












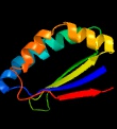

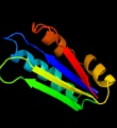






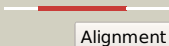

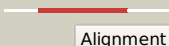


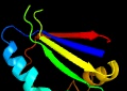





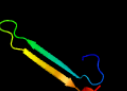



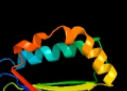




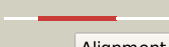
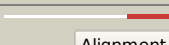






Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2557 (-) _2877082_2877756
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	b04570b5e0c9a3d7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mcsB_	 Alignment		98.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of putative monooxygenase (fn1347) from2 fusobacterium nucleatum subsp. nucleatum atcc 25586 at 2.55 a3 resolution
2	c5f9pA_	 Alignment		98.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: anthrone oxidase-like protein; PDBTitle: crystal structure study of anthrone oxidase-like protein
3	c3f44A_	 Alignment		98.3	7	PDB header: oxidoreductase Chain: A: PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of putative monooxygenase (yp_193413.1) from2 lactobacillus acidophilus ncfm at 1.55 a resolution
4	d1iuja_	 Alignment		98.0	21	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
5	c3gz7B_	 Alignment		97.9	22	PDB header: biosynthetic protein Chain: B: PDB Molecule: putative antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of putative antibiotic biosynthesis monooxygenase2 (np_888398.1) from bordetella bronchiseptica at 2.15 a resolution
6	c3bm7A_	 Alignment		97.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: protein of unknown function with ferredoxin-like fold; PDBTitle: crystal structure of a putative antibiotic biosynthesis monooxygenase2 (cc_2132) from caulobacter crescentus cb15 at 1.35 a resolution
7	c2gffB_	 Alignment		97.9	14	PDB header: sugar binding protein Chain: B: PDB Molecule: lsrg protein; PDBTitle: crystal structure of yersinia pestis lsrg
8	c2omoC_	 Alignment		97.9	14	PDB header: oxidoreductase Chain: C: PDB Molecule: duf176; PDBTitle: putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
9	c4dpoA_	 Alignment		97.8	8	PDB header: unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: crystal structure of a conserved protein mm_1583 from methanosarcina2 mazei go1
10	d2zdpa1	 Alignment		97.7	8	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
11	d2omoa1	 Alignment		97.6	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like

12	c3fgvB_	 Alignment		97.3	14	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein with ferredoxin-like fold; PDBTitle: crystal structure of a putative antibiotic biosynthesis monooxygenase2 (spo2313) from silicibacter pomeroyi dss-3 at 1.30 a resolution
13	c4zosA_	 Alignment		97.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein ye0340 from yersinia enterocolitica subsp. PDBTitle: 2.20 angstrom resolution crystal structure of protein ye0340 of2 unidentified function from yersinia enterocolitica subsp.3 enterocolitica 8081]
14	c3hx9B_	 Alignment		97.3	17	PDB header: oxidoreductase Chain: B: PDB Molecule: protein rv3592; PDBTitle: structure of heme-degrader, mhud (rv3592), from2 mycobacterium tuberculosis with two hemes bound in its3 active site
15	c2bbeA_	 Alignment		97.1	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein so0527; PDBTitle: crystal structure of protein so0527 from shewanella oneidensis
16	d2pd1a1	 Alignment		97.0	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
17	d2go8a1	 Alignment		97.0	26	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
18	d1y0ha_	 Alignment		96.9	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
19	c4dn9B_	 Alignment		96.9	16	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of putative antibiotic biosynthesis monooxygenase2 from chloroflexus aurantiacus j-10-fl
20	c3e8oB_	 Alignment		96.9	17	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized protein with ferredoxin-like fold; PDBTitle: crystal structure of a putative antibiotic biosynthesis monooxygenase2 (dr_2100) from deinococcus radiodurans at 1.40 a resolution
21	c2riiA_	 Alignment	not modelled	96.7	8	PDB header: oxidoreductase Chain: A: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of a putative monooxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
22	c3tvzA_	 Alignment	not modelled	96.7	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein yhgc; PDBTitle: structure of bacillus subtilis hmob
23	c2fb0A_	 Alignment	not modelled	96.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of conserved protein of unknown function from2 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
24	d1lq9a_	 Alignment	not modelled	96.6	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Actinorhodin biosynthesis monooxygenase ActVa-Orf6
25	d1x7va_	 Alignment	not modelled	96.6	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
26	d1tz0a_	 Alignment	not modelled	96.6	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
27	c4hl9B_	 Alignment	not modelled	96.5	16	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of antibiotic biosynthesis monooxygenase
28	c3kkfA_	 Alignment	not modelled	96.2	10	PDB header: oxidoreductase Chain: A: PDB Molecule: putative antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of putative antibiotic biosynthesis monooxygenase2 (np_810307.1) from bacteriodes thetaiotaomicron

