
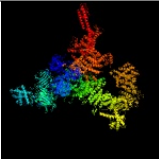
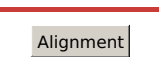
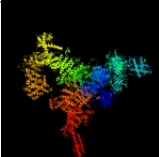
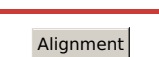
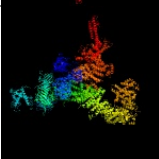


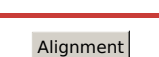
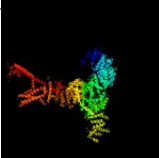

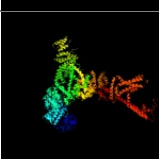

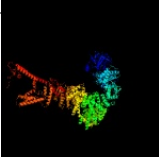
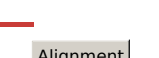
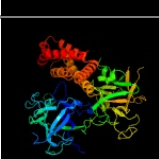

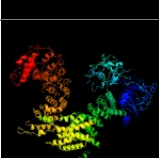

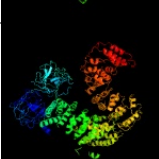

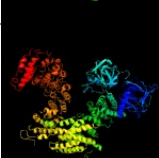

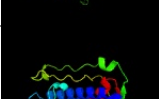
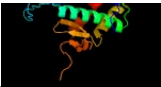

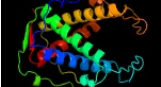




Phyre2.2

Email katiecmorrison@gmail.com
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Date Tue Oct 21 22:34:15 BST 2025
Unique Job ID d93b978a3eaf5ed7

Detailed template information



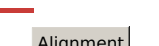



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c8vjkA_	 Alignment		100.0	98	PDB header: membrane protein Chain: A: PDB Molecule: Ryanodine receptor 1 PDBTitle: structure of mouse ryr1 (high-ca2+/cfl/atp dataset) PDB Entry: PDBe RCSB PDBj
2	c8vjkH_	 Alignment		100.0	98	PDB header: membrane protein Chain: H: PDB Molecule: Ryanodine receptor 1 PDBTitle: structure of mouse ryr1 (high-ca2+/cfl/atp dataset) PDB Entry: PDBe RCSB PDBj
3	c9c1eB_	 Alignment		100.0	72	PDB header: membrane protein Chain: B: PDB Molecule: Ryanodine receptor 3 PDBTitle: mink ryr3 in closed conformation PDB Entry: PDBe RCSB PDBj
4	c8tk8D_	 Alignment		100.0	22	PDB header: transport protein Chain: D: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 3 PDBTitle: human type 3 ip3 receptor - resting state (+ip3/atp) PDB Entry: PDBe RCSB PDBj
5	c8tk8A_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 3 PDBTitle: human type 3 ip3 receptor - resting state (+ip3/atp) PDB Entry: PDBe RCSB PDBj
6	c6mu2A_	 Alignment		100.0	22	PDB header: membrane protein Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1 PDBTitle: structure of full-length ip3r1 channel in the apo-state PDB Entry: PDBe RCSB PDBj
7	c6uqkA_	 Alignment		100.0	22	PDB header: transport protein Chain: A: PDB Molecule: inositol 1, 4, 5-trisphosphate receptor, type 3 PDBTitle: cryo-em structure of type 3 ip3 receptor revealing presence of a self-binding peptide PDB Entry: PDBe RCSB PDBj
8	c4jkqA_	 Alignment		100.0	71	PDB header: unknown function Chain: A: PDB Molecule: Ryanodine receptor 2 PDBTitle: crystal structure of the n-terminal region of the human ryanodine receptor 2 PDB Entry: PDBe RCSB PDBj
9	c5xa0A_	 Alignment		100.0	20	PDB header: metal transport Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1 PDBTitle: crystal structure of inositol 1,4,5-trisphosphate receptor cytosolic domain PDB Entry: PDBe RCSB PDBj
10	c5xa0B_	 Alignment		100.0	20	PDB header: metal transport Chain: B: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1 PDBTitle: crystal structure of inositol 1,4,5-trisphosphate receptor cytosolic domain PDB Entry: PDBe RCSB PDBj
11	c5xa1A_	 Alignment		100.0	20	PDB header: metal transport Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1 PDBTitle: crystal structure of inositol 1,4,5-trisphosphate receptor cytosolic domain with inositol 1,4,5-trisphosphate PDB Entry: PDBe RCSB PDBj
12	c5c20A_	 Alignment		100.0	20	PDB header: contractile protein Chain: A: PDB Molecule: Ryanodine receptor 1







