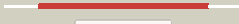



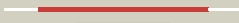



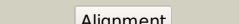

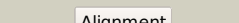

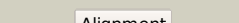











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1445c_(devB)_1623720_1624463
Date	Fri Aug 2 13:30:02 BST 2019
Unique Job ID	35a564f5bb2f51e2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3icoA_	 Alignment		100.0	100	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from mycobacterium2 tuberculosis
2	c3oc6A_	 Alignment		100.0	66	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from mycobacterium2 smegmatis, apo form
3	c2j0eA_	 Alignment		100.0	29	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: three dimensional structure and catalytic mechanism of 6-2 phosphogluconolactonase from trypanosoma brucei
4	c3hn6D_	 Alignment		100.0	22	PDB header: isomerase Chain: D: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: crystal structure of glucosamine-6-phosphate deaminase from borrelia2 burgdorferi
5	d1ne7a_	 Alignment		100.0	24	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: NagB-like
6	c1y89B_	 Alignment		100.0	31	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: devb protein; PDBTitle: crystal structure of devb protein
7	c3cssA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from leishmania2 guyanensis
8	d1fsfa_	 Alignment		100.0	22	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: NagB-like
9	c6nbgD_	 Alignment		100.0	22	PDB header: unknown function Chain: D: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: 2.05 angstrom resolution crystal structure of hypothetical protein2 kp1_5497 from klebsiella pneumoniae.
10	c1pbtA_	 Alignment		100.0	29	PDB header: hydrolase, oxidoreductase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: the crystal structure of tm1154, oxidoreductase, sol/devb2 family from thermotoga maritima
11	d1vl1a_	 Alignment		100.0	29	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: NagB-like

12	c3lwdA_	Alignment		100.0	26	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-phosphogluconolactonase (yp_574786.1)2 from chromohalobacter salexigens dsm 3043 at 1.88 a resolution
13	c3e15D_	Alignment		100.0	21	PDB header: hydrolase Chain: D: PDB Molecule: glucose-6-phosphate 1-dehydrogenase; PDBTitle: 6-phosphogluconolactonase from plasmodium vivax
14	c3nwpA_	Alignment		100.0	27	PDB header: hydrolase Chain: A: PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of a 6-phosphogluconolactonase (sbal_2240) from2 shewanella baltica os155 at 1.40 a resolution
15	c3lhiA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: putative 6-phosphogluconolactonase; PDBTitle: crystal structure of putative 6-phosphogluconolactonase(yp_207848.1)2 from neisseria gonorrhoeae fa 1090 at 1.33 a resolution
16	c2bkxB_	Alignment		100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: structure and kinetics of a monomeric glucosamine-6-2 phosphate deaminase: missing link of the nagb superfamily
17	c2ri0B_	Alignment		100.0	22	PDB header: hydrolase Chain: B: PDB Molecule: glucosamine-6-phosphate deaminase; PDBTitle: crystal structure of glucosamine 6-phosphate deaminase (nagb) from s.2 mutans
18	c4oqqA_	Alignment		99.8	14	PDB header: transcription Chain: A: PDB Molecule: deoxyribonucleoside regulator; PDBTitle: structure of the effector-binding domain of deoxyribonucleoside2 regulator deor from bacillus subtilis
19	d2gnpa1	Alignment		99.7	11	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
20	c2w48D_	Alignment		99.6	14	PDB header: transcription Chain: D: PDB Molecule: sorbitol operon regulator; PDBTitle: crystal structure of the full-length sorbitol operon2 regulator sorc from klebsiella pneumoniae
21	d2o0ma1	Alignment	not modelled	99.5	15	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
22	c2o0mA_	Alignment	not modelled	99.5	15	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator, sorc family; PDBTitle: the crystal structure of the putative sorc family transcriptional2 regulator from enterococcus faecalis
23	d3efba1	Alignment	not modelled	99.5	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
24	c3nzeB_	Alignment	not modelled	99.4	17	PDB header: transcription regulator Chain: B: PDB Molecule: putative transcriptional regulator, sugar-binding family; PDBTitle: the crystal structure of a domain of a possible sugar-binding2 transcriptional regulator from arthrobacter aurescens tc1.
25	c4r9nA_	Alignment	not modelled	99.4	15	PDB header: transcription Chain: A: PDB Molecule: lmo0547 protein; PDBTitle: deor family transcriptional regulator from listeria monocytogenes.
26	c4go1A_	Alignment	not modelled	98.7	22	PDB header: transcription Chain: A: PDB Molecule: transcriptional regulator lsr; PDBTitle: crystal structure of full length transcription repressor lsr from e.2 coli.
27	d2okga1	Alignment	not modelled	98.5	14	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
28	c3kv1A_	Alignment	not modelled	97.5	13	PDB header: transcription Chain: A: PDB Molecule: transcriptional repressor; PDBTitle: crystal structure of putative sugar-binding domain of transcriptional2 repressor from vibrio fischeri
						Fold: NagB/RpiA/CoA transferase-like