						vpi-5482 at 1.30 a3 resolution
29	d1xbwa_	Alignment	not modelled	96.2	8	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
30	c3kngA_	Alignment	not modelled	95.7	9	PDB header: oxidoreductase Chain: A: PDB Molecule: snoab; PDBTitle: crystal structure of snoab, a cofactor-independent oxygenase2 from streptomyces nogalater, determined to 1.9 resolution
31	c3fj2A_	Alignment	not modelled	95.6	11	PDB header: unknown function Chain: A: PDB Molecule: monooxygenase-like protein; PDBTitle: crystal structure of a monooxygenase-like protein (lin2316) from2 listeria innocua at 1.85 a resolution
32	c4ae5C_	Alignment	not modelled	95.1	20	PDB header: signaling protein Chain: C: PDB Molecule: signal transduction protein trap; PDBTitle: structure of a major regulator of staphylococcal pathogenesis
33	d1tuva_	Alignment	not modelled	94.9	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
34	d2hiqa1	Alignment	not modelled	91.1	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YdhR
35	d2ftra1	Alignment	not modelled	88.9	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: EthD-like
36	d1vqsa_	Alignment	not modelled	87.8	10	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
37	d1vqya1	Alignment	not modelled	78.4	9	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
38	d1q8ba_	Alignment	not modelled	76.2	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YjCS
39	c5k9fA_	Alignment	not modelled	72.5	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nipsnap domain protein; PDBTitle: crystal structure of a nipsnap domain protein from burkholderia2 xenovorans
40	c5kakE_	Alignment	not modelled	68.7	10	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap-like domain protein2 from burkholderia xenovorans
41	c5ixuA_	Alignment	not modelled	65.0	16	PDB header: structural genomics/unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap domain protein from2 burkholderia xenovorans
42	c3gvzB_	Alignment	not modelled	59.0	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein cv2077; PDBTitle: crystal structure of the protein cv2077 from chromobacterium2 violaceum. northeast structural genomics consortium target cvr62
43	c6fxdB_	Alignment	not modelled	49.6	5	PDB header: biosynthetic protein Chain: B: PDB Molecule: mupz; PDBTitle: crystal structure of mupz from pseudomonas fluorescens
44	c1wd6B_	Alignment	not modelled	39.5	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli
45	c5qziB_	Alignment	not modelled	34.3	16	PDB header: lyase Chain: B: PDB Molecule: lysine cyclodeaminase; PDBTitle: cyclodeaminase_pa
46	c2qlwA_	Alignment	not modelled	27.0	12	PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
47	c2qlxA_	Alignment	not modelled	27.0	12	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
48	d2q49a2	Alignment	not modelled	26.2	26	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
49	c3bf4B_	Alignment	not modelled	24.3	15	PDB header: unknown function Chain: B: PDB Molecule: ethyl tert-butyl ether degradation ethd protein; PDBTitle: crystal structure of an ethd-like protein (reut_b5694) from ralstonia2 eutropha jmp134 at 2.10 a resolution
50	d1vq3a_	Alignment	not modelled	19.2	19	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
51	d1vkna2	Alignment	not modelled	18.5	7	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
52	d3b48a1	Alignment	not modelled	15.0	11	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
53	d2hwja1	Alignment	not modelled	13.3	23	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Atu1540-like
54	d1x8da1	Alianment	not modelled	13.2	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel

						Family:Yiil-like
55	d1j9ia_	Alignment	not modelled	12.9	16	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
56	d3ct6a1	Alignment	not modelled	11.0	19	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
57	c5wwoB_	Alignment	not modelled	10.6	12	PDB header: rna binding protein Chain: B: PDB Molecule: essential nuclear protein 1; PDBTitle: crystal structure of enp1
58	c3iabA_	Alignment	not modelled	9.4	11	PDB header: hydrolase/rna Chain: A: PDB Molecule: ribonucleases p/mrp protein subunit pop6; PDBTitle: crystal structure of rnase p /rnase mrp proteins pop6, pop72 in a complex with the p3 domain of rnase mrp rna
59	c6hvpA_	Alignment	not modelled	9.0	32	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: fetuin-b; PDBTitle: crystal structure of mouse fetuin-b
60	c2i7gA_	Alignment	not modelled	9.0	25	PDB header: oxidoreductase Chain: A: PDB Molecule: monooxygenase; PDBTitle: crystal structure of monooxygenase from agrobacterium tumefaciens
61	c3gdwA_	Alignment	not modelled	8.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sigma-54 interaction domain protein; PDBTitle: crystal structure of sigma-54 interaction domain protein from 2 enterococcus faecalis
62	c3j0iF_	Alignment	not modelled	8.2	29	PDB header: structural protein Chain: F: PDB Molecule: phikz029; PDBTitle: fitting of the phikz gp29pr structure into the cryo-em density map of 2 the phikz polysheath
63	c3dm3A_	Alignment	not modelled	8.2	20	PDB header: replication Chain: A: PDB Molecule: replication factor a; PDBTitle: crystal structure of a domain of a replication factor a2 protein, from methanocaldococcus jannaschii. northeast3 structural genomics target mjrl18e
64	c3a4tA_	Alignment	not modelled	8.0	4	PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase mj0026; PDBTitle: crystal structure of atrm4 from m.jannaschii with sinefungin
65	c3gx1A_	Alignment	not modelled	7.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1832 protein; PDBTitle: crystal structure of a domain of lin1832 from listeria innocua
66	d1mjta_	Alignment	not modelled	7.6	19	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
67	c3sdoB_	Alignment	not modelled	7.5	24	PDB header: oxidoreductase Chain: B: PDB Molecule: nitritotriacetate monooxygenase; PDBTitle: structure of a nitritotriacetate monooxygenase from burkholderia2 pseudomallei
68	c6g4ww_	Alignment	not modelled	7.4	21	PDB header: ribosome Chain: W: PDB Molecule: 40s ribosomal protein s15a; PDBTitle: cryo-em structure of a late human pre-40s ribosomal subunit - state a
69	d1m9ma_	Alignment	not modelled	7.4	16	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
70	d2p0va1	Alignment	not modelled	6.8	38	Fold: alpha/alpha toroid Superfamily: Six-hairpin glycosidases Family: CPF0428-like
71	c2p0vA_	Alignment	not modelled	6.8	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein bt3781; PDBTitle: crystal structure of bt3781 protein from bacteroides thetaiotaomicron,2 northeast structural genomics target btr58
72	c5m72B_	Alignment	not modelled	6.8	54	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle subunit srp68; PDBTitle: structure of the human srp68-72 protein-binding domain complex
73	c4za1A_	Alignment	not modelled	6.7	19	PDB header: transferase Chain: A: PDB Molecule: nosa; PDBTitle: crystal structure of nosa involved in nosiheptide biosynthesis
74	d2bnma1	Alignment	not modelled	6.6	41	Fold: lambda repressor-like DNA-binding domains Superfamily: lambda repressor-like DNA-binding domains Family: SinR domain-like
75	c5wrvA_	Alignment	not modelled	6.6	54	PDB header: protein transport Chain: A: PDB Molecule: signal recognition particle subunit srp68; PDBTitle: complex structure of human srp72/srp68
76	d1q2oa_	Alignment	not modelled	6.5	16	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
77	c5u47A_	Alignment	not modelled	6.4	16	PDB header: lipid-binding protein Chain: A: PDB Molecule: penicillin binding protein 2x; PDBTitle: 1.95 angstrom resolution crystal structure of penicillin binding2 protein 2x from streptococcus thermophilus
78	d3e7ma1	Alignment	not modelled	6.3	16	Fold: Nitric oxide (NO) synthase oxygenase domain Superfamily: Nitric oxide (NO) synthase oxygenase domain Family: Nitric oxide (NO) synthase oxygenase domain
79	c2y0fD_	Alignment	not modelled	6.3	10	PDB header: oxidoreductase Chain: D: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
80	d1s0aa_	Alignment	not modelled	6.3	12	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like

81	d1k25a4	Alignment	not modelled	6.3	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
82	d1j4wa2	Alignment	not modelled	5.9	17	Fold: Eukaryotic type KH-domain (KH-domain type I) Superfamily: Eukaryotic type KH-domain (KH-domain type I) Family: Eukaryotic type KH-domain (KH-domain type I)
83	c2zw2B_	Alignment	not modelled	5.7	15	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfolobus tokodaii (stpurs)
84	c2rpsA_	Alignment	not modelled	5.6	47	PDB header: immune system Chain: A: PDB Molecule: chemokine; PDBTitle: solution structure of a novel insect chemokine isolated from2 integument
85	c2jsxA_	Alignment	not modelled	5.6	31	PDB header: chaperone Chain: A: PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
86	d1vj1a1	Alignment	not modelled	5.5	19	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
87	d2bi0a2	Alignment	not modelled	5.5	19	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
88	d2ivda2	Alignment	not modelled	5.2	29	Fold: FAD-linked reductases, C-terminal domain Superfamily: FAD-linked reductases, C-terminal domain Family: L-aminoacid/polyamine oxidase
89	c1fooA_	Alignment	not modelled	5.1	17	PDB header: oxidoreductase Chain: A: PDB Molecule: nitric-oxide synthase; PDBTitle: bovine endothelial nitric oxide synthase heme domain complexed with I-2 arg and no(h4b-free)