSB PDBJ   |
| 4  | c8tk8D_  |                    |          | 100.0      | 22     | PDB header: transport protein<br>Chain: D: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 3<br>PDBTitle: human type 3 ip3 receptor - resting state (+ip3/atp)<br>PDB Entry: PDBe RCSB PDBJ  |
| 5  | c8tk8A_  |                    |          | 100.0      | 22     | PDB header: transport protein<br>Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 3<br>PDBTitle: human type 3 ip3 receptor - resting state (+ip3/atp)<br>PDB Entry: PDBe RCSB PDBJ  |
| 6  | c6mu2A_  |                    |          | 100.0      | 22     | PDB header: membrane protein<br>Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1<br>PDBTitle: structure of full-length ip3r1 channel in the apo-state<br>PDB Entry: PDBe RCSB PDBJ  |
| 7  | c6uqkA_  |                    |          | 100.0      | 22     | PDB header: transport protein<br>Chain: A: PDB Molecule: inositol 1, 4, 5-triphosphate receptor, type 3<br>PDBTitle: cryo-em structure of type 3 ip3 receptor revealing presence of a self-binding peptide<br>PDB Entry: PDBe RCSB PDBJ                       |
| 8  | c4jkkA_  |                    |          | 100.0      | 71     | PDB header: unknown function<br>Chain: A: PDB Molecule: Ryanodine receptor 2<br>PDBTitle: crystal structure of the n-terminal region of the human ryanodine receptor 2<br>PDB Entry: PDBe RCSB PDBJ   |
| 9  | c5xa0A_  |                    |          | 100.0      | 20     | PDB header: metal transport<br>Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1<br>PDBTitle: crystal structure of inositol 1,4,5-trisphosphate receptor cytosolic domain<br>PDB Entry: PDBe RCSB PDBJ                                   |
| 10 | c5xa0B_  |                    |          | 100.0      | 20     | PDB header: metal transport<br>Chain: B: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1<br>PDBTitle: crystal structure of inositol 1,4,5-trisphosphate receptor cytosolic domain<br>PDB Entry: PDBe RCSB PDBJ                                   |
| 11 | c5xa1A_  |                    |          | 100.0      | 20     | PDB header: metal transport<br>Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1<br>PDBTitle: crystal structure of inositol 1,4,5-trisphosphate receptor cytosolic domain with inositol 1,4,5-trisphosphate<br>PDB Entry: PDBe RCSB PDBJ |
| 12 | c5xa0A_  |                    |          | 100.0      | 20     | PDB header: contractile protein<br>Chain: A: PDB Molecule: Ryanodine receptor 1   |

|    |         |                           |   |       |    |   |
|----|---------|---------------------------|---|-------|----|---|
| 12 | c0cova_ | <a href="#">Alignment</a> |   | 99.9  | 50 | PDB header: transport protein<br>Chain: A: PDB Molecule: Ryanodine receptor 1<br>PDBTitle: crystal structure of rabbit ryanodine receptor 1 repeat12 domain<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>          |
| 13 | c4p9jA_ | <a href="#">Alignment</a> |  | 99.9  | 99 | PDB header: transport protein<br>Chain: A: PDB Molecule: Ryanodine receptor 1<br>PDBTitle: crystal structure of rabbit ryanodine receptor 1 spry2 domain (1070-1246)<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a> |
| 14 | c6uheC_ | <a href="#">Alignment</a> |  | 100.0 | 71 | PDB header: metal transport<br>Chain: C: PDB Molecule: Ryanodine receptor 3<br>PDBTitle: closed-form crystal structure of human ryr receptor 3 (848-1055)<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>            |
| 15 | c6uhA_  | <a href="#">Alignment</a> |  | 99.9  | 71 | PDB header: metal transport<br>Chain: A: PDB Molecule: Ryanodine receptor 3<br>PDBTitle: open-form crystal structure of human ryr receptor 3 (848-1055)<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>              |

