
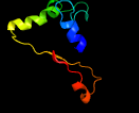
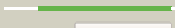














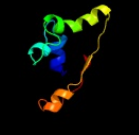

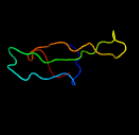




Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2901c (-)_3211813_3212118
Date	Thu Aug 8 16:20:05 BST 2019
Unique Job ID	7c60b5178c7b63c6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2cg9A_	 Alignment		61.6	21	PDB header: chaperone Chain: A: PDB Molecule: atp-dependent molecular chaperone hsp82; PDBTitle: crystal structure of an hsp90-sba1 closed chaperone complex
2	c5ulsA_	 Alignment		53.3	27	PDB header: chaperone Chain: A: PDB Molecule: endoplasmic; PDBTitle: structure of grp94 in the active conformation
3	d2fa8a1	 Alignment		45.9	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
4	c5fwkA_	 Alignment		42.6	21	PDB header: signaling protein Chain: A: PDB Molecule: heat shock protein hsp 90 beta; PDBTitle: atomic cryoem structure of hsp90-cdc37-cdk4 complex
5	c2ojlB_	 Alignment		40.3	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
6	c4ipeA_	 Alignment		37.1	32	PDB header: chaperone Chain: A: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: crystal structure of mitochondrial hsp90 (trap1) with amppnp
7	c2p0gB_	 Alignment		36.3	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: selenoprotein w-related protein; PDBTitle: crystal structure of selenoprotein w-related protein from vibrio2 cholerae. northeast structural genomics target vcr75
8	c5tthA_	 Alignment		29.7	34	PDB header: chaperone Chain: A: PDB Molecule: c-terminal spycatcher fusion of wildtype zebrafish tnf PDBTitle: heterodimeric spycatcher/spytag-fused zebrafish trap1 in atp/adp-2 hybrid state
9	c4j0bB_	 Alignment		21.6	29	PDB header: chaperone Chain: B: PDB Molecule: tnf receptor-associated protein 1; PDBTitle: structure of mitochondrial hsp90 (trap1) with adp-bef3
10	c3metB_	 Alignment		19.4	29	PDB header: transcription Chain: B: PDB Molecule: saga-associated factor 29 homolog; PDBTitle: crystal structure of sgf29 in complex with h3k4me2
11	c2obkE_	 Alignment		14.1	16	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: sel1/selw/selh selenoprotein domain; PDBTitle: x-ray structure of the putative se binding protein from pseudomonas2 fluorescens. northeast structural genomics consortium target plr6.

12	c3pehB_	Alignment		13.2	29	PDB header: chaperone Chain: B: PDB Molecule: endoplasmin homolog; PDBTitle: crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pfl1070c in the presence of a thienopyrimidine derivative
13	c3dupB_	Alignment		11.2	33	PDB header: hydrolase Chain: B: PDB Molecule: mutt/nudix family protein; PDBTitle: crystal structure of mutt/nudix family hydrolase from rhodospirillum2 rubrum atcc 11170
14	c3oq0D_	Alignment		11.2	39	PDB header: cell cycle Chain: D: PDB Molecule: dbf4; PDBTitle: crystal structure of motif n of saccharomyces cerevisiae dbf4
15	c6qpiA_	Alignment		10.5	37	PDB header: membrane protein Chain: A: PDB Molecule: anoctamin-6; PDBTitle: cryo-em structure of calcium-free mtmem16f lipid scramblase in2 nanodisc
16	c6bgiA_	Alignment		9.2	27	PDB header: membrane protein Chain: A: PDB Molecule: anoctamin-1; PDBTitle: cryo-em structure of the tmem16a calcium-activated chloride channel in2 nanodisc
17	c5nl2A_	Alignment		8.8	26	PDB header: membrane protein Chain: A: PDB Molecule: anoctamin-1; PDBTitle: cryo-em structure of the mtmem16a ion channel at 6.6 a resolution.
18	c1wwtA_	Alignment		7.9	33	PDB header: ligase Chain: A: PDB Molecule: threonyl-trna synthetase, cytoplasmic; PDBTitle: solution structure of the tgs domain from human threonyl-2 trna synthetase
19	c2npbA_	Alignment		7.2	29	PDB header: oxidoreductase Chain: A: PDB Molecule: selenoprotein w; PDBTitle: nmr solution structure of mouse selw
20	c2o1uA_	Alignment		7.0	28	PDB header: chaperone Chain: A: PDB Molecule: endoplasmin; PDBTitle: structure of full length grp94 with amp-pnp bound
21	c3q8jA_	Alignment	not modelled	6.2	45	PDB header: toxin Chain: A: PDB Molecule: asteropsin a; PDBTitle: crystal structure of asteropsin a from marine sponge asteropus sp.
22	c6qpbB_	Alignment	not modelled	6.2	37	PDB header: membrane protein Chain: B: PDB Molecule: anoctamin-6; PDBTitle: cryo-em structure of calcium-free mtmem16f lipid scramblase in2 digitonin
23	c4witB_	Alignment	not modelled	6.1	41	PDB header: lipid transport Chain: B: PDB Molecule: predicted protein; PDBTitle: tmem16 lipid scramblase in crystal form 2
24	d1ogmx1	Alignment	not modelled	6.1	32	Fold: Dextranase, N-terminal domain Superfamily: Dextranase, N-terminal domain Family: Dextranase, N-terminal domain
25	c2o1wB_	Alignment	not modelled	5.9	25	PDB header: chaperone Chain: B: PDB Molecule: endoplasmin; PDBTitle: structure of n-terminal plus middle domains (n+m) of grp94
26	c6qpcB_	Alignment	not modelled	5.7	37	PDB header: membrane protein Chain: B: PDB Molecule: anoctamin-6; PDBTitle: cryo-em structure of calcium-bound mtmem16f lipid scramblase in2 nanodisc
27	d2iwgb1	Alignment	not modelled	5.5	23	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: SPRY domain
28	c5oygA_	Alignment	not modelled	5.4	27	PDB header: membrane protein Chain: A: PDB Molecule: anoctamin-1; PDBTitle: structure of calcium-free mtmem16a chloride channel at 4.06 a2 resolution