
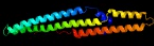

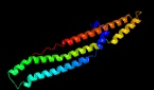

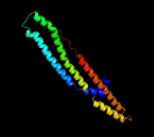

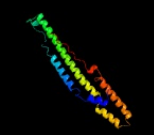

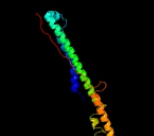

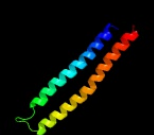

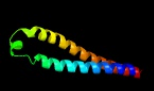










Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1917c_(PPE34)_2162939_2167318
 Date Fri Aug 2 13:30:53 BST 2019
 Unique Job ID 7eda22ad27de1089

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5xfsB_	 Alignment		100.0	51	PDB header: protein transport Chain: B; PDB Molecule: ppe family protein ppe15; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
2	c2g38B_	 Alignment		100.0	34	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: ppe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
3	d2g38b1	 Alignment		100.0	34	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PPE
4	c4xy3A_	 Alignment		100.0	19	PDB header: protein transport Chain: A; PDB Molecule: esx-1 secretion-associated protein espb; PDBTitle: structure of esx-1 secreted protein espb
5	c4wj2A_	 Alignment		96.7	21	PDB header: unknown function Chain: A; PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
6	c4iogD_	 Alignment		95.7	16	PDB header: unknown function Chain: D; PDB Molecule: secreted protein esxb; PDBTitle: the crystal structure of a secreted protein esxb (wild-type, in p212 space group) from bacillus anthracis str. Sterne
7	c2vs0B_	 Alignment		95.5	9	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	c3gvmA_	 Alignment		94.4	11	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
9	c3zbhC_	 Alignment		94.2	16	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
10	d1wa8a1	 Alignment		92.4	15	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
11	c3jywF_	 Alignment		69.2	43	PDB header: ribosome Chain: F; PDB Molecule: 60s ribosomal protein l7(a); PDBTitle: structure of the 60s proteins for eukaryotic ribosome based on cryo-em2 map of thermomyces lanuginosus ribosome at 8.9a resolution

12	c4lwsA_	Alignment		65.7	19	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
13	d1wa8b1	Alignment		58.8	16	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
14	c4i0xA_	Alignment		47.6	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: esat-6-like protein mab_3112; PDBTitle: crystal structure of the mycobacterium abscessus esxef (mab_3112-2 mab_3113) complex
15	c2vsnB_	Alignment		45.7	12	PDB header: transferase Chain: B: PDB Molecule: xcogt; PDBTitle: structure and topological arrangement of an o-glcna2 transferase homolog: insight into molecular control of f3 intracellular glycosylation
16	c4lwsB_	Alignment		37.8	9	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
17	c2kg7B_	Alignment		31.5	16	PDB header: unknown function Chain: B: PDB Molecule: esat-6-like protein eshx; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
18	c4bgoA_	Alignment		29.0	12	PDB header: hydrolase Chain: A: PDB Molecule: efem m75 peptidase; PDBTitle: structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
19	c5djsA_	Alignment		24.0	18	PDB header: transferase Chain: A: PDB Molecule: tetratricopeptide tpr_2 repeat protein; PDBTitle: thermobaculum terrenum o-glcna2 transferase mutant - k341m
20	c5uz9B_	Alignment		21.5	21	PDB header: immune system/rna Chain: B: PDB Molecule: crispr-associated protein csy2; PDBTitle: cryo em structure of anti-crisprs, acrf1 and acrf2, bound to type i-f2 crrna-guided crispr surveillance complex
21	c2lyyB_	Alignment	not modelled	20.5	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of the protein nb7890a from shewanella sp
22	d1ui5a2	Alignment	not modelled	20.0	20	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
23	c3pe3D_	Alignment	not modelled	19.9	14	PDB header: transferase Chain: D: PDB Molecule: udp-n-acetylglucosamine--peptide n- PDBTitle: structure of human o-glcna2 transferase and its complex with a peptide2 substrate
24	c3at7B_	Alignment	not modelled	19.9	9	PDB header: structural protein Chain: B: PDB Molecule: alginate-binding flagellin; PDBTitle: crystal structure of bacterial cell-surface alginate-binding protein2 algp7
25	c4lrV_	Alignment	not modelled	18.2	40	PDB header: dna binding protein Chain: L: PDB Molecule: dna sulfur modification protein dnde; PDBTitle: crystal structure of dnde from escherichia coli b7a involved in dna2 phosphorothioation modification
26	c3fpjA_	Alignment	not modelled	17.6	11	PDB header: biosynthetic protein, transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of e81q mutant of mtas in complex with s-2 adenosylmethionine
27	c6ghrF_	Alignment	not modelled	17.1	53	PDB header: photosynthesis Chain: F: PDB Molecule: cp12 polypeptide; PDBTitle: cyanobacterial gapdh with full-length cp12
28	c3lhoA_	Alignment	not modelled	16.2	28	PDB header: hydrolase Chain: A: PDB Molecule: putative hydrolase; PDBTitle: crystal structure of putative hydrolase (yp_751971.1) from shewanella2 frigidimarina ncimb 400 at 1.80 a resolution
						PDB header: hydrolase

