
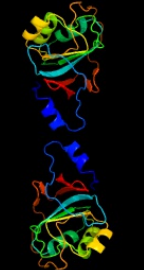

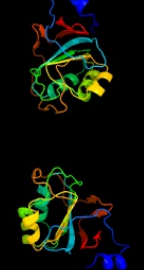

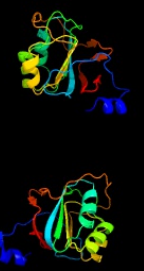

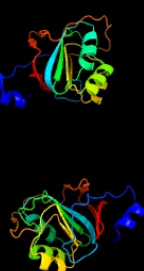





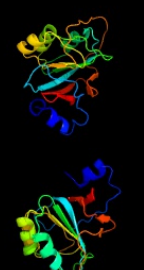



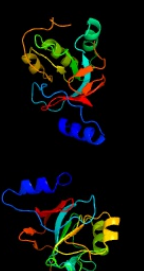



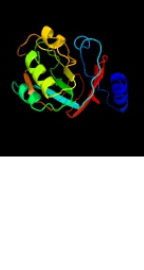










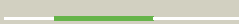
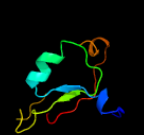

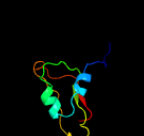





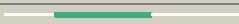


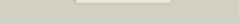
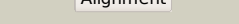

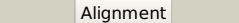
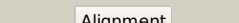


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3853_(menG)_4325673_4326146
Date	Sat Aug 10 22:05:03 BST 2019
Unique Job ID	d41279bee7a2b93e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1nxjA_	 Alignment		100.0	100	PDB header: unknown function Chain: A: PDB Molecule: probable s-adenosylmethionine:2- PDBTitle: structure of rv3853 from mycobacterium tuberculosis
2	d1nxja_	 Alignment		100.0	100	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
3	c2pcnA_	 Alignment		100.0	44	PDB header: transferase Chain: A: PDB Molecule: s-adenosylmethionine:2- demethylmenaquinone PDBTitle: crystal structure of s-adenosylmethionine: 2- dimethylmenaquinone2 methyltransferase (gk_1813) from geobacillus kaustophilus hta426
4	d1vi4a_	 Alignment		100.0	47	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
5	d1q5xa_	 Alignment		100.0	45	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
6	c3c8oB_	 Alignment		100.0	44	PDB header: hydrolase regulator Chain: B: PDB Molecule: regulator of ribonuclease activity a; PDBTitle: the crystal structure of rraa from pao1
7	c3noja_	 Alignment		100.0	27	PDB header: lyase Chain: A: PDB Molecule: 4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate PDBTitle: the structure of hmg/cha aldolase from the protocatechuate degradation2 pathway of pseudomonas putida
8	d1j3la_	 Alignment		100.0	45	Fold: The "swivelling" beta/beta/alpha domain Superfamily: RraA-like Family: RraA-like
9	c5ir2A_	 Alignment		100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: cellulase; PDBTitle: crystal structure of novel cellulases from microbes associated with2 the gut ecosystem
10	c3k4iC_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
11	c5x15C_	 Alignment		100.0	28	PDB header: transferase inhibitor Chain: C: PDB Molecule: putative transferase; PDBTitle: crystal structure of streptomyces coelicolor rraas2, an unusual member2 of the rnase es inhibitor rraa protein family

12	c2c5qE_	 Alignment		100.0	20	PDB header: structural genomics,unknown function Chain: E: PDB Molecule: rraa-like protein yer010c; PDBTitle: crystal structure of yeast yer010cp
13	d2gp4a1	 Alignment		72.3	17	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: IlvD/EDD C-terminal domain-like
14	c2gp4A_	 Alignment		70.7	16	PDB header: lyase Chain: A: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
15	c2gp4B_	 Alignment		66.8	16	PDB header: lyase Chain: B: PDB Molecule: 6-phosphogluconate dehydratase; PDBTitle: structure of [fes]cluster-free apo form of 6-phosphogluconate2 dehydratase from shewanella oneidensis
16	c6ovtD_	 Alignment		56.9	18	PDB header: lyase Chain: D: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of ilvd from mycobacterium tuberculosis
17	c5j84A_	 Alignment		55.7	14	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
18	c5oynB_	 Alignment		53.1	20	PDB header: lyase Chain: B: PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
19	d1kbla2	 Alignment		48.9	23	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
20	c5ze4A_	 Alignment		48.4	26	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
21	c5hdjA_	 Alignment	not modelled	47.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: nfra1; PDBTitle: structure of b. megaterium nfra1
22	c5ym0A_	 Alignment	not modelled	45.8	26	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the crystal structure of dhad
23	d1f5va_	 Alignment	not modelled	44.4	21	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
24	c3n2sD_	 Alignment	not modelled	41.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: nadph-dependent nitro/flavin reductase; PDBTitle: structure of nfra1 nitroreductase from b. subtilis
25	d1e8ca2	 Alignment	not modelled	41.2	20	Fold: MurD-like peptide ligases, peptide-binding domain Superfamily: MurD-like peptide ligases, peptide-binding domain Family: MurCDEF C-terminal domain
26	d1zcha1	 Alignment	not modelled	39.2	10	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
27	d1vfga2	 Alignment	not modelled	32.7	35	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
28	c5heiE_	 Alignment	not modelled	32.7	15	PDB header: oxidoreductase Chain: E: PDB Molecule: nfra2; PDBTitle: structure of b. megaterium nfra2
29	c3eofB_	 Alignment	not modelled	32.4	15	PDB header: oxidoreductase Chain: B: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase

						(yp_213212.1) from2 bacteroides fragilis nctc 9343 at 1.99 a resolution
30	d1bkja_	Alignment	not modelled	32.3	18	Fold: FMN-dependent nitroreductase-like Superfamily: FMN-dependent nitroreductase-like Family: NADH oxidase/flavin reductase
31	c1vfgB_	Alignment	not modelled	31.7	35	PDB header: transferase/rna Chain: B: PDB Molecule: poly a polymerase; PDBTitle: crystal structure of trna nucleotidyltransferase complexed2 with a primer trna and an incoming atp analog
32	c1ou5A_	Alignment	not modelled	30.8	36	PDB header: translation, transferase Chain: A: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of human cca-adding enzyme
33	c1dbgA_	Alignment	not modelled	27.4	20	PDB header: lyase Chain: A: PDB Molecule: chondroitinase b; PDBTitle: crystal structure of chondroitinase b
34	d1ofla_	Alignment	not modelled	26.9	26	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Chondroitinase B
35	d1vbga2_	Alignment	not modelled	26.9	13	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Phosphohistidine domain Family: Pyruvate phosphate dikinase, central domain
36	c2vpiA_	Alignment	not modelled	25.8	24	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
37	d1ou5a2_	Alignment	not modelled	25.7	36	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
38	d1miwa2_	Alignment	not modelled	19.3	36	Fold: Nucleotidyltransferase Superfamily: Nucleotidyltransferase Family: Poly A polymerase head domain-like
39	c6odm5_	Alignment	not modelled	17.3	33	PDB header: viral protein Chain: 5: PDB Molecule: triple capsid protein 1; PDBTitle: herpes simplex virus type 1 (hsv-1) portal vertex-adjacent2 capsid/catc, asymmetric unit
40	c4x4wB_	Alignment	not modelled	15.3	36	PDB header: rna binding protein Chain: B: PDB Molecule: cca trna nucleotidyltransferase 1, mitochondrial; PDBTitle: crystal structure of the full-length human mitochondrial cca-adding2 enzyme
41	c3aqnA_	Alignment	not modelled	15.1	27	PDB header: transferase Chain: A: PDB Molecule: poly(a) polymerase; PDBTitle: complex structure of bacterial protein (apo form ii)
42	c5gkdA_	Alignment	not modelled	14.9	8	PDB header: lyase Chain: A: PDB Molecule: alygc; PDBTitle: structure of pl6 family alginate lyase alygc
43	c1e8cB_	Alignment	not modelled	14.1	20	PDB header: ligase Chain: B: PDB Molecule: udp-n-acetylmuramoylalanyl-d-glutamate-2,6-diaminopimelate PDBTitle: structure of mure the udp-n-acetylmuramyl tripeptide synthetase from2 e. coli
44	c3mvaA_	Alignment	not modelled	13.9	18	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo- PDBTitle: crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp
45	d1vzwa1_	Alignment	not modelled	13.7	17	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
46	c3h37B_	Alignment	not modelled	12.9	21	PDB header: transferase Chain: B: PDB Molecule: trna nucleotidyl transferase-related protein; PDBTitle: the structure of cca-adding enzyme apo form i
47	c3l7oB_	Alignment	not modelled	12.6	12	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from streptococcus2 mutans ua159
48	c3tbiB_	Alignment	not modelled	11.1	33	PDB header: transcription Chain: B: PDB Molecule: dna-directed rna polymerase subunit beta; PDBTitle: crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
49	c6q52A_	Alignment	not modelled	10.8	36	PDB header: rna binding protein Chain: A: PDB Molecule: cca-adding enzyme; PDBTitle: structure of a psychrophilic cca-adding enzyme in complex with cmpcpp2 at room temperature in chipx microfluidic device
50	c3bm2B_	Alignment	not modelled	10.7	15	PDB header: oxidoreductase Chain: B: PDB Molecule: protein ydja; PDBTitle: crystal structure of a minimal nitroreductase ydja from escherichia2 coli k12 with and without fmn cofactor
51	c2pjmA_	Alignment	not modelled	10.4	15	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: structure of ribose 5-phosphate isomerase a from2 methanocaldococcus jannaschii
52	d1thfd_	Alignment	not modelled	10.2	8	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
53	c3k6hB_	Alignment	not modelled	10.2	13	PDB header: oxidoreductase Chain: B: PDB Molecule: nitroreductase family protein; PDBTitle: crystal structure of a nitroreductase family protein from2 agrobacterium tumefaciens str. c58
54	c2xrfA_	Alignment	not modelled	9.5	38	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase 2; PDBTitle: crystal structure of human uridine phosphorylase 2

55	c1y43B	Alignment	not modelled	9.3	21	PDB header: hydrolase Chain: B: PDB Molecule: aspergillopepsin ii heavy chain; PDBTitle: crystal structure of aspergilloglutamic peptidase from aspergillus2 niger
56	c3i28A	Alignment	not modelled	8.8	15	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
57	d1i1qb	Alignment	not modelled	8.6	25	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
58	c1miyB	Alignment	not modelled	8.5	36	PDB header: translation, transferase Chain: B: PDB Molecule: trna cca-adding enzyme; PDBTitle: crystal structure of bacillus stearothermophilus cca-adding enzyme in2 complex with ctp
59	d1ka9f	Alignment	not modelled	8.4	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
60	c5z9tB	Alignment	not modelled	8.2	26	PDB header: lyase Chain: B: PDB Molecule: alginate lyase alyf-ou02; PDBTitle: a new pl6 alginate lyase complex with trisaccharide
61	c2wzvB	Alignment	not modelled	7.6	8	PDB header: oxidoreductase Chain: B: PDB Molecule: nfnb protein; PDBTitle: crystal structure of the fnm-dependent nitroreductase nfnb2 from mycobacterium smegmatis
62	d3bi1a2	Alignment	not modelled	7.5	16	Fold: The "swivelling" beta/beta/alpha domain Superfamily: PA domain Family: PA domain
63	c2xjaD	Alignment	not modelled	7.4	20	PDB header: ligase Chain: D: PDB Molecule: udp-n-acetylmuramoyl-l-alanyl-d-glutamate--2,6- PDBTitle: structure of mure from m.tuberculosis with dipeptide and adp
64	c3cioA	Alignment	not modelled	7.4	22	PDB header: signaling protein, transferase Chain: A: PDB Molecule: tyrosine-protein kinase etk; PDBTitle: the kinase domain of escherichia coli tyrosine kinase etk
65	c2lktA	Alignment	not modelled	6.9	32	PDB header: hydrolase Chain: A: PDB Molecule: retinoic acid receptor responder protein 3; PDBTitle: solution structure of n-terminal domain of human tig3 in 2 m urea
66	c1vdzA	Alignment	not modelled	6.9	21	PDB header: hydrolase Chain: A: PDB Molecule: a-type atpase subunit a; PDBTitle: crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
67	c4gmkB	Alignment	not modelled	6.9	15	PDB header: isomerase Chain: B: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose 5-phosphate isomerase from the probiotic2 bacterium lactobacillus salivarius ucc118
68	d1j5ya1	Alignment	not modelled	6.8	38	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Biotin repressor-like
69	c6cslA	Alignment	not modelled	6.6	30	PDB header: metal binding protein Chain: A: PDB Molecule: histidine triad protein d; PDBTitle: pneumococcal phtd protein 269-339 fragment with bound zn(ii)
70	c1gqqA	Alignment	not modelled	6.5	22	PDB header: cell wall biosynthesis Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: murc - crystal structure of the apo-enzyme from haemophilus influenzae
71	d2cs7a1	Alignment	not modelled	6.5	35	Fold: IL8-like Superfamily: PhtA domain-like Family: PhtA domain-like
72	c3mogA	Alignment	not modelled	6.2	13	PDB header: oxidoreductase Chain: A: PDB Molecule: probable 3-hydroxybutyryl-coa dehydrogenase; PDBTitle: crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
73	d1bvp12	Alignment	not modelled	6.1	30	Fold: Viral protein domain Superfamily: Viral protein domain Family: Top domain of virus capsid protein
74	d1ahsa	Alignment	not modelled	6.0	22	Fold: Viral protein domain Superfamily: Viral protein domain Family: Top domain of virus capsid protein
75	c6iunB	Alignment	not modelled	5.9	7	PDB header: oxidoreductase Chain: B: PDB Molecule: enoyl-coa hydratase/delta(3)-cis-delta(2)-trans-enoyl-coa PDBTitle: crystal structure of enoyl-coa hydratase (ech) from ralstonia eutropha2 h16 in complex with nad
76	c2kyaA	Alignment	not modelled	5.9	24	PDB header: hydrolase Chain: A: PDB Molecule: group xvi phospholipase a2; PDBTitle: solution structure of the h-rev107 n-terminal domain
77	c2d3tB	Alignment	not modelled	5.7	12	PDB header: lyase, oxidoreductase/transferase Chain: B: PDB Molecule: fatty oxidation complex alpha subunit; PDBTitle: fatty acid beta-oxidation multienzyme complex from2 pseudomonas fragi, form v
78	d1eara1	Alignment	not modelled	5.6	35	Fold: Urease metallochaperone UreE, N-terminal domain Superfamily: Urease metallochaperone UreE, N-terminal domain Family: Urease metallochaperone UreE, N-terminal domain
79	c3bemA	Alignment	not modelled	5.5	27	PDB header: oxidoreductase Chain: A: PDB Molecule: putative nad(p)h nitroreductase ydfn; PDBTitle: crystal structure of putative nitroreductase ydfn (2632848) from2 bacillus subtilis at 1.65 a resolution
80	c4ifdl	Alignment	not modelled	5.5	56	PDB header: hydrolase/rna Chain: I: PDB Molecule: exosome complex component csl4; PDBTitle: crystal structure of an 11-subunit eukaryotic exosome complex bound to2 rna

81 [clzciA_](#)

Alignment

not modelled

5.2

12

PDB header: oxidoreductase
Chain: A: **PDB Molecule:** peroxisomal bifunctional enzyme;
PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase