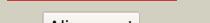
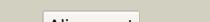
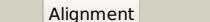
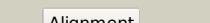


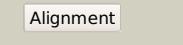
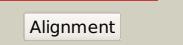
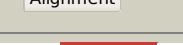
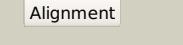
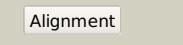
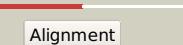
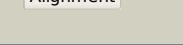
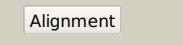
Phyre²

Email	mdejesus@rockefeller.edu
Description	RVBD2977c_(thiL)_3332797_3333798
Date	Thu Aug 8 16:20:14 BST 2019
Unique Job ID	2d4e93a8917bba4d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3c9uB_			100.0	30	PDB header: transferase Chain: B; PDB Molecule: thiamine monophosphate kinase; PDBTitle: aathil complexed with adp and tpp
2	c1vqvB_			100.0	30	PDB header: transferase Chain: B; PDB Molecule: thiamine monophosphate kinase; PDBTitle: crystal structure of thiamine monophosphate kinase (thiL)2 from aquifex aeolicus
3	c5cm7A_			100.0	31	PDB header: transferase Chain: A; PDB Molecule: thiamine-monophosphate kinase; PDBTitle: structure of thiamine-monophosphate kinase from acinetobacter2 baumannii in complex with adenosine diphosphate (adp) and thiamine3 diphosphate (tpp)
4	c2yxzA_			100.0	27	PDB header: transferase Chain: A; PDB Molecule: thiamin-monophosphate kinase; PDBTitle: crystal structure of tt0281 from thermus thermophilus hb8
5	c5vk4B_			100.0	16	PDB header: ligase Chain: B; PDB Molecule: phosphoribosylformylglycinamide cycloligase; PDBTitle: crystal structure of a phosphoribosylformylglycinamide cyclo-ligase2 from neisseria gonorrhoeae bound to amppnp and magnesium
6	c3mcqA_			100.0	30	PDB header: transferase Chain: A; PDB Molecule: thiamine-monophosphate kinase; PDBTitle: crystal structure of thiamine-monophosphate kinase (mfla_0573) from2 methylbacillus flagellatus kt at 1.91 a resolution
7	c2btuB_			100.0	16	PDB header: synthase Chain: B; PDB Molecule: phosphoribosyl-aminoimidazole synthetase; PDBTitle: crystal structure of phosphoribosylformylglycinamide cyclo-ligase2 from bacillus anthracis at 2.3a resolution.
8	c1cliD_			100.0	18	PDB header: ligase Chain: D; PDB Molecule: protein (phosphoribosyl-aminoimidazole synthetase); PDBTitle: x-ray crystal structure of aminoimidazole ribonucleotide synthetase2 (purm), from the e. coli purine biosynthetic pathway, at 2.5 a3 resolution
9	c3vtiD_			100.0	20	PDB header: transferase Chain: D; PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of hype-hypf complex
10	c2rb9D_			100.0	25	PDB header: structural genomics, unknown function Chain: D; PDB Molecule: hype protein; PDBTitle: crystal structure of e.coli hype
11	c2z1tA_			100.0	21	PDB header: lyase Chain: A; PDB Molecule: hydrogenase expression/formation protein hype; PDBTitle: crystal structure of hydrogenase maturation protein hype

12	c3fd5B_		100.0	21	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase 1; PDBTitle: crystal structure of human selenophosphate synthetase 12 complex with ampcp	
13	c3vysC_		100.0	23	PDB header: metal binding protein/transferase Chain: C: PDB Molecule: hydrogenase expression/formation protein hype; PDBTitle: crystal structure of the hycp-hypd-hype complex (form i)	
14	c3u0oA_		100.0	21	PDB header: transferase Chain: A: PDB Molecule: selenide, water dikinase; PDBTitle: the crystal structure of selenophosphate synthetase from e. coli	
15	c2zodB_		100.0	15	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of selenophosphate synthetase from aquifex aeolicus	
16	c2zauB_		100.0	14	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of an n-terminally truncated2 selenophosphate synthetase from aquifex aeolicus	
17	c2z01A_		100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cycloligase; PDBTitle: crystal structure of phosphoribosylaminoimidazole synthetase from2 geobacillus kaustophilus	
18	c3m84A_		100.0	15	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cycloligase; PDBTitle: crystal structure of phosphoribosylaminoimidazole synthetase from2 francisella tularensis	
19	c2z1eA_		100.0	25	PDB header: transferase Chain: A: PDB Molecule: hydrogenase expression/formation protein hype; PDBTitle: crystal structure of hype from thermococcus kodakaraensis (outward2 form)	
20	c2v9yA_		100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide cycloligase; PDBTitle: human aminoimidazole ribonucleotide synthetase	
21	c5avmE_		not modelled	100.0	17	PDB header: ligase Chain: E: PDB Molecule: phosphoribosylformylglycinamide cycloligase; PDBTitle: crystal structures of 5-aminoimidazole ribonucleotide (air)2 synthetase, purm, from thermus thermophilus
