
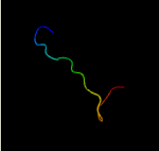
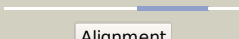
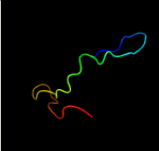
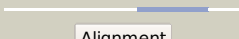
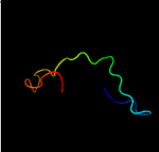



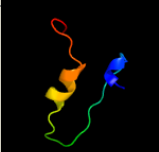

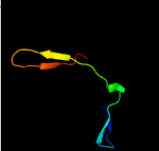





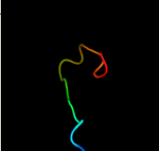



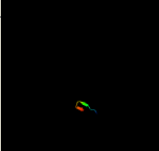
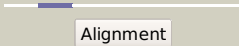
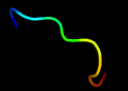




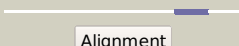

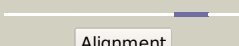

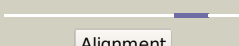

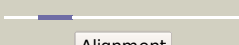
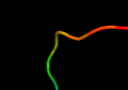




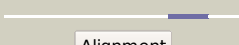
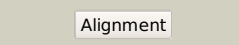

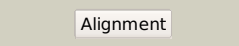

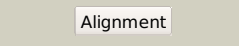

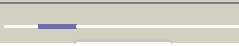


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1954A_(RVBD1954A)_2201284_2201586
Date	Mon Aug 5 13:25:05 BST 2019
Unique Job ID	2cfd192050eb7e86

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2m0oA_	 Alignment		30.5	41	PDB header: peptide binding protein Chain: A: PDB Molecule: phd finger protein 1; PDBTitle: the solution structure of human phf1 in complex with h3k36me3
2	d1iu4a_	 Alignment		28.3	38	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Microbial transglutaminase
3	c3iu0A_	 Alignment		27.1	38	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: structural basis for zymogen activation and substrate binding of 2 transglutaminase from streptomyces mobaraense
4	c1rfoC_	 Alignment		25.7	40	PDB header: viral protein Chain: C: PDB Molecule: whisker antigen control protein; PDBTitle: trimeric foldon of the t4 phagehead fibrin
5	c3co5B_	 Alignment		24.7	28	PDB header: transcription regulator Chain: B: PDB Molecule: putative two-component system transcriptional response PDBTitle: crystal structure of sigma-54 interaction domain of putative 2 transcriptional response regulator from neisseria gonorrhoeae
6	c6g49A_	 Alignment		24.3	33	PDB header: transferase Chain: A: PDB Molecule: protein-glutamine gamma-glutamyltransferase; PDBTitle: crystal structure of the periplasmic domain of tgpa from pseudomonas 2 aeruginosa
7	c2lp7C_	 Alignment		19.4	40	PDB header: viral protein Chain: C: PDB Molecule: envelope glycoprotein; PDBTitle: structure of gp41-m-mat, a membrane associated mper trimer from hiv-12 gp41.
8	c6dkuA_	 Alignment		18.9	40	PDB header: unknown function Chain: A: PDB Molecule: vp35; PDBTitle: crystal structure of myotis vp35 mutant of interferon inhibitory 2 domain
9	c3isrB_	 Alignment		18.6	29	PDB header: hydrolase Chain: B: PDB Molecule: transglutaminase-like enzymes, putative cysteine protease; PDBTitle: the crystal structure of a putative cysteine protease from cytophaga 2 hutchinsonii to 1.9a
10	c4gh9A_	 Alignment		16.9	40	PDB header: viral protein,rna binding protein Chain: A: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of marburg virus vp35 rna binding domain
11	c4xhiB_	 Alignment		15.7	33	PDB header: transcription Chain: B: PDB Molecule: rna-dependent rna polymerase; PDBTitle: crystal structure of native thosea asigna virus rna-dependent rna 2 polymerase (rdrp) at 2.15 angstrom resolution