|    |         |                           |   |       |    |  |
|----|---------|---------------------------|---|-------|----|--|
| 16 | c5c33A_ | <a href="#">Alignment</a> |    | 99.9  | 78 | PDB header: contractile protein<br>Chain: A: PDB Molecule: Ryanodine receptor 2<br>PDBTitle: crystal structure of mouse ryanodine receptor 2 spry1 domain<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>   |
| 17 | c4p9iA_ | <a href="#">Alignment</a> |  | 99.9  | 64 | PDB header: transport protein<br>Chain: A: PDB Molecule: Ryanodine receptor 2<br>PDBTitle: crystal structure of mouse ryanodine receptor 2 spry2 domain (1080-1253)<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>   |
| 18 | c6lt9A_ | <a href="#">Alignment</a> |  | 99.9  | 56 | PDB header: membrane protein<br>Chain: A: PDB Molecule: Ryanodine receptor 1<br>PDBTitle: the crystal structure of diamondback moth ryanodine receptor spry1 domain<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>   |
| 19 | c3uj4B_ | <a href="#">Alignment</a> |  | 100.0 | 22 | PDB header: signaling protein<br>Chain: B: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1<br>PDBTitle: crystal structure of the apo-inositol 1,4,5-trisphosphate receptor<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>                     |
| 20 | c3uj0A_ | <a href="#">Alignment</a> |  | 100.0 | 21 | PDB header: signaling protein<br>Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1<br>PDBTitle: crystal structure of the inositol 1,4,5-trisphosphate receptor with ligand bound form.<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a> |
| 21 | c6kimA_ | <a href="#">Alignment</a> | not modelled  | 99.8  | 51 | PDB header: transport protein<br>Chain: A: PDB Molecule: Ryanodine receptor<br>PDBTitle: crystal structure of diamondback moth ryanodine receptor spry2 domain<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>  |
| 22 | c6uhsA_ | <a href="#">Alignment</a> | not modelled  | 99.9  | 42 | PDB header: metal transport<br>Chain: A: PDB Molecule: Ryanodine receptor 1 chimera<br>PDBTitle: open-form crystal structure of chimera bt-hryr_12 from bacteroides thetaiotaomicron /human<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>                 |
| 23 | c6uhia_ | <a href="#">Alignment</a> | not modelled  | 99.9  | 39 | PDB header: metal transport<br>Chain: A: PDB Molecule: Ryanodine receptor 1 chimera<br>PDBTitle: closed-form crystal structure of chimera bt-hryr_12 from bacteroides thetaiotaomicron /human<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>               |
| 24 | c4ervA_ | <a href="#">Alignment</a> | not modelled  | 100.0 | 34 | PDB header: metal transport<br>Chain: A: PDB Molecule: Ryanodine receptor 3<br>PDBTitle: crystal structure of human ryanodine receptor 3 (2597-2800)<br>PDB Entry: <a href="#">PDBe RCSB PDBj</a>  |

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|----|--------|---------------------------|--------------|-------|----|---|
| 25 | nc1caA | <a href="#">Alignment</a> | not modelled | 100.0 | 20 | PDB header: metal transport<br>Chain: A: PDB Molecule: Ryanodine receptor<br>PDBTitle: crystal structure of diamondback moth ryanodine receptor |
|----|--------|---------------------------|--------------|-------|----|---|

|    |         |                           |              |       |    |   |
|----|---------|---------------------------|--------------|-------|----|---|
| 25 | c0jouR_ | <a href="#">Alignment</a> | not modelled | 100.0 | 50 | <b>PDB header:</b> crystal structure of diamondback moth tyramide receptor phosphorylation domain(2836-3050)<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 26 | c3jrrB_ | <a href="#">Alignment</a> | not modelled | 99.9  | 26 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> Inositol 1, 4, 5-trisphosphate receptor type 3<br><b>PDBTitle:</b> crystal structure of the ligand binding suppressor domain of type 3 inositol 1,4,5-trisphosphate receptor<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 27 | c1xzzA_ | <a href="#">Alignment</a> | not modelled | 99.8  | 25 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Inositol 1, 4, 5-trisphosphate receptor type 1<br><b>PDBTitle:</b> crystal structure of the ligand binding suppressor domain of type 1 inositol 1,4,5-trisphosphate receptor<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 28 | c7nscA_ | <a href="#">Alignment</a> | not modelled | 99.5  | 27 | <b>PDB header:</b> ligase<br><b>Chain:</b> A: <b>PDB Molecule:</b> Ran-binding protein 9<br><b>PDBTitle:</b> substrate receptor scaffolding module of human cth e3 ubiquitin ligase<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 29 | c5jiaD_ | <a href="#">Alignment</a> | not modelled | 99.0  | 28 | <b>PDB header:</b> ran-binding protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> Ran-binding protein 10<br><b>PDBTitle:</b> the crystal structure of ius-spry domain from ranbp10<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 30 | c5ji7A_ | <a href="#">Alignment</a> | not modelled | 98.9  | 29 | <b>PDB header:</b> ran-binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Ran-binding protein 9<br><b>PDBTitle:</b> the crystal structure of ius-spry domain from ranbp10<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 31 | c5jiuA_ | <a href="#">Alignment</a> | not modelled | 99.0  | 29 | <b>PDB header:</b> ran binding protein/peptide<br><b>Chain:</b> A: <b>PDB Molecule:</b> Ran-binding protein 9<br><b>PDBTitle:</b> the crystal structure of ranbp10 ius-spry domain in complex with ddx-4 peptide<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 32 | c6e2hA_ | <a href="#">Alignment</a> | not modelled | 99.0  | 29 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> Set1/Ash2 histone methyltransferase complex subunit ASH2<br><b>PDBTitle:</b> crystal structure of human ash2l (spry domain and sdi motif) in complex with full length dpy-30<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 33 | c5f6IB_ | <a href="#">Alignment</a> | not modelled | 98.9  | 26 | <b>PDB header:</b> protein binding/transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> Set1/Ash2 histone methyltransferase complex subunit ASH2<br><b>PDBTitle:</b> the crystal structure of mll1 (n3861i/q3867l) in complex with rbbp5 and ash2l<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 34 | c6w5iD_ | <a href="#">Alignment</a> | not modelled | 99.3  | 28 | <b>PDB header:</b> transferase/structural protein/dna<br><b>Chain:</b> D: <b>PDB Molecule:</b> Set1/Ash2 histone methyltransferase complex subunit ASH2<br><b>PDBTitle:</b> cryo-em structure of mll1 in complex with rbbp5, wdr5, set1, and ash2l bound to the nucleosome (class01)<br><b>PDB Entry:</b> PDBe RCSB PDB                                       |
| 35 | c6kizN_ | <a href="#">Alignment</a> | not modelled | 98.9  | 28 | <b>PDB header:</b> transcription/dna<br><b>Chain:</b> N: <b>PDB Molecule:</b> Set1/Ash2 histone methyltransferase complex subunit ASH2<br><b>PDBTitle:</b> cryo-em structure of human mll1-ncp complex, binding mode2<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 36 | c7wgC_  | <a href="#">Alignment</a> | not modelled | 99.2  | 24 | <b>PDB header:</b> ligase<br><b>Chain:</b> C: <b>PDB Molecule:</b> Vacuolar import and degradation protein 30<br><b>PDBTitle:</b> gid subcomplex: gid12 bound substrate receptor scaffolding module<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 37 | c6ug5D_ | <a href="#">Alignment</a> | not modelled | 99.4  | 36 | <b>PDB header:</b> metal transport<br><b>Chain:</b> D: <b>PDB Molecule:</b> Putative ryanodine receptor<br><b>PDBTitle:</b> closed dimer of y77a mutant putative ryanodine receptor from bacteroides thetaiotaomicron vpi-5482<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 38 | c6ug5C_ | <a href="#">Alignment</a> | not modelled | 99.4  | 36 | <b>PDB header:</b> metal transport<br><b>Chain:</b> C: <b>PDB Molecule:</b> Putative ryanodine receptor<br><b>PDBTitle:</b> closed dimer of y77a mutant putative ryanodine receptor from bacteroides thetaiotaomicron vpi-5482<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 39 | c2yyoA_ | <a href="#">Alignment</a> | not modelled | 99.1  | 27 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> SPRY domain-containing protein 3<br><b>PDBTitle:</b> crystal structure of human spry domain<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 40 | c6venO_ | <a href="#">Alignment</a> | not modelled | 99.5  | 23 | <b>PDB header:</b> transferase/structural protein/dna<br><b>Chain:</b> O: <b>PDB Molecule:</b> COMPASS component BRE2<br><b>PDBTitle:</b> yeast compass in complex with a ubiquitinated nucleosome<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 41 | c4xw3B_ | <a href="#">Alignment</a> | not modelled | 98.7  | 22 | <b>PDB header:</b> hydrolase<br><b>Chain:</b> B: <b>PDB Molecule:</b> ATP-dependent RNA helicase DDX1<br><b>PDBTitle:</b> crystal structure of the spry domain of the human dead-box protein ddx1<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 42 | c8bv0B_ | <a href="#">Alignment</a> | not modelled | 99.0  | 26 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: <b>PDB Molecule:</b> Truncated secreted SPRY domain-containing protein 15 (Fragment)<br><b>PDBTitle:</b> :binary complex between the nb-arc domain from the tomato immune receptor nrc1 and the spry domain-containing effector ss15 from the potato cyst nematode;<br><b>PDB Entry:</b> PDBe RCSB PDB |
| 43 | c8bv0D_ | <a href="#">Alignment</a> | not modelled | 99.0  | 26 | <b>PDB header:</b> protein binding<br><b>Chain:</b> D: <b>PDB Molecule:</b> Truncated secreted SPRY domain-containing protein 15 (Fragment)<br><b>PDBTitle:</b> :binary complex between the nb-arc domain from the tomato immune receptor nrc1 and the spry domain-containing effector ss15 from the potato cyst nematode;<br><b>PDB Entry:</b> PDBe RCSB PDB |
| 44 | c7ccbA_ | <a href="#">Alignment</a> | not modelled | 98.9  | 23 | <b>PDB header:</b> unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> SPRY domain-containing protein 7<br><b>PDBTitle:</b> crystal structure of the spry domain-containing protein 7 (spry7)<br><b>PDB Entry:</b> PDBe RCSB PDB  |

|    |         |   |              |      |    |   |
|----|---------|---|--------------|------|----|---|
| 45 | c1ij5A_ |  | not modelled | 94.6 | 12 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> PLASMODIAL SPECIFIC LAV1-2 PROTEIN<br><b>PDBTitle:</b> metal-free structure of multidomain ef-hand protein, cbp40, from true slime mold<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>      |
| 46 | c1ij6A_ |  | not modelled | 94.6 | 12 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> PLASMODIAL SPECIFIC LAV1-2 PROTEIN<br><b>PDBTitle:</b> ca2+-bound structure of multidomain ef-hand protein, cbp40, from true slime mold<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>      |
| 47 | c3malA_ |  | not modelled | 98.0 | 18 | <b>PDB header:</b> plant protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Stromal cell-derived factor 2-like protein<br><b>PDBTitle:</b> crystal structure of the sdf2-like protein from arabidopsis thaliana<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>                  |
| 48 | c6zqqA_ |  | not modelled | 97.3 | 21 | <b>PDB header:</b> peptide binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> PMT3 isoform 1<br><b>PDBTitle:</b> structure of the pmt3-mir domain with bound ligands<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>   |
| 49 | c1t9fA_ |  | not modelled | 98.7 | 21 | <b>PDB header:</b> structural genomics, unknown function<br><b>Chain:</b> A: <b>PDB Molecule:</b> protein 1d10<br><b>PDBTitle:</b> structural genomics of caenorhabditis elegans: structure of a protein with unknown function<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a> |
| 50 | c6chgB_ |  | not modelled | 99.6 | 20 | <b>PDB header:</b> transferase<br><b>Chain:</b> B: <b>PDB Molecule:</b> KLLA0C10945p<br><b>PDBTitle:</b> crystal structure of the yeast compass catalytic module<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>   |

|    |         |   |              |      |    |  |
|----|---------|---|--------------|------|----|--|
| 51 | c5hvdA_ |  | not modelled | 95.5 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Ion transport protein<br><b>PDBTitle:</b> full length open-form sodium channel navms i218c<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>  |
| 52 | c6j8eB_ |  | not modelled | 85.3 | 19 | <b>PDB header:</b> membrane protein/toxin<br><b>Chain:</b> B: <b>PDB Molecule:</b> Sodium channel protein type 2 subunit alpha<br><b>PDBTitle:</b> human nav1.2-beta2-kiila ternary complex<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>   |
| 53 | c6t9nB_ |  | not modelled | 91.8 | 19 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> Polycystin-2<br><b>PDBTitle:</b> cryoem structure of human polycystin-2/pkd2 in udm supplemented with pi(4,5)p2<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>  |
| 54 | c4rgjA_ |  | not modelled | 96.4 | 16 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> Calcium-dependent protein kinase 4<br><b>PDBTitle:</b> apo crystal structure of cdpk4 from plasmodium falciparum, pf3d7_0717500<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>   |
| 55 | c7vfuA_ |  | not modelled | 92.6 | 19 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Voltage-dependent N-type calcium channel subunit alpha-1B<br><b>PDBTitle:</b> human n-type voltage gated calcium channel cav2.2-alpha2/delta1-beta1 complex, bound to ziconotide<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a> |
| 56 | c6a70D_ |  | not modelled | 95.1 | 18 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> Polycystin-2<br><b>PDBTitle:</b> structure of the human pkd1/pkd2 complex<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>  |
| 57 | c6p28A_ |  | not modelled | 97.3 | 19 | <b>PDB header:</b> transferase<br><b>Chain:</b> A: <b>PDB Molecule:</b> Dolichyl-phosphate-mannose--protein mannosyltransferase 2<br><b>PDBTitle:</b> crystal structure of the mir domain (aa 337-532) of the s. cerevisiae mannosyltransferase pmf2<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>          |
| 58 | c6n4qB_ |  | not modelled | 94.9 | 20 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> Nav1.7 VSD2-NavAb chimera<br><b>PDBTitle:</b> cryoem structure of nav1.7 vsd2 (activated state) in complex with the gating modifier toxin protx2<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>                                 |
| 59 | c7mijA_ |  | not modelled | 91.5 | 15 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Transient receptor potential cation channel subfamily V member 3<br><b>PDBTitle:</b> mouse trpv3 in msp2n2 nanodiscs, closed state at 4 degrees celsius<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>                          |
| 60 | c7mijD_ |  | not modelled | 91.4 | 15 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> Transient receptor potential cation channel subfamily V member 3<br><b>PDBTitle:</b> mouse trpv3 in msp2n2 nanodiscs, closed state at 4 degrees celsius<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>                          |
| 61 | c6t9nD_ |  | not modelled | 92.9 | 18 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> D: <b>PDB Molecule:</b> Polycystin-2<br><b>PDBTitle:</b> cryoem structure of human polycystin-2/pkd2 in udm supplemented with pi(4,5)p2<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>  |
| 62 | c7xsuA_ |  | not modelled | 87.9 | 15 | <b>PDB header:</b> membrane protein/toxin<br><b>Chain:</b> A: <b>PDB Molecule:</b> Sodium channel protein type 5 subunit alpha, G protein/GFP fusion protein<br><b>PDBTitle:</b> cardiac sodium channel in complex with lqhiii<br><b>PDB Entry:</b> <a href="#">PDBe RCSB PDB</a>                                |

|    |         |   |              |      |    |  |
|----|---------|---|--------------|------|----|--|
| 63 | c8ep1A_ |  | not modelled | 92.8 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Voltage-dependent R-type calcium channel subunit alpha-1E<br><b>PDBTitle:</b> human r-type voltage-gated calcium channel cav2.3 at 3.1 angstrom resolution |
|----|---------|---|--------------|------|----|--|

