


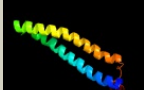

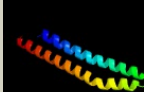



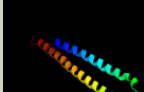














Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD1197_(esxK)_1340665_1340961
 Date Wed Jul 31 22:05:28 BST 2019
 Unique Job ID 0bec90beaa9a80f3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ogiD_	 Alignment		100.0	92	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		96.1	14	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: esxa : esxb (semet) hetero-dimer from thermomonospora curvata
10	c2kg7B_	 Alignment		95.4	22	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		76.3	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		66.6	19	PDB header: protein binding Chain: F: PDB Molecule: tnf receptor-associated factor 2; PDBTitle: crystal structure of traf2
13	c2dw3A_	Alignment		51.2	38	PDB header: photosynthesis Chain: A: PDB Molecule: intrinsic membrane protein pufx; PDBTitle: solution structure of the rhodobacter sphaeroides pufx2 membrane protein
14	c3ag7A_	Alignment		28.3	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
15	d1pqua2	Alignment		26.9	54	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
16	d1wtea_	Alignment		25.6	42	Fold: Restriction endonuclease-like Superfamily: Restriction endonuclease-like Family: Restriction endonuclease EcoO109IR
17	d1mb4a2	Alignment		19.8	54	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
18	d1t4ba2	Alignment		19.7	46	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
19	c2la2A_	Alignment		19.5	27	PDB header: antimicrobial protein Chain: A: PDB Molecule: cecropin; PDBTitle: solution structure of papilicocin isolated from the swallowtail2 butterfly, papilio xuthus
20	d2gz1a2	Alignment		19.5	46	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
21	c3gtzA_	Alignment	not modelled	16.6	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
22	c5a3kA_	Alignment	not modelled	16.6	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
23	c3h6pD_	Alignment	not modelled	12.7	28	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
24	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
25	d1xbla_	Alignment	not modelled	10.3	12	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
26	c2dn9A_	Alignment	not modelled	9.2	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
27	c3kjl_	Alignment	not modelled	8.7	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)
28	c3l32B_	Alignment	not modelled	8.5	35	PDB header: viral protein Chain: B: PDB Molecule: phosphoprotein; PDBTitle: structure of the dimerisation domain of the rabies virus2 phosphoprotein
						Fold: Ribosomal protein L6

29	d1vqpe1	Alignment	not modelled	8.3	41	Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
30	d2qamq1	Alignment	not modelled	8.2	35	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
31	d2j01h1	Alignment	not modelled	8.1	23	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
32	c4m70A_	Alignment	not modelled	7.7	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
33	c2vq7B_	Alignment	not modelled	7.7	53	PDB header: oxidoreductase Chain: B: PDB Molecule: flavin-containing monooxygenase; PDBTitle: bacterial flavin-containing monooxygenase in complex with2 nadp: native data
34	c2bi8A_	Alignment	not modelled	7.5	47	PDB header: isomerase Chain: A: PDB Molecule: udp-galactopyranose mutase; PDBTitle: udp-galactopyranose mutase from klebsiella pneumoniae with reduced fad
35	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
36	c3k0tA_	Alignment	not modelled	7.5	14	PDB header: sugar binding protein Chain: A: PDB Molecule: endoribonuclease I-psp, putative; PDBTitle: crystal structure of pspto -psp protein in complex with d-beta-glucose2 from pseudomonas syringae pv. tomato str. dc3000
37	d1jd1a_	Alignment	not modelled	7.4	18	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
38	c5nmwA_	Alignment	not modelled	7.3	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	c5j7xA_	Alignment	not modelled	7.1	40	PDB header: oxidoreductase Chain: A: PDB Molecule: dimethylaniline monooxygenase, putative; PDBTitle: baeyer-villiger monooxygenase bvmoaff838 from aspergillus flavus
40	d2k49a2	Alignment	not modelled	7.1	43	Fold: YegP-like Superfamily: YegP-like Family: YegP-like
41	c3we0A_	Alignment	not modelled	6.9	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	6.9	27	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
43	c3bj4B_	Alignment	not modelled	6.9	39	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
44	d1nz6a_	Alignment	not modelled	6.8	20	Fold: Long alpha-hairpin Superfamily: Chaperone J-domain Family: Chaperone J-domain
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	c2ym9D_	Alignment	not modelled	6.6	23	PDB header: cell invasion Chain: D: PDB Molecule: cell invasion protein sipd; PDBTitle: sipd from salmonella typhimurium
48	d1j7ha_	Alignment	not modelled	6.6	18	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
49	c4ap3A_	Alignment	not modelled	6.3	27	PDB header: oxidoreductase Chain: A: PDB Molecule: steroid monooxygenase; PDBTitle: oxidized steroid monooxygenase bound to nadp
50	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)
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	d2ewca1	Alignment	not modelled	6.0	23	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: YjgF/L-PSP
55	d2bi7a1	Alignment	not modelled	5.9	47	Fold: Nucleotide-binding domain Superfamily: Nucleotide-binding domain Family: UDP-galactopyranose mutase, N-terminal domain

56	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
57	c3lmeE_	Alignment	not modelled	5.8	13	PDB header: translation Chain: E; PDB Molecule: possible translation initiation inhibitor; PDBTitle: structure of probable translation initiation inhibitor from (rpa2473)2 from rhodopseudomonas palustris
58	c1bq0A_	Alignment	not modelled	5.7	12	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
59	c3r0pB_	Alignment	not modelled	5.6	29	PDB header: hydrolase Chain: B; PDB Molecule: l-psp putative endoribonuclease; PDBTitle: crystal structure of l-psp putative endoribonuclease from uncultured2 organism
60	c3nj2B_	Alignment	not modelled	5.6	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
61	c2ip6A_	Alignment	not modelled	5.6	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	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
64	c6fe8D_	Alignment	not modelled	5.1	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
65	c2bbrA_	Alignment	not modelled	5.0	44	PDB header: viral protein Chain: A; PDB Molecule: viral casp8 and fadd-like apoptosis regulator; PDBTitle: crystal structure of mc159 reveals molecular mechanism of2 disc assembly and vflip inhibition
66	c3uteB_	Alignment	not modelled	5.0	40	PDB header: isomerase Chain: B; PDB Molecule: udp-galactopyranose mutase; PDBTitle: crystal structure of aspergillus fumigatus udp galactopyranose mutase2 sulfate complex