12	c2m5tA	 Alignment		15.5	50	PDB header: viral protein Chain: A: PDB Molecule: human rhinovirus 2a proteinase; PDBTitle: solution structure of the 2a proteinase from a common cold agent,2 human rhinovirus rv-c02, strain w12
13	c6d9oA	 Alignment		15.2	70	PDB header: toxin Chain: A: PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant e25a
14	c1avyA	 Alignment		14.6	40	PDB header: coiled coil Chain: A: PDB Molecule: fibritin; PDBTitle: fibritin deletion mutant m (bacteriophage t4)
15	c3fkeB	 Alignment		14.4	53	PDB header: rna binding protein Chain: B: PDB Molecule: polymerase cofactor vp35; PDBTitle: structure of the ebola vp35 interferon inhibitory domain
16	c3ks8D	 Alignment		14.0	47	PDB header: viral protein/rna Chain: D: PDB Molecule: polymerase cofactor vp35; PDBTitle: crystal structure of reston ebolavirus vp35 rna binding domain in2 complex with 18bp dsrna
17	c1ox3A	 Alignment		13.8	40	PDB header: chaperone Chain: A: PDB Molecule: fibritin; PDBTitle: crystal structure of mini-fibritin
18	c1z8rA	 Alignment		13.6	60	PDB header: hydrolase Chain: A: PDB Molecule: coxssackievirus b4 polyprotein; PDBTitle: 2a cysteine proteinase from human coxsackievirus b4 (strain2 jvb / benschten / new york / 51)
19	c4p78D	 Alignment		13.5	14	PDB header: toxin Chain: D: PDB Molecule: hica3 toxin; PDBTitle: hica3 and hicb3 toxin-antitoxin complex
20	c3rp7A	 Alignment		13.4	56	PDB header: oxidoreductase Chain: A: PDB Molecule: flavoprotein monooxygenase; PDBTitle: crystal structure of klebsiella pneumoniae hpxo complexed with fad and2 uric acid
21	c1v1hB	 Alignment	not modelled	13.3	39	PDB header: adenovirus Chain: B: PDB Molecule: fibritin, fiber protein; PDBTitle: adenovirus fibre shaft sequence n-terminally fused to the2 bacteriophage t4 fibritin foldon trimerisation motif with a short3 linker
22	c5fn0C	 Alignment	not modelled	12.9	38	PDB header: oxidoreductase Chain: C: PDB Molecule: kynurenine 3-monooxygenase; PDBTitle: crystal structure of pseudomonas fluorescens kynurenine-3-2 monooxygenase (kmo) in complex with gsk180
23	c3j21B	 Alignment	not modelled	12.5	19	PDB header: ribosome Chain: B: PDB Molecule: 50s ribosomal protein l2p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (50s3 ribosomal proteins)
24	d2hrva	 Alignment	not modelled	12.4	40	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
25	c3c4aA	 Alignment	not modelled	12.0	31	PDB header: oxidoreductase Chain: A: PDB Molecule: probable tryptophan hydroxylase viod; PDBTitle: crystal structure of viod hydroxylase in complex with fad from2 chromobacterium violaceum. northeast structural genomics consortium3 target cvr158
26	c211sA	 Alignment	not modelled	11.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yohn; PDBTitle: yp_001336205.1
27	c2dkhA	 Alignment	not modelled	11.6	33	PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of 3-hydroxybenzoate hydroxylase from comamonas2 testosteroni, in complex with the substrate
						PDB header: oxidoreductase Chain: B: PDB Molecule: 2-methyl-3-hydroxypyridine-5-carboxylic

