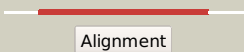

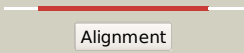



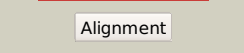



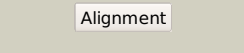
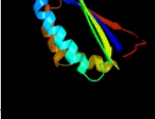
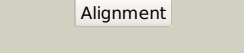



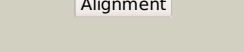

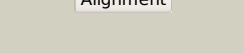

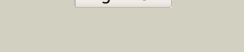



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1117_(-)_1241638_1241961
Date	Wed Jul 31 22:05:20 BST 2019
Unique Job ID	f61134800b0c6eaa

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bm7A_	 Alignment		99.9	20	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
2	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 mazei go1
3	d2pd1a1	 Alignment		99.9	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
4	c2omoC_	 Alignment		99.9	21	PDB header: oxidoreductase Chain: C: PDB Molecule: duf176; PDBTitle: putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
5	c3e8oB_	 Alignment		99.9	20	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
6	c3mcsB_	 Alignment		99.9	18	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
7	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
8	d2omoa1	 Alignment		99.9	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
9	d1tuva_	 Alignment		99.9	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
10	c4zosA_	 Alignment		99.9	25	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]
11	c4dn9B_	 Alignment		99.9	12	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of putative antibiotic biosynthesis monooxygenase2 from chloroflexus aurantiacus j-10-fl

12	c2gffB_	Alignment		99.9	19	PDB header: sugar binding protein Chain: B: PDB Molecule: lsrg protein; PDBTitle: crystal structure of yersinia pestis lsrg
13	c3gz7B_	Alignment		99.9	16	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
14	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 bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution, possible3 oxidoreductase
15	c4hl9B_	Alignment		99.9	19	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of antibiotic biosynthesis monooxygenase
16	d1y0ha_	Alignment		99.9	21	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
17	c3fgvB_	Alignment		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
18	d1x7va_	Alignment		99.9	23	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
19	c3kkfA_	Alignment		99.8	17	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
20	c3f44A_	Alignment		99.8	18	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	d1iuja_	Alignment	not modelled	99.8	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
22	c3kngA_	Alignment	not modelled	99.8	16	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
23	d1q8ba_	Alignment	not modelled	99.8	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YjCS
24	c3hx9B_	Alignment	not modelled	99.7	14	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
25	d2zdpal	Alignment	not modelled	99.5	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
26	c6fxdB_	Alignment	not modelled	99.5	18	PDB header: biosynthetic protein Chain: B: PDB Molecule: mupz; PDBTitle: crystal structure of mupz from pseudomonas fluorescens
27	c3tvzA_	Alignment	not modelled	99.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein yhgc; PDBTitle: structure of bacillus subtilis hmob
28	c5f9pA_	Alignment	not modelled	99.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: anthrone oxidase-like protein; PDBTitle: crystal structure study of anthrone oxidase-like protein
						PDB header: unknown function

29	c3fj2A_	Alignment	not modelled	99.3	6	Chain: A: PDB Molecule: monoxygenase-like protein; PDBTitle: crystal structure of a monoxygenase-like protein (lin2316) from2 listeria innocua at 1.85 a resolution
30	c2riIA_	Alignment	not modelled	99.3	13	PDB header: oxidoreductase Chain: A: PDB Molecule: antibiotic biosynthesis monoxygenase; PDBTitle: crystal structure of a putative monoxygenase (yp_001095275.1) from2 shewanella loihica pv-4 at 1.26 a resolution
31	d1xbwa_	Alignment	not modelled	99.1	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
32	d1tz0a_	Alignment	not modelled	99.1	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
33	c4ae5C_	Alignment	not modelled	99.1	15	PDB header: signaling protein Chain: C: PDB Molecule: signal transduction protein trap; PDBTitle: structure of a major regulator of staphylococcal pathogenesis
34	d1lq9a_	Alignment	not modelled	98.8	21	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Actinorhodin biosynthesis monoxygenase ActVa-Orf6
35	c5ixuA_	Alignment	not modelled	98.3	7	PDB header: structural genomics/unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap domain protein from2 burkholderia xenovorans
36	c3bn7A_	Alignment	not modelled	98.0	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
37	c5y02D_	Alignment	not modelled	98.0	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
38	d1tr0a_	Alignment	not modelled	98.0	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
39	c5k9fA_	Alignment	not modelled	97.9	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
40	d1vqsa_	Alignment	not modelled	97.7	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
41	c2qycA_	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 (bb1511) from2 bordetella bronchiseptica rb50 at 1.90 a resolution
42	d1vqya1	Alignment	not modelled	97.7	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
43	c3hfkB_	Alignment	not modelled	97.7	18	PDB header: isomerase Chain: B: PDB Molecule: 4-methylmuconolactone methylisomerase; PDBTitle: crystal structure of 4-methylmuconolactone methylisomerase (h52a) in2 complex with 4-methylmuconolactone
44	c3bdeA_	Alignment	not modelled	97.6	16	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
45	d1q4ra_	Alignment	not modelled	97.6	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
46	d2cb2a1	Alignment	not modelled	97.5	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: SOR-like
47	c3bguA_	Alignment	not modelled	97.5	14	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
48	c5kakE_	Alignment	not modelled	97.5	13	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap-like domain protein2 from burkholderia xenovorans
49	d1rja_	Alignment	not modelled	97.3	7	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
50	c3bb5B_	Alignment	not modelled	97.2	14	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
51	d1x8da1	Alignment	not modelled	97.2	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Yjil-like
52	c3fmbA_	Alignment	not modelled	97.2	12	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
53	c5b0aA_	Alignment	not modelled	96.7	9	PDB header: lyase Chain: A: PDB Molecule: olivetolic acid cyclase; PDBTitle: polyketide cyclase oac from cannabis sativa, h5q mutant
						Fold: Ferredoxin-like

54	d2ftra1	Alignment	not modelled	96.5	11	Superfamily: Dimeric alpha+beta barrel Family: EthD-like
55	c2qlwA	Alignment	not modelled	96.3	6	PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
56	c2qlxA	Alignment	not modelled	96.3	6	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
57	d2go8a1	Alignment	not modelled	96.0	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
58	c2djbB	Alignment	not modelled	94.7	14	PDB header: biosynthetic protein Chain: B: PDB Molecule: redy-like protein; PDBTitle: crystal structure of hapk from hahella chejuensis
59	c3bf4B	Alignment	not modelled	91.9	10	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
60	c3a16C	Alignment	not modelled	90.4	8	PDB header: lyase Chain: C: PDB Molecule: aldoxime dehydratase; PDBTitle: crystal structure of aldoxime dehydratase (oxdre) in complex2 with propionaldoxime
61	c6hnnA	Alignment	not modelled	89.3	6	PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of l-rhamnose mutarotase fa22100 from formosa2 agariphila
62	d2fiua1	Alignment	not modelled	87.3	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
63	c3lo3E	Alignment	not modelled	87.1	14	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.
64	c3dcaC	Alignment	not modelled	83.3	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
65	d2hiqa1	Alignment	not modelled	83.2	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YdhR
66	c2e1aD	Alignment	not modelled	78.1	7	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
67	c3gn6B	Alignment	not modelled	76.9	13	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	c2djwF	Alignment	not modelled	71.7	14	PDB header: unknown function Chain: F: PDB Molecule: probable transcriptional regulator, asnc family; PDBTitle: crystal structure of ttha0845 from thermus thermophilus hb8
69	c2kl8A	Alignment	not modelled	69.0	9	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
70	c1wd6B	Alignment	not modelled	63.0	14	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: protein ydhr; PDBTitle: crystal structure of jw1657 from escherichia coli
71	c4ky3A	Alignment	not modelled	56.4	10	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
72	c4hhuA	Alignment	not modelled	42.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: or280; PDBTitle: crystal structure of engineered protein. northeast structural genomics2 consortium target or280.
73	c5cw9A	Alignment	not modelled	32.1	8	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
74	d2cs4a1	Alignment	not modelled	30.8	38	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
75	d2cfxa2	Alignment	not modelled	28.7	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
76	c1zr9A	Alignment	not modelled	19.1	19	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	19.1	19	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: HkH motif-containing C2H2 finger
78	d2ifxa1	Alignment	not modelled	18.0	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: MmlI-like