22	c3ac6A_		not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase 2; PDBTitle: crystal structure of purl from thermus thermophilus
23	c5l16A_		not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: putative selenophosphate synthetase; PDBTitle: crystal structure of n-terminus truncated selenophosphate synthetase2 from leishmania major
24	c2hs0A_		not modelled	100.0	19	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase ii; PDBTitle: t. maritima purl complexed with atp
25	c3d54I_		not modelled	100.0	18	PDB header: ligase Chain: I: PDB Molecule: phosphoribosylformylglycinamide synthase ii; PDBTitle: structure of purlqs from thermotoga maritima
26	d3c9ua1		not modelled	100.0	26	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
27	c1t3tA_		not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
28	d1clib1		not modelled	100.0	21	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like

29	d1clia1		Alignment	not modelled	100.0	20	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
30	d2zua1		Alignment	not modelled	100.0	15	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
31	d3c9ua2		Alignment	not modelled	100.0	34	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
32	d2zoda1		Alignment	not modelled	100.0	17	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
33	c3mdoB_		Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: putative phosphoribosylformylglycinamidine cyclo-ligase; PDBTitle: crystal structure of a putative phosphoribosylformylglycinamidine2 cyclo-ligase (bdi_2101) from parabacteroides distasonis atcc 8503 at 3.91 a resolution
34	d2z1ea1		Alignment	not modelled	100.0	24	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
35	d1vk3a2		Alignment	not modelled	99.9	14	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
36	d2zoda2		Alignment	not modelled	99.9	15	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
37	c3kizA_		Alignment	not modelled	99.9	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamidine cyclo-ligase; PDBTitle: crystal structure of putative phosphoribosylformylglycinamidine cyclo-2 ligase (yp_676759.1) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
38	d2z1ea2		Alignment	not modelled	99.9	25	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
39	d1vk3a1		Alignment	not modelled	99.9	23	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
40	d1clia2		Alignment	not modelled	99.9	17	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
41	d1vk3a3		Alignment	not modelled	99.8	13	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
42	d1t3ta4		Alignment	not modelled	99.6	18	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
43	d1t3ta6		Alignment	not modelled	99.6	14	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
44	d1t3ta5		Alignment	not modelled	99.2	16	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like
45	d1t3ta7		Alignment	not modelled	99.2	23	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
46	c3fokH_		Alignment	not modelled	86.2	17	PDB header: structural genomics, unknown function Chain: H: PDB Molecule: uncharacterized protein cgl0159; PDBTitle: crystal structure of cgl0159 from corynebacterium2 glutamicum (brevibacterium flavum). northeast structural3 genomics target cgr115
47	c3jrkG_		Alignment	not modelled	84.1	15	PDB header: lyase Chain: G: PDB Molecule: tagatose 1,6-diphosphate aldolase 2; PDBTitle: a putative tagatose 1,6-diphosphate aldolase from streptococcus2 pyogenes
48	d1to3a_		Alignment	not modelled	76.9	23	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
49	c3qi7A_		Alignment	not modelled	73.1	16	PDB header: transcription Chain: A: PDB Molecule: putative transcriptional regulator; PDBTitle: crystal structure of a putative transcriptional regulator2 (yp_001089212.1) from clostridium difficile 630 at 1.86 a resolution
50	c3dzvB_		Alignment	not modelled	42.9	20	PDB header: transferase Chain: B: PDB Molecule: 4-methyl-5-(beta-hydroxyethyl)thiazole kinase; PDBTitle: crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole kinase2 (np_816404.1) from enterococcus faecalis v583 at 2.57 a resolution
51	c2qjhH_		Alignment	not modelled	42.6	19	PDB header: lyase Chain: H: PDB Molecule: putative aldolase mj0400; PDBTitle: m. jannaschii adh synthase covalently bound to2 dihydroxyacetone phosphate
52	c4ru1C_		Alignment	not modelled	41.2	5	PDB header: transport protein Chain: C: PDB Molecule: monosaccharide abc transporter substrate-binding protein, PDBTitle: crystal structure of carbohydrate transporter acei_1806 from2 acidothermus cellulolyticus 11b, target efi-510965, in complex with3 myo-inositol
