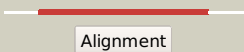

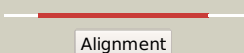

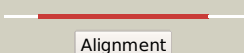

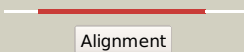





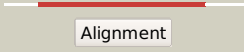

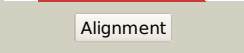



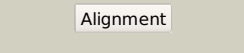

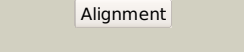



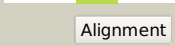

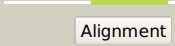

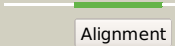

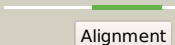

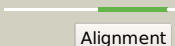

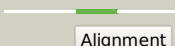

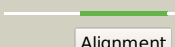





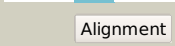
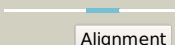

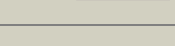
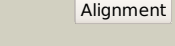
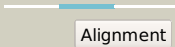


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2987c_(leuD)_3344043_3344639
Date	Thu Aug 8 16:20:15 BST 2019
Unique Job ID	56d8134cbb6d5053

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h5jA_	 Alignment		100.0	100	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
2	c3q3wB_	 Alignment		100.0	43	PDB header: transferase Chain: B: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from campylobacter jejuni.
3	c2hcuA_	 Alignment		100.0	42	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus mutans
4	d1v7la_	 Alignment		100.0	31	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IIVD-like Family: LeuD-like
5	c3vbaE_	 Alignment		100.0	33	PDB header: lyase Chain: E: PDB Molecule: isopropylmalate/citramalate isomerase small subunit; PDBTitle: crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit
6	c2pkpA_	 Alignment		100.0	32	PDB header: lyase Chain: A: PDB Molecule: homoaconitase small subunit; PDBTitle: crystal structure of 3-isopropylmalate dehydratase (leud)2 from methanocaldococcus jannaschii dsm2661 (mj1271)
7	d1acoa1	 Alignment		100.0	21	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IIVD-like Family: LeuD-like
8	d2b3ya1	 Alignment		100.0	24	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IIVD-like Family: LeuD-like
9	d1l5ja2	 Alignment		100.0	23	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IIVD-like Family: LeuD-like
10	c2b3yB_	 Alignment		100.0	22	PDB header: lyase Chain: B: PDB Molecule: iron-responsive element binding protein 1; PDBTitle: structure of a monoclinic crystal form of human cytosolic aconitase2 (irp1)
11	c5acnA_	 Alignment		100.0	19	PDB header: lyase(carbon-oxygen) Chain: A: PDB Molecule: aconitase; PDBTitle: structure of activated aconitase. formation of the (4fe-4s) cluster in2 the crystal

12	c1l5jB	 Alignment		99.6	20	PDB header: lyase Chain: B: PDB Molecule: aconitate hydratase 2; PDBTitle: crystal structure of e. coli aconitase b.
13	c1t6zB	 Alignment		63.0	24	PDB header: transferase Chain: B: PDB Molecule: riboflavin kinase/fmn adenyllyltransferase; PDBTitle: crystal structure of riboflavin bound tm379
14	d1e01a	 Alignment		61.3	20	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
15	c2yx6C	 Alignment		59.5	9	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein ph0822; PDBTitle: crystal structure of ph0822
16	d1o13a	 Alignment		54.0	14	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
17	c2qtdA	 Alignment		51.9	12	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein mj0327; PDBTitle: crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution
18	c3op1A	 Alignment		51.1	25	PDB header: transferase Chain: A: PDB Molecule: macrolide-efflux protein; PDBTitle: crystal structure of macrolide-efflux protein sp_1110 from2 streptococcus pneumoniae
19	d1rdua	 Alignment		50.7	16	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
20	d1t3va	 Alignment		48.3	13	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
21	d1jx4a1	 Alignment	not modelled	41.6	23	Fold: Lesion bypass DNA polymerase (Y-family), little finger domain Superfamily: Lesion bypass DNA polymerase (Y-family), little finger domain Family: Lesion bypass DNA polymerase (Y-family), little finger domain
22	c2wfbA	 Alignment	not modelled	39.7	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange2 protein (orp) from desulfovibrio gigas
23	d1nyta1	 Alignment	not modelled	38.5	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Aminoacid dehydrogenase-like, C-terminal domain
24	c2dlnA	 Alignment	not modelled	32.2	30	PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine ligase at 2.32 angstroms resolution
25	c6et5u	 Alignment	not modelled	30.7	27	PDB header: photosynthesis Chain: U: PDB Molecule: light-harvesting protein b-1015 gamma chain; PDBTitle: reaction centre light harvesting complex 1 from blc. viridis
26	c3c3jA	 Alignment	not modelled	30.4	18	PDB header: isomerase Chain: A: PDB Molecule: putative tagatose-6-phosphate ketose/aldose isomerase; PDBTitle: crystal structure of tagatose-6-phosphate ketose/aldose isomerase from2 escherichia coli
27	c3vh3A	 Alignment	not modelled	30.2	33	PDB header: metal binding protein/protein transport Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme atg7; PDBTitle: crystal structure of atg7ctd-atg8 complex
		 Alignment				PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein ta1041;

