
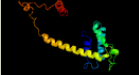



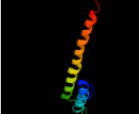
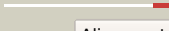









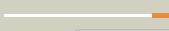
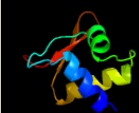




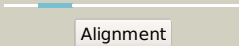





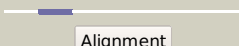
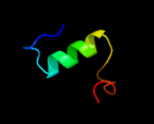
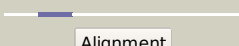
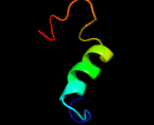
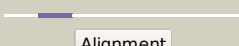

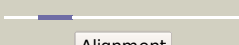
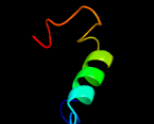





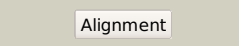




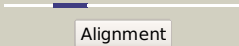



# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1709_(-)_1937320_1938156
Date	Fri Aug 2 13:30:31 BST 2019
Unique Job ID	ddb3b7cd916afd57

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4i98A_</a>	 Alignment		100.0	25	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> segregation and condensation protein a; <b>PDBTitle:</b> crystal structure of the complex between scpa(residues 1-160)-2 scpb(residues 1-183)
2	<a href="#">c3w6jA_</a>	 Alignment		100.0	32	<b>PDB header:</b> cell cycle <b>Chain:</b> A; <b>PDB Molecule:</b> scpa; <b>PDBTitle:</b> crystal structure of scpab core complex
3	<a href="#">c3zgxZ_</a>	 Alignment		99.9	40	<b>PDB header:</b> cell cycle <b>Chain:</b> Z; <b>PDB Molecule:</b> segregation and condensation protein a; <b>PDBTitle:</b> crystal structure of the kleisin-n smc interface in2 prokaryotic condensin
4	<a href="#">c5h67C_</a>	 Alignment		99.5	25	<b>PDB header:</b> dna binding protein/cell cycle <b>Chain:</b> C; <b>PDB Molecule:</b> segregation and condensation protein a; <b>PDBTitle:</b> crystal structure of the bacillus subtilis smc head domain complexed2 with the cognate scpa c-terminal domain and soaked atp
5	<a href="#">c1w1wF_</a>	 Alignment		98.6	18	<b>PDB header:</b> cell adhesion <b>Chain:</b> F; <b>PDB Molecule:</b> sister chromatid cohesion protein 1; <b>PDBTitle:</b> sc smc1hd:scc1-c complex, atpgs
6	<a href="#">d1w1we_</a>	 Alignment		98.6	18	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> "Winged helix" DNA-binding domain <b>Family:</b> Rad21/Rec8-like
7	<a href="#">c4i99C_</a>	 Alignment		98.3	32	<b>PDB header:</b> dna binding protein <b>Chain:</b> C; <b>PDB Molecule:</b> putative uncharacterized protein; <b>PDBTitle:</b> crystal structure of the smchead bound to the c-winged helix domain of2 scpa
8	<a href="#">c6qj4E_</a>	 Alignment		86.6	23	<b>PDB header:</b> cell cycle <b>Chain:</b> E; <b>PDB Molecule:</b> condensin complex subunit 2; <b>PDBTitle:</b> crystal structure of the c. thermophilum condensin ycs4-brn12 subcomplex bound to the smc4 atpase head in complex with the c-3 terminal domain of brn1
9	<a href="#">c2i01A_</a>	 Alignment		84.1	17	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein bvu3908 from bacteroides vulgatus,2 northeast structural genomics consortium target bvr153
10	<a href="#">c2i02B_</a>	 Alignment		62.8	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of protein bt2368 from bacteroides2 thetaiotaomicron, northeast structural genomics consortium target3 btr375
11	<a href="#">c3f41B_</a>	 Alignment		57.5	7	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> structure of the tandemly repeated protein tyrosine2 phosphatase like phytase from mitsuokella multacida

