



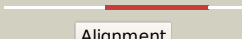


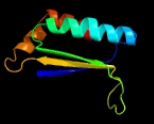
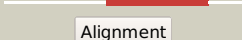



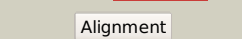

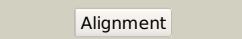

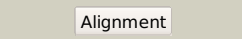

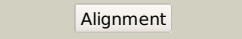

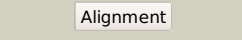



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1874 (-)_2123691_2124377
Date	Fri Aug 2 13:30:49 BST 2019
Unique Job ID	300c9df6f9be7ce9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hfkB_	 Alignment		99.9	15	PDB header: isomerase Chain: B: PDB Molecule: 4-methylmuconolactone methylisomerase; PDBTitle: crystal structure of 4-methylmuconolactone methylisomerase (h52a) in2 complex with 4-methylmuconolactone
2	d2ftra1	 Alignment		99.4	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: EthD-like
3	c3bf4B_	 Alignment		98.1	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
4	d2ifxa1	 Alignment		95.8	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Mmll-like
5	c3dcaC_	 Alignment		95.8	12	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
6	d1rjja_	 Alignment		94.8	7	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
7	d1tr0a_	 Alignment		91.2	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
8	c2jdjB_	 Alignment		90.8	13	PDB header: biosynthetic protein Chain: B: PDB Molecule: redy-like protein; PDBTitle: crystal structure of hapk from hahella chejuensis
9	c5y02D_	 Alignment		90.2	15	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
10	c2qycA_	 Alignment		89.7	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
11	c3bguA_	 Alignment		89.2	16	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

12	c3bb5B_	Alignment		85.4	12	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
13	d1q4ra_	Alignment		83.0	9	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Plant stress-induced protein
14	c3kngA_	Alignment		75.1	5	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
15	c3fmbA_	Alignment		68.8	11	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
16	d2fiua1	Alignment		67.4	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
17	d1x7va_	Alignment		67.1	8	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
18	c4dpoA_	Alignment		64.1	11	PDB header: unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: crystal structure of a conserved protein mm_1583 from methanosarcina2 mazei go1
19	c4zosA_	Alignment		63.8	9	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]
20	c3hx9B_	Alignment		62.5	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
21	c3bn7A_	Alignment	not modelled	61.1	8	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
22	c3lo3E_	Alignment	not modelled	53.3	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.
23	c2bbeA_	Alignment	not modelled	48.7	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein so0527; PDBTitle: crystal structure of protein so0527 from shewanella oneidensis
24	c3zphA_	Alignment	not modelled	44.7	11	PDB header: isomerase Chain: A: PDB Molecule: chalcone isomerase; PDBTitle: bacterial chalcone isomerase in closed conformation from2 eubacterium ramulus at 2.8 a resolution
25	d1tuva_	Alignment	not modelled	44.4	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
26	c2fb0A_	Alignment	not modelled	43.3	11	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
27	c3f44A_	Alignment	not modelled	37.5	9	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
28	d1y0ha_	Alignment	not modelled	36.2	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like

