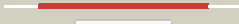



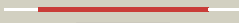



















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2749 (-)_3062515_3062829
Date	Wed Aug 7 12:50:40 BST 2019
Unique Job ID	7f59c7de36ea9f85

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2pd1a1	 Alignment		100.0	23	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
2	c2omoC	 Alignment		99.9	14	PDB header: oxidoreductase Chain: C: PDB Molecule: duf176; PDBTitle: putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
3	d1y0ha	 Alignment		99.9	27	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
4	d2omoa1	 Alignment		99.9	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
5	c2bbeA	 Alignment		99.9	26	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein so0527; PDBTitle: crystal structure of protein so0527 from shewanella oneidensis
6	c3e8oB	 Alignment		99.9	26	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
7	c3bm7A	 Alignment		99.9	30	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
8	c4dpoA	 Alignment		99.9	26	PDB header: unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: crystal structure of a conserved protein mm_1583 from methanosarcina2 mazeri go1
9	c2gffB	 Alignment		99.9	17	PDB header: sugar binding protein Chain: B: PDB Molecule: lsrg protein; PDBTitle: crystal structure of yersinia pestis lsrg
10	c3fgvB	 Alignment		99.9	22	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
11	c4zosA	 Alignment		99.9	26	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]

12	c4dn9B_	Alignment		99.9	21	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of putative antibiotic biosynthesis monooxygenase2 from chloroflexus aurantiacus j-10-fl
13	d1tuva_	Alignment		99.9	27	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
14	c3mcsB_	Alignment		99.9	16	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
15	c4hl9B_	Alignment		99.9	26	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of antibiotic biosynthesis monooxygenase
16	c3kkfA_	Alignment		99.9	20	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
17	c2fb0A_	Alignment		99.9	17	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
18	d1x7va_	Alignment		99.9	28	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
19	c3gz7B_	Alignment		99.9	19	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
20	c3f44A_	Alignment		99.9	15	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
21	d1q8ba_	Alignment	not modelled	99.8	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YjcS
22	c3hx9B_	Alignment	not modelled	99.8	19	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
23	c6fxdB_	Alignment	not modelled	99.8	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: mupz; PDBTitle: crystal structure of mupz from pseudomonas fluorescens
24	c3kngA_	Alignment	not modelled	99.8	18	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
25	d1iuja_	Alignment	not modelled	99.8	18	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
26	c5f9pA_	Alignment	not modelled	99.5	21	PDB header: oxidoreductase Chain: A: PDB Molecule: anthrone oxidase-like protein; PDBTitle: crystal structure study of anthrone oxidase-like protein
27	c3tvzA_	Alignment	not modelled	99.4	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein yhgc; PDBTitle: structure of bacillus subtilis hmob
28	d2zdpal	Alignment	not modelled	99.3	7	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
						PDB header: oxidoreductase

29	c2ri1A_	Alignment	not modelled	99.3	16	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
30	c3fj2A_	Alignment	not modelled	99.3	15	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	d1xbwa_	Alignment	not modelled	99.1	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
32	d1lq9a_	Alignment	not modelled	99.1	23	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Actinorhodin biosynthesis monooxygenase ActVa-Orf6
33	c4ae5C_	Alignment	not modelled	99.0	15	PDB header: signaling protein Chain: C: PDB Molecule: signal transduction protein trap; PDBTitle: structure of a major regulator of staphylococcal pathogenesis
34	d1tz0a_	Alignment	not modelled	99.0	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
35	c3bn7A_	Alignment	not modelled	97.7	11	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	97.5	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
37	c3bdeA_	Alignment	not modelled	97.5	14	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	c5y02D_	Alignment	not modelled	97.5	10	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
39	d1tr0a_	Alignment	not modelled	97.4	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
40	c2qycA_	Alignment	not modelled	97.4	18	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
41	c3bguA_	Alignment	not modelled	97.2	13	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
42	c3bb5B_	Alignment	not modelled	97.1	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
43	d1rja_	Alignment	not modelled	97.0	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
44	d2cb2a1	Alignment	not modelled	96.9	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: SOR-like
45	c3hfkB_	Alignment	not modelled	96.9	17	PDB header: isomerase Chain: B: PDB Molecule: 4-methylmuconolactone methylisomerase; PDBTitle: crystal structure of 4-methylmuconolactone methylisomerase (h52a) in2 complex with 4-methylmuconolactone
46	c2qlwA_	Alignment	not modelled	96.5	12	PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
47	c2qlxA_	Alignment	not modelled	96.5	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	c3fmbA_	Alignment	not modelled	96.4	9	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
49	d1x8da1	Alignment	not modelled	96.4	10	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Yiil-like
50	c5ixuA_	Alignment	not modelled	96.2	12	PDB header: structural genomics/unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap domain protein from2 burkholderia xenovorans
51	d2go8a1	Alignment	not modelled	96.1	17	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
52	d1vqya1	Alignment	not modelled	95.8	7	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
53	c5k9fA_	Alignment	not modelled	95.4	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nipsnap domain protein; PDBTitle: crystal structure of a nipsnap domain protein from burkholderia2 xenovorans
						Fold: Ferredoxin-like