12	c6c3uA_	Alignment		99.9	98	PDBTitle: crystal structure of rabbit ryanodine receptor 1 repeat12 domain PDB Entry: PDBe RCSB PDBj
13	c4p9jA_	Alignment		99.9	99	PDB header: transport protein Chain: A; PDB Molecule: Ryanodine receptor 1 PDBTitle: crystal structure of rabbit ryanodine receptor 1 spry2 domain (1070-1246) PDB Entry: PDBe RCSB PDBj
14	c6uheC_	Alignment		100.0	71	PDB header: metal transport Chain: C; PDB Molecule: Ryanodine receptor 3 PDBTitle: closed-form crystal structure of human ryr receptor 3 (848-1055) PDB Entry: PDBe RCSB PDBj
15	c6uhaA_	Alignment		99.9	71	PDB header: metal transport Chain: A; PDB Molecule: Ryanodine receptor 3 PDBTitle: open-form crystal structure of human ryr receptor 3 (848-1055) PDB Entry: PDBe RCSB PDBj

16	c5c33A_	Alignment		99.9	78	PDB header: contractile protein Chain: A; PDB Molecule: Ryanodine receptor 2 PDBTitle: crystal structure of mouse ryanodine receptor 2 spry1 domain PDB Entry: PDBe RCSB PDBj
17	c4p9iA_	Alignment		99.9	64	PDB header: transport protein Chain: A; PDB Molecule: Ryanodine receptor 2 PDBTitle: crystal structure of mouse ryanodine receptor 2 spry2 domain (1080-1253) PDB Entry: PDBe RCSB PDBj
18	c6lt9A_	Alignment		99.9	56	PDB header: membrane protein Chain: A; PDB Molecule: Ryanodine receptor 1 PDBTitle: the crystal structure of diamondback moth ryanodine receptor spry1 domain PDB Entry: PDBe RCSB PDBj
19	c3uj4B_	Alignment		100.0	22	PDB header: signaling protein Chain: B; PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1 PDBTitle: crystal structure of the apo-inositol 1,4,5-trisphosphate receptor PDB Entry: PDBe RCSB PDBj
20	c3uj0A_	Alignment		100.0	21	PDB header: signaling protein Chain: A; PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1 PDBTitle: crystal structure of the inositol 1,4,5-trisphosphate receptor with ligand bound form. PDB Entry: PDBe RCSB PDBj
21	c6kimA_	Alignment	not modelled	99.8	51	PDB header: transport protein Chain: A; PDB Molecule: Ryanodine receptor PDBTitle: crystal structure of diamondback moth ryanodine receptor spry2 domain PDB Entry: PDBe RCSB PDBj
22	c6uhsA_	Alignment	not modelled	99.9	42	PDB header: metal transport Chain: A; PDB Molecule: Ryanodine receptor 1 chimera PDBTitle: open-form crystal structure of chimera bt-hyr_12 from bacteroides thetaiotaomicron /human PDB Entry: PDBe RCSB PDBj
23	c6uhiA_	Alignment	not modelled	99.9	39	PDB header: metal transport Chain: A; PDB Molecule: Ryanodine receptor 1 chimera PDBTitle: closed-form crystal structure of chimera bt-hyr_12 from bacteroides thetaiotaomicron /human PDB Entry: PDBe RCSB PDBj
24	c4ervA_	Alignment	not modelled	100.0	34	PDB header: metal transport Chain: A; PDB Molecule: Ryanodine receptor 3 PDBTitle: crystal structure of human ryanodine receptor 3 (2597-2800) PDB Entry: PDBe RCSB PDBj