12	<a href="#">d1whqa_</a>	 Alignment		34.5	22	<b>Fold:</b> dsRBD-like <b>Superfamily:</b> dsRNA-binding domain-like <b>Family:</b> Double-stranded RNA-binding domain (dsRBD)
13	<a href="#">c2qdoC_</a>	 Alignment		20.9	21	<b>PDB header:</b> photosynthesis <b>Chain:</b> C; <b>PDB Molecule:</b> nbla protein; <b>PDBTitle:</b> nbla protein from t. vulcanus
14	<a href="#">c1u24A_</a>	 Alignment		19.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> myo-inositol hexaphosphate phosphohydrolase; <b>PDBTitle:</b> crystal structure of selenomonas ruminantium phytase
15	<a href="#">c2bbrA_</a>	 Alignment		19.9	17	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> viral casp8 and fadd-like apoptosis regulator; <b>PDBTitle:</b> crystal structure of mc159 reveals molecular mechanism of 2 disc assembly and vflip inhibition
16	<a href="#">d2gf5a2</a>	 Alignment		18.8	20	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH effector domain, DED
17	<a href="#">c2bbzC_</a>	 Alignment		18.1	17	<b>PDB header:</b> viral protein <b>Chain:</b> C; <b>PDB Molecule:</b> viral casp8 and fadd-like apoptosis regulator; <b>PDBTitle:</b> crystal structure of mc159 reveals molecular mechanism of 2 disc assembly and vflip inhibition
18	<a href="#">c2ls7A_</a>	 Alignment		16.8	10	<b>PDB header:</b> apoptosis <b>Chain:</b> A; <b>PDB Molecule:</b> astrocytic phosphoprotein pea-15; <b>PDBTitle:</b> high definition solution structure of ped/pea-15 death effector domain
19	<a href="#">d1locka_</a>	 Alignment		14.3	17	<b>Fold:</b> Amidase signature (AS) enzymes <b>Superfamily:</b> Amidase signature (AS) enzymes <b>Family:</b> Amidase signature (AS) enzymes
20	<a href="#">d2ixma1</a>	 Alignment		13.8	18	<b>Fold:</b> PTPA-like <b>Superfamily:</b> PTPA-like <b>Family:</b> PTPA-like
21	<a href="#">c3mhcC_</a>	 Alignment	not modelled	13.7	3	<b>PDB header:</b> protein transport <b>Chain:</b> C; <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4; <b>PDBTitle:</b> crystal structure of vps4 and vta1
22	<a href="#">d1h99a2</a>	 Alignment	not modelled	10.4	18	<b>Fold:</b> PTS-regulatory domain, PRD <b>Superfamily:</b> PTS-regulatory domain, PRD <b>Family:</b> PTS-regulatory domain, PRD
23	<a href="#">d1b34b_</a>	 Alignment	not modelled	10.1	27	<b>Fold:</b> Sm-like fold <b>Superfamily:</b> Sm-like ribonucleoproteins <b>Family:</b> Sm motif of small nuclear ribonucleoproteins, SNRNP
24	<a href="#">c1b34B_</a>	 Alignment	not modelled	10.1	27	<b>PDB header:</b> rna binding protein <b>Chain:</b> B; <b>PDB Molecule:</b> protein (small nuclear ribonucleoprotein sm d2); <b>PDBTitle:</b> crystal structure of the d1d2 sub-complex from the human snrnp core2 domain
25	<a href="#">c2g62A_</a>	 Alignment	not modelled	9.9	18	<b>PDB header:</b> hydrolase activator <b>Chain:</b> A; <b>PDB Molecule:</b> protein phosphatase 2a, regulatory subunit b' (pr 53); <b>PDBTitle:</b> crystal structure of human ptpa
26	<a href="#">c5h6tB_</a>	 Alignment	not modelled	9.6	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> amidase; <b>PDBTitle:</b> crystal structure of hydrazidase from microbacterium sp. strain hm58-2
27	<a href="#">c4xypA_</a>	 Alignment	not modelled	9.5	15	<b>PDB header:</b> viral protein <b>Chain:</b> A; <b>PDB Molecule:</b> fusion protein; <b>PDBTitle:</b> crystal structure of a piscine viral fusion protein
28	<a href="#">c1ydnA_</a>	 Alignment	not modelled	9.3	17	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of the hmg-coa lyase from brucella melitensis,2 northeast structural genomics target lr35.