28	c2re2A_	Alignment	not modelled	28.5	19	PDBTitle: crystal structure of a putative iron-molybdenum cofactor (femo-co) ₂ dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
29	d1xjha_	Alignment	not modelled	28.1	32	Fold: HSP33 redox switch-like Superfamily: HSP33 redox switch-like Family: HSP33 redox switch-like
30	c1vkzA_	Alignment	not modelled	27.7	38	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
31	d1a9xa3	Alignment	not modelled	27.4	41	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
32	c4wwsE_	Alignment	not modelled	26.7	23	PDB header: oxidoreductase Chain: E: PDB Molecule: putative heme-dependent peroxidase lmo2113; PDBTitle: structure of chlorite dismutase-like protein from listeria2 monocytogenes
33	c5xf2B_	Alignment	not modelled	26.7	21	PDB header: transferase Chain: B: PDB Molecule: putative cytidyltransferase; PDBTitle: crystal structure of semet-hldc from burkholderia pseudomallei
34	d2gp4a1	Alignment	not modelled	26.5	14	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/llvD-like Family: llvD/EDD C-terminal domain-like
35	c3uvzB_	Alignment	not modelled	26.3	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
36	c1yriD_	Alignment	not modelled	25.7	17	PDB header: oxidoreductase Chain: D: PDB Molecule: ketol-acid reductoisomerase; PDBTitle: escherichia coli ketol-acid reductoisomerase
37	c2amIB_	Alignment	not modelled	25.6	13	PDB header: transferase Chain: B: PDB Molecule: sis domain protein; PDBTitle: crystal structure of lmo0035 protein (46906266) from listeria2 monocytogenes 4b f2365 at 1.50 a resolution
38	c3ax6C_	Alignment	not modelled	25.5	12	PDB header: ligase Chain: C: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of n5-carboxyaminoimidazole ribonucleotide2 synthetase from thermotoga maritima
39	c3bgdB_	Alignment	not modelled	25.1	17	PDB header: transferase Chain: B: PDB Molecule: thiopurine s-methyltransferase; PDBTitle: thiopurine s-methyltransferase
40	c4dtfA_	Alignment	not modelled	24.5	32	PDB header: toxin Chain: A: PDB Molecule: vgrg protein; PDBTitle: structure of a vgrg vibrio cholerae toxin acd domain in complex with2 amp-pnp and mg++
41	c2ip4A_	Alignment	not modelled	24.5	41	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
42	d1fe0a_	Alignment	not modelled	23.8	9	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
43	c4uc0A_	Alignment	not modelled	23.7	19	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of a purine nucleoside phosphorylase (psi-nysgrc-2 029736) from agrobacterium vitis
44	c3fj1A_	Alignment	not modelled	23.2	18	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of putative phosphosugar isomerase (yp_167080.1)2 from silicibacter pomeroyi dss-3 at 1.75 a resolution
45	c5d6sB_	Alignment	not modelled	23.0	33	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
46	d1vkza2	Alignment	not modelled	22.4	40	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
47	c5d0bB_	Alignment	not modelled	21.8	42	PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
48	c3la8A_	Alignment	not modelled	21.6	15	PDB header: transferase Chain: A: PDB Molecule: putative purine nucleoside phosphorylase; PDBTitle: the crystal structure of smu.1229 from streptococcus mutans ua159
49	c5ym0A_	Alignment	not modelled	21.5	21	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the crystal structure of dhad
50	d1a9xa4	Alignment	not modelled	21.1	26	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
51	c5xeiA_	Alignment	not modelled	20.9	39	PDB header: dna binding protein, cell cycle Chain: A: PDB Molecule: chromosome partition protein smc; PDBTitle: crystal structure of the smc head domain with a coiled coil and joint2 derived from pyrococcus yayanosii
52	c3t07D_	Alignment	not modelled	20.5	16	PDB header: transferase/transferase inhibitor Chain: D: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of s. aureus pyruvate kinase in complex with a2 naturally occurring bis-indole alkaloid
53	c2zj3A_	Alignment	not modelled	20.4	9	PDB header: transferase Chain: A: PDB Molecule: glucosamine--fructose-6-phosphate PDBTitle: isomerase domain of human glucose:fructose-6-

						phosphate2 amidotransferase
54	d1okkd2	Alignment	not modelled	20.4	33	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
55	d1t0tv	Alignment	not modelled	19.9	23	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
56	c3hrpA	Alignment	not modelled	18.6	38	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of structural genomics protein of unknown function2 (np_812590.1) from bacteroides thetaiotaomicron vpi-5482 at 1.70 a3 resolution
57	d1j9ba	Alignment	not modelled	18.3	16	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: ArsC-like
58	c3idwA	Alignment	not modelled	18.3	14	PDB header: endocytosis Chain: A: PDB Molecule: actin cytoskeleton-regulatory complex protein sla1; PDBTitle: crystal structure of sla1 homology domain 2
59	c4uy5A	Alignment	not modelled	18.2	20	PDB header: transferase Chain: A: PDB Molecule: histidine-specific methyltransferase egt2; PDBTitle: crystal structure of histidine-specific methyltransferase egt2 from2 mycobacterium smegmatis
60	c4I5cE	Alignment	not modelled	18.0	38	PDB header: transferase Chain: E: PDB Molecule: s-methyl-5'-thioadenosine phosphorylase; PDBTitle: methylthioadenosine phosphorylase from schistosoma mansoni in complex2 with adenine in space group p212121
61	c5j84A	Alignment	not modelled	17.9	39	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
62	c4o0lA	Alignment	not modelled	17.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-dependent 3-quinuclidinone reductase; PDBTitle: crystal structure of nadph-dependent 3-quinuclidinone reductase from2 rhodotorula rubra
63	c3knzA	Alignment	not modelled	17.7	15	PDB header: sugar binding protein Chain: A: PDB Molecule: putative sugar binding protein; PDBTitle: crystal structure of putative sugar binding protein (np_459565.1) from2 salmonella typhimurium lt2 at 2.50 a resolution
64	d1vdha	Alignment	not modelled	17.6	27	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Chlorite dismutase-like
65	d1vmaa2	Alignment	not modelled	17.4	36	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
66	c5ze4A	Alignment	not modelled	17.4	21	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
67	d2hi6a1	Alignment	not modelled	17.3	13	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IlvD-like Family: AF0055-like
68	c1z34A	Alignment	not modelled	17.2	12	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of trichomonas vaginalis purine nucleoside2 phosphorylase complexed with 2-fluoro-2'-deoxyadenosine
69	d2bzga1	Alignment	not modelled	16.9	17	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Thiopurine S-methyltransferase
70	c1tcbB	Alignment	not modelled	16.5	10	PDB header: transferase Chain: B: PDB Molecule: purine-nucleoside phosphorylase; PDBTitle: crystal structure of the purine nucleoside phosphorylase2 from schistosoma mansoni in complex with non-detergent3 sulfobetaine 195 and acetate
71	c3pg8B	Alignment	not modelled	16.4	26	PDB header: transferase Chain: B: PDB Molecule: phospho-2-dehydro-3-deoxyheptonate aldolase; PDBTitle: truncated form of 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase2 from thermotoga maritima
72	c5oynB	Alignment	not modelled	16.4	27	PDB header: lyase Chain: B: PDB Molecule: dehydratase, ilvD/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
73	c4s1wA	Alignment	not modelled	16.0	11	PDB header: transferase Chain: A: PDB Molecule: glutamine--fructose-6-phosphate aminotransferase PDBTitle: structure of a putative glutamine--fructose-6-phosphate2 aminotransferase from staphylococcus aureus dsubsp. aureus mu50
74	c5onkA	Alignment	not modelled	15.9	21	PDB header: hydrolase Chain: A: PDB Molecule: ynd1; PDBTitle: native ynd1
75	c2xd4A	Alignment	not modelled	15.9	34	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
76	c5ojgB	Alignment	not modelled	15.8	28	PDB header: oxidoreductase Chain: B: PDB Molecule: dehydrogenase/reductase sdr family member 4; PDBTitle: crystal structure of the dehydrogenase/reductase sdr family member 42 (dhrs4) from caenorhabditis elegans
77	d1oqya1	Alignment	not modelled	15.1	31	Fold: RuvA C-terminal domain-like Superfamily: UBA-like Family: UBA domain
78	c2gusA	Alignment	not modelled	15.1	18	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate kinase;

