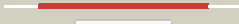
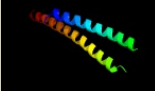


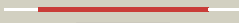
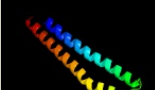













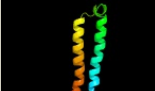

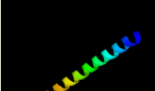


Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1038c_(esx)_1160859_1161155
 Date Wed Jul 31 22:05:11 BST 2019
 Unique Job ID 64c906b673bfce25

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	24	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	c4lwsB_	 Alignment		96.0	14	PDB header: unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c2kg7B_	 Alignment		95.5	21	PDB header: unknown function Chain: B; PDB Molecule: esat-6-like protein esxh; PDBTitle: structure and features of the complex formed by the tuberculosis2 virulence factors rv0287 and rv0288
11	c3m0dC_	 Alignment		76.8	19	PDB header: signaling protein Chain: C; PDB Molecule: tnf receptor-associated factor 1; PDBTitle: crystal structure of the traf1:traf2:ciap2 complex

12	c3m06F_	Alignment		66.9	19	PDB header: protein binding Chain: F: PDB Molecule: tnf receptor-associated factor 2; PDBTitle: crystal structure of traf2
13	c2dw3A_	Alignment		51.6	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		30.4	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		27.3	54	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
16	d1wtea_	Alignment		26.1	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease EcoO109IR
17	c3ag7A_	Alignment		20.6	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		20.0	54	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
19	d1t4ba2	Alignment		19.9	46	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
20	d2gz1a2	Alignment		19.7	46	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
21	c2la2A_	Alignment	not modelled	19.6	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: cecropin; PDBTitle: solution structure of papilioicin isolated from the swallowtail2 butterfly, papilio xuthus
22	c3gtzA_	Alignment	not modelled	13.7	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	12.7	23	PDB header: cell invasion Chain: D: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium
24	c5a3kA_	Alignment	not modelled	11.3	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	10.8	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	9.9	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	9.8	42	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
28	d2zjre2	Alignment	not modelled	9.5	45	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
						Fold: Ribosomal protein L6

29	d2qamg1	Alignment	not modelled	9.0	33	Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
30	d1vqoe1	Alignment	not modelled	8.6	58	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
31	c3l32B_	Alignment	not modelled	8.3	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	8.2	12	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
33	c2vq7B_	Alignment	not modelled	7.8	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	7.8	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	7.6	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	7.5	40	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
37	c2dn9A_	Alignment	not modelled	7.4	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
38	c5nmwA_	Alignment	not modelled	7.4	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
39	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
40	c5j7xA_	Alignment	not modelled	7.2	40	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylaniline monooxygenase, putative; PDBTitle: baeyer-villiger monooxygenase bvmoaf838 from aspergillus flavus
41	d2k49a2	Alignment	not modelled	7.1	43	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
42	c3we0A_	Alignment	not modelled	7.0	47	PDB header: oxidoreductase Chain: A: PDB Molecule: l-amino acid oxidase/monooxygenase; PDBTitle: l-amino acid oxidase/monooxygenase from pseudomonas sp. aiu 813
43	d2hjsa2	Alignment	not modelled	7.0	27	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
44	d1rl6a1	Alignment	not modelled	7.0	45	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
45	d2k8ea1	Alignment	not modelled	6.8	71	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
46	c1v0jB_	Alignment	not modelled	6.6	27	PDB header: isomerase Chain: B: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from mycobacterium tuberculosis
47	d2cq1a1	Alignment	not modelled	6.6	45	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
48	c4ap3A_	Alignment	not modelled	6.3	27	PDB header: oxidoreductase Chain: A: PDB Molecule: steroid monooxygenase; PDBTitle: oxidized steroid monooxygenase bound to nadp
49	c3uoyB_	Alignment	not modelled	6.2	33	PDB header: oxidoreductase Chain: B: PDB Molecule: otemo; PDBTitle: crystal structure of otemo complex with fad and nadp (form 1)
50	d1jd1a_	Alignment	not modelled	6.1	14	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
51	c5gsnD_	Alignment	not modelled	6.1	40	PDB header: flavoprotein Chain: D: PDB Molecule: flavin-containing monooxygenase; PDBTitle: tmm in complex with methimazole
52	c3gwdA_	Alignment	not modelled	6.1	33	PDB header: oxidoreductase Chain: A: PDB Molecule: cyclohexanone monooxygenase; PDBTitle: closed crystal structure of cyclohexanone monooxygenase
53	c4tlxC_	Alignment	not modelled	6.0	27	PDB header: oxidoreductase Chain: C: PDB Molecule: ktzi; PDBTitle: kutzneria sp. 744 ornithine n-hydroxylase, ktzi-fadred-nadp+-l-orn
54	c3nj2B_	Alignment	not modelled	6.0	18	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
						Fold: Nucleotide-binding domain

55	d2bi7a1	Alignment	not modelled	5.9	47	Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain
56	c3zqbB	Alignment	not modelled	5.9	20	PDB header: cell invasion Chain: B: PDB Molecule: protein prgi, cell invasion protein sipd; PDBTitle: prgi-sipd from salmonella typhimurium
57	c5o60G	Alignment	not modelled	5.9	42	PDB header: ribosome Chain: G: PDB Molecule: 50s ribosomal protein l6; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
58	c2jb1B	Alignment	not modelled	5.8	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
59	c2i2vG	Alignment	not modelled	5.7	33	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.
60	c3k0tA	Alignment	not modelled	5.5	11	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	c2ip6A	Alignment	not modelled	5.5	29	PDB header: antimicrobial protein Chain: A: PDB Molecule: papb; PDBTitle: crystal structure of pedb
62	c5jwcA	Alignment	not modelled	5.3	38	PDB header: membrane protein Chain: A: PDB Molecule: nadh dehydrogenase, putative; PDBTitle: structure of ndh2 from plasmodium falciparum in complex with ryl-552
63	c1vw4F	Alignment	not modelled	5.2	42	PDB header: ribosome Chain: F: PDB Molecule: 54s ribosomal protein l6, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
64	c5o8rA	Alignment	not modelled	5.2	20	PDB header: biosynthetic protein Chain: A: PDB Molecule: l-lysine 6-monooxygenase involved in desferrioxamine PDBTitle: the crystal structure of dfoa bound to fad and nadp; the2 desferrioxamine biosynthetic pathway cadaverine monooxygenase from3 the fire blight disease pathogen erwinia amylovora
65	c3kjlL	Alignment	not modelled	5.1	18	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	c2hguH	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.
67	c6fe8D	Alignment	not modelled	5.0	42	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