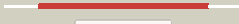



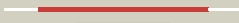



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3592_(TB11.2)_4034236_4034553
Date	Fri Aug 9 18:20:27 BST 2019
Unique Job ID	d81eabf0ec04ed19

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hx9B_	 Alignment		100.0	100	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
2	c3e8oB_	 Alignment		99.9	15	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
3	d1luja_	 Alignment		99.9	36	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
4	c3gz7B_	 Alignment		99.9	18	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
5	c2omoC_	 Alignment		99.9	12	PDB header: oxidoreductase Chain: C: PDB Molecule: duf176; PDBTitle: putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
6	c2bbeA_	 Alignment		99.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein so0527; PDBTitle: crystal structure of protein so0527 from shewanella oneidensis
7	c4dpoA_	 Alignment		99.9	5	PDB header: unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: crystal structure of a conserved protein mm_1583 from methanosarcina2 mazei go1
8	c4zosA_	 Alignment		99.9	15	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]
9	d2omoa1	 Alignment		99.9	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
10	c2gffB_	 Alignment		99.9	15	PDB header: sugar binding protein Chain: B: PDB Molecule: lsrg protein; PDBTitle: crystal structure of yersinia pestis lsrg
11	c3bm7A_	 Alignment		99.9	23	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

12	c2fb0A_	Alignment		99.9	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of conserved protein of unknown function from2 bacteriodes thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
13	d1y0ha_	Alignment		99.9	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
14	d1x7va_	Alignment		99.9	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
15	c3mcsB_	Alignment		99.9	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
16	c3kngA_	Alignment		99.9	27	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
17	d1xbwa_	Alignment		99.9	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
18	c4hl9B_	Alignment		99.9	9	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of antibiotic biosynthesis monooxygenase
19	d2zdpa1	Alignment		99.9	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
20	d2pd1a1	Alignment		99.9	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
21	c3fgvB_	Alignment	not modelled	99.9	16	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
22	c4dn9B_	Alignment	not modelled	99.8	17	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of putative antibiotic biosynthesis monooxygenase2 from chloroflexus aurantiacus j-10-fl
23	d1tuva_	Alignment	not modelled	99.8	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
24	d1tz0a_	Alignment	not modelled	99.8	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
25	c3kkfA_	Alignment	not modelled	99.8	11	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
26	c3f44A_	Alignment	not modelled	99.8	11	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
27	c5f9pA_	Alignment	not modelled	99.8	19	PDB header: oxidoreductase Chain: A: PDB Molecule: anthrone oxidase-like protein; PDBTitle: crystal structure study of anthrone oxidase-like protein
						PDB header: oxidoreductase

28	c2riIA_	Alignment	not modelled	99.8	23	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
29	d1q8ba_	Alignment	not modelled	99.7	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YjCS
30	c3fj2A_	Alignment	not modelled	99.7	16	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
31	c3tvzA_	Alignment	not modelled	99.7	32	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein yhgc; PDBTitle: structure of bacillus subtilis hmob
32	c4ae5C_	Alignment	not modelled	99.7	22	PDB header: signaling protein Chain: C: PDB Molecule: signal transduction protein trap; PDBTitle: structure of a major regulator of staphylococcal pathogenesis
33	d1lq9a_	Alignment	not modelled	99.6	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Actinorhodin biosynthesis monooxygenase ActVa-Orf6
34	c6fxdB_	Alignment	not modelled	99.5	12	PDB header: biosynthetic protein Chain: B: PDB Molecule: mpuz; PDBTitle: crystal structure of mpuz from pseudomonas fluorescens
35	c3bn7A_	Alignment	not modelled	98.3	7	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (cc_2267) from2 caulobacter crescentus cb15 at 1.64 a resolution
36	d1q4ra_	Alignment	not modelled	98.2	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
37	c3bdeA_	Alignment	not modelled	98.1	11	PDB header: unknown function Chain: A: PDB Molecule: mll5499 protein; PDBTitle: crystal structure of a dabb family protein with a ferredoxin-like fold2 (mll5499) from mesorhizobium loti maff303099 at 1.79 a resolution
38	c3bb5B_	Alignment	not modelled	98.1	17	PDB header: unknown function Chain: B: PDB Molecule: stress responsive alpha-beta protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein of unknown2 function (jann_3925) from jannaschia sp. ccs1 at 2.30 a resolution
39	c2qycA_	Alignment	not modelled	98.0	15	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein; PDBTitle: crystal structure of a dimeric ferredoxin-like protein (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
40	c3bguA_	Alignment	not modelled	97.9	12	PDB header: unknown function Chain: A: PDB Molecule: ferredoxin-like protein of unknown function; PDBTitle: crystal structure of a dimeric ferredoxin-like protein of unknown2 function (tfu_0763) from thermobifida fusca yx at 1.50 a resolution
41	d1tr0a_	Alignment	not modelled	97.9	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
42	d2cb2a1	Alignment	not modelled	97.9	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: SOR-like
43	c5y02D_	Alignment	not modelled	97.8	12	PDB header: lyase Chain: D: PDB Molecule: hydroxynitrile lyase; PDBTitle: c-terminal peptide depleted mutant of hydroxynitrile lyase from2 passiflora edulis (pehnl) bound with (r)-mandelonitrile
44	d1rja_	Alignment	not modelled	97.7	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
45	c3fmbA_	Alignment	not modelled	97.6	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dimeric protein of unknown function and ferredoxin-like PDBTitle: crystal structure of dimeric protein of unknown function and2 ferredoxin-like fold (yp_212648.1) from bacteroides fragilis nctc3 9343 at 1.85 a resolution
46	c3hfkB_	Alignment	not modelled	97.4	12	PDB header: isomerase Chain: B: PDB Molecule: 4-methylmuconolactone methylisomerase; PDBTitle: crystal structure of 4-methylmuconolactone methylisomerase (h52a) in2 complex with 4-methylmuconolactone
47	c3dcaC_	Alignment	not modelled	97.3	18	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: rpa0582; PDBTitle: crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
48	c5b0aA_	Alignment	not modelled	97.2	13	PDB header: lyase Chain: A: PDB Molecule: olivetolic acid cyclase; PDBTitle: polyketide cyclase oac from cannabis sativa, h5q mutant
49	d2go8a1	Alignment	not modelled	96.9	26	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
50	d2ftra1	Alignment	not modelled	96.9	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: EthD-like
51	c5ixuA_	Alignment	not modelled	96.9	13	PDB header: structural genomics/unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap domain protein from2 burkholderia xenovorans
52	d2hiqa1	Alignment	not modelled	96.6	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein Ydhr
						Fold: Ferredoxin-like

53	dlvqsa_	Alignment	not modelled	96.1	11	Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
54	dlvqya1	Alignment	not modelled	96.0	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
55	dlx8da1	Alignment	not modelled	95.6	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Yiil-like
56	c5k9fA_	Alignment	not modelled	95.3	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nipsnap domain protein; PDBTitle: crystal structure of a nipsnap domain protein from burkholderia2 xenovorans
57	c5kakE_	Alignment	not modelled	95.1	10	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap-like domain protein2 from burkholderia xenovorans
58	d2fiua1	Alignment	not modelled	95.0	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
59	c3lo3E_	Alignment	not modelled	94.8	13	PDB header: structure genomics, unknown function Chain: E: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 colwellia psychrethraea 34h.
60	c2qlwA_	Alignment	not modelled	94.1	16	PDB header: isomerase Chain: A: PDB Molecule: rhaui; PDBTitle: crystal structure of rhamnose mutarotase rhaui of rhizobium2 leguminosarum
61	c2qlxA_	Alignment	not modelled	94.1	16	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of rhamnose mutarotase rhaui of rhizobium2 leguminosarum in complex with l-rhamnose
62	c3bf4B_	Alignment	not modelled	94.0	17	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
63	c1wd6B_	Alignment	not modelled	93.3	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli
64	c3a16C_	Alignment	not modelled	92.6	16	PDB header: lyase Chain: C: PDB Molecule: aldoxime dehydratase; PDBTitle: crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime
65	c2djb_	Alignment	not modelled	85.5	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: redy-like protein; PDBTitle: crystal structure of hapk from hahella chejuensis
66	c6hhnA_	Alignment	not modelled	75.1	9	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of l-rhamnose mutarotase fa22100 from formosa2 agariphila
67	c3gn6B_	Alignment	not modelled	69.7	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: ct0912, orfan protein with a ferredoxin-like domain repeat; PDBTitle: crystal structure of ct0912, orfan protein from chlorobium tepidum2 with a ferredoxin-like domain repeat (np_661805.1) from chlorobium3 tepidum t1s at 1.80 a resolution
68	d2cfxa2	Alignment	not modelled	51.5	21	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
69	c5cw9A_	Alignment	not modelled	23.4	18	PDB header: de novo protein Chain: A: PDB Molecule: de novo designed ferredoxin-ferredoxin domain insertion PDBTitle: crystal structure of de novo designed ferredoxin-ferredoxin domain2 insertion protein
70	dlilga2	Alignment	not modelled	22.4	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
71	c2e1aD_	Alignment	not modelled	21.7	16	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
72	c2kl8A_	Alignment	not modelled	20.7	15	PDB header: de novo protein Chain: A: PDB Molecule: or15; PDBTitle: solution nmr structure of de novo designed ferredoxin-like fold2 protein, northeast structural genomics consortium target or15
73	d2cs4a1	Alignment	not modelled	20.3	24	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
74	c2djwF_	Alignment	not modelled	17.1	13	PDB header: unknown function Chain: F: PDB Molecule: probable transcriptional regulator, asnc family; PDBTitle: crystal structure of ttha0845 from thermus thermophilus hb8
75	d2cyya2	Alignment	not modelled	14.4	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
76	c1zr9A_	Alignment	not modelled	10.4	0	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 593; PDBTitle: solution structure of a human c2h2-type zinc finger protein
77	d1zr9a1	Alignment	not modelled	10.4	0	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
						PDB header: isomerase Chain: B: PDB Molecule: 4-oxalocrotonate tautomerase;

78	c2x4kB_	Alignment	not modelled	9.6	22	PDBTitle: crystal structure of sar1376, a putative 4-oxalocrotonate2 tautomerase from the methicillin-resistant staphylococcus3 aureus (mrsa)
79	c3lygA_	Alignment	not modelled	9.5	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: ntf2-like protein of unknown function; PDBTitle: crystal structure of ntf2-like protein of unknown function2 (yp_270605.1) from colwellia psychrerythraea 34h at 1.61 a resolution
80	c4p6iB_	Alignment	not modelled	8.9	16	PDB header: hydrolase Chain: B: PDB Molecule: crispr-associated endoribonuclease cas2; PDBTitle: crystal structure of the cas1-cas2 complex from escherichia coli
81	d2okqa1	Alignment	not modelled	7.2	25	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YbaA-like
82	c4lbaA_	Alignment	not modelled	6.7	14	PDB header: lyase Chain: A: PDB Molecule: 5-chloro-2-hydroxyhydroquinone dehydrochlorinase (tftg); PDBTitle: 5-chloro-2-hydroxyhydroquinone dehydrochlorinase (tftg) from2 burkholderia phenoliruptrix ac1100: apo-form
83	d1r2aa_	Alignment	not modelled	6.6	25	Fold: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Superfamily: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit Family: Dimerization-anchoring domain of cAMP-dependent PK regulatory subunit
84	c3qzcA_	Alignment	not modelled	6.5	8	PDB header: signaling protein Chain: A: PDB Molecule: periplasmic protein cpxp; PDBTitle: structure of the periplasmic stress response protein cpxp
85	c4h0aB_	Alignment	not modelled	5.7	13	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a cysteine-rich secretory protein (sav1118) from2 staphylococcus aureus subsp. aureus mu50 at 1.90 a resolution
86	c3zpnD_	Alignment	not modelled	5.3	4	PDB header: photosynthesis Chain: D: PDB Molecule: photosystem ii reaction center psb28 protein; PDBTitle: structure of psb28
87	c4ky3A_	Alignment	not modelled	5.2	13	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or327; PDBTitle: three-dimensional structure of the orthorhombic crystal of2 computationally designed insertion domain , northeast structural3 genomics consortium (nesg) target or327