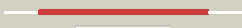


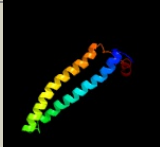



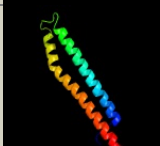

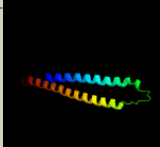



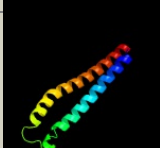

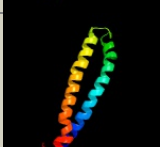

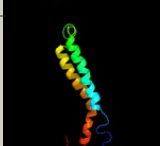






Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD3620c_esxW_4060474_4060770
 Date Fri Aug 9 18:20:30 BST 2019
 Unique Job ID 1e6716550d462678

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ogiD_	 Alignment		100.0	91	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: putative esat-6-like protein 7; PDBTitle: crystal structure of the mycobacterium tuberculosis h37rv esxop2 complex (rv2346c-rv2347c)
2	d1wa8a1	 Alignment		98.6	20	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
3	c3zbhC_	 Alignment		97.9	20	PDB header: unknown function Chain: C; PDB Molecule: esxa; PDBTitle: geobacillus thermodenitrificans esxa crystal form i
4	c3gvmA_	 Alignment		97.7	16	PDB header: viral protein Chain: A; PDB Molecule: putative uncharacterized protein sag1039; PDBTitle: structure of the homodimeric wxg-100 family protein from streptococcus2 agalactiae
5	c4lwsA_	 Alignment		97.6	22	PDB header: unknown function Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
6	c4iogD_	 Alignment		97.6	22	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		97.5	14	PDB header: cell invasion Chain: B; PDB Molecule: virulence factor esxa; PDBTitle: structural analysis of homodimeric staphylococcal aureus2 virulence factor esxa
8	d1wa8b1	 Alignment		96.6	10	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
9	c2kg7B_	 Alignment		95.6	21	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
10	c4lwsB_	 Alignment		95.3	14	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
11	c3m0dC_	 Alignment		77.1	19	PDB header: signaling protein Chain: C; PDB Molecule: tnfr receptor-associated factor 1; PDBTitle: crystal structure of the traf1:traf2:ciap2 complex

12	c3m06F_	Alignment		67.4	19	PDB header: protein binding Chain: F: PDB Molecule: tnf receptor-associated factor 2; PDBTitle: crystal structure of traf2
13	c2dw3A_	Alignment		52.5	38	PDB header: photosynthesis Chain: A: PDB Molecule: intrinsic membrane protein pufx; PDBTitle: solution structure of the rhodobacter sphaeroides pufx2 membrane protein
14	c3bj4B_	Alignment		30.2	44	PDB header: signaling protein Chain: B: PDB Molecule: potassium voltage-gated channel subfamily kqt PDBTitle: the kcnq1 (kv7.1) c-terminus, a multi-tiered scaffold for2 subunit assembly and protein interaction
15	d1pqua2	Alignment		28.2	54	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
16	d1wtea_	Alignment		26.5	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease EcoO109IR
17	c3ag7A_	Alignment		21.4	16	PDB header: plant protein Chain: A: PDB Molecule: putative uncharacterized protein f9e10.5; PDBTitle: an auxilin-like j-domain containing protein, jac1 j-domain
18	d1mb4a2	Alignment		20.7	54	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
19	d1t4ba2	Alignment		20.6	46	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
20	d2gz1a2	Alignment		20.4	46	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
21	c2la2A_	Alignment	not modelled	20.2	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: cecropin; PDBTitle: solution structure of papiliocin isolated from the swallowtail2 butterfly, papilio xuthus
22	c3gtzA_	Alignment	not modelled	13.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative translation initiation inhibitor; PDBTitle: crystal structure of a putative translation initiation inhibitor from2 salmonella typhimurium
23	c2ym9D_	Alignment	not modelled	12.8	23	PDB header: cell invasion Chain: D: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium
24	c5a3kA_	Alignment	not modelled	11.6	31	PDB header: oxidoreductase Chain: A: PDB Molecule: putative pteridine-dependent dioxygenase; PDBTitle: chorismatase mechanisms reveal fundamentally different types of2 reaction in a single conserved protein fold
25	c1i8tB_	Alignment	not modelled	11.3	40	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: strcuture of udp-galactopyranose mutase from e.coli
26	c3h6pD_	Alignment	not modelled	10.2	30	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
27	d2j01h1	Alignment	not modelled	9.9	42	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
28	d2zjre2	Alignment	not modelled	9.6	45	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
						Fold: Ribosomal protein L6

29	d2qamg1	Alignment	not modelled	9.1	33	Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
30	d1vqoe1	Alignment	not modelled	8.7	58	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
31	c3l32B_	Alignment	not modelled	8.4	35	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the dimerisation domain of the rabies virus2 phosphoprotein
32	d1xbla_	Alignment	not modelled	8.3	12	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
33	c2vq7B_	Alignment	not modelled	8.1	53	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-containing monooxygenase; PDBTitle: bacterial flavin-containing monooxygenase in complex with2 nadp: native data
34	c4m70A_	Alignment	not modelled	8.0	39	PDB header: plant protein Chain: A: PDB Molecule: rx protein; PDBTitle: crystal structure of potato rx-cc domain in complex with rangap2-wpp2 domain
35	c2bi8A_	Alignment	not modelled	7.9	47	PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad
36	d1w4xa1	Alignment	not modelled	7.9	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
37	c5nmwA_	Alignment	not modelled	7.7	47	PDB header: oxidoreductase Chain: A: PDB Molecule: flavin-containing monooxygenase; PDBTitle: crystal structure of the pyrrolizidine alkaloid n-oxygenase from2 zonocerus variegatus in complex with fad
38	c2dn9A_	Alignment	not modelled	7.5	14	PDB header: apoptosis, chaperone Chain: A: PDB Molecule: dnaj homolog subfamily a member 3; PDBTitle: solution structure of j-domain from the dnaj homolog, human2 tid1 protein
39	c5j7xA_	Alignment	not modelled	7.5	40	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylaniline monooxygenase, putative; PDBTitle: baeyer-villiger monooxygenase bvmoaf1838 from aspergillus flavus
40	d2k49a2	Alignment	not modelled	7.3	43	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
41	c3we0A_	Alignment	not modelled	7.3	47	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase/monooxygenase; PDBTitle: l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813
42	d2hjsa2	Alignment	not modelled	7.3	27	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
43	c487dJ_	Alignment	not modelled	7.2	42	PDB header: ribosome Chain: J: PDB Molecule: protein (50s l6 ribosomal protein); PDBTitle: seven ribosomal proteins fitted to a cryo-electron2 microscopic map of the large 50s subunit at 7.5 angstroms3 resolution
44	d2k8ea1	Alignment	not modelled	7.1	71	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
45	d1rl6a1	Alignment	not modelled	7.1	45	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
46	c1v0jB_	Alignment	not modelled	6.9	27	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis
47	d2cqla1	Alignment	not modelled	6.6	45	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
48	c4ap3A_	Alignment	not modelled	6.6	27	PDB header: oxidoreductase Chain: A: PDB Molecule: steroid monooxygenase; PDBTitle: oxidized steroid monooxygenase bound to nadp
49	c3uoyB_	Alignment	not modelled	6.5	33	PDB header: oxidoreductase Chain: B: PDB Molecule: otemo; PDBTitle: crystal structure of otemo complex with fad and nadp (form 1)
50	c5gsnD_	Alignment	not modelled	6.4	40	PDB header: flavoprotein Chain: D: PDB Molecule: flavin-containing monooxygenase; PDBTitle: tmm in complex with methimazole
51	c3gwdA_	Alignment	not modelled	6.4	33	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: closed crystal structure of cyclohexanone monooxygenase
52	d1jd1a_	Alignment	not modelled	6.3	14	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
53	c4tlxC_	Alignment	not modelled	6.3	27	PDB header: oxidoreductase Chain: C: PDB Molecule: ktzi; PDBTitle: kutzneria sp. 744 ornithine n-hydroxylase, ktzi-fadred-nadp+-l-orn
54	d2bi7a1	Alignment	not modelled	6.2	47	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
55	c2jb1B_	Alignment	not modelled	6.1	33	PDB header: oxidoreductase Chain: B: PDB Molecule: l-amino acid oxidase; PDBTitle: the l-amino acid oxidase from rhodococcus opacus in

						complex2 with l-alanine PDB header: unknown function Chain: B: PDB Molecule: duf269-containing protein; PDBTitle: crystal structure of cce_0566 from the cyanobacterium cyanothece2 51142, a protein associated with nitrogen fixation from the duf2693 family
56	c3nj2B_	Alignment	not modelled	6.0	18	PDB header: cell invasion Chain: B: PDB Molecule: protein prgi, cell invasion protein sipd; PDBTitle: prgi-sipd from salmonella typhimurium
57	c3zqbB_	Alignment	not modelled	6.0	20	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
58	c5o60G_	Alignment	not modelled	5.9	42	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: crystal structure of ribosome with messenger rna and the anticodon2 stem-loop of p-site trna. this file contains the 50s subunit of one3 70s ribosome. the entire crystal structure contains two 70s ribosomes4 and is described in remark 400.
59	c2i2vG_	Alignment	not modelled	5.7	33	PDB header: antimicrobial protein Chain: A: PDB Molecule: papb; PDBTitle: crystal structure of pedb
60	c2ip6A_	Alignment	not modelled	5.6	29	PDB header: sugar binding protein Chain: A: PDB Molecule: endoribonuclease l-psp, putative; PDBTitle: crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
61	c3k0tA_	Alignment	not modelled	5.5	11	PDB header: membrane protein Chain: A: PDB Molecule: nadh dehydrogenase, putative; PDBTitle: structure of ndh2 from plasmodium falciparum in complex with ryl-552
62	c5jwcA_	Alignment	not modelled	5.5	38	PDB header: biosynthetic protein Chain: A: PDB Molecule: l-lysine 6-monoxygenase involved in desferrioxamine PDBTitle: the crystal structure of dfoa bound to fad and nadp; the2 desferrioxamine biosynthetic pathway cadaverine monoxygenase from3 the fire blight disease pathogen erwinia amylovora
63	c5o8rA_	Alignment	not modelled	5.4	20	PDB header: ribosome Chain: F: PDB Molecule: 54s ribosomal protein l6, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
64	c1vw4F_	Alignment	not modelled	5.3	42	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex
65	c3uteB_	Alignment	not modelled	5.2	40	PDB header: unknown function Chain: L: PDB Molecule: nmb1025 protein; PDBTitle: crystal structure of nmb1025, a member of yjgf protein family, from2 neisseria meningitidis (hexagonal crystal form)
66	c3kjlL_	Alignment	not modelled	5.2	18	PDB header: dna binding protein Chain: D: PDB Molecule: centromere dna-binding protein complex cbf3 subunit c; PDBTitle: cryo-em structure of the core centromere binding factor 3 complex
67	c6fe8D_	Alignment	not modelled	5.1	42	PDB header: ribosome Chain: H: PDB Molecule: 50s ribosomal protein l6; PDBTitle: 70s t.th. ribosome functional complex with mrna and e- and p-site2 trnas at 4.5a. this entry 2hgu contains 50s ribosomal subunit. the3 30s ribosomal subunit can be found in pdb entry 2hgr.
68	c2hguH_	Alignment	not modelled	5.1	42	PDB header: chaperone Chain: A: PDB Molecule: dnaj; PDBTitle: j-domain (residues 1-77) of the escherichia coli n-terminal2 fragment (residues 1-104) of the molecular chaperone dnaj,3 nmr, 20 structures
69	c1bq0A_	Alignment	not modelled	5.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: baeyer-villiger monoxygenase; PDBTitle: crystal structure of baeyer-villiger monoxygenase from parvibaculum2 lavamentivorans
70	c6jdkA_	Alignment	not modelled	5.1	40	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monoxygenase from thermocrispum municipale.;
71	c5m0zA_	Alignment	not modelled	5.1	33	PDBTitle: cyclohexanone monoxygenase from t. municipale: reduced enzyme bound2 to nadp+
72	d2dw4a2	Alignment	not modelled	5.0	53	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD-linked reductases, N-terminal domain