|    |         |           |              |      |    |  |
|----|---------|-----------|--------------|------|----|--|
|    |         |           |              |      |    | <b>PDB Entry:</b> PDBe RCSB PDBj   |
| 64 | c8vgmF_ | Alignment | not modelled | 95.4 | 19 | <b>PDB header:</b> transport protein<br><b>Chain:</b> F: PDB Molecule: Chimeric Nav1.7-NavAb<br><b>PDBTitle:</b> cryoem structure of nav1.7 in complex with engineered conformationally rigid fab 7a9.4ds<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 65 | c5mkfA_ | Alignment | not modelled | 91.8 | 19 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: PDB Molecule: Polycystin-2<br><b>PDBTitle:</b> cryoem structure of polycystin-2 in complex with calcium and lipids<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 66 | c8dj1A_ | Alignment | not modelled | 95.2 | 19 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: PDB Molecule: Ion transport protein<br><b>PDBTitle:</b> crystal structure of navab v126t as a basis for the human nav1.7 inherited erythromelalgia s241t mutation<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 67 | c7vfaA_ | Alignment | not modelled | 92.0 | 18 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: PDB Molecule: Voltage-dependent N-type calcium channel subunit alpha-1B<br><b>PDBTitle:</b> human n-type voltage gated calcium channel cav2.2-alpha2/delta1-beta1 complex, apo state<br><b>PDB Entry:</b> PDBe RCSB PDBj                                   |
| 68 | c7w77C_ | Alignment | not modelled | 83.9 | 19 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C: PDB Molecule: Sodium channel protein type 3 subunit alpha<br><b>PDBTitle:</b> cryo-em structure of human nav1.3/beta1/beta2-bulleyaconitine<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 69 | c8e5bA_ | Alignment | not modelled | 92.1 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1D<br><b>PDBTitle:</b> human l-type voltage-gated calcium channel cav1.3 in the presence of amiodarone and sofosbuvir at 3.3 angstrom resolution<br><b>PDB Entry:</b> PDBe RCSB PDBj |
| 70 | c6zqpA_ | Alignment | not modelled | 97.3 | 15 | <b>PDB header:</b> peptide binding protein<br><b>Chain:</b> A: PDB Molecule: PMT2 isoform 1<br><b>PDBTitle:</b> structure of the pmt2-mir domain with bound ligands<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 71 | c7uhgB_ | Alignment | not modelled | 90.9 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> B: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1D<br><b>PDBTitle:</b> human l-type voltage-gated calcium channel cav1.3 at 3.0 angstrom resolution<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 72 | c6dn7A_ | Alignment | not modelled | 96.8 | 21 | <b>PDB header:</b> immune system/inhibitor<br><b>Chain:</b> A: PDB Molecule: SPRY domain-containing SOCS box protein 4<br><b>PDBTitle:</b> spry domain-containing socs box protein 2 complexed with wdinnn(bal) cyclic peptide inhibitor<br><b>PDB Entry:</b> PDBe RCSB PDBj                                       |
| 73 | c8okxB_ | Alignment | not modelled | 98.3 | 21 | <b>PDB header:</b> immune system<br><b>Chain:</b> B: PDB Molecule: SPRY domain-containing SOCS box protein 3<br><b>PDBTitle:</b> structure of egas in complex with spsb3-elobc<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 74 | c8hmaA_ | Alignment | not modelled | 91.6 | 17 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha<br><b>PDBTitle:</b> cryo-em structure of human high-voltage activated l-type calcium channel cav1.2 in complex with tetrandrine (tet)<br><b>PDB Entry:</b> PDBe RCSB PDBj             |

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|----|---------|-----------|--------------|------|----|--|
|    |         |           |              |      |    | <b>PDB header:</b> membrane protein<br><b>Chain:</b> D: PDB Molecule: Maltose/maltodextrin-binding periplasmic protein, ion transport protein, Sodium channel protein type 9 subunit alpha chimera<br><b>PDBTitle:</b> structure of navab/nav1.7-vs2a chimera trapped in the resting state by tarantula toxin m3-huwentoxin-iv<br><b>PDB Entry:</b> PDBe RCSB PDBj |
| 75 | c7k48D_ | Alignment | not modelled | 92.9 | 19 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1S<br><b>PDBTitle:</b> rabbit l-type voltage-gated calcium channel cav1.1 in the presence of amiodarone and 100 microm mni-1 at 2.8 angstrom resolution<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 76 | c8e57A_ | Alignment | not modelled | 93.5 | 16 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: PDB Molecule: Voltage-dependent P/Q-type calcium channel subunit alpha-1A<br><b>PDBTitle:</b> p/q type calcium channel<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 77 | c8x90A_ | Alignment | not modelled | 88.7 | 18 | <b>PDB header:</b> transport protein<br><b>Chain:</b> D: PDB Molecule: Polycystin-2<br><b>PDBTitle:</b> cryoem structure of polycystin-2 in complex with calcium and lipids<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 78 | c5mkfD_ | Alignment | not modelled | 92.4 | 17 | <b>PDB header:</b> protein transport<br><b>Chain:</b> B: PDB Molecule: Cation channel sperm-associated protein 2<br><b>PDBTitle:</b> structure of the catpermasome<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 79 | c7eebB_ | Alignment | not modelled | 96.9 | 15 | <b>PDB header:</b> protein binding<br><b>Chain:</b> B: PDB Molecule: SPRY domain-containing SOCS box protein 2<br><b>PDBTitle:</b> crystal structure of human spsb2 in the apo-state<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 80 | c6jkjB_ | Alignment | not modelled | 96.1 | 18 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: PDB Molecule: SPRY domain-containing SOCS box protein 2<br><b>PDBTitle:</b> crystal structure of human spsb2 in the apo-state<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 81 | c3emwA_ | Alignment | not modelled | 97.0 | 19 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: PDB Molecule: SPRY domain-containing SOCS box protein 2<br><b>PDBTitle:</b> crystal structure of human splat/ryanodine receptor domain and socs box containing 2 (spsb2) in complex with a 20-residue vasa peptide;<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 82 | c8fd7B_ | Alignment | not modelled | 90.5 | 16 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1C<br><b>PDBTitle:</b> structure of the human l-type voltage-gated calcium channel cav1.2 complexed with cahapantin   |