28	c3gmbB_	Alignment	not modelled	10.1	39	acid oxygenase; PDBTitle: crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase
29	c1vw4d_	Alignment	not modelled	10.0	86	PDB header: ribosome Chain: D: PDB Molecule: PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
30	c2qa1A_	Alignment	not modelled	10.0	39	PDB header: oxidoreductase Chain: A: PDB Molecule: polyketide oxygenase pgae; PDBTitle: crystal structure of pgae, an aromatic hydroxylase involved in2 angucycline biosynthesis
31	c1pn0A_	Alignment	not modelled	9.9	38	PDB header: oxidoreductase Chain: A: PDB Molecule: phenol 2-monooxygenase; PDBTitle: phenol hydroxylase from trichosporon cutaneum
32	d1pn0a1	Alignment	not modelled	9.9	38	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain
33	c6h3jA_	Alignment	not modelled	9.5	32	PDB header: protein transport Chain: A: PDB Molecule: protein involved in gliding motility spr; PDBTitle: structural snapshots of the type 9 protein translocon plug-complex
34	d1m1ha1	Alignment	not modelled	9.3	64	Fold: N-utilization substance G protein NusG, insert domain Superfamily: N-utilization substance G protein NusG, insert domain Family: N-utilization substance G protein NusG, insert domain
35	c2a56A_	Alignment	not modelled	9.2	27	PDB header: luminescent protein Chain: A: PDB Molecule: gfp-like non-fluorescent chromoprotein fp595 chain 1; PDBTitle: fluorescent protein asfp595, a143s, on-state, 5min irradiation
36	c1phhA_	Alignment	not modelled	9.2	39	PDB header: oxidoreductase Chain: A: PDB Molecule: p-hydroxybenzoate hydroxylase; PDBTitle: crystal structure of p-hydroxybenzoate hydroxylase complexed with its2 reaction product 3,4-dihydroxybenzoate
37	d1jmab2	Alignment	not modelled	9.0	55	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
38	c3kzsD_	Alignment	not modelled	8.8	21	PDB header: hydrolase Chain: D: PDB Molecule: glycosyl hydrolase family 5; PDBTitle: crystal structure of glycosyl hydrolase family 5 (np_809925.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
39	c6h3iA_	Alignment	not modelled	8.7	32	PDB header: protein transport Chain: A: PDB Molecule: protein involved in gliding motility spr; PDBTitle: structural snapshots of the type 9 protein translocon
40	c3lf4A_	Alignment	not modelled	8.7	33	PDB header: fluorescent protein Chain: A: PDB Molecule: fluorescent timer precursor blue102; PDBTitle: crystal structure of fluorescent timer precursor blue102
41	c4c26A_	Alignment	not modelled	8.6	29	PDB header: toxin Chain: A: PDB Molecule: hica; PDBTitle: solution nmr structure of the hica toxin from burkholderia2 pseudomallei
42	c2e6iA_	Alignment	not modelled	8.5	32	PDB header: transferase Chain: A: PDB Molecule: tyrosine-protein kinase itk/tsk; PDBTitle: solution structure of the btk motif of tyrosine-protein2 kinase itk from human
43	c2l62A_	Alignment	not modelled	8.4	58	PDB header: metal binding protein Chain: A: PDB Molecule: ec protein i/ii; PDBTitle: protein and metal cluster structure of the wheat metallothionein2 domain g-ec-1. the second part of the puzzle.
44	c4yl5A_	Alignment	not modelled	8.0	40	PDB header: transferase Chain: A: PDB Molecule: putative phosphomethylpyrimidine kinase; PDBTitle: structure of a putative phosphomethylpyrimidine kinase from2 acinetobacter baumannii
45	c3es4B_	Alignment	not modelled	7.8	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein duf861 with a rmlc-like cupin fold; PDBTitle: crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
46	c3e1tA_	Alignment	not modelled	7.7	28	PDB header: flavoprotein Chain: A: PDB Molecule: halogenase; PDBTitle: structure and action of the myxobacterial chondrochloren2 halogenase cndh, a new variant of fad-dependent halogenases
47	c4k22A_	Alignment	not modelled	7.7	33	PDB header: oxidoreductase Chain: A: PDB Molecule: protein visc; PDBTitle: structure of the c-terminal truncated form of e.coli c5-hydroxylase2 ubii involved in ubiquinone (q8) biosynthesis
48	c2gw4C_	Alignment	not modelled	7.6	40	PDB header: luminescent protein Chain: C: PDB Molecule: kaede; PDBTitle: crystal structure of stony coral fluorescent protein kaede, red form
49	c2m2rA_	Alignment	not modelled	7.5	75	PDB header: unknown function Chain: A: PDB Molecule: inhibitor cystine knot peptide mch-2; PDBTitle: solution structure of mch-2: a novel inhibitor cystine knot peptide2 from momordica charantia
50	c2l61A_	Alignment	not modelled	7.4	58	PDB header: metal binding protein Chain: A: PDB Molecule: ec protein i/ii; PDBTitle: protein and metal cluster structure of the wheat metallothionein2 domain g-ec-1. the second part of the puzzle.
51	d1k8kb1	Alignment	not modelled	7.2	22	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Actin/HSP70
52	c3i3iA_	Alignment	not modelled	7.1	33	PDB header: hydrolase Chain: A: PDB Molecule: alkylhalidase cmls; PDBTitle: crystal structure of cmls, a flavin-dependent halogenase
						PDB header: metal binding protein

