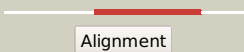
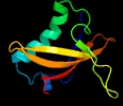
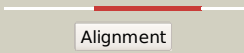



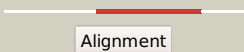

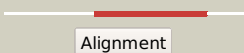

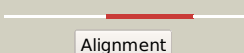

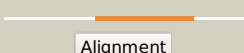


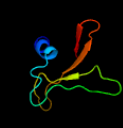


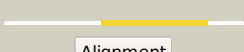

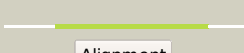



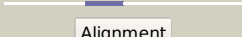
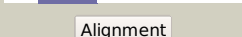
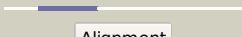

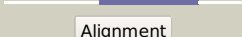
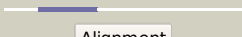
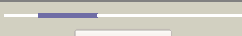
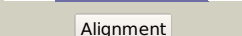
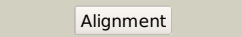
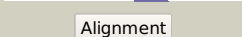
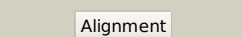
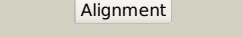
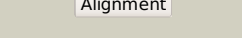

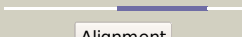
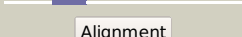

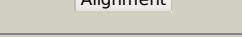


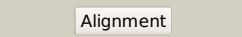
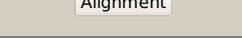

Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2022c (-)_2267127_2267732
Date	Mon Aug 5 13:25:13 BST 2019
Unique Job ID	2709157a58773cc9

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kheA_	 Alignment		97.6	15	PDB header: hydrolase Chain: A; PDB Molecule: toxin-like protein; PDBTitle: solution structure of the bacterial toxin rele from thermus2 thermophilus hb8
2	d1wmia1	 Alignment		97.4	15	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
3	c3bpqD_	 Alignment		96.5	11	PDB header: toxin Chain: D; PDB Molecule: toxin rele3; PDBTitle: crystal structure of relb-rele antitoxin-toxin complex from2 methanococcus jannaschii
4	c3g5oC_	 Alignment		96.2	14	PDB header: toxin/antitoxin Chain: C; PDB Molecule: uncharacterized protein rv2866; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
5	c3kixy_	 Alignment		95.8	18	PDB header: ribosome Chain: Y; PDB Molecule: PDBTitle: structure of rele nuclease bound to the 70s ribosome (postcleavage2 state; part 3 of 4)
6	c3oeiH_	 Alignment		90.4	16	PDB header: toxin, protein binding Chain: H; PDB Molecule: relk (toxin rv3358); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
7	d2a6sa1	 Alignment		88.9	13	Fold: RelE-like Superfamily: RelE-like Family: YoeB/Txe-like
8	c2otrA_	 Alignment		82.6	14	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: hypothetical protein hp0892; PDBTitle: solution structure of conserved hypothetical protein hp0892 from2 helicobacter pylori
9	c5cegB_	 Alignment		81.0	15	PDB header: toxin Chain: B; PDB Molecule: plasmid stabilization system; PDBTitle: x-ray structure of toxin/anti-toxin complex from mesorhizobium2 opportunistum
10	c5ja9D_	 Alignment		72.9	22	PDB header: toxin Chain: D; PDB Molecule: toxin higb-2; PDBTitle: crystal structure of the higb2 toxin in complex with nb6
11	c6feuj_	 Alignment		67.9	19	PDB header: oxidoreductase Chain: J; PDB Molecule: peroxiredoxin; PDBTitle: prxq2, a 1-cys peroxiredoxin of the thermo-acidophilic archaeon2 sulfobolus islandicus