25	c6ifeA_	Alignment	not modelled	100.0	30	PDB header: metal transport Chain: A; PDB Molecule: Ryanodine receptor PDBTitle: crystal structure of diamondback moth ryanodine receptor
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25	c3p0A_	Alignment	not modelled	100.0	30	PDB title: crystal structure of diatomback moth ryanodine receptor phosphorylation domain(2836-3050) PDB Entry: PDBe RCSB PDBj
26	c3jrrB_	Alignment	not modelled	99.9	26	PDB header: transport protein Chain: B: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 3 PDBTitle: crystal structure of the ligand binding suppressor domain of type 3 inositol 1,4,5-trisphosphate receptor PDB Entry: PDBe RCSB PDBj
27	c1xzzA_	Alignment	not modelled	99.8	25	PDB header: membrane protein Chain: A: PDB Molecule: Inositol 1, 4, 5-trisphosphate receptor type 1 PDBTitle: crystal structure of the ligand binding suppressor domain of type 1 inositol 1,4,5-trisphosphate receptor PDB Entry: PDBe RCSB PDBj
28	c7nscA_	Alignment	not modelled	99.5	27	PDB header: ligase Chain: A: PDB Molecule: Ran-binding protein 9 PDBTitle: substrate receptor scaffolding module of human ctth e3 ubiquitin ligase PDB Entry: PDBe RCSB PDBj
29	c5jiaD_	Alignment	not modelled	99.0	28	PDB header: ran-binding protein Chain: D: PDB Molecule: Ran-binding protein 10 PDBTitle: the crystal structure of ius-spry domain from ranbp10 PDB Entry: PDBe RCSB PDBj
30	c5ji7A_	Alignment	not modelled	98.9	29	PDB header: ran-binding protein Chain: A: PDB Molecule: Ran-binding protein 9 PDBTitle: the crystal structure of ius-spry domain from ranbpm/9 PDB Entry: PDBe RCSB PDBj
31	c5jiuA_	Alignment	not modelled	99.0	29	PDB header: ran binding protein/peptide Chain: A: PDB Molecule: Ran-binding protein 9 PDBTitle: the crystal structure of ranbpm/9 ius-spry domain in complex with ddx-4 peptide PDB Entry: PDBe RCSB PDBj
32	c6e2hA_	Alignment	not modelled	99.0	29	PDB header: protein binding Chain: A: PDB Molecule: Set1/Ash2 histone methyltransferase complex subunit ASH2 PDBTitle: crystal structure of human ash2l (spry domain and sdi motif) in complex with full length dpy-30 PDB Entry: PDBe RCSB PDBj
33	c5f6lB_	Alignment	not modelled	98.9	26	PDB header: protein binding/transferase Chain: B: PDB Molecule: Set1/Ash2 histone methyltransferase complex subunit ASH2 PDBTitle: the crystal structure of mll1 (n3861i/q3867l) in complex with rbbp5 and ash2l PDB Entry: PDBe RCSB PDBj
34	c6w5iD_	Alignment	not modelled	99.3	28	PDB header: transferase/structural protein/dna Chain: D: PDB Molecule: Set1/Ash2 histone methyltransferase complex subunit ASH2 PDBTitle: cryo-em structure of mll1 in complex with rbbp5, wdr5, set1, and ash2l bound to the nucleosome (class01) PDB Entry: PDBe RCSB PDBj
35	c6kizN_	Alignment	not modelled	98.9	28	PDB header: transcription/dna Chain: N: PDB Molecule: Set1/Ash2 histone methyltransferase complex subunit ASH2 PDBTitle: cryo-em structure of human mll1-ncp complex, binding mode2 PDB Entry: PDBe RCSB PDBj
36	c7wugC_	Alignment	not modelled	99.2	24	PDB header: ligase Chain: C: PDB Molecule: Vacuolar import and degradation protein 30 PDBTitle: gid subcomplex: gid12 bound substrate receptor scaffolding module PDB Entry: PDBe RCSB PDBj
37	c6ug5D_	Alignment	not modelled	99.4	36	PDB header: metal transport Chain: D: PDB Molecule: Putative ryanodine receptor PDBTitle: closed dimer of y77a mutant putative ryanodine receptor from bacteroides thetaiotaomicron vpi-5482 PDB Entry: PDBe RCSB PDBj
38	c6ug5C_	Alignment	not modelled	99.4	36	PDB header: metal transport Chain: C: PDB Molecule: Putative ryanodine receptor PDBTitle: closed dimer of y77a mutant putative ryanodine receptor from bacteroides thetaiotaomicron vpi-5482 PDB Entry: PDBe RCSB PDBj
39	c2yyoA_	Alignment	not modelled	99.1	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: SPRY domain-containing protein 3 PDBTitle: crystal structure of human spry domain PDB Entry: PDBe RCSB PDBj
40	c6venO_	Alignment	not modelled	99.5	23	PDB header: transferase/structural protein/dna Chain: O: PDB Molecule: COMPASS component BRE2 PDBTitle: yeast compass in complex with a ubiquitinated nucleosome PDB Entry: PDBe RCSB PDBj
41	c4xw3B_	Alignment	not modelled	98.7	22	PDB header: hydrolase Chain: B: PDB Molecule: ATP-dependent RNA helicase DDX1 PDBTitle: crystal structure of the spry domain of the human dead-box protein ddx1 PDB Entry: PDBe RCSB PDBj
42	c8bv0B_	Alignment	not modelled	99.0	26	PDB header: protein binding Chain: B: PDB Molecule: Truncated secreted SPRY domain-containing protein 15 (Fragment) PDBTitle: ;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; PDB Entry: PDBe RCSB PDBj
43	c8bv0D_	Alignment	not modelled	99.0	26	PDB header: protein binding Chain: D: PDB Molecule: Truncated secreted SPRY domain-containing protein 15 (Fragment) PDBTitle: ;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; PDB Entry: PDBe RCSB PDBj
44	c7ccbA_	Alignment	not modelled	98.9	23	PDB header: unknown function Chain: A: PDB Molecule: SPRY domain-containing protein 7 PDBTitle: crystal structure of the spry domain-containing protein 7 (spry7) PDB Entry: PDBe RCSB PDBj