29	<a href="#">d2ozza1</a>	Alignment	not modelled	9.0	38	<b>Fold:</b> Periplasmic binding protein-like II <b>Superfamily:</b> Periplasmic binding protein-like II <b>Family:</b> Phosphate binding protein-like
30	<a href="#">d1wg8a1</a>	Alignment	not modelled	8.7	23	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Putative methyltransferase TM0872, insert domain <b>Family:</b> Putative methyltransferase TM0872, insert domain
31	<a href="#">d1n3ka</a>	Alignment	not modelled	8.5	10	<b>Fold:</b> DEATH domain <b>Superfamily:</b> DEATH domain <b>Family:</b> DEATH effector domain, DED
32	<a href="#">c3r6uA</a>	Alignment	not modelled	8.2	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> choline-binding protein; <b>PDBTitle:</b> crystal structure of choline binding protein opubc from bacillus2 subtilis
33	<a href="#">d1m6ya1</a>	Alignment	not modelled	8.2	30	<b>Fold:</b> SAM domain-like <b>Superfamily:</b> Putative methyltransferase TM0872, insert domain <b>Family:</b> Putative methyltransferase TM0872, insert domain
34	<a href="#">c2l2iB</a>	Alignment	not modelled	8.2	86	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> krueppel-like factor 1; <b>PDBTitle:</b> nmr structure of the complex between the tfb1 subunit of tfiih and the2 activation domain of ekf
35	<a href="#">c3pccX</a>	Alignment	not modelled	7.9	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem i 4.8k protein; <b>PDBTitle:</b> femtosecond x-ray protein nanocrystallography
36	<a href="#">c5j0fA</a>	Alignment	not modelled	7.8	32	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> superoxide dismutase [cu-zn],oxidoreductase,superoxide <b>PDBTitle:</b> monomeric human cu,zn superoxide dismutase, loops iv and vii deleted,2 apo form, circular permutant p4/5
37	<a href="#">c5ganm</a>	Alignment	not modelled	7.6	20	<b>PDB header:</b> transcription <b>Chain:</b> M: <b>PDB Molecule:</b> <b>PDBTitle:</b> the overall structure of the yeast spliceosomal u4/u6.u5 tri-snrnp at2 3.7 angstrom
38	<a href="#">c1jb0X</a>	Alignment	not modelled	7.2	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem i subunit psax; <b>PDBTitle:</b> crystal structure of photosystem i: a photosynthetic reaction center2 and core antenna system from cyanobacteria
39	<a href="#">c4fe1X</a>	Alignment	not modelled	7.2	44	<b>PDB header:</b> photosynthesis <b>Chain:</b> X: <b>PDB Molecule:</b> photosystem i 4.8k protein; <b>PDBTitle:</b> improving the accuracy of macromolecular structure refinement at 7 a2 resolution
40	<a href="#">d1jb0x</a>	Alignment	not modelled	7.2	44	<b>Fold:</b> Single transmembrane helix <b>Superfamily:</b> Subunit Psax of photosystem I reaction centre <b>Family:</b> Subunit Psax of photosystem I reaction centre
41	<a href="#">d2pt0a1</a>	Alignment	not modelled	7.2	15	<b>Fold:</b> (Phosphotyrosine protein) phosphatases II <b>Superfamily:</b> (Phosphotyrosine protein) phosphatases II <b>Family:</b> Myo-inositol hexaphosphate phosphohydrolase (phytase) PhyA
42	<a href="#">c4z7eB</a>	Alignment	not modelled	7.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> lmo1422 protein; <b>PDBTitle:</b> soluble binding domain of lmo1422 abc-transporter
43	<a href="#">c4tvvA</a>	Alignment	not modelled	6.9	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> tyrosine phosphatase ii superfamily protein; <b>PDBTitle:</b> crystal structure of lppa from legionella pneumophila
44	<a href="#">d2azeb1</a>	Alignment	not modelled	6.8	35	<b>Fold:</b> E2F-DP heterodimerization region <b>Superfamily:</b> E2F-DP heterodimerization region <b>Family:</b> E2F dimerization segment
45	<a href="#">d1v2za</a>	Alignment	not modelled	6.8	15	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
46	<a href="#">c1xhoB</a>	Alignment	not modelled	6.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> chorismate mutase; <b>PDBTitle:</b> chorismate mutase from clostridium thermocellum cth-682
47	<a href="#">d1xhoa</a>	Alignment	not modelled	6.7	18	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> Chorismate mutase
48	<a href="#">c2gppD</a>	Alignment	not modelled	6.5	36	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> nuclear receptor-interacting protein 1; <b>PDBTitle:</b> estrogen related receptor-gamma ligand binding domain2 complexed with a rip140 peptide and synthetic ligand3 gsk4716
49	<a href="#">c4ljoA</a>	Alignment	not modelled	6.5	39	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> e3 ubiquitin-protein ligase rnf31; <b>PDBTitle:</b> structure of an active ligase (hoip)/ubiquitin transfer complex
50	<a href="#">c3l6gA</a>	Alignment	not modelled	6.3	27	<b>PDB header:</b> glycine betaine-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> betaine abc transporter permease and substrate binding <b>PDBTitle:</b> crystal structure of lactococcal opuac in its open conformation
51	<a href="#">c5jqeA</a>	Alignment	not modelled	6.3	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> sugar abc transporter substrate-binding protein,caspase-8 <b>PDBTitle:</b> crystal structure of caspase8 tded
52	<a href="#">d1fnja</a>	Alignment	not modelled	6.3	24	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> Chorismate mutase
53	<a href="#">c5ir0B</a>	Alignment	not modelled	6.3	33	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein orf19; <b>PDBTitle:</b> crystal structure of protein of unknown function orf19 from vibrio2 cholerae o1 picl-like element, c57s i109m mutant
54	<a href="#">c2do5A</a>	Alignment	not modelled	6.2	38	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> splicing factor 3b subunit 2; <b>PDBTitle:</b> solution structure of the sap domain of human splicing2 factor 3b subunit 2