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|----|---------|--|--------------|------|----|--|
|    |         |  |              |      |    | complexed with gustavustin<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 83 | c8eogB_ |  | not modelled | 90.5 | 16 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> Isoform 20 of Voltage-dependent L-type calcium channel subunit alpha-1C<br><b>PDBTitle:</b> structure of the human l-type voltage-gated calcium channel cav1.2 complexed with l-leucine<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 84 | c7u0uA_ |  | not modelled | 95.0 | 14 | <b>PDB header:</b> antifungal protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Serine/threonine-protein phosphatase 2B catalytic subunit, Asf1uA.00174.a.TQ11 + Asf1uA.01011.a.TR11<br><b>PDBTitle:</b> crystal structure of a aspergillus fumigatus calcineurin a - calcineurin b fusion bound to fkbp12 and fk-506<br><b>PDB Entry:</b> PDBe RCSB PDBj |
| 85 | c6dn5A_ |  | not modelled | 96.4 | 19 | <b>PDB header:</b> immune system/inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> SPRY domain-containing SOCS box protein 2<br><b>PDBTitle:</b> spry domain-containing socs box protein 2 complexed with wdinnn(bal) cyclic peptide inhibitor<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 86 | c6c9aA_ |  | not modelled | 89.5 | 16 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Two pore calcium channel protein 1<br><b>PDBTitle:</b> cryo-em structure of mouse tpc1 channel in the ptdins(3,5)p2-bound state<br><b>PDB Entry:</b> PDBe RCSB PDBj   |

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|----|---------|--|--------------|------|----|--|
| 87 | c5xn3A_ |  | not modelled | 96.2 | 19 | <b>PDB header:</b> protein binding/inhibitor<br><b>Chain:</b> A: <b>PDB Molecule:</b> SPRY domain-containing SOCS box protein 2<br><b>PDBTitle:</b> crystal structure of spsb2 in complex with a rational designed rgd containing cyclic peptide inhibitor of spsb2-inos interaction<br><b>PDB Entry:</b> PDBe RCSB PDBj |
| 88 | c3sjqA_ |  | not modelled | 95.2 | 20 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Calmodulin<br><b>PDBTitle:</b> crystal structure of a small conductance potassium channel splice variant complexed with calcium-calmodulin<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 89 | c2o5gA_ |  | not modelled | 95.2 | 20 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Calmodulin<br><b>PDBTitle:</b> calmodulin-smooth muscle light chain kinase peptide complex<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 90 | c2afjA_ |  | not modelled | 97.4 | 18 | <b>PDB header:</b> gene regulation<br><b>Chain:</b> A: <b>PDB Molecule:</b> gene rich cluster, C9 gene<br><b>PDBTitle:</b> spry domain-containing socs box protein 2 (ssb-2)<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 91 | c7tbgA_ |  | not modelled | 91.5 | 16 | <b>PDB header:</b> transport protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Two pore calcium channel protein 1<br><b>PDBTitle:</b> attpc1 d454n with 1 mm ca2+<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 92 | c2lmuA_ |  | not modelled | 96.1 | 19 | <b>PDB header:</b> metal binding protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Calmodulin-related protein 97A<br><b>PDBTitle:</b> androcan at high calcium<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 93 | c2fnjA_ |  | not modelled | 97.1 | 18 | <b>PDB header:</b> protein transport/signaling protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> CG2944-PF, isoform F<br><b>PDBTitle:</b> crystal structure of a b30.2/spry domain-containing protein gustavus in complex with elongin b and elongin c<br><b>PDB Entry:</b> PDBe RCSB PDBj                                |
| 94 | c3ek9A_ |  | not modelled | 95.0 | 19 | <b>PDB header:</b> protein binding<br><b>Chain:</b> A: <b>PDB Molecule:</b> SPRY domain-containing SOCS box protein 2<br><b>PDBTitle:</b> spry domain-containing socs box protein 2: crystal structure and residues critical for protein binding<br><b>PDB Entry:</b> PDBe RCSB PDBj                                     |
| 95 | c7uswC_ |  | not modelled | 92.1 | 22 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> C: <b>PDB Molecule:</b> CALMyrin (Calcium and Integrin Binding protein) homolog<br><b>PDBTitle:</b> structure of expanded c. elegans tmc-1 complex<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 96 | c8tkpB_ |  | not modelled | 92.1 | 23 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> B: <b>PDB Molecule:</b> CALMyrin (Calcium and Integrin Binding protein) homolog<br><b>PDBTitle:</b> structure of the c. elegans tmc-2 complex<br><b>PDB Entry:</b> PDBe RCSB PDBj   |
| 97 | c2jk9A_ |  | not modelled | 97.0 | 19 | <b>PDB header:</b> apoptosis<br><b>Chain:</b> A: <b>PDB Molecule:</b> SPRY DOMAIN-CONTAINING SOCS BOX PROTEIN 1<br><b>PDBTitle:</b> the structure of spla-ryanodine receptor domain and socs box containing 1 in complex with a par-4 peptide<br><b>PDB Entry:</b> PDBe RCSB PDBj  |
| 98 | c7kaaA_ |  | not modelled | 93.3 | 22 | <b>PDB header:</b> contractile protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Troponin C, skeletal muscle, Troponin I, fast skeletal muscle chimera<br><b>PDBTitle:</b> nmr solution structures of tirasemtiv drug bound to a fast skeletal troponin c-troponin i complex<br><b>PDB Entry:</b> PDBe RCSB PDBj          |

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| 99 | c8we8A_ |  | not modelled | 92.8 | 13 | <b>PDB header:</b> membrane protein<br><b>Chain:</b> A: <b>PDB Molecule:</b> Voltage-dependent L-type calcium channel subunit alpha-1C<br><b>PDBTitle:</b> human l-type voltage-gated calcium channel cav1.2 in the presence of calciseptine, amlodipine and pinaverium at 2.9 angstrom resolution;<br><b>PDB Entry:</b> PDBe RCSB PDBj |
|----|---------|--|--------------|------|----|---|

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| 100 | c8rx8A_ |  | not modelled | 96.5 | 15 | <b>PDB header:</b> signaling protein<br><b>Chain: A: PDB Molecule:</b> Probable calcium-binding protein CML18<br><b>PDBTitle:</b> the structure of cml18 in complex with 4 ca2+ ions<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 101 | c8we7A_ |  | not modelled | 93.5 | 13 | <b>PDB header:</b> membrane protein<br><b>Chain: A: PDB Molecule:</b> Voltage-dependent L-type calcium channel subunit alpha-1C<br><b>PDBTitle:</b> human I-type voltage-gated calcium channel cav1.2 in the presence of calciseptine at 3.2 angstrom resolution<br><b>PDB Entry:</b> PDBe RCSB PDB              |
| 102 | c8uwwC_ |  | not modelled | 96.0 | 15 | <b>PDB header:</b> motor protein<br><b>Chain: C: PDB Molecule:</b> Troponin C, slow skeletal and cardiac muscles<br><b>PDBTitle:</b> the structure of the native cardiac thin filament troponin core in ca2+-free state from the upper strand<br><b>PDB Entry:</b> PDBe RCSB PDB                                 |
| 103 | c8v0kC_ |  | not modelled | 96.0 | 15 | <b>PDB header:</b> motor protein<br><b>Chain: C: PDB Molecule:</b> Troponin C, slow skeletal and cardiac muscles<br><b>PDBTitle:</b> the structure of the native cardiac thin filament troponin core in ca2+-bound partially activated state from the lower strand<br><b>PDB Entry:</b> PDBe RCSB PDB            |
| 104 | c7tdfB_ |  | not modelled | 92.4 | 15 | <b>PDB header:</b> transport protein<br><b>Chain: B: PDB Molecule:</b> Two pore calcium channel protein 1<br><b>PDBTitle:</b> atpc1 d454n with 1 mm edta state i<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 105 | c6uw4C_ |  | not modelled | 89.8 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain: C: PDB Molecule:</b> Transient receptor potential cation channel subfamily V member 3<br><b>PDBTitle:</b> cryo-em structure of human trpv3 determined in lipid nanodisc<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 106 | c6uw4D_ |  | not modelled | 89.8 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain: D: PDB Molecule:</b> Transient receptor potential cation channel subfamily V member 3<br><b>PDBTitle:</b> cryo-em structure of human trpv3 determined in lipid nanodisc<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 107 | c8f0pA_ |  | not modelled | 88.9 | 14 | <b>PDB header:</b> membrane protein/inhibitor<br><b>Chain: A: PDB Molecule:</b> Sodium channel protein PaFPC1, Sodium channel protein type 9 subunit alpha chimera<br><b>PDBTitle:</b> structure of vsd4-nav1.7-navpas channel chimera bound to the hybrid inhibitor gne-1305<br><b>PDB Entry:</b> PDBe RCSB PDB |
| 108 | c1ggzA_ |  | not modelled | 95.3 | 18 | <b>PDB header:</b> metal binding protein<br><b>Chain: A: PDB Molecule:</b> CALMODULIN-RELATED PROTEIN NB-1<br><b>PDBTitle:</b> crystal structure of the calmodulin-like protein (hclp) from human epithelial cells<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 109 | c8v6nD_ |  | not modelled | 89.4 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain: D: PDB Molecule:</b> Transient receptor potential cation channel subfamily V member 3<br><b>PDBTitle:</b> open-state cryo-em structure of human trpv3 in presence of 2-apb in cnw30 nanodiscs<br><b>PDB Entry:</b> PDBe RCSB PDB                                |
| 110 | c8v6mD_ |  | not modelled | 87.8 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain: D: PDB Molecule:</b> Transient receptor potential cation channel subfamily V member 3<br><b>PDBTitle:</b> inactivated-state cryo-em structure of human trpv3 in presence of tetrahydrocannabinol (thcv) in cnw30 nanodiscs<br><b>PDB Entry:</b> PDBe RCSB PDB   |