45	c1ij5A_	 Alignment	not modelled	94.6	12	PDB header: metal binding protein Chain: A: PDB Molecule: PLASMODIAL SPECIFIC LAV1-2 PROTEIN PDBTitle: metal-free structure of multidomain ef-hand protein, cbp40, from true slime mold PDB Entry: PDBe RCSB PDBj
46	c1ij6A_	 Alignment	not modelled	94.6	12	PDB header: metal binding protein Chain: A: PDB Molecule: PLASMODIAL SPECIFIC LAV1-2 PROTEIN PDBTitle: ca2+-bound structure of multidomain ef-hand protein, cbp40, from true slime mold PDB Entry: PDBe RCSB PDBj
47	c3maIA_	 Alignment	not modelled	98.0	18	PDB header: plant protein Chain: A: PDB Molecule: Stromal cell-derived factor 2-like protein PDBTitle: crystal structure of the sdf2-like protein from arabidopsis thaliana PDB Entry: PDBe RCSB PDBj
48	c6zqqA_	 Alignment	not modelled	97.3	21	PDB header: peptide binding protein Chain: A: PDB Molecule: PMT3 isoform 1 PDBTitle: structure of the pmt3-mir domain with bound ligands PDB Entry: PDBe RCSB PDBj
49	c1t9fA_	 Alignment	not modelled	98.7	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein 1d10 PDBTitle: structural genomics of caenorhabditis elegans: structure of a protein with unknown function PDB Entry: PDBe RCSB PDBj
50	c6chgB_	 Alignment	not modelled	99.6	20	PDB header: transferase Chain: B: PDB Molecule: KLLA0C10945p PDBTitle: crystal structure of the yeast compass catalytic module PDB Entry: PDBe RCSB PDBj

