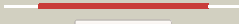











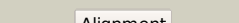












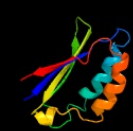











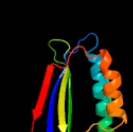

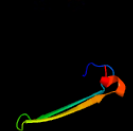




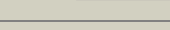





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2558 (-)_2877841_2878551
Date	Wed Aug 7 12:50:19 BST 2019
Unique Job ID	846fc142ad96d9a9

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5f9pA_	 Alignment		98.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: anthrone oxidase-like protein; PDBTitle: crystal structure study of anthrone oxidase-like protein
2	c3mcsB_	 Alignment		98.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of putative monooxygenase (fn1347) from <i>Fusobacterium nucleatum</i> subsp. <i>nucleatum</i> atcc 25586 at 2.55 Å resolution
3	c2gffB_	 Alignment		98.0	15	PDB header: sugar binding protein Chain: B: PDB Molecule: lsrg protein; PDBTitle: crystal structure of yersinia pestis lsrg
4	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 <i>Bordetella bronchiseptica</i> at 2.15 Å resolution
5	c3f44A_	 Alignment		97.9	5	PDB header: oxidoreductase Chain: A: PDB Molecule: putative monooxygenase; PDBTitle: crystal structure of putative monooxygenase (yp_193413.1) from <i>Mycobacterium acidophilus</i> ncfm at 1.55 Å resolution
6	c2omoC_	 Alignment		97.9	13	PDB header: oxidoreductase Chain: C: PDB Molecule: duf176; PDBTitle: putative antibiotic biosynthesis monooxygenase from <i>Nitrosomonas europaea</i>
7	c3bm7A_	 Alignment		97.9	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 <i>Caulobacter crescentus</i> cb15 at 1.35 Å resolution
8	d1iuja_	 Alignment		97.8	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
9	c4dpoA_	 Alignment		97.7	8	PDB header: unknown function Chain: A: PDB Molecule: conserved protein; PDBTitle: crystal structure of a conserved protein mm_1583 from <i>Methanosarcina mazei</i> go1
10	d2omoa1	 Alignment		97.7	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
11	d2zdpa1	 Alignment		97.5	10	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like

12	c3fgvB_	 Alignment		97.3	13	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		97.2	12	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		97.2	20	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	d1y0ha_	 Alignment		96.9	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
18	c3e8oB_	 Alignment		96.9	16	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
19	c4dn9B_	 Alignment		96.9	18	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	d2go8a1	 Alignment		96.7	26	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
21	c4hl9B_	 Alignment	not modelled	96.7	17	PDB header: oxidoreductase Chain: B: PDB Molecule: antibiotic biosynthesis monooxygenase; PDBTitle: crystal structure of antibiotic biosynthesis monooxygenase
22	c2riiA_	 Alignment	not modelled	96.7	9	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
23	c2fb0A_	 Alignment	not modelled	96.5	10	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	d1tz0a_	 Alignment	not modelled	96.4	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
25	d1x7va_	 Alignment	not modelled	96.4	20	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
26	c3tvzA_	 Alignment	not modelled	96.3	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative uncharacterized protein yhgc; PDBTitle: structure of bacillus subtilis hmob
27	c3kkfA_	 Alignment	not modelled	96.2	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
28	d1lq9a_	 Alignment	not modelled	96.1	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel

						Family: Actinorhodin biosynthesis monooxygenase ActVa-Orf6
29	d1xbwa_	Alignment	not modelled	95.9	10	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
30	c3kngA_	Alignment	not modelled	95.7	13	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	95.2	9	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	94.9	10	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	94.6	21	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PA3566-like
34	d2ftra1	Alignment	not modelled	90.5	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: EthD-like
35	d1vqsa_	Alignment	not modelled	87.2	15	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
36	d2hiqa1	Alignment	not modelled	87.0	8	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YdhR
37	c5kakE_	Alignment	not modelled	81.6	11	PDB header: unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized nipsnap-like domain protein2 from burkholderia xenovorans
38	d1q8ba_	Alignment	not modelled	77.5	12	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Hypothetical protein YjcS
39	d1vqya1	Alignment	not modelled	71.5	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: NIPSNAP
40	c5k9fA_	Alignment	not modelled	56.9	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
41	c6fxdB_	Alignment	not modelled	51.9	8	PDB header: biosynthetic protein Chain: B: PDB Molecule: mupz; PDBTitle: crystal structure of mupz from pseudomonas fluorescens
42	c5ixuA_	Alignment	not modelled	50.9	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
43	c2qlxA_	Alignment	not modelled	39.0	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
44	c2qlwA_	Alignment	not modelled	39.0	12	PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
45	c3gvzB_	Alignment	not modelled	33.9	13	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
46	c5gziB_	Alignment	not modelled	32.2	16	PDB header: lyase Chain: B: PDB Molecule: lysine cyclodeaminase; PDBTitle: cyclodeaminase_pa
47	c6a4mA_	Alignment	not modelled	29.1	18	PDB header: hydrolase Chain: A: PDB Molecule: uric acid degradation bifunctional protein pucl; PDBTitle: structure of urate oxidase from bacillus subtilis 168
48	c3bf4B_	Alignment	not modelled	28.1	11	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
49	d1x8da1	Alignment	not modelled	27.3	13	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Yiil-like
50	d2hwja1	Alignment	not modelled	22.7	23	Fold: ParB/Sulfiredoxin Superfamily: ParB/Sulfiredoxin Family: Atu1540-like
51	d3b48a1	Alignment	not modelled	16.7	13	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
52	c3iabA_	Alignment	not modelled	15.6	15	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
53	c2mntA_	Alignment	not modelled	15.2	54	PDB header: transferase/protein binding Chain: A: PDB Molecule: histone-lysine n-methyltransferase 2a, pc4 and sfrs1- PDBTitle: solution structure of mll-ibd complex
						PDB header: isomerase Chain: B: PDB Molecule: hypothetical aldose 1-epimerase;

54	c3ty1B_	Alignment	not modelled	14.6	24	PDBTitle: crystal structure of a putative aldose 1-epimerase (kpn_04629) from <i>Klebsiella pneumoniae</i> subsp. <i>pneumoniae</i> mgh 78578 at 1.90 Å resolution
55	c3sdoB_	Alignment	not modelled	13.3	20	PDB header: oxidoreductase Chain: B; PDB Molecule: nitritotriacetate monooxygenase; PDBTitle: structure of a nitritotriacetate monooxygenase from <i>Burkholderia pseudomallei</i>
56	d2q49a2	Alignment	not modelled	12.7	25	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
57	d1vq3a_	Alignment	not modelled	12.4	18	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
58	c4mp6A_	Alignment	not modelled	12.3	13	PDB header: oxidoreductase Chain: A; PDB Molecule: putative ornithine cyclodeaminase; PDBTitle: staphyloferrin B precursor biosynthetic enzyme sbnb bound to citrate2 and nad+
59	c6hhnA_	Alignment	not modelled	12.2	13	PDB header: isomerase Chain: A; PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of l-rhamnose mutarotase fa22100 from <i>Formosa2</i> agariphila
60	d3ct6a1	Alignment	not modelled	11.9	23	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
61	c3dm3A_	Alignment	not modelled	11.7	20	PDB header: replication Chain: A; PDB Molecule: replication factor a; PDBTitle: crystal structure of a domain of a replication factor a2 protein, from <i>Methanocaldococcus jannaschii</i> . northeast3 structural genomics target mjrl18e
62	c3bt7A_	Alignment	not modelled	11.2	9	PDB header: transferase/rna Chain: A; PDB Molecule: trna (uracil-5-)-methyltransferase; PDBTitle: structure of <i>E. coli</i> 5-methyluridine methyltransferase trna in complex2 with 19 nucleotide t-arm analogue
63	d1vkna2	Alignment	not modelled	10.5	10	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
64	d1o7ia_	Alignment	not modelled	10.4	14	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
65	c2mfpA_	Alignment	not modelled	10.4	44	PDB header: metal binding protein Chain: A; PDB Molecule: ec protein i/ii; PDBTitle: solution structure of the circular g-domain analog from the wheat2 metallothionein ec-1
66	c3j0iF_	Alignment	not modelled	10.2	32	PDB header: structural protein Chain: F; PDB Molecule: phikz029; PDBTitle: fitting of the phikz gp29pr structure into the cryo-em density map of2 the phikz polysheath
67	d1k25a4	Alignment	not modelled	9.1	20	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: beta-Lactamase/D-ala carboxypeptidase
68	c5u47A_	Alignment	not modelled	9.0	16	PDB header: lipid-binding protein Chain: A; PDB Molecule: penicillin binding protein 2x; PDBTitle: 1.95 Å resolution crystal structure of penicillin binding2 protein 2x from <i>Streptococcus thermophilus</i>
69	c3gx1A_	Alignment	not modelled	8.9	13	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: lin1832 protein; PDBTitle: crystal structure of a domain of lin1832 from <i>Listeria innocua</i>
70	c6hvpA_	Alignment	not modelled	8.7	32	PDB header: hydrolase inhibitor Chain: A; PDB Molecule: fetuin-b; PDBTitle: crystal structure of mouse fetuin-b
71	c3gdwA_	Alignment	not modelled	8.7	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 from2 <i>Enterococcus faecalis</i>
72	c2zw2B_	Alignment	not modelled	8.6	10	PDB header: ligase Chain: B; PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from <i>Sulfolobus tokodaii</i> (stpsurs)
73	c4owxB_	Alignment	not modelled	8.2	24	PDB header: dna binding protein/dna Chain: B; PDB Molecule: soss complex subunit b1; PDBTitle: structural basis of soss1 in complex with a 12nt ssdna
74	c2jsxA_	Alignment	not modelled	8.2	25	PDB header: chaperone Chain: A; PDB Molecule: protein napd; PDBTitle: solution structure of the <i>E. coli</i> tat proofreading2 chaperone protein napd
75	c4otmB_	Alignment	not modelled	7.8	58	PDB header: transferase Chain: B; PDB Molecule: serine/threonine-protein kinase gcn2; PDBTitle: crystal structure of the c-terminal domain from yeast gcn2
76	d1eg7a_	Alignment	not modelled	7.8	60	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
77	c3kxtA_	Alignment	not modelled	7.8	19	PDB header: dna binding protein/dna Chain: A; PDB Molecule: chromatin protein cren7; PDBTitle: crystal structure of <i>Sulfolobus cren7</i> -dsdna complex
78	c3a4tA_	Alignment	not modelled	7.6	4	PDB header: transferase Chain: A; PDB Molecule: putative methyltransferase mj0026; PDBTitle: crystal structure of atrm4 from <i>M. jannaschii</i> with sinefungin
79	c3do6B_	Alignment	not modelled	7.6	60	PDB header: ligase Chain: B; PDB Molecule: formate--tetrahydrofolate ligase; PDBTitle: crystal structure of putative formyltetrahydrofolate synthetase2 (tm1766) from <i>Thermotoga maritima</i> at 1.85 Å resolution

80	c2jtmA_	Alignment	not modelled	7.3	19	PDB header: dna binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of sso6901 from sulfobolus solfataricus2 p2
81	d1j4wa2	Alignment	not modelled	7.3	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)
82	c6h3zB_	Alignment	not modelled	6.6	25	PDB header: gene regulation Chain: B: PDB Molecule: ccr4-not transcription complex subunit 1; PDBTitle: crystal structure of a c-terminal mif4g domain in not1
83	c5hb8B_	Alignment	not modelled	6.6	22	PDB header: transport protein Chain: B: PDB Molecule: nucleoporin nup53; PDBTitle: crystal structure of chaetomium thermophilum nup53 rrm (space group2 p3121)
84	d1v3va1	Alignment	not modelled	6.5	15	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
85	c5m72B_	Alignment	not modelled	6.1	46	PDB header: protein transport Chain: B: PDB Molecule: signal recognition particle subunit srp68; PDBTitle: structure of the human srp68-72 protein-binding domain complex
86	d2axya1	Alignment	not modelled	6.1	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)
87	c6cmhA_	Alignment	not modelled	6.1	56	PDB header: contractile protein Chain: A: PDB Molecule: protein (endothelin-1); PDBTitle: synthetic linear modified endothelin-1 agonist
88	c2n37A_	Alignment	not modelled	6.1	40	PDB header: unknown function Chain: A: PDB Molecule: avr-pia protein; PDBTitle: solution structure of avr-pia
89	c5wrvA_	Alignment	not modelled	6.1	46	PDB header: protein transport Chain: A: PDB Molecule: signal recognition particle subunit srp68; PDBTitle: complex structure of human srp72/srp68
90	d1vj1a1	Alignment	not modelled	6.0	20	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
91	d1j9ia_	Alignment	not modelled	6.0	16	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Terminase gpNU1 subunit domain
92	c2ckcA_	Alignment	not modelled	6.0	5	PDB header: hydrolase Chain: A: PDB Molecule: chromodomain-helicase-dna-binding protein 7; PDBTitle: solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
93	d2ckca1	Alignment	not modelled	6.0	5	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
94	d1mk0a_	Alignment	not modelled	5.8	12	Fold: GIY-YIG endonuclease Superfamily: GIY-YIG endonuclease Family: GIY-YIG endonuclease
95	c3ue3A_	Alignment	not modelled	5.8	16	PDB header: transferase Chain: A: PDB Molecule: septum formation, penicillin binding protein 3, PDBTitle: crystal structure of acinetobacter baumannii pbb3
96	d1ec6a_	Alignment	not modelled	5.7	22	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)
97	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
98	d1wjja_	Alignment	not modelled	5.6	20	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
99	d1s0aa_	Alignment	not modelled	5.5	21	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: GABA-aminotransferase-like