55	<a href="#">d1sv1a_</a>	Alignment	not modelled	6.0	15	<b>Fold:</b> KaiA/RbsU domain <b>Superfamily:</b> KaiA/RbsU domain <b>Family:</b> Circadian clock protein KaiA, C-terminal domain
56	<a href="#">c5gveA_</a>	Alignment	not modelled	5.7	16	<b>PDB header:</b> isomerase/protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> dna topoisomerase 3-beta-1; <b>PDBTitle:</b> human top3b-ttdr3 complex
57	<a href="#">d2iboa1</a>	Alignment	not modelled	5.7	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
58	<a href="#">c2v6xA_</a>	Alignment	not modelled	5.7	14	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> vacuolar protein sorting-associated protein 4; <b>PDBTitle:</b> structural insight into the interaction between escrt-iii and vps4
59	<a href="#">c5jwrE_</a>	Alignment	not modelled	5.7	15	<b>PDB header:</b> transcription regulator <b>Chain:</b> E: <b>PDB Molecule:</b> circadian clock protein kaia; <b>PDBTitle:</b> crystal structure of foldswitch-stabilized kaib in complex with the n-2 terminal ci domain of kaic and a dimer of kaia c-terminal domains3 from thermosynechococcus elongatus
60	<a href="#">c5j2yA_</a>	Alignment	not modelled	5.6	26	<b>PDB header:</b> gene regulation/dna <b>Chain:</b> A: <b>PDB Molecule:</b> regulatory protein; <b>PDBTitle:</b> molecular insight into the regulatory mechanism of the quorum-sensing2 repressor rsal in pseudomonas aeruginosa
61	<a href="#">d1yqha1</a>	Alignment	not modelled	5.6	33	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
62	<a href="#">c3d7aB_</a>	Alignment	not modelled	5.5	19	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> upf0201 protein ph1010; <b>PDBTitle:</b> crystal structure of duf54 family protein ph1010 from2 hyperthermophilic archaea pyrococcus horikoshii ot3
63	<a href="#">d1lxna_</a>	Alignment	not modelled	5.4	27	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> MTH1187/YkoF-like <b>Family:</b> MTH1187-like
64	<a href="#">d1dbfa_</a>	Alignment	not modelled	5.4	24	<b>Fold:</b> Bacillus chorismate mutase-like <b>Superfamily:</b> YjgF-like <b>Family:</b> Chorismate mutase
65	<a href="#">d1pdza1</a>	Alignment	not modelled	5.2	27	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> Enolase
66	<a href="#">c3bw1A_</a>	Alignment	not modelled	5.2	33	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> u6 snrna-associated sm-like protein lsm3; <b>PDBTitle:</b> crystal structure of homomeric yeast lsm3 exhibiting novel octameric2 ring organisation
67	<a href="#">d1g8fa3</a>	Alignment	not modelled	5.1	11	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> ATP sulfurylase C-terminal domain