51	c5hvdA_	 Alignment	not modelled	95.5	18	PDB header: transport protein Chain: A: PDB Molecule: Ion transport protein PDBTitle: full length open-form sodium channel navms i218c PDB Entry: PDBe RCSB PDBj
52	c6j8eB_	 Alignment	not modelled	85.3	19	PDB header: membrane protein/toxin Chain: B: PDB Molecule: Sodium channel protein type 2 subunit alpha PDBTitle: human nav1.2-beta2-kiiia ternary complex PDB Entry: PDBe RCSB PDBj
53	c6t9nB_	 Alignment	not modelled	91.8	19	PDB header: membrane protein Chain: B: PDB Molecule: Polycystin-2 PDBTitle: cryoem structure of human polycystin-2/pkd2 in udm supplemented with pi(4,5)p2 PDB Entry: PDBe RCSB PDBj
54	c4rgjA_	 Alignment	not modelled	96.4	16	PDB header: transferase Chain: A: PDB Molecule: Calcium-dependent protein kinase 4 PDBTitle: apo crystal structure of cdpk4 from plasmodium falciparum, pf3d7_0717500 PDB Entry: PDBe RCSB PDBj
55	c7vfuA_	 Alignment	not modelled	92.6	19	PDB header: membrane protein Chain: A: PDB Molecule: Voltage-dependent N-type calcium channel subunit alpha-1B PDBTitle: human n-type voltage gated calcium channel cav2.2-alpha2/delta1-beta1 complex, bound to ziconotide PDB Entry: PDBe RCSB PDBj
56	c6a70D_	 Alignment	not modelled	95.1	18	PDB header: membrane protein Chain: D: PDB Molecule: Polycystin-2 PDBTitle: structure of the human pkd1/pkd2 complex PDB Entry: PDBe RCSB PDBj
57	c6p28A_	 Alignment	not modelled	97.3	19	PDB header: transferase Chain: A: PDB Molecule: Dolichyl-phosphate-mannose--protein mannosyltransferase 2 PDBTitle: crystal structure of the mir domain (aa 337-532) of the s. cerevisiae mannosyltransferase pmt2 PDB Entry: PDBe RCSB PDBj
58	c6n4qB_	 Alignment	not modelled	94.9	20	PDB header: membrane protein Chain: B: PDB Molecule: Nav1.7 VSD2-NavAb chimera PDBTitle: cryoem structure of nav1.7 vsd2 (activated state) in complex with the gating modifier toxin protx2 PDB Entry: PDBe RCSB PDBj
59	c7mijA_	 Alignment	not modelled	91.5	15	PDB header: membrane protein Chain: A: PDB Molecule: Transient receptor potential cation channel subfamily V member 3 PDBTitle: mouse trpv3 in msp2n2 nanodiscs, closed state at 4 degrees celsius PDB Entry: PDBe RCSB PDBj
60	c7mijD_	 Alignment	not modelled	91.4	15	PDB header: membrane protein Chain: D: PDB Molecule: Transient receptor potential cation channel subfamily V member 3 PDBTitle: mouse trpv3 in msp2n2 nanodiscs, closed state at 4 degrees celsius PDB Entry: PDBe RCSB PDBj
61	c6t9nD_	 Alignment	not modelled	92.9	18	PDB header: membrane protein Chain: D: PDB Molecule: Polycystin-2 PDBTitle: cryoem structure of human polycystin-2/pkd2 in udm supplemented with pi(4,5)p2 PDB Entry: PDBe RCSB PDBj
62	c7xsuA_	 Alignment	not modelled	87.9	15	PDB header: membrane protein/toxin Chain: A: PDB Molecule: Sodium channel protein type 5 subunit alpha, G protein/GFP fusion protein PDBTitle: cardiac sodium channel in complex with lqhiii PDB Entry: PDBe RCSB PDBj