78	c2cuaA	Alignment	not modelled	13.1	48	PDBTitle: crystal structure of phosphoglycerate kinase from pyrococcus2 horikoshii ot3
79	c4ds1C	Alignment	not modelled	14.5	33	PDB header: structural protein/transport protein Chain: C: PDB Molecule: dynein light chain 1, cytoplasmic; PDBTitle: the structure of a yeast dyn2-nup159 complex and the molecular basis2 for the dynein light chain - nuclear pore interaction
80	c5uqiA	Alignment	not modelled	14.3	13	PDB header: isomerase Chain: A: PDB Molecule: phosphosugar isomerase; PDBTitle: e. coli cft073 c3406 in complex with a5p
81	c4lkrA	Alignment	not modelled	14.2	10	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of deo-3 gene product from shewanella oneidensis2 mr-1, nysgrc target 029437
82	d1c55a	Alignment	not modelled	14.0	31	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Scorpion toxin-like Family: Short-chain scorpion toxins
83	d1assa	Alignment	not modelled	13.8	24	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: Group II chaperonin (CCT, TRIC), apical domain
84	c3m4qA	Alignment	not modelled	13.7	20	PDB header: ligase Chain: A: PDB Molecule: asparaginyl-trna synthetase, putative; PDBTitle: entamoeba histolytica asparaginyl-trna synthetase (asnrs)
85	c4q0rB	Alignment	not modelled	13.5	10	PDB header: hydrolase/dna Chain: B: PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
86	c3g68A	Alignment	not modelled	13.5	20	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerase; PDBTitle: crystal structure of a putative phosphosugar isomerase (cd3275) from2 clostridium difficile 630 at 1.80 a resolution
87	d1uadc	Alignment	not modelled	13.5	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: Other IPT/TIG domains
88	d1cmia	Alignment	not modelled	13.5	33	Fold: DLC Superfamily: DLC Family: DLC
89	c2jgqB	Alignment	not modelled	13.4	8	PDB header: isomerase Chain: B: PDB Molecule: triosephosphate isomerase; PDBTitle: kinetics and structural properties of triosephosphate2 isomerase from helicobacter pylori
90	c3bk7A	Alignment	not modelled	13.4	38	PDB header: hydrolyase/translation Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of the complete abc1/rnaase-i inhibitor protein from2 pyrococcus abyssi
91	c2d2aA	Alignment	not modelled	13.4	26	PDB header: metal transport Chain: A: PDB Molecule: sufa protein; PDBTitle: crystal structure of escherichia coli sufa involved in biosynthesis of2 iron-sulfur clusters
92	d2btma	Alignment	not modelled	13.4	21	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
93	d1d3va	Alignment	not modelled	13.4	31	Fold: Arginase/deacetylase Superfamily: Arginase/deacetylase Family: Arginase-like amidino hydrolases
94	c4yqyA	Alignment	not modelled	12.7	21	PDB header: oxidoreductase Chain: A: PDB Molecule: putative dehydrogenase; PDBTitle: crystal structure of a putative dehydrogenase from sulfitolobacter sp.2 (cog1028) (target efi-513936) in its apo form
95	c5e38D	Alignment	not modelled	12.3	21	PDB header: transferase Chain: D: PDB Molecule: uracil phosphoribosyltransferase; PDBTitle: structural basis of mapping the spontaneous mutations with 5-2 flourouracil in uracil phosphoribosyltransferase from mycobacterium3 tuberculosis
96	c3uekA	Alignment	not modelled	12.1	33	PDB header: hydrolase Chain: A: PDB Molecule: poly(adp-ribose) glycohydrolase; PDBTitle: crystal structure of the catalytic domain of rat poly (adp-ribose)2 glycohydrolase
97	d3e2ba1	Alignment	not modelled	12.1	33	Fold: DLC Superfamily: DLC Family: DLC
98	c1wj9A	Alignment	not modelled	11.6	43	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: crispr-associated protein; PDBTitle: crystal structure of a crispr-associated protein from2 thermus thermophilus
99	c3fkjA	Alignment	not modelled	11.6	15	PDB header: isomerase Chain: A: PDB Molecule: putative phosphosugar isomerases; PDBTitle: crystal structure of a putative phosphosugar isomerase (stm_0572) from2 salmonella typhimurium lt2 at 2.12 a resolution