29	c4jzaB_	Alignment	not modelled	15.9	58	Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a legionella phosphoinositide phosphatase:2 insights into lipid metabolism in pathogen host interaction
30	d1fnda2	Alignment	not modelled	15.9	26	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
31	d2a15a1	Alignment	not modelled	15.1	24	Fold: Cystatin-like Superfamily: NTF2-like Family: Ketosteroid isomerase-like
32	d1knca_	Alignment	not modelled	14.5	19	Fold: AhpD-like Superfamily: AhpD-like Family: AhpD
33	d1rzoa_	Alignment	not modelled	13.8	10	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Plant cytotoxins
34	c3kb4D_	Alignment	not modelled	13.2	14	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr8543 protein; PDBTitle: crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
35	c4fbaC_	Alignment	not modelled	13.2	25	PDB header: hydrolase Chain: C: PDB Molecule: protein synthesis inhibitor i; PDBTitle: structure of mutant rip from barley seeds in complex with adenine
36	d1hi9a_	Alignment	not modelled	12.4	26	Fold: Dipeptide transport protein Superfamily: Dipeptide transport protein Family: Dipeptide transport protein
37	d2fr1a1	Alignment	not modelled	12.0	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
38	d1rp4a_	Alignment	not modelled	11.6	21	Fold: ERO1-like Superfamily: ERO1-like Family: ERO1-like
39	c3ahrA_	Alignment	not modelled	11.1	28	PDB header: oxidoreductase Chain: A: PDB Molecule: ero1-like protein alpha; PDBTitle: inactive human ero1
40	c2pqjC_	Alignment	not modelled	11.0	24	PDB header: hydrolase Chain: C: PDB Molecule: ribosome-inactivating protein 3; PDBTitle: crystal structure of active ribosome inactivating protein from maize2 (b-32), complex with adenine
41	c4o94B_	Alignment	not modelled	10.4	15	PDB header: transport protein Chain: B: PDB Molecule: trap dicarboxylate transporter dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 rhodospseudomonas palustris haa2 (rpb_3329), target efi-510223, with3 bound succinate
42	c3q3hA_	Alignment	not modelled	10.3	10	PDB header: transferase Chain: A: PDB Molecule: hmw1c-like glycosyltransferase; PDBTitle: crystal structure of the actinobacillus pleuropneumoniae hmw1c2 glycosyltransferase in complex with udp-glc
43	d1uq5a_	Alignment	not modelled	10.2	10	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Plant cytotoxins
44	d1f20a2	Alignment	not modelled	9.9	26	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: NADPH-cytochrome p450 reductase-like
45	c5frgA_	Alignment	not modelled	9.8	75	PDB header: protein binding Chain: A: PDB Molecule: formin-binding protein 1-like; PDBTitle: the nmr structure of the cdc42-interacting region of toca1
46	d1yf8a1	Alignment	not modelled	9.7	13	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Plant cytotoxins
47	c4co6A_	Alignment	not modelled	9.6	37	PDB header: chaperone Chain: A: PDB Molecule: nucleoprotein; PDBTitle: crystal structure of the nipah virus rna free2 nucleoprotein-phosphoprotein complex
48	c4rqoB_	Alignment	not modelled	9.6	25	PDB header: lyase Chain: B: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure of l-serine dehydratase from legionella pneumophila
49	c1trfB_	Alignment	not modelled	9.5	28	PDB header: hydrolase (metalloprotease) Chain: B: PDB Molecule: thermolysin fragment 255 - 316; PDBTitle: nmr solution structure of the c-terminal fragment 255-3162 of thermolysin: a dimer formed by subunits having the3 native structure
50	d1g03a_	Alignment	not modelled	9.2	19	Fold: Retrovirus capsid protein, N-terminal core domain Superfamily: Retrovirus capsid protein, N-terminal core domain Family: Retrovirus capsid protein, N-terminal core domain
51	d1vefa1	Alignment	not modelled	9.1	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like
52	c1bkvA_	Alignment	not modelled	9.0	38	PDB header: structural protein Chain: A: PDB Molecule: t3-785; PDBTitle: collagen
53	d1umka2	Alignment	not modelled	8.9	21	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
54	c5ddwD_	Alignment	not modelled	8.8	22	PDB header: transferase Chain: D: PDB Molecule: crmg; PDBTitle: crystal structure of aminotransferase crmg from