53	d2csua1		Alignment	not modelled	38.6	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain

54	c4mozC	Alignment	not modelled	34.1	18	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDB Title: fructose-bisphosphate aldolase from slackia heliotrichireducens dsm 20476
55	c2hqbA	Alignment	not modelled	33.7	16	PDB header: transcription Chain: A: PDB Molecule: transcriptional activator of comk gene; PDB Title: crystal structure of a transcriptional activator of comk2 gene from bacillus halodurans
56	c5jxpA	Alignment	not modelled	32.7	27	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDB Title: crystal structure of porphyromonas endodontalis dpp11 in alternate2 conformation
57	c5jxfA	Alignment	not modelled	29.2	27	PDB header: hydrolase Chain: A: PDB Molecule: asp/glu-specific dipeptidyl-peptidase; PDB Title: crystal structure of flavobacterium psychrophilum dpp11 in complex2 with dipeptide arg-asp
58	c5kdmD	Alignment	not modelled	28.2	15	PDB header: chaperone / dna binding protein Chain: D: PDB Molecule: major tegument protein; PDB Title: crystal structure of ebv tegument protein bnrf1 in complex with2 histone chaperone daxx and histones h3.3-h4
59	c3gndC	Alignment	not modelled	24.6	18	PDB header: lyase Chain: C: PDB Molecule: aldolase lsrf; PDB Title: crystal structure of e. coli lsrf in complex with ribulose-5-phosphate
60	d1fnnda1	Alignment	not modelled	23.3	25	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferrodoxin reductase FAD-binding domain-like
61	d1wf8a1	Alignment	not modelled	22.5	11	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
62	c3g85A	Alignment	not modelled	21.4	5	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulator (laci family); PDB Title: crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
63	d1v8aa	Alignment	not modelled	21.0	29	Fold: Ribokinase-like Superfamily: Ribokinase-like Family: Thiamin biosynthesis kinases
64	c3eggC	Alignment	not modelled	20.7	12	PDB header: hydrolase Chain: C: PDB Molecule: spinophilin; PDB Title: crystal structure of a complex between protein phosphatase 1 alpha2 (pp1) and the pp1 binding and pdz domains of spinophilin
65	c3lukB	Alignment	not modelled	20.5	9	PDB header: rna binding protein Chain: B: PDB Molecule: protein argonaute-2; PDB Title: crystal structure of mid domain from hago2
66	d1gawa1	Alignment	not modelled	20.1	17	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferrodoxin reductase FAD-binding domain-like
67	c5mvra	Alignment	not modelled	19.9	40	PDB header: transferase Chain: A: PDB Molecule: tRNA threonylcarbamoyladenosine biosynthesis protein tsae; PDB Title: crystal structure of bacillus subtilis ydib
68	d2bmwa1	Alignment	not modelled	19.8	22	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferrodoxin reductase FAD-binding domain-like
69	c5braA	Alignment	not modelled	19.4	14	PDB header: solute-binding protein Chain: A: PDB Molecule: putative periplasmic binding protein with substrate ribose; PDB Title: crystal structure of a putative periplasmic solute binding protein2 (ipr025997) from ochrobactrum anthropi atcc49188 (oant 2843, target3 efi-511085)
70	d1htwa	Alignment	not modelled	19.4	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: YjeE-like
71	c4y01B	Alignment	not modelled	18.9	14	PDB header: hydrolase Chain: B: PDB Molecule: peptidase s46; PDB Title: crystal structure of dipeptidyl peptidase 11 (dpp11) from2 porphyromonas gingivalis
72	d1ep3b1	Alignment	not modelled	18.7	32	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferrodoxin reductase FAD-binding domain-like
73	c2jreA	Alignment	not modelled	18.3	16	PDB header: de novo protein Chain: A: PDB Molecule: c60-1 pdz domain peptide; PDB Title: c60-1, a pdz domain designed using statistical coupling2 analysis
74	c3rotA	Alignment	not modelled	18.1	10	PDB header: transport protein Chain: A: PDB Molecule: abc sugar transporter, periplasmic sugar binding protein; PDB Title: crystal structure of abc sugar transporter (periplasmic sugar binding2 protein) from legionella pneumophila
75	d2byga1	Alignment	not modelled	18.0	23	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
76	c5f67A	Alignment	not modelled	17.9	23	PDB header: protein binding Chain: A: PDB Molecule: inactivation-no-after-potential d protein; PDB Title: an exquisitely specific pdz/target recognition revealed by the2 structure of inad pdz3 in complex with trp channel tail
77	c6ndiB	Alignment	not modelled	17.7	15	PDB header: sugar binding protein Chain: B: PDB Molecule: transcriptional regulator; PDB Title: 2.60 angstrom resolution crystal structure of periplasmic binding and2 sugar binding domain of laci family protein from klebsiella3 pneumoniae.