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|-----|---------|---|--------------|------|----|--|
| 111 | c8g3dQ_ |  | not modelled | 95.3 | 12 | <b>PDB header:</b> structural protein<br><b>Chain: Q: PDB Molecule:</b> RIB57<br><b>PDBTitle:</b> 48-nm doublet microtubule from tetrahymena thermophila strain k40r<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 112 | c2ro8A_ |  | not modelled | 88.9 | 33 | <b>PDB header:</b> metal binding protein<br><b>Chain: A: PDB Molecule:</b> Calmodulin<br><b>PDBTitle:</b> solution structure of calcium bound soybean calmodulin isoform 1 n-terminal domain<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 113 | c7wlkA_ |  | not modelled | 90.2 | 11 | <b>PDB header:</b> membrane protein<br><b>Chain: A: PDB Molecule:</b> Voltage-dependent T-type calcium channel subunit alpha-1I<br><b>PDBTitle:</b> cryoem structure of human low-voltage activated t-type calcium channel cav3.3 in complex with oltionium bromide(ob)<br><b>PDB Entry:</b> PDBe RCSB PDB |
| 114 | c7dtcA_ |  | not modelled | 88.2 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain: A: PDB Molecule:</b> Sodium channel protein type 5 subunit alpha<br><b>PDBTitle:</b> voltage-gated sodium channel nav1.5-e1784k<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 115 | c1sjjB_ |  | not modelled | 87.9 | 10 | <b>PDB header:</b> contractile protein<br><b>Chain: B: PDB Molecule:</b> actinin<br><b>PDBTitle:</b> cryo-em structure of chicken gizzard smooth muscle alpha-actinin<br><b>PDB Entry:</b> PDBe RCSB PDB   |
| 116 | c2scpA_ |  | not modelled | 93.8 | 15 | <b>PDB header:</b> binding protein<br><b>Chain: A: PDB Molecule:</b> SARCOPLASMIC CALCIUM-BINDING PROTEIN<br><b>PDBTitle:</b> structure of a sarcoplasmic calcium-binding protein from nereis diversicolor refined at 2.0 angstroms resolution<br><b>PDB Entry:</b> PDBe RCSB PDB                          |
| 117 | c6xqoA_ |  | not modelled | 94.1 | 15 | <b>PDB header:</b> calcium binding protein<br><b>Chain: A: PDB Molecule:</b> Calcium uptake protein 1, mitochondrial<br><b>PDBTitle:</b> structure of the human mico1-mico2 heterodimer, calcium bound, in association with a lipid nanodisc<br><b>PDB Entry:</b> PDBe RCSB PDB                            |
| 118 | c5xsyA_ |  | not modelled | 93.5 | 14 | <b>PDB header:</b> membrane protein<br><b>Chain: A: PDB Molecule:</b> Sodium channel protein<br><b>PDBTitle:</b> structure of the nav1.4-beta1 complex from electric eel<br><b>PDB Entry:</b> PDBe RCSB PDB  |
| 119 | c7qioE_ |  | not modelled | 95.1 | 17 | <b>PDB header:</b> motor protein<br><b>Chain: E: PDB Molecule:</b> Myosin regulatory light chain 2, skeletal muscle isoform<br><b>PDBTitle:</b> homology model of myosin neck domain in skeletal sarcomere   |

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| 120 | c1q80A_ | Alignment | not modelled | 92.9 | 15 | PDB ID: homology model of myosin neck domain in skeletal sarcomere<br>PDB Entry: PDBe RCSB PDB <br><b>PDB header:</b> metal binding protein<br><b>Chain:</b> A <b>PDB Molecule:</b> Sarcoplasmic calcium-binding protein<br><b>PDBTitle:</b> solution structure and dynamics of nereis sarcoplasmic calcium binding protein<br><b>PDB Entry:</b> PDBe RCSB PDB |
|-----|---------|-----------|--------------|------|----|--|