54	d1vqsa_	Alignment	not modelled	95.3	8	Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
55	c5b0aA_	Alignment	not modelled	95.3	15	PDB header: lyase Chain: A: PDB Molecule: olivetolic acid cyclase; PDBTitle: polyketide cyclase oac from cannabis sativa, h5q mutant
56	c2djB_	Alignment	not modelled	95.0	11	PDB header: biosynthetic protein Chain: B: PDB Molecule: redy-like protein; PDBTitle: crystal structure of hapk from hahella chejuensis
57	d2ftra1	Alignment	not modelled	94.3	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: EthD-like
58	c5kakE_	Alignment	not modelled	93.4	13	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap-like domain protein2 from burkholderia xenovorans
59	c6hhaA_	Alignment	not modelled	93.3	9	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of l-rhamnose mutarotase fa22100 from formosa2 agariphila
60	d2hiqa1	Alignment	not modelled	93.1	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YdHR
61	c1wd6B_	Alignment	not modelled	91.9	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli
62	c3lo3E_	Alignment	not modelled	72.9	10	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 psychrerythraea 34h.
63	d2fiua1	Alignment	not modelled	64.8	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
64	c3bf4B_	Alignment	not modelled	63.1	13	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
65	c3dcaC_	Alignment	not modelled	61.1	13	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
66	c3a16C_	Alignment	not modelled	60.7	17	PDB header: lyase Chain: C: PDB Molecule: aldoxime dehydratase; PDBTitle: crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime
67	c3gn6B_	Alignment	not modelled	59.0	17	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	c5cw9A_	Alignment	not modelled	54.6	15	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
69	d2cfxa2	Alignment	not modelled	29.8	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
70	c2kl8A_	Alignment	not modelled	23.6	10	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
71	d2ifxa1	Alignment	not modelled	22.2	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Mml1-like
72	d2pbza2	Alignment	not modelled	20.4	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
73	d2okqa1	Alignment	not modelled	16.2	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YbaA-like
74	c4hhuA_	Alignment	not modelled	15.8	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: or280; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
75	d2cs4a1	Alignment	not modelled	15.0	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
76	c4o8uE_	Alignment	not modelled	13.1	14	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein pf2046; PDBTitle: structure of pf2046
77	c3x37A_	Alignment	not modelled	11.0	13	PDB header: replication regulator Chain: A: PDB Molecule: zyro0c14696p; PDBTitle: crystal structure of the n-terminal domain of sld7 in complex with2 sld3
78	d1zr9a1	Alignment	not modelled	10.8	15	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
79	c1zr9A_	Alignment	not modelled	10.8	15	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 593; PDBTitle: solution structure of a human c2h2-type zinc finger protein

80	c4ky3A_	 Alignment	not modelled	9.3	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
81	c2kllA_	 Alignment	not modelled	9.0	21	PDB header: cytokine Chain: A: PDB Molecule: interleukin-33; PDBTitle: solution structure of human interleukin-33
82	c2k9hA_	 Alignment	not modelled	7.2	28	PDB header: metal binding protein Chain: A: PDB Molecule: glycoprotein; PDBTitle: the hantavirus glycoprotein g1 tail contains a dual cchc-2 type classical zinc fingers
83	c3maeA_	 Alignment	not modelled	6.7	6	PDB header: transferase Chain: A: PDB Molecule: 2-oxoisovalerate dehydrogenase e2 component, PDBTitle: crystal structure of probable dihydrolipoamide acetyltransferase from2 listeria monocytogenes 4b f2365
84	d2pc6a1	 Alignment	not modelled	6.7	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
85	c2e1aD_	 Alignment	not modelled	6.5	11	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
86	d2f1fa2	 Alignment	not modelled	6.4	9	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
87	c3rqcB_	 Alignment	not modelled	5.9	7	PDB header: transferase Chain: B: PDB Molecule: probable lipoamide acyltransferase; PDBTitle: crystal structure of the catalytic core of the 2-oxoacid dehydrogenase2 multienzyme complex from thermoplasma acidophilum
88	c6ip4A_	 Alignment	not modelled	5.5	9	PDB header: gene regulation Chain: A: PDB Molecule: arabidopsis jmj13; PDBTitle: crystal structure of arabidopsis thaliana jmj13 catalytic domain in2 complex with nog and an h3k27me3 peptide
89	d2fgca1	 Alignment	not modelled	5.4	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
90	c2pbzC_	 Alignment	not modelled	5.3	17	PDB header: ligase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis