
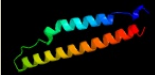

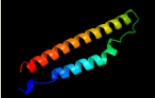
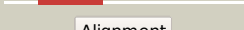




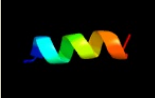






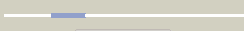




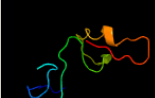






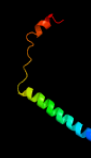
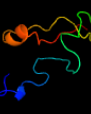



Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD2408_(PE24)_2706027_2706746
 Date Wed Aug 7 12:50:02 BST 2019
 Unique Job ID 19a93b9061cb3cd9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2g38A_	 Alignment		99.9	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pe family protein; PDBTitle: a pe/ppe protein complex from mycobacterium tuberculosis
2	d2g38a1	 Alignment		99.9	27	Fold: Ferritin-like Superfamily: PE/PPE dimer-like Family: PE
3	c5xfsA_	 Alignment		99.9	30	PDB header: protein transport Chain: A: PDB Molecule: pe family protein pe8; PDBTitle: crystal structure of pe8-ppe15 in complex with esp95 from m.2 tuberculosis
4	c4wj2A_	 Alignment		41.3	13	PDB header: unknown function Chain: A: PDB Molecule: antigen mtb48; PDBTitle: mycobacterial protein
5	d1lghb_	 Alignment		27.9	29	Fold: Light-harvesting complex subunits Superfamily: Light-harvesting complex subunits Family: Light-harvesting complex subunits
6	c4f82A_	 Alignment		25.1	62	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin reductase; PDBTitle: x-ray crystal structure of a putative thioredoxin reductase from 2 burkholderia cenocepacia
7	c4or8A_	 Alignment		24.2	38	PDB header: viral protein Chain: A: PDB Molecule: membrane-associated protein vp24; PDBTitle: crystal structure of marburg virus vp24
8	c4m0qB_	 Alignment		23.1	31	PDB header: viral protein Chain: B: PDB Molecule: membrane-associated protein vp24; PDBTitle: ebola virus vp24 structure
9	c3oniA_	 Alignment		21.3	17	PDB header: protein transport Chain: A: PDB Molecule: t-snare vti1; PDBTitle: crystal structure of yeast vti1p_habc domain
10	c1wrgA_	 Alignment		17.6	14	PDB header: membrane protein Chain: A: PDB Molecule: light-harvesting protein b-880, beta chain; PDBTitle: light-harvesting complex 1 beta subunit from wild-type2 rhodospirillum rubrum
11	c5hzbE_	 Alignment		14.8	37	PDB header: hydrolase Chain: E: PDB Molecule: non-structural protein 11; PDBTitle: structure of eav nsp11 k170a mutant at 3.10a

12	c6i52A_	Alignment		14.6	64	PDB header: dna binding protein Chain: A: PDB Molecule: replication factor a protein 3; PDBTitle: yeast rpa bound to ssdna
13	c6et5u_	Alignment		12.0	21	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
14	c2w0cR_	Alignment		11.8	14	PDB header: virus Chain: R: PDB Molecule: protein p3; PDBTitle: x-ray structure of the entire lipid-containing bacteriophage pm2
15	c2drtA_	Alignment		11.0	70	PDB header: structural protein Chain: A: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
16	c2drtB_	Alignment		11.0	70	PDB header: structural protein Chain: B: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
17	c2drtC_	Alignment		10.8	70	PDB header: structural protein Chain: C: PDB Molecule: collagen like peptide; PDBTitle: structure analysis of (pog)4-log-(pog)5
18	d1wa8a1	Alignment		10.8	17	Fold: Ferritin-like Superfamily: EsxAB dimer-like Family: ESAT-6 like
19	d1o65a_	Alignment		10.6	19	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: MOSC (MOCO sulphurase C-terminal) domain
20	c3u9iA_	Alignment		10.4	15	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing enzyme, c-terminal PDBTitle: the crystal structure of mandelate racemase/muconate lactonizing2 enzyme from roseiflexus sp.
21	c2bfuL_	Alignment	not modelled	9.8	20	PDB header: virus Chain: L: PDB Molecule: cowpea mosaic virus, large (l) subunit; PDBTitle: x-ray structure of cpmv top component
22	c4agrB_	Alignment	not modelled	9.5	47	PDB header: sugar binding protein Chain: B: PDB Molecule: galectin; PDBTitle: structure of a tetrameric galectin from cinachyrella sp. (ball2 sponge)
23	c4rqlA_	Alignment	not modelled	8.5	21	PDB header: dna binding protein Chain: A: PDB Molecule: filamentation induced by camp protein fic; PDBTitle: crystal structure of a fic family protein (dde_2494) from2 desulfovibrio desulfuricans g20 at 2.70 a resolution
24	c2k9yB_	Alignment	not modelled	8.5	73	PDB header: transferase Chain: B: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
25	c2k9yA_	Alignment	not modelled	8.3	73	PDB header: transferase Chain: A: PDB Molecule: ephrin type-a receptor 2; PDBTitle: epha2 dimeric structure in the lipidic bicelle at ph 5.0
26	d1ua7a1	Alignment	not modelled	8.2	60	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
27	c3sqsA_	Alignment	not modelled	7.9	28	PDB header: isomerase Chain: A: PDB Molecule: mandelate racemase/muconate lactonizing protein; PDBTitle: crystal structure of a putative mandelate racemase/muconate2 lactonizing protein from dinoroseobacter shibae dfl 12
28	d1wuea1	Alignment	not modelled	7.6	27	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like

29	c4k2xB	Alignment	not modelled	7.5	42	PDB header: oxidoreductase, flavoprotein Chain: B: PDB Molecule: polyketide oxygenase/hydroxylase; PDBTitle: oxys anhydrotetracycline hydroxylase from streptomyces rimosus
30	c4cy8A	Alignment	not modelled	7.4	37	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-hydroxybiphenyl 3-monooxygenase; PDBTitle: 2-hydroxybiphenyl 3-monooxygenase (hbpa) in complex with fad
31	d1vkma	Alignment	not modelled	7.4	33	Fold: Indigoidine synthase A-like Superfamily: Indigoidine synthase A-like Family: Indigoidine synthase A-like
32	c3cawB	Alignment	not modelled	7.2	23	PDB header: oxidoreductase Chain: B: PDB Molecule: o-succinylbenzoate synthase; PDBTitle: crystal structure of o-succinylbenzoate synthase from bdellovibrio2 bacteriovirus liganded with mg
33	d2h85a2	Alignment	not modelled	6.8	46	Fold: EndoU-like Superfamily: EndoU-like Family: Nsp15 C-terminal domain-like
34	c5cupB	Alignment	not modelled	6.7	44	PDB header: transferase Chain: B: PDB Molecule: phosphate propanoyltransferase; PDBTitle: structure of rhodopseudomonas palustris pdul - phosphate bound form
35	c5dnIA	Alignment	not modelled	6.6	46	PDB header: lyase Chain: A: PDB Molecule: imidazoleglycerol-phosphate dehydratase; PDBTitle: crystal structure of igpd from pyrococcus furiosus in complex with2 (s)-c348
36	d1mioa	Alignment	not modelled	6.5	25	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
37	c1cwxA	Alignment	not modelled	6.4	47	PDB header: viral protein Chain: A: PDB Molecule: hepatitis c virus capsid protein; PDBTitle: solution structure of the hepatitis c virus n-terminal2 capsid protein 2-45 [c-hcv(2-45)]
38	d1pgw21	Alignment	not modelled	6.3	25	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
39	c5x2hA	Alignment	not modelled	6.2	34	PDB header: hydrolase/rna/dna Chain: A: PDB Molecule: crispr-associated endonuclease cas9; PDBTitle: crystal structure of campylobacter jejuni cas9 in complex with sgRNA2 and target dna (agaaaac pam)
40	c2r0gB	Alignment	not modelled	6.2	48	PDB header: oxidoreductase Chain: B: PDB Molecule: rebc; PDBTitle: chromopyrrolic acid-soaked rebc with bound 7-carboxy-k252c
41	c4mitG	Alignment	not modelled	6.2	50	PDB header: signaling protein Chain: G: PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpa4 pbd
42	d1pgl21	Alignment	not modelled	6.1	25	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
43	d1r0ma1	Alignment	not modelled	6.1	32	Fold: TIM beta/alpha-barrel Superfamily: Enolase C-terminal domain-like Family: D-glucarate dehydratase-like
44	c4mitE	Alignment	not modelled	6.0	50	PDB header: signaling protein Chain: E: PDB Molecule: serine/threonine protein kinase pak, putative; PDBTitle: crystal structure of e. histolytica racc bound to the ehpa4 pbd
45	d1c1yb	Alignment	not modelled	6.0	49	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
46	c2boiA	Alignment	not modelled	5.9	31	PDB header: lectin Chain: A: PDB Molecule: cv-ii lectin; PDBTitle: 1.1a structure of chromobacterium violaceum lectin cv21 in2 complex with alpha-methyl-fucoside
47	d1ny721	Alignment	not modelled	5.8	20	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Comoviridae-like VP
48	c3lwzC	Alignment	not modelled	5.7	57	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinatase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-dehydroquinatase2 dehydratase (aroq) from yersinia pestis
49	d1h05a	Alignment	not modelled	5.7	43	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinatase dehydratase Family: Type II 3-dehydroquinatase dehydratase
50	c3iv4A	Alignment	not modelled	5.5	27	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: a putative oxidoreductase with a thioredoxin fold
51	c6cv6L	Alignment	not modelled	5.5	29	PDB header: lyase Chain: L: PDB Molecule: 3-dehydroquinatase dehydratase; PDBTitle: crystal structure of 3-dehydroquinatase dehydratase, type ii, from2 burkholderia phymatum stm815
52	d1gqoa	Alignment	not modelled	5.5	21	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinatase dehydratase Family: Type II 3-dehydroquinatase dehydratase
53	c3u80A	Alignment	not modelled	5.4	43	PDB header: unknown function Chain: A: PDB Molecule: 3-dehydroquinatase dehydratase, type ii; PDBTitle: 1.60 angstrom resolution crystal structure of a 3-dehydroquinatase2 dehydratase-like protein from bifidobacterium longum
54	c5n6yD	Alignment	not modelled	5.3	24	PDB header: oxidoreductase Chain: D: PDB Molecule: nitrogenase vanadium-iron protein alpha chain;

					PDBTitle: azotobacter vinelandii vanadium nitrogenase
55	c3n8kG_	Alignment	not modelled	5.3	PDB header: lyase Chain: G: PDB Molecule: 3-dehydroquinatate dehydratase; PDBTitle: type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
56	c2uygF_	Alignment	not modelled	5.3	PDB header: lyase Chain: F: PDB Molecule: 3-dehydroquinatate dehydratase; PDBTitle: crystallogaphic structure of the typeii 3-dehydroquinase from thermus2 thermophilus
57	d1m3ya1	Alignment	not modelled	5.2	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Major capsid protein vp54
58	c5yhhA_	Alignment	not modelled	5.1	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized conserved protein yiim; PDBTitle: crystal structure of yiim from geobacillus stearothermophilus
59	c3witA_	Alignment	not modelled	5.1	PDB header: structural protein Chain: A: PDB Molecule: putative vgr protein; PDBTitle: crystal structure of the c-terminal region of vgrg1 from e. coli o1572 edl933
60	c3kipU_	Alignment	not modelled	5.1	PDB header: lyase Chain: U: PDB Molecule: 3-dehydroquinase, type ii; PDBTitle: crystal structure of type-ii 3-dehydroquinase from c. albicans