12	c3m3iC_	Alignment		54.0	29	PDB header: unknown function Chain: C: PDB Molecule: putative uncharacterized protein; PDBTitle: hypothetical protein from leishmania major
13	dlyuda1	Alignment		52.3	42	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like
14	d1znpa1	Alignment		48.8	39	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like
15	c5ovqL_	Alignment		48.3	21	PDB header: oxidoreductase Chain: L: PDB Molecule: peroxiredoxin; PDBTitle: crystal structure of the peroxiredoxin (ahpc2) from the2 hyperthermophilic bacteria aquifex aeolicus vf
16	c1psvA_	Alignment		48.3	39	PDB header: designed peptide Chain: A: PDB Molecule: pda8d; PDBTitle: computationally designed peptide with a beta-beta-alpha2 fold selection, nmr, 32 structures
17	c3lzzB_	Alignment		47.6	21	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structures of cupin superfamily bbduf985 from branchiostoma2 belcheri tsingtauense in apo and gdp-bound forms
18	c1y96C_	Alignment		29.8	24	PDB header: rna binding protein Chain: C: PDB Molecule: gem-associated protein 6; PDBTitle: crystal structure of the gemin6/gemin7 heterodimer from the2 human smn complex
19	d1xcca_	Alignment		27.5	14	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
20	c5f3xB_	Alignment		27.4	17	PDB header: structural protein/protein binding Chain: B: PDB Molecule: ankyrin repeat and sam domain-containing protein 4b; PDBTitle: crystal structure of harmonin npdz1 in complex with anks4b sam-pbm
21	d1xe7a_	Alignment	not modelled	26.2	24	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: YML079-like
22	d1z8ma1	Alignment	not modelled	26.1	16	Fold: RelE-like Superfamily: RelE-like Family: RelE-like
23	d1prxa_	Alignment	not modelled	22.5	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
24	c2w1oA_	Alignment	not modelled	22.3	34	PDB header: translation Chain: A: PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: nmr structure of dimerization domain of human ribosomal2 protein p2
25	c2jx3A_	Alignment	not modelled	22.1	45	PDB header: dna binding protein Chain: A: PDB Molecule: protein dek; PDBTitle: nmr solution structure of the n-terminal domain of dek
26	c2v2gC_	Alignment	not modelled	20.7	13	PDB header: oxidoreductase Chain: C: PDB Molecule: peroxiredoxin 6; PDBTitle: crystal structure of the c45s mutant of the peroxiredoxin 62 of arenicola marina. monoclinic form
27	d1phza2	Alignment	not modelled	20.4	17	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
28	c3iz5w_	Alignment	not modelled	19.8	23	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein l22 (l22e); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome

29	c3izcw_	 Alignment	not modelled	19.3	23	PDB header: ribosome Chain: W: PDB Molecule: 60s ribosomal protein rpI22 (I22e); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
30	c3e2tA_	 Alignment	not modelled	18.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 5-hydroxylase 1; PDBTitle: the catalytic domain of chicken tryptophan hydroxylase 12 with bound tryptophan
31	d1toha_	 Alignment	not modelled	18.3	23	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
32	c5x90B_	 Alignment	not modelled	17.3	29	PDB header: protein transport Chain: B: PDB Molecule: icmw; PDBTitle: structure of dotI(656-783)-icms-icmw-lvga derived from legionella2 pneumophila
33	c5cw7H_	 Alignment	not modelled	17.0	19	PDB header: toxin Chain: H: PDB Molecule: plasmid stabilization protein pare; PDBTitle: crystal structure of the paaa2-pare2 antitoxin-toxin complex
34	d1mlwa_	 Alignment	not modelled	16.5	23	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
35	c5jk5A_	 Alignment	not modelled	16.1	19	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: phenylalanine hydroxylase from dictyostelium - bh2 complex
36	d2zcta1	 Alignment	not modelled	15.5	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
37	c1fsdA_	 Alignment	not modelled	15.5	35	PDB header: novel sequence Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures
38	c1fsvA_	 Alignment	not modelled	15.5	35	PDB header: beta beta alpha motif Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, minimized average structure
39	c4v06A_	 Alignment	not modelled	15.4	25	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 5-hydroxylase 2; PDBTitle: crystal structure of human tryptophan hydroxylase 2 (tph2), catalytic2 domain
40	c2pnmA_	 Alignment	not modelled	15.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated
41	c5denA_	 Alignment	not modelled	15.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine-4-hydroxylase; PDBTitle: the first structure of a full-length mammalian phenylalanine2 hydroxylase reveals the architecture of an auto-inhibited tetramer
42	d1j8ua_	 Alignment	not modelled	14.9	17	Fold: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monooxygenases, catalytic and oligomerization domains
43	c3rriB_	 Alignment	not modelled	14.5	15	PDB header: metal binding protein Chain: B: PDB Molecule: glyoxalase/bleomycin resistance protein/dioxygenase; PDBTitle: crystal structure of glyoxalase/bleomycin resistance2 protein/dioxygenase from alicyclobacillus acidocaldarius
44	c5abrB_	 Alignment	not modelled	14.1	39	PDB header: electron transport Chain: B: PDB Molecule: ferredoxin, 2fe-2s; PDBTitle: structure of fes1 protein from azotobacter vinelandii
45	c4ii1A_	 Alignment	not modelled	14.0	36	PDB header: transcription Chain: A: PDB Molecule: zinc finger ccch-type with g patch domain-containing PDBTitle: crystal structure of the zinc finger of zgpat
46	c5hy7D_	 Alignment	not modelled	13.9	19	PDB header: protein binding Chain: D: PDB Molecule: ysf3; PDBTitle: sf3b10-sf3b130 from chaetomium thermophilum
47	c3kxeB_	 Alignment	not modelled	12.8	21	PDB header: protein binding Chain: B: PDB Molecule: toxin protein pare-1; PDBTitle: a conserved mode of protein recognition and binding in a2 pard-pare toxin-antitoxin complex
48	c5vwzB_	 Alignment	not modelled	12.7	75	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3pc
49	c5vwzD_	 Alignment	not modelled	12.7	75	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3pc
50	d1prtF_	 Alignment	not modelled	12.6	20	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
51	d1ttza_	 Alignment	not modelled	12.0	38	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
52	c5ifeB_	Alianment	not modelled	11.7	17	PDB header: splicing Chain: B: PDB Molecule: splicing factor 3b subunit 5;