53	c2mfpA	Alignment	not modelled	7.0	43	Chain: A; PDB Molecule: ec protein I/ii; PDBTitle: solution structure of the circular g-domain analog from the wheat2 metallothionein ec-1
54	c2vouA	Alignment	not modelled	7.0	50	PDB header: oxidoreductase Chain: A; PDB Molecule: 2,6-dihydroxypyridine hydroxylase; PDBTitle: structure of 2,6-dihydroxypyridine-3-hydroxylase from2 arthrobacter nicotinovorans
55	c6fviA	Alignment	not modelled	7.0	58	PDB header: cell cycle Chain: A; PDB Molecule: centrosomal protein of 192 kda; PDBTitle: ash / papd-like domain of human cep192 (papd-like domain 7)
56	d1d0gr2	Alignment	not modelled	6.9	42	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
57	c6d93A	Alignment	not modelled	6.9	60	PDB header: toxin Chain: A; PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant y31a
58	c2m2gA	Alignment	not modelled	6.9	75	PDB header: unknown function Chain: A; PDB Molecule: inhibitor cystine knot peptide mch-1; PDBTitle: solution structure of mch-1: a novel inhibitor cystine knot peptide2 from momordica charantia
59	c3fmwC	Alignment	not modelled	6.7	44	PDB header: oxidoreductase Chain: C; PDB Molecule: oxygenase; PDBTitle: the crystal structure of mtmoiv, a baeyer-villiger monooxygenase from2 the mithramycin biosynthetic pathway in streptomyces argillaceus.
60	c4xa9g	Alignment	not modelled	6.7	62	PDB header: structural genomics, unknown function Chain: G; PDB Molecule: gala protein type 1, 3 or 4; PDBTitle: crystal structure of the complex between the n-terminal domain of ravj2 and legl1 from legionella pneumophila str. philadelphia
61	c5evyX	Alignment	not modelled	6.7	50	PDB header: oxidoreductase Chain: X; PDB Molecule: salicylate hydroxylase; PDBTitle: salicylate hydroxylase substrate complex
62	d2nn6c2	Alignment	not modelled	6.6	40	Fold: Ribonuclease PH domain 2-like Superfamily: Ribonuclease PH domain 2-like Family: Ribonuclease PH domain 2-like
63	c2r0gB	Alignment	not modelled	6.5	39	PDB header: oxidoreductase Chain: B; PDB Molecule: rebc; PDBTitle: chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
64	d1bkta	Alignment	not modelled	6.5	100	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
65	c5kowA	Alignment	not modelled	6.4	39	PDB header: oxidoreductase Chain: A; PDB Molecule: pentachlorophenol 4-monooxygenase; PDBTitle: structure of rifampicin monooxygenase
66	c2rgiA	Alignment	not modelled	6.4	39	PDB header: oxidoreductase Chain: A; PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of flavin-containing monooxygenase phzs
67	c2xdoC	Alignment	not modelled	6.2	28	PDB header: oxidoreductase Chain: C; PDB Molecule: tetx2 protein; PDBTitle: structure of the tetracycline degrading monooxygenase tetx2 from2 bacteroides thetaiotaomicron
68	c4hb9A	Alignment	not modelled	5.9	33	PDB header: oxidoreductase Chain: A; PDB Molecule: similarities with probable monooxygenase; PDBTitle: crystal structure of a putative fad containing monooxygenase from2 photorhabdus luminescens subsp. laumondii tto1 (target psi-012791)
69	c5c0rA	Alignment	not modelled	5.8	40	PDB header: viral protein/immune system Chain: A; PDB Molecule: hemagglutinin, envelope glycoprotein, fibrinin fusion PDBTitle: crystal structure of a generation 3 influenza hemagglutinin stabilized2 stem complexed with the broadly neutralizing antibody c179
70	d1g2ra	Alignment	not modelled	5.8	44	Fold: YlxR-like Superfamily: YlxR-like Family: YlxR-like
71	c4n9xA	Alignment	not modelled	5.7	39	PDB header: oxidoreductase Chain: A; PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of the octaprenyl-methyl-methoxy-benzo molecule from2 erwina carotovora subsp. atroseptica strain scri 1043 / atcc baa-672,3 northeast structural genomics consortium (nesg) target ewr161
72	c6c6rA	Alignment	not modelled	5.7	28	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A; PDB Molecule: squalene monooxygenase; PDBTitle: human squalene epoxidase (sqle, squalene monooxygenase) structure with2 fad
73	c6d8tA	Alignment	not modelled	5.7	60	PDB header: toxin Chain: A; PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant e25k/k27e
74	c4bk2A	Alignment	not modelled	5.6	28	PDB header: oxidoreductase Chain: A; PDB Molecule: probable salicylate monooxygenase; PDBTitle: crystal structure of 3-hydroxybenzoate 6-hydroxylase2 uncovers lipid-assisted flavoprotein strategy for3 regioselective aromatic hydroxylation: q301e mutant
75	c6d8sA	Alignment	not modelled	5.5	60	PDB header: toxin Chain: A; PDB Molecule: potassium channel toxin alpha-ktx 5.4; PDBTitle: nmr solution structure of tamapin, mutant k27e
76	c4ebuA	Alignment	not modelled	5.4	26	PDB header: transferase Chain: A; PDB Molecule: 2-dehydro-3-deoxygluconokinase; PDBTitle: crystal structure of a sugar kinase (target efi-502312) from2 oceanicola granulosis, with bound amp/adp crystal form i
77	c6aioA	Alignment	not modelled	5.4	44	PDB header: flavoprotein Chain: A; PDB Molecule: pnpa; PDBTitle: crystal structure of p-nitrophenol 4-monooxygenase pnpa

						from2 pseudomonas putida dll-e4
78	c5dbjA_	Alignment	not modelled	5.3	33	PDB header: flavoprotein Chain: A: PDB Molecule: fadh2-dependent halogenase plta; PDBTitle: crystal structure of halogenase plta
79	c3nvnA_	Alignment	not modelled	5.3	71	PDB header: viral protein/signaling protein Chain: A: PDB Molecule: evm139; PDBTitle: molecular mechanism of guidance cue recognition
80	d2ktxa_	Alignment	not modelled	5.2	80	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
81	c4k2xB_	Alignment	not modelled	5.1	39	PDB header: oxidoreductase, flavoprotein Chain: B: PDB Molecule: polyketide oxygenase/hydroxylase; PDBTitle: oxys anhydrotetracycline hydroxylase from streptomyces rimosus
82	c3ihgA_	Alignment	not modelled	5.1	39	PDB header: flavoprotein, oxidoreductase Chain: A: PDB Molecule: rdme; PDBTitle: crystal structure of a ternary complex of aklavinone-11 hydroxylase2 with fad and aklavinone
83	c1dmfA_	Alignment	not modelled	5.1	71	PDB header: metallothionein Chain: A: PDB Molecule: cd6 metallothionein-1; PDBTitle: the three-dimensional solution structure of callinectes2 sapidus metallothionein-i determined by homonuclear and3 heteronuclear magnetic resonance spectroscopy