29	d2pd1a1	Alignment	not modelled	33.3	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
30	d2omoa1	Alignment	not modelled	23.0	8	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
31	d2zdpa1	Alignment	not modelled	23.0	11	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
32	c3bm7A	Alignment	not modelled	18.1	14	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
33	c3bdeA	Alignment	not modelled	17.2	4	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
34	c2gffb	Alignment	not modelled	16.5	9	PDB header: sugar binding protein Chain: B: PDB Molecule: lsrg protein; PDBTitle: crystal structure of yersinia pestis lsrg
35	c3h6pD	Alignment	not modelled	16.4	21	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: esat-6-like protein esxr; PDBTitle: crystal structure of rv3019c-rv3020c from mycobacterium tuberculosis
36	c3q4hB	Alignment	not modelled	15.7	14	PDB header: metal transport Chain: B: PDB Molecule: slow molecular weight protein antigen 7; PDBTitle: crystal structure of the mycobacterium smegmatis esxh complex2 (msmeg_0620-msmeg_0621)
37	c2bjeA	Alignment	not modelled	15.6	29	PDB header: hydrolase Chain: A: PDB Molecule: acylphosphatase; PDBTitle: acylphosphatase from sulfobolus solfataricus. monoclinic p212 space group
38	d1dqaa1	Alignment	not modelled	15.4	19	Fold: Ferredoxin-like Superfamily: NAD-binding domain of HMG-CoA reductase Family: NAD-binding domain of HMG-CoA reductase
39	c3fgvB	Alignment	not modelled	15.3	9	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
40	c3gz7B	Alignment	not modelled	15.3	14	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
41	c5b0aA	Alignment	not modelled	14.6	13	PDB header: lyase Chain: A: PDB Molecule: olivetolic acid cyclase; PDBTitle: polyketide cyclase oac from cannabis sativa, h5q mutant
42	c2jrtA	Alignment	not modelled	14.0	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
43	c5f9pA	Alignment	not modelled	13.4	9	PDB header: oxidoreductase Chain: A: PDB Molecule: anthrone oxidase-like protein; PDBTitle: crystal structure study of anthrone oxidase-like protein
44	c6d0hA	Alignment	not modelled	12.7	12	PDB header: toxin Chain: A: PDB Molecule: part: cog5654 (res domain) toxin; PDBTitle: part: prs adp-ribosylating toxin bound to cognate antitoxin pars
45	d2oa4a1	Alignment	not modelled	12.7	23	Fold: DNA/RNA-binding 3-helical bundle Superfamily: TrpR-like Family: SPO1678-like
46	c2riiA	Alignment	not modelled	12.4	10	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
47	c2kj5A	Alignment	not modelled	12.1	5	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phage integrase; PDBTitle: solution nmr structure of a domain from a putative phage integrase2 protein nmul_a0064 from nitrosospora multiformis, northeast3 structural genomics consortium target nmr46c
48	d1kyfa2	Alignment	not modelled	11.8	16	Fold: Subdomain of clathrin and coatamer appendage domain Superfamily: Subdomain of clathrin and coatamer appendage domain Family: Clathrin adaptor appendage, alpha and beta chain-specific domain
49	c4dn9B	Alignment	not modelled	11.5	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
50	c2n5xA	Alignment	not modelled	10.8	21	PDB header: chaperone Chain: A: PDB Molecule: hsp90 co-chaperone cdc37; PDBTitle: c-terminal domain of cdc37 cochaperone
51	c2mbhB	Alignment	not modelled	10.3	27	PDB header: transcription Chain: B: PDB Molecule: krueppel-like factor 1; PDBTitle: nmr structure of eklf(22-40)/ubiquitin complex
52	c5x90B	Alignment	not modelled	9.7	11	PDB header: protein transport Chain: B: PDB Molecule: icmw; PDBTitle: structure of dotl(656-783)-icms-icmw-lvga derived from legionella2 pneumophila

53	d2hg6a1	Alignment	not modelled	9.5	22	Fold: PA1123-like Superfamily: PA1123-like Family: PA1123-like
54	c1cojA	Alignment	not modelled	8.8	4	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (superoxide dismutase); PDBTitle: fe-sod from aquifex pyrophilus, a hyperthermophilic bacterium
55	c5k8zB	Alignment	not modelled	8.1	22	PDB header: oxidoreductase Chain: B: PDB Molecule: chlorite dismutase; PDBTitle: crystal structure of dimeric chlorite dismutase from cyanothece sp.2 pcc7425 (ph 8.5)
56	c3kkfA	Alignment	not modelled	7.9	8	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
57	d2acya	Alignment	not modelled	7.7	24	Fold: Ferredoxin-like Superfamily: Acylphosphatase/BLUF domain-like Family: Acylphosphatase-like
58	d1mhna	Alignment	not modelled	7.3	14	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
59	c1i7fA	Alignment	not modelled	7.0	18	PDB header: chaperone Chain: A: PDB Molecule: heat shock protein 33; PDBTitle: crystal structure of the hsp33 domain with constitutive chaperone2 activity
60	c2omoC	Alignment	not modelled	6.7	8	PDB header: oxidoreductase Chain: C: PDB Molecule: duf176; PDBTitle: putative antibiotic biosynthesis monooxygenase from nitrosomonas2 europaea
61	c2gpcB	Alignment	not modelled	6.6	13	PDB header: oxidoreductase Chain: B: PDB Molecule: iron superoxide dismutase; PDBTitle: the crystal structure of the enzyme fe-superoxide dismutase2 from trypanosoma cruzi
62	d1whza	Alignment	not modelled	6.5	25	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: YcfA-like
63	d1iuja	Alignment	not modelled	6.4	5	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
64	c6gw6A	Alignment	not modelled	6.4	20	PDB header: toxin Chain: A: PDB Molecule: res toxin; PDBTitle: structure of the pseudomonas putida res-xre toxin-antitoxin complex
65	d1xbwa	Alignment	not modelled	6.4	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
66	c3al6C	Alignment	not modelled	6.4	12	PDB header: unknown function Chain: C: PDB Molecule: jmjc domain-containing protein c2orf60; PDBTitle: crystal structure of human tyw5
67	c5cuvB	Alignment	not modelled	6.2	7	PDB header: metal binding protein Chain: B: PDB Molecule: acidocalcisomal pyrophosphatase; PDBTitle: crystal structure of trypanosoma cruzi vacuolar soluble2 pyrophosphatases in apo form
68	c4ou6A	Alignment	not modelled	6.1	30	PDB header: replication/dna Chain: A: PDB Molecule: primosomal protein 1; PDBTitle: crystal structure of dnat84-153-dt10 ssdna complex form 1