79	c2w2iC_	Alignment	not modelled	16.0	20	PDB header: oxidoreductase Chain: C: PDB Molecule: 2-oxoglutarate oxygenase; PDBTitle: crystal structure of the human 2-oxoglutarate oxygenase2 loc390245
80	d1i1ga2	Alignment	not modelled	13.3	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
81	c3or8A_	Alignment	not modelled	10.0	10	PDB header: transcription Chain: A: PDB Molecule: transcription elongation factor spt6; PDBTitle: a tandem sh2 domain in transcription elongation factor spt6
82	c3opwA_	Alignment	not modelled	8.3	4	PDB header: oxidoreductase Chain: A: PDB Molecule: dna damage-responsive transcriptional repressor rph1; PDBTitle: crystal structure of the rph1 catalytic core
83	d2pbza2	Alignment	not modelled	8.2	10	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
84	c4jcuC_	Alignment	not modelled	7.7	11	PDB header: isomerase Chain: C: PDB Molecule: 5-carboxymethyl-2-hydroxyuconate isomerase; PDBTitle: crystal structure of a 5-carboxymethyl-2-hydroxyuconate isomerase2 from deinococcus radiodurans r1
85	d2cyya2	Alignment	not modelled	7.7	7	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
86	c1bmxA_	Alignment	not modelled	7.3	28	PDB header: viral protein Chain: A: PDB Molecule: human immunodeficiency virus type 1 capsid; PDBTitle: hiv-1 capsid protein major homology region peptide analog,2 nmr, 8 structures
87	d1fo8a_	Alignment	not modelled	7.1	13	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: N-acetylglucosaminyltransferase I
88	c2dcjA_	Alignment	not modelled	6.7	20	PDB header: hydrolase Chain: A: PDB Molecule: xylanase j; PDBTitle: a two-domain structure of alkaliphilic xynj from bacillus sp. 41m-1
89	c5yknA_	Alignment	not modelled	6.6	9	PDB header: gene regulation Chain: A: PDB Molecule: probable lysine-specific demethylase jmj14; PDBTitle: crystal structure of arabidopsis thaliana jmj14 catalytic domain
90	c2os2A_	Alignment	not modelled	6.4	15	PDB header: oxidoreductase Chain: A: PDB Molecule: jmjc domain-containing histone demethylation protein 3a; PDBTitle: crystal structure of jmjd2a complexed with histone h3 peptide2 trimethylated at lys36
91	c4lhbA_	Alignment	not modelled	6.4	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
92	c4igpA_	Alignment	not modelled	6.2	13	PDB header: structural protein Chain: A: PDB Molecule: os05g0196500 protein; PDBTitle: histone h3 lysine 4 demethylating rice jmj703 apo enzyme
93	c3bpjD_	Alignment	not modelled	5.9	8	PDB header: translation Chain: D: PDB Molecule: eukaryotic translation initiation factor 3 subunit j; PDBTitle: crystal structure of human translation initiation factor 3, subunit 12 alpha
94	c2zbcH_	Alignment	not modelled	5.7	9	PDB header: transcription Chain: H: PDB Molecule: 83aa long hypothetical transcriptional regulator asnc; PDBTitle: crystal structure of sts042, a stand-alone ram module protein, from2 hyperthermophilic archaeon sulfolobus tokodaii strain7.
95	c4npbA_	Alignment	not modelled	5.6	11	PDB header: isomerase Chain: A: PDB Molecule: protein disulfide isomerase ii; PDBTitle: the crystal structure of thiol:disulfide interchange protein dsbc from2 yersinia pestis co92
96	c2uwqA_	Alignment	not modelled	5.5	17	PDB header: apoptosis Chain: A: PDB Molecule: apoptosis-stimulating of p53 protein 2; PDBTitle: solution structure of aspp2 n-terminus
97	d1f5ja_	Alignment	not modelled	5.4	26	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Xylanase/endoglucanase 11/12