						actinoalloteichus sp.2 wh1-2216-6 in complex with the pmp external aldimine adduct with 3 caerulomycin m
55	d3cx5d1	Alignment	not modelled	8.6	35	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
56	d1byra	Alignment	not modelled	8.6	22	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Nuclease
57	d1oc7a	Alignment	not modelled	8.6	14	Fold: 7-stranded beta/alpha barrel Superfamily: Glycosyl hydrolases family 6, cellulases Family: Glycosyl hydrolases family 6, cellulases
58	d1spgb	Alignment	not modelled	8.5	29	Fold: Globin-like Superfamily: Globin-like Family: Globins
59	c1qcrD	Alignment	not modelled	8.5	30	PDB header: oxidoreductase Chain: D: PDB Molecule: ubiquinol cytochrome c oxidoreductase; PDBTitle: crystal structure of bovine mitochondrial cytochrome bc12 complex, alpha carbon atoms only
60	c1bkvC	Alignment	not modelled	8.3	38	PDB header: structural protein Chain: C: PDB Molecule: t3-785; PDBTitle: collagen
61	c1bkvB	Alignment	not modelled	8.3	38	PDB header: structural protein Chain: B: PDB Molecule: t3-785; PDBTitle: collagen
62	c3fyqA	Alignment	not modelled	8.3	21	PDB header: cell adhesion Chain: A: PDB Molecule: cg6831-pa (talin); PDBTitle: structure of drosophila melanogaster talin 1bs2 domain (residues 1981-2 2168)
63	c3vohA	Alignment	not modelled	8.3	18	PDB header: hydrolase Chain: A: PDB Molecule: cellobiohydrolase; PDBTitle: ccel6a catalytic domain complexed with cellobiose
64	c3bkhA	Alignment	not modelled	8.2	20	PDB header: hydrolase Chain: A: PDB Molecule: lytic transglycosylase; PDBTitle: crystal structure of the bacteriophage phikz lytic2 transglycosylase, gp144
65	d1ppid1	Alignment	not modelled	8.1	30	Fold: Cytochrome c Superfamily: Cytochrome c Family: Cytochrome bc1 domain
66	d1luaa2	Alignment	not modelled	7.9	36	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Methylene-tetrahydrodihydropterin dehydrogenase
67	c1sseB	Alignment	not modelled	7.9	18	PDB header: transcription activator Chain: B: PDB Molecule: ap-1 like transcription factor yap1; PDBTitle: solution structure of the oxidized form of the yap1 redox2 domain
68	c2pheC	Alignment	not modelled	7.9	31	PDB header: transcription Chain: C: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to pc4
69	c6efvA	Alignment	not modelled	7.9	28	PDB header: flavoprotein Chain: A: PDB Molecule: sulfite reductase [nadph] flavoprotein alpha-component; PDBTitle: the nadph-dependent sulfite reductase flavoprotein adopts an extended2 conformation that is unique to this diflavin reductase
70	c6fhjA	Alignment	not modelled	7.9	20	PDB header: hydrolase Chain: A: PDB Molecule: protein,protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase, native.
71	c6rdf7	Alignment	not modelled	7.8	30	PDB header: proton transport Chain: 7: PDB Molecule: mitochondrial atp synthase associated protein asa7; PDBTitle: cryoem structure of polytomella f-atp synthase, primary rotary state2 3, monomer-masked refinement
72	c4xjnM	Alignment	not modelled	7.7	32	PDB header: viral protein/rna Chain: M: PDB Molecule: nucleocapsid; PDBTitle: structure of the parainfluenza virus 5 nucleocapsid-rna complex: an2 insight into paramyxovirus polymerase activity
73	c5lzkB	Alignment	not modelled	7.6	6	PDB header: structural genomics Chain: B: PDB Molecule: protein fam83b; PDBTitle: structure of the domain of unknown function duf1669 from human fam83b
74	c2phgB	Alignment	not modelled	7.4	33	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: model for vp16 binding to tfiib
75	d1dwna	Alignment	not modelled	7.4	38	Fold: RNA bacteriophage capsid protein Superfamily: RNA bacteriophage capsid protein Family: RNA bacteriophage capsid protein
76	c3a64A	Alignment	not modelled	7.1	17	PDB header: hydrolase Chain: A: PDB Molecule: cellobiohydrolase; PDBTitle: crystal structure of ccel6c, a glycoside hydrolase family 62 enzyme, from coprinopsis cinerea
77	c5jn6A	Alignment	not modelled	7.1	67	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the nmr solution structure of rpa3313
78	c5cgaC	Alignment	not modelled	7.0	33	PDB header: transferase Chain: C: PDB Molecule: hydroxyethylthiazole kinase; PDBTitle: structure of hydroxyethylthiazole kinase thim from staphylococcus2 aureus in complex with substrate analog 2-(1,3,5-trimethyl-1h-3 pyrazole-4-yl)ethanol
79	c5e4vA	Alignment	not modelled	7.0	32	PDB header: viral protein Chain: A: PDB Molecule: nucleoprotein,phosphoprotein; PDBTitle: crystal structure of measles n0-p complex
						PDB header: hydrolase

80	c3ktzA_	Alignment	not modelled	7.0	15	Chain: A: PDB Molecule: ribosome-inactivating protein gelonin; PDBTitle: structure of gap31
81	d1ndha2	Alignment	not modelled	6.9	22	Fold: Ferredoxin reductase-like, C-terminal NADP-linked domain Superfamily: Ferredoxin reductase-like, C-terminal NADP-linked domain Family: Reductases
82	c6fhnA_	Alignment	not modelled	6.9	20	PDB header: hydrolase Chain: A: PDB Molecule: protein; PDBTitle: structural dynamics and catalytic properties of a multi-modular2 xanthanase (pt derivative)
83	c3i5tB_	Alignment	not modelled	6.9	18	PDB header: transferase Chain: B: PDB Molecule: aminotransferase; PDBTitle: crystal structure of aminotransferase prk07036 from rhodobacter2 sphaeroides kd131
84	c2k2uB_	Alignment	not modelled	6.8	33	PDB header: transcription Chain: B: PDB Molecule: alpha trans-inducing protein; PDBTitle: nmr structure of the complex between tfb1 subunit of tfiih2 and the activation domain of vp16
85	c3fy6A_	Alignment	not modelled	6.8	67	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: integron cassette protein; PDBTitle: structure from the mobile metagenome of v. cholerae. integron cassette2 protein vch_cass3
86	d1x7da_	Alignment	not modelled	6.8	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Ornithine cyclodeaminase-like
87	c1tlla_	Alignment	not modelled	6.7	23	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase, brain; PDBTitle: crystal structure of rat neuronal nitric-oxide synthase2 reductase module at 2.3 a resolution.
88	c6m9sC_	Alignment	not modelled	6.6	12	PDB header: oxidoreductase Chain: C: PDB Molecule: sznf; PDBTitle: crystal structure of semet sznf from streptomyces achromogenes var.2 streptozoticus nrri 2697
89	d1qtma1	Alignment	not modelled	6.5	44	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: DnaQ-like 3'-5' exonuclease
90	d2c7fa1	Alignment	not modelled	6.5	21	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: Composite domain of glycosyl hydrolase families 5, 30, 39 and 51
91	c4nn3A_	Alignment	not modelled	6.5	11	PDB header: transport protein Chain: A: PDB Molecule: trap dicarboxylate transporter, dctp subunit; PDBTitle: crystal structure of a trap periplasmic solute binding protein from2 desulfovibrio salexigens (desal_2161), target efi-510109, with bound3 otrotic acid
92	c3b5oA_	Alignment	not modelled	6.4	36	PDB header: oxidoreductase Chain: A: PDB Molecule: cadd-like protein of unknown function; PDBTitle: crystal structure of a cadd-like protein of unknown function2 (npun_f6505) from nostoc punctiforme pcc 73102 at 1.35 a resolution
93	c6cboB_	Alignment	not modelled	6.4	16	PDB header: transferase Chain: B: PDB Molecule: c-6' aminotransferase; PDBTitle: x-ray structure of genb1 from micromonospora echinospora in complex2 with neamine and plp (as the external aldimine)
94	c1zrtD_	Alignment	not modelled	6.3	39	PDB header: oxidoreductase/metal transport Chain: D: PDB Molecule: cytochrome c1; PDBTitle: rhodobacter capsulatus cytochrome bc1 complex with2 stigmatellin bound
95	d1abra_	Alignment	not modelled	6.3	19	Fold: Ribosome inactivating proteins (RIP) Superfamily: Ribosome inactivating proteins (RIP) Family: Plant cytotoxins
96	c2ke4A_	Alignment	not modelled	6.3	75	PDB header: membrane protein Chain: A: PDB Molecule: cdc42-interacting protein 4; PDBTitle: the nmr structure of the tc10 and cdc42 interacting domain2 of cip4
97	c2bn5B_	Alignment	not modelled	6.2	63	PDB header: nuclear protein Chain: B: PDB Molecule: u1 small nuclear ribonucleoprotein 70 kda; PDBTitle: p-element somatic inhibitor protein complex with u1-70k2 proline-rich peptide
98	d1b93a_	Alignment	not modelled	6.1	29	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
99	c6ajrA_	Alignment	not modelled	6.1	18	PDB header: dna binding protein Chain: A: PDB Molecule: uracil dna glycosylase superfamily protein; PDBTitle: complex form of uracil dna glycosylase x and uracil