						PDBTitle: crystal structure of the human sf3b core complex
53	c3vejB_	Alignment	not modelled	11.5	28	PDB header: protein binding Chain: B; PDB Molecule: ubiquitin-like protein mdy2; PDBTitle: crystal structure of the get5 carboxyl domain from s. cerevisiae
54	d2ctka1	Alignment	not modelled	10.6	19	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
55	c4n6bB_	Alignment	not modelled	10.4	18	PDB header: transferase Chain: B; PDB Molecule: serine acetyltransferase apoenzyme; PDBTitle: soybean serine acetyltransferase complexed with coa
56	d1js8a1	Alignment	not modelled	10.3	27	Fold: Di-copper centre-containing domain Superfamily: Di-copper centre-containing domain Family: Hemocyanin middle domain
57	c2m46A_	Alignment	not modelled	10.3	19	PDB header: oxidoreductase Chain: A; PDB Molecule: arsenate reductase, putative; PDBTitle: solution nmr structure of saclo0876 from staphylococcus aureus col,2 nesg target zr353 and csgid target idp00841
58	c5vx3B_	Alignment	not modelled	10.1	78	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
59	d1q1aa_	Alignment	not modelled	9.8	35	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Sir2 family of transcriptional regulators
60	c4q2uH_	Alignment	not modelled	9.7	8	PDB header: toxin/toxin repressor Chain: H; PDB Molecule: mrna interferase yafq; PDBTitle: crystal structure of the e. coli dinj-yafq toxin-antitoxin complex
61	c3qz3A_	Alignment	not modelled	9.6	13	PDB header: oxidoreductase Chain: A; PDB Molecule: ferritin; PDBTitle: the crystal structure of ferritin from vibrio cholerae o1 biovar el2 tor str. n16961
62	d1i2ta_	Alignment	not modelled	9.6	19	Fold: PABP domain-like Superfamily: PABC (PABP) domain Family: PABC (PABP) domain
63	c2hjhB_	Alignment	not modelled	9.5	27	PDB header: hydrolase Chain: B; PDB Molecule: nad-dependent histone deacetylase sir2; PDBTitle: crystal structure of the sir2 deacetylase
64	c3g9dB_	Alignment	not modelled	9.4	38	PDB header: hydrolase Chain: B; PDB Molecule: dinitrogenase reductase activacting PDBTitle: crystal structure glycohydrolase
65	c5gapG_	Alignment	not modelled	9.3	18	PDB header: transcription Chain: G; PDB Molecule: u4/u6 small nuclear ribonucleoprotein prp3; PDBTitle: body region of the u4/u6.u5 tri-snrnp
66	c3b50A_	Alignment	not modelled	9.2	15	PDB header: transport protein Chain: A; PDB Molecule: sialic acid-binding periplasmic protein siap; PDBTitle: structure of h. influenzae sialic acid binding protein2 bound to neu5ac.
67	c4nb2B_	Alignment	not modelled	9.0	16	PDB header: transferase Chain: B; PDB Molecule: metallothiol transferase fosb; PDBTitle: crystal structure of fosb from staphylococcus aureus at 1.89 angstrom2 resolution - apo structure
68	c5vwxB_	Alignment	not modelled	8.9	86	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-h0-h3glt
69	c5vwxD_	Alignment	not modelled	8.9	86	PDB header: apoptosis Chain: D; PDB Molecule: bcl-2-like protein 11; PDBTitle: bak core latch dimer in complex with bim-h0-h3glt
70	c5vx3H_	Alignment	not modelled	8.9	86	PDB header: apoptosis Chain: H; PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
71	c4behB_	Alignment	not modelled	8.9	35	PDB header: translation Chain: B; PDB Molecule: 60s acidic ribosomal protein p2; PDBTitle: solution structure of human ribosomal protein p1.p2 heterodimer
72	c3zi1A_	Alignment	not modelled	8.9	20	PDB header: isomerase Chain: A; PDB Molecule: glyoxalase domain-containing protein 4; PDBTitle: crystal structure of human glyoxalase domain-containing protein 42 (glod4)
73	c3sbcG_	Alignment	not modelled	8.9	21	PDB header: oxidoreductase Chain: G; PDB Molecule: peroxiredoxin tsa1; PDBTitle: crystal structure of saccharomyces cerevisiae tsa1c47s mutant protein
74	c4f52F_	Alignment	not modelled	8.9	14	PDB header: cell cycle/ligase/signaling protein Chain: F; PDB Molecule: glomulin; PDBTitle: structure of a glomulin-rbx1-cul1 complex
75	c5vx0D_	Alignment	not modelled	8.9	86	PDB header: apoptosis Chain: D; PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3glt
76	c5vx3F_	Alignment	not modelled	8.8	86	PDB header: apoptosis Chain: F; PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
77	c5vx3D_	Alignment	not modelled	8.8	86	PDB header: apoptosis Chain: D; PDB Molecule: bcl-2-like protein 11; PDBTitle: bcl-xl in complex with bim-h3pc-rt
78	c5vx2B_	Alignment	not modelled	8.8	86	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim-h3pc-rt
79	c5vvyB_	Alignment	not modelled	8.7	86	PDB header: apoptosis Chain: B; PDB Molecule: bcl-2-like protein 11;

						PDBTitle: bak core latch dimer in complex with bim-h3pc-rt
80	c5vx2D_	Alignment	not modelled	8.7	86	PDB header: apoptosis Chain: D: PDB Molecule: bcl-2-like protein 11; PDBTitle: mcl-1 in complex with bim-h3pc-rt
81	c5vx0B_	Alignment	not modelled	8.7	86	PDB header: apoptosis Chain: B: PDB Molecule: bcl-2-like protein 11; PDBTitle: bak in complex with bim-h3glg
82	c3k1rB_	Alignment	not modelled	8.6	13	PDB header: structural protein Chain: B: PDB Molecule: usher syndrome type-1g protein; PDBTitle: structure of harmonin npdz1 in complex with the sam-pbm of 2 sans
83	c2k6rA_	Alignment	not modelled	8.4	43	PDB header: de novo protein Chain: A: PDB Molecule: full sequence design 1 synthetic superstable; PDBTitle: protein folding on a highly rugged landscape: experimental observation2 of glassy dynamics and structural frustration
84	c5lqwZ_	Alignment	not modelled	8.3	17	PDB header: splicing Chain: Z: PDB Molecule: rds3 complex subunit 10; PDBTitle: yeast activated spliceosome
85	c4ntqB_	Alignment	not modelled	8.2	19	PDB header: toxin Chain: B: PDB Molecule: ecdii; PDBTitle: cdia-ct/cdii toxin and immunity complex from enterobacter cloacae
86	d1qmva_	Alignment	not modelled	8.0	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
87	c2m60A_	Alignment	not modelled	8.0	64	PDB header: antimicrobial protein Chain: A: PDB Molecule: enterocin jsb; PDBTitle: enterocin 7b
88	c3v0rA_	Alignment	not modelled	7.7	29	PDB header: unknown function Chain: A: PDB Molecule: major allergen alt a 1; PDBTitle: crystal structure of alternaria alternata allergen alt a 1
89	c3l6wB_	Alignment	not modelled	7.6	29	PDB header: oxygen binding Chain: B: PDB Molecule: hemocyanin 1; PDBTitle: structure of the collar functional unit (klh1-h) of keyhole limpet2 hemocyanin
90	c1jzpA_	Alignment	not modelled	7.6	45	PDB header: signaling protein Chain: A: PDB Molecule: skeletal dihydropyridine receptor; PDBTitle: modified peptide a (d18-a1) of the rabbit skeletal2 dihydropyridine receptor
91	c1du1A_	Alignment	not modelled	7.6	45	PDB header: signaling protein Chain: A: PDB Molecule: skeletal dihydropyridine receptor; PDBTitle: peptide fragment thr671-leu690 of the rabbit skeletal2 dihydropyridine receptor
92	c5itiA_	Alignment	not modelled	7.3	30	PDB header: signaling protein Chain: A: PDB Molecule: tankyrase-1; PDBTitle: crystal structure of the human tankyrase 1 (tnks) sam domain (d1055r),2 crystal form 2
93	c2kl4A_	Alignment	not modelled	7.3	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2032 protein; PDBTitle: nmr structure of the protein nb7804a
94	c2lkqA_	Alignment	not modelled	7.3	60	PDB header: immune system Chain: A: PDB Molecule: immunoglobulin lambda-like polypeptide 1; PDBTitle: nmr structure of the lambda 5 22-45 peptide
95	d1jk0a_	Alignment	not modelled	7.3	13	Fold: Ferritin-like Superfamily: Ferritin-like Family: Ribonucleotide reductase-like
96	c2v27A_	Alignment	not modelled	7.3	24	PDB header: oxidoreductase Chain: A: PDB Molecule: phenylalanine hydroxylase; PDBTitle: structure of the cold active phenylalanine hydroxylase from colwellia2 psychrerythraea 34h
97	c2h66G_	Alignment	not modelled	7.2	17	PDB header: structural genomics/oxidoreductase Chain: G: PDB Molecule: pv-pf14_0368; PDBTitle: the crystal structure of plasmodium vivax 2-cys2 peroxiredoxin
98	c4nq8B_	Alignment	not modelled	7.0	20	PDB header: protein transport Chain: B: PDB Molecule: putative periplasmic substrate-binding transport protein; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 bordetella bronchiseptica (bb3421), target efi-510039, with density3 modeled as pantoate
99	c4q51A_	Alignment	not modelled	7.0	29	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative molybdenum cofactor biosynthesis2 protein f from burkholderia cenocepacia j2315