78	c3wolB	Alignment	not modelled	17.5	23	PDB header: hydrolase Chain: B: PDB Molecule: dipeptidyl aminopeptidase bii; PDB Title: crystal structure of the dap bii dipeptide complex i
						Fold: Periplasmic binding protein-like I

79	d1jyea_	Alignment	not modelled	17.2	21	Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
80	c1jyeA_	Alignment	not modelled	17.2	21	PDB header: transcription Chain: A: PDB Molecule: lactose operon repressor; PDBTitle: structure of a dimeric lac repressor with c-terminal deletion and k84I2 substitution
81	c6dspB_	Alignment	not modelled	17.1	17	PDB header: signaling protein Chain: B: PDB Molecule: autoinducer 2-binding protein lsrB; PDBTitle: lsrB from clostridium saccharobutylicum in complex with ai-2
82	c3d02A_	Alignment	not modelled	17.1	3	PDB header: sugar binding protein Chain: A: PDB Molecule: putative laci-type transcriptional regulator; PDBTitle: crystal structure of periplasmic sugar-binding protein2 (yp_001338366.1) from klebsiella pneumoniae subsp. pneumoniae mgm3 78578 at 1.30 a resolution
83	d2f0aa1	Alignment	not modelled	16.7	25	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
84	d1ujda_	Alignment	not modelled	16.6	17	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
85	c3qz6A_	Alignment	not modelled	16.6	13	PDB header: lyase Chain: A: PDB Molecule: hpch/hpaI aldolase; PDBTitle: the crystal structure of hpch/hpaI aldolase from desulfobacterium2 hafniense dcb-2
86	d1oi7a1	Alignment	not modelled	16.0	19	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
87	d1x5qa1	Alignment	not modelled	15.8	23	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
88	c6fpeE_	Alignment	not modelled	15.6	30	PDB header: rna binding protein Chain: E: PDB Molecule: atpase yjee, predicted to have essential role in cell wall PDBTitle: bacterial protein complex
89	c6hyhA_	Alignment	not modelled	15.4	17	PDB header: sugar binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of msmeg_1712 from mycobacterium smegmatis in2 complex with beta-d-fucofuranose
90	c3gbvB_	Alignment	not modelled	15.3	9	PDB header: transcription regulator Chain: B: PDB Molecule: putative laci-family transcriptional regulator; PDBTitle: crystal structure of a putative laci transcriptional regulator from2 bacteroides fragilis
91	d1tjya_	Alignment	not modelled	14.3	14	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
92	d1wfga_	Alignment	not modelled	13.9	17	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
93	c3dbiA_	Alignment	not modelled	13.8	13	PDB header: transcription regulator Chain: A: PDB Molecule: sugar-binding transcriptional regulator, laci family; PDBTitle: crystal structure of sugar-binding transcriptional regulator (laci2 family) from escherichia coli complexed with phosphate
94	c4ywka_	Alignment	not modelled	13.8	31	PDB header: cell cycle Chain: A: PDB Molecule: cell division control protein 21; PDBTitle: pyrococcus furiosus mcm n-terminal domain with zinc-binding subdomain2 b deleted
95	c4wzza_	Alignment	not modelled	13.7	10	PDB header: transport protein Chain: A: PDB Molecule: putative sugar abc transporter, substrate-binding protein; PDBTitle: crystal structure of an abc transporter solute binding protein2 (ipr025997) from clostridium phytofermentas (cpphy_0583, target efi-3 511148) with bound L-rhamnose
96	c5hqjA_	Alignment	not modelled	13.6	15	PDB header: solute-binding protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of abc transporter solute binding protein b1g1h72 from burkholderia graminis c4d1m, target efi-511179, in complex with3 d-arabinose
97	d1whaa_	Alignment	not modelled	13.6	14	Fold: PDZ domain-like Superfamily: PDZ domain-like Family: PDZ domain
98	c3d8uA_	Alignment	not modelled	13.5	6	PDB header: transcription regulator Chain: A: PDB Molecule: purr transcriptional regulator; PDBTitle: the crystal structure of a purr family transcriptional regulator from2 vibrio parahaemolyticus rimp 2210633
99	c4kzkA_	Alignment	not modelled	13.5	12	PDB header: sugar binding protein Chain: A: PDB Molecule: l-arabinose abc transporter, periplasmic l-arabinose- PDBTitle: the structure of the periplasmic l-arabinose binding protein from2 burkholderia thailandensis