63	c8eplA_	 Alignment	not modelled	92.8	18	PDB header: transport protein Chain: A: PDB Molecule: Voltage-dependent R-type calcium channel subunit alpha-1E PDBTitle: human r-type voltage-gated calcium channel cav2.3 at 3.1 angstrom resolution
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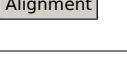
						PDB Entry: PDB RCSB PDBj
64	c8vgmF_	Alignment	not modelled	95.4	19	PDB header: transport protein Chain: F: PDB Molecule: Chimeric Nav1.7-NavAb PDBTitle: cryoem structure of nav1.7 in complex with engineered conformationally rigid fab 7a9.4ds PDB Entry: PDB RCSB PDBj
65	c5mkfA_	Alignment	not modelled	91.8	19	PDB header: transport protein Chain: A: PDB Molecule: Polycystin-2 PDBTitle: cryoem structure of polycystin-2 in complex with calcium and lipids PDB Entry: PDB RCSB PDBj
66	c8dj1A_	Alignment	not modelled	95.2	19	PDB header: membrane protein Chain: A: PDB Molecule: Ion transport protein PDBTitle: crystal structure of navab v126t as a basis for the human nav1.7 inherited erythromelalgia s241t mutation PDB Entry: PDB RCSB PDBj
67	c7visA_	Alignment	not modelled	92.0	18	PDB header: membrane protein Chain: A: PDB Molecule: Voltage-dependent N-type calcium channel subunit alpha-1B PDBTitle: human n-type voltage gated calcium channel cav2.2-alpha2/delta1-beta1 complex, apo state PDB Entry: PDB RCSB PDBj
68	c7w77C_	Alignment	not modelled	83.9	19	PDB header: membrane protein Chain: C: PDB Molecule: Sodium channel protein type 3 subunit alpha PDBTitle: cryo-em structure of human nav1.3/beta1/beta2-bulleyaconitinea PDB Entry: PDB RCSB PDBj
69	c8e5bA_	Alignment	not modelled	92.1	16	PDB header: transport protein Chain: A: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1D PDBTitle: human l-type voltage-gated calcium channel cav1.3 in the presence of amiodarone and sofosbuvir at 3.3 angstrom resolution PDB Entry: PDB RCSB PDBj
70	c6zqpA_	Alignment	not modelled	97.3	15	PDB header: peptide binding protein Chain: A: PDB Molecule: PMT2 isoform 1 PDBTitle: structure of the pmt2-mir domain with bound ligands PDB Entry: PDB RCSB PDBj
71	c7uhgB_	Alignment	not modelled	90.9	16	PDB header: transport protein Chain: B: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1D PDBTitle: human l-type voltage-gated calcium channel cav1.3 at 3.0 angstrom resolution PDB Entry: PDB RCSB PDBj
72	c6dn7A_	Alignment	not modelled	96.8	21	PDB header: immune system/inhibitor Chain: A: PDB Molecule: SPRY domain-containing SOCS box protein 4 PDBTitle: spry domain-containing socs box protein 2 complexed with wdlnnn(bal) cyclic peptide inhibitor PDB Entry: PDB RCSB PDBj
73	c8okxB_	Alignment	not modelled	98.3	21	PDB header: immune system Chain: B: PDB Molecule: SPRY domain-containing SOCS box protein 3 PDBTitle: structure of cgas in complex with spsb3-elobc PDB Entry: PDB RCSB PDBj
74	c8hmaA_	Alignment	not modelled	91.6	17	PDB header: membrane protein Chain: A: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha PDBTitle: cryo-em structure of human high-voltage activated l-type calcium channel cav1.2 in complex with tetrandrine (tet) PDB Entry: PDB RCSB PDBj










75	c7k48D_	Alignment	not modelled	92.9	19	PDB header: membrane protein Chain: D: PDB Molecule: Maltose/maltodextrin-binding periplasmic protein, ion transport protein, Sodium channel protein type 9 subunit alpha chimera PDBTitle: structure of navab/nav1.7-vs2a chimera trapped in the resting state by tarantula toxin m3-huwentoxin-iv PDB Entry: PDB RCSB PDBj
76	c8e57A_	Alignment	not modelled	93.5	16	PDB header: transport protein Chain: A: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1S PDBTitle: rabbit l-type voltage-gated calcium channel cav1.1 in the presence of amiodarone and 100 microm mni-1 at 2.8 angstrom resolution PDB Entry: PDB RCSB PDBj
77	c8x90A_	Alignment	not modelled	88.7	18	PDB header: membrane protein Chain: A: PDB Molecule: Voltage-dependent P/Q-type calcium channel subunit alpha-1A PDBTitle: p/q type calcium channel PDB Entry: PDB RCSB PDBj
78	c5mkfD_	Alignment	not modelled	92.4	17	PDB header: transport protein Chain: D: PDB Molecule: Polycystin-2 PDBTitle: cryoem structure of polycystin-2 in complex with calcium and lipids PDB Entry: PDB RCSB PDBj
79	c7eebB_	Alignment	not modelled	96.9	15	PDB header: protein transport Chain: B: PDB Molecule: Cation channel sperm-associated protein 2 PDBTitle: structure of the catspermasome PDB Entry: PDB RCSB PDBj
80	c6kjB_	Alignment	not modelled	96.1	18	PDB header: protein binding Chain: B: PDB Molecule: SPRY domain-containing SOCS box protein 2 PDBTitle: crystal structure of human spsb2 in the apo-state PDB Entry: PDB RCSB PDBj
81	c3emwA_	Alignment	not modelled	97.0	19	PDB header: apoptosis Chain: A: PDB Molecule: SPRY domain-containing SOCS box protein 2 PDBTitle: :crystal structure of human spla/ryanodine receptor domain and socs box containing 2 (spsb2) in complex with a 20-residue vasa peptide; PDB Entry: PDB RCSB PDBj
82	c8fd7B_	Alignment	not modelled	90.5	16	PDB header: membrane protein Chain: B: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1C PDBTitle: structure of the human l-type voltage-gated calcium channel cav1.2 complexed with rananentin

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

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

99	c8we8A_	Alignment	not modelled	92.8	13	PDB header: membrane protein Chain: A: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1C PDBTitle: ;human l-type voltage-gated calcium channel cav1.2 in the presence of calciseptine, amlodipine and pinaverium at 2.9 angstrom resolution; PDB Entry: PDBe RCSB PDBj
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100	c8rx8A_		not modelled	96.5	15	PDB header: signaling protein Chain: A: PDB Molecule: Probable calcium-binding protein CML18 PDBTitle: the structure of cml18 in complex with 4 ca2+ ions PDB Entry: PDBe RCSB PDBj
101	c8we7A_		not modelled	93.5	13	PDB header: membrane protein Chain: A: PDB Molecule: Voltage-dependent L-type calcium channel subunit alpha-1C PDBTitle: human l-type voltage-gated calcium channel cav1.2 in the presence of calciseptine at 3.2 angstrom resolution PDB Entry: PDBe RCSB PDBj
102	c8uwwC_		not modelled	96.0	15	PDB header: motor protein Chain: C: PDB Molecule: Troponin C, slow skeletal and cardiac muscles PDBTitle: the structure of the native cardiac thin filament troponin core in ca2+-free state from the upper strand PDB Entry: PDBe RCSB PDBj
103	c8v0kC_		not modelled	96.0	15	PDB header: motor protein Chain: C: PDB Molecule: Troponin C, slow skeletal and cardiac muscles PDBTitle: the structure of the native cardiac thin filament troponin core in ca2+-bound partially activated state from the lower strand PDB Entry: PDBe RCSB PDBj
104	c7tdfB_		not modelled	92.4	15	PDB header: transport protein Chain: B: PDB Molecule: Two pore calcium channel protein 1 PDBTitle: attpc1 d454n with 1 mm edta state i PDB Entry: PDBe RCSB PDBj
105	c6uw4C_		not modelled	89.8	14	PDB header: membrane protein Chain: C: PDB Molecule: Transient receptor potential cation channel subfamily V member 3 PDBTitle: cryo-em structure of human trpv3 determined in lipid nanodisc PDB Entry: PDBe RCSB PDBj
106	c6uw4D_		not modelled	89.8	14	PDB header: membrane protein Chain: D: PDB Molecule: Transient receptor potential cation channel subfamily V member 3 PDBTitle: cryo-em structure of human trpv3 determined in lipid nanodisc PDB Entry: PDBe RCSB PDBj
107	c8f0pA_		not modelled	88.9	14	PDB header: membrane protein/inhibitor Chain: A: PDB Molecule: Sodium channel protein PaFPC1, Sodium channel protein type 9 subunit alpha chimera PDBTitle: structure of vsd4-nav1.7-navpas channel chimera bound to the hybrid inhibitor gne-1305 PDB Entry: PDBe RCSB PDBj
108	c1ggzA_		not modelled	95.3	18	PDB header: metal binding protein Chain: A: PDB Molecule: CALMODULIN-RELATED PROTEIN NB-1 PDBTitle: crystal structure of the calmodulin-like protein (hclp) from human epithelial cells PDB Entry: PDBe RCSB PDBj
109	c8v6nD_		not modelled	89.4	14	PDB header: membrane protein Chain: D: PDB Molecule: Transient receptor potential cation channel subfamily V member 3 PDBTitle: open-state cryo-em structure of human trpv3 in presence of 2-apb in cnw30 nanodiscs PDB Entry: PDBe RCSB PDBj
110	c8v6mD_		not modelled	87.8	14	PDB header: membrane protein Chain: D: PDB Molecule: Transient receptor potential cation channel subfamily V member 3 PDBTitle: inactivated-state cryo-em structure of human trpv3 in presence of tetrahydrocannabivarin (thcv) in cnw30 nanodiscs PDB Entry: PDBe RCSB PDBj

111	c8g3dQ_		not modelled	95.3	12	PDB header: structural protein Chain: Q: PDB Molecule: RIB57 PDBTitle: 48-nm doublet microtubule from tetrahymena thermophila strain k40r PDB Entry: PDBe RCSB PDBj
112	c2ro8A_		not modelled	88.9	33	PDB header: metal binding protein Chain: A: PDB Molecule: Calmodulin PDBTitle: solution structure of calcium bound soybean calmodulin isoform 1 n-terminal domain PDB Entry: PDBe RCSB PDBj
113	c7wlkA_		not modelled	90.2	11	PDB header: membrane protein Chain: A: PDB Molecule: Voltage-dependent T-type calcium channel subunit alpha-1I PDBTitle: cryoem structure of human low-voltage activated t-type calcium channel cav3.3 in complex with otilonium bromide(ob) PDB Entry: PDBe RCSB PDBj
114	c7dtcA_		not modelled	88.2	14	PDB header: membrane protein Chain: A: PDB Molecule: Sodium channel protein type 5 subunit alpha PDBTitle: voltage-gated sodium channel nav1.5-e1784k PDB Entry: PDBe RCSB PDBj
115	c1sjjB_		not modelled	87.9	10	PDB header: contractile protein Chain: B: PDB Molecule: actinin PDBTitle: cryo-em structure of chicken gizzard smooth muscle alpha-actinin PDB Entry: PDBe RCSB PDBj
116	c2scpA_		not modelled	93.8	15	PDB header: binding protein Chain: A: PDB Molecule: SARCOPLASMIC CALCIUM-BINDING PROTEIN PDBTitle: structure of a sarcoplasmic calcium-binding protein from nereis diversicolor refined at 2.0 angstroms resolution PDB Entry: PDBe RCSB PDBj
117	c6xqoA_		not modelled	94.1	15	PDB header: calcium binding protein Chain: A: PDB Molecule: Calcium uptake protein 1, mitochondrial PDBTitle: structure of the human micu1-micu2 heterodimer, calcium bound, in association with a lipid nanodisc PDB Entry: PDBe RCSB PDBj
118	c5xsyA_		not modelled	93.5	14	PDB header: membrane protein Chain: A: PDB Molecule: Sodium channel protein PDBTitle: structure of the nav1.4-beta1 complex from electric eel PDB Entry: PDBe RCSB PDBj
119	c7qioE_		not modelled	95.1	17	PDB header: motor protein Chain: E: PDB Molecule: Myosin regulatory light chain 2, skeletal muscle isoform PDBTitle: homology model of myosin neck domain in skeletal sarcomere PDB Entry: PDBe RCSB PDBj

				PDB Entry: PDBe RCSB PDBj	
				PDB header: metal binding protein	
				Chain: A: PDB Molecule: Sarcoplasmic calcium-binding protein	
				PDBTitle: solution structure and dynamics of nereis sarcoplasmic calcium binding protein	
				PDB Entry: PDBe RCSB PDBj	
120	c1q80A_	Alignment	not modelled	92.9	15