29	d2r5fa1	Alignment	not modelled	97.4	16	Superfamily: NagB/RpiA/CoA transferase-like Family: SorC sugar-binding domain-like
30	c2e21A	Alignment	not modelled	91.9	14	PDB header: ligase Chain: A: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils in a complex with amppnp from aquifex2 aeolicus.
31	d1zuna1	Alignment	not modelled	86.9	8	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PAPS reductase-like
32	c1ni5A	Alignment	not modelled	81.5	14	PDB header: cell cycle Chain: A: PDB Molecule: putative cell cycle protein mesj; PDBTitle: structure of the mesj pp-atpase from escherichia coli
33	d1wy5a1	Alignment	not modelled	77.0	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
34	c3vrhA	Alignment	not modelled	76.2	9	PDB header: rna binding protein Chain: A: PDB Molecule: putative uncharacterized protein ph0300; PDBTitle: crystal structure of ph0300
35	c5udwB	Alignment	not modelled	73.4	11	PDB header: transferase Chain: B: PDB Molecule: lactate racemization operon protein lare; PDBTitle: lare, a sulfur transferase involved in synthesis of the cofactor for2 lactate racemase, in complex with nickel
36	c3a2kB	Alignment	not modelled	72.8	15	PDB header: ligase/rna Chain: B: PDB Molecule: trna(ile)-lysine synthase; PDBTitle: crystal structure of tils complexed with trna
37	c2oq2B	Alignment	not modelled	66.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: crystal structure of yeast paps reductase with pap, a product complex
38	d1ni5a1	Alignment	not modelled	56.5	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: PP-loop ATPase
39	c2goyC	Alignment	not modelled	53.5	18	PDB header: oxidoreductase Chain: C: PDB Molecule: adenosine phosphosulfate reductase; PDBTitle: crystal structure of assimilatory adenosine 5'-2 phosphosulfate reductase with bound aps
40	c1zunA	Alignment	not modelled	52.1	8	PDB header: transferase Chain: A: PDB Molecule: sulfate adenylyltransferase subunit 2; PDBTitle: crystal structure of a gtp-regulated atp sulfurylase2 heterodimer from pseudomonas syringae
41	c2q4dB	Alignment	not modelled	48.6	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: lysine decarboxylase-like protein at5g11950; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at5g11950
42	c3uowB	Alignment	not modelled	48.2	8	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
43	d1wxia1	Alignment	not modelled	46.5	9	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
44	d1pjqa3	Alignment	not modelled	45.9	19	Fold: Siroheme synthase middle domains-like Superfamily: Siroheme synthase middle domains-like Family: Siroheme synthase middle domains-like
45	c5tw7E	Alignment	not modelled	45.5	15	PDB header: ligase Chain: E: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of a gmp synthase (glutamine-hydrolyzing) from2 neisseria gonorrhoeae
46	c4xgIA	Alignment	not modelled	43.4	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a domain of unknown function (duf1537) from2 pectobacterium atrosepticum (eca3761), target efi-511609, apo3 structure, domain swapped dimer
47	d1gpmA1	Alignment	not modelled	43.3	15	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
48	d1ydha	Alignment	not modelled	41.7	22	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
49	c1gpmD	Alignment	not modelled	39.3	18	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
50	c2dplA	Alignment	not modelled	38.3	16	PDB header: ligase Chain: A: PDB Molecule: gmp synthase [glutamine-hydrolyzing] subunit b; PDBTitle: crystal structure of the gmp synthase from pyrococcus horikoshii ot3
51	c3dpiA	Alignment	not modelled	38.0	17	PDB header: ligase Chain: A: PDB Molecule: nad+ synthetase; PDBTitle: crystal structure of nad+ synthetase from burkholderia pseudomallei
52	d3bzka5	Alignment	not modelled	37.1	13	Fold: Ribonuclease H-like motif Superfamily: Ribonuclease H-like Family: Tex RuvX-like domain-like
53	c3u7jA	Alignment	not modelled	36.8	20	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
54	c3tqiB	Alignment	not modelled	36.7	13	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella

						burnetii
55	d1xnga1	Alignment	not modelled	36.7	12	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
56	c5hujB	Alignment	not modelled	36.4	12	PDB header: transferase Chain: B: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of nade from streptococcus pyogenes
57	d1uj4a1	Alignment	not modelled	35.9	19	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: D-ribose-5-phosphate isomerase (RpiA), catalytic domain
58	c4bwvB	Alignment	not modelled	35.2	12	PDB header: oxidoreductase Chain: B: PDB Molecule: phosphoadenosine-phosphosulphate reductase; PDBTitle: structure of adenosine 5-prime-phosphosulfate reductase apr-b from2 physcomitrella patens
59	c4xfdA	Alignment	not modelled	33.0	20	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: crystal structure of a nh(3)-dependent nad(+) synthetase from2 pseudomonas aeruginosa
60	c4q16C	Alignment	not modelled	32.5	18	PDB header: ligase Chain: C: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad+ synthetase from deinococcus radiodurans
61	c5itsD	Alignment	not modelled	32.1	25	PDB header: hydrolase Chain: D: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal structure of log from corynebacterium glutamicum
62	c3sftA	Alignment	not modelled	31.9	15	PDB header: hydrolase Chain: A: PDB Molecule: chemotaxis response regulator protein-glutamate PDBTitle: crystal structure of thermotoga maritima cheb methylesterase catalytic2 domain
63	d1q15a1	Alignment	not modelled	31.7	19	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
64	d1t35a	Alignment	not modelled	31.3	19	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
65	c5zjbA	Alignment	not modelled	29.6	17	PDB header: hydrolase Chain: A: PDB Molecule: putative cytokinin riboside 5'-monophosphate PDBTitle: crystal structure of type-i log from pseudomonas aeruginosa pao1
66	c2o8vA	Alignment	not modelled	29.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: phosphoadenosine phosphosulfate reductase; PDBTitle: paps reductase in a covalent complex with thioredoxin c35a
67	d1xhoa	Alignment	not modelled	26.0	21	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
68	c2q4oA	Alignment	not modelled	25.3	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein at2g37210/t2n18.3; PDBTitle: ensemble refinement of the crystal structure of a lysine2 decarboxylase-like protein from arabidopsis thaliana gene at2g37210
69	d2q4oa1	Alignment	not modelled	25.3	21	Fold: MCP/YpsA-like Superfamily: MCP/YpsA-like Family: MoCo carrier protein-like
70	c1xhoB	Alignment	not modelled	24.2	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: chorismate mutase; PDBTitle: chorismate mutase from clostridium thermocellum cth-682
71	d1kqpa	Alignment	not modelled	24.2	13	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
72	c6c6kD	Alignment	not modelled	23.9	43	PDB header: rna binding protein/rna Chain: D: PDB Molecule: interferon-induced protein with tetratricopeptide repeats PDBTitle: structural basis for preferential recognition of cap 0 rna by a human2 ifit1-ffit3 protein complex
73	c1uj6A	Alignment	not modelled	23.3	19	PDB header: isomerase Chain: A: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: crystal structure of thermus thermophilus ribose-5-phosphate isomerase2 complexed with arabinose-5-phosphate
74	c2vzaD	Alignment	not modelled	23.1	14	PDB header: cell adhesion Chain: D: PDB Molecule: cell filamentation protein; PDBTitle: type iv secretion system effector protein bepa
75	c4gmkB	Alignment	not modelled	22.1	11	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
76	d1ct9a1	Alignment	not modelled	21.4	14	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
77	c1x3IA	Alignment	not modelled	21.3	19	PDB header: transferase Chain: A: PDB Molecule: hypothetical protein ph0495; PDBTitle: crystal structure of the ph0495 protein from pyrococcus horikoshii2 ot3
78	c4x84C	Alignment	not modelled	21.1	16	PDB header: isomerase Chain: C: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from pseudomonas2 aeruginosa
						Fold: Adenine nucleotide alpha hydrolase-like

79	d1jgta1	Alignment	not modelled	19.9	20	Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
80	d1yzya1	Alignment	not modelled	19.7	14	Fold: YgbK-like Superfamily: YgbK-like Family: YgbK-like
81	c3q4gA	Alignment	not modelled	19.6	13	PDB header: ligase Chain: A: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nad synthetase from vibrio cholerae
82	d2jm6b1	Alignment	not modelled	19.6	8	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
83	d2fvta1	Alignment	not modelled	19.5	25	Fold: MTH938-like Superfamily: MTH938-like Family: MTH938-like
84	c3e59A	Alignment	not modelled	19.5	16	PDB header: transferase Chain: A: PDB Molecule: pyoverdine biosynthesis protein pvca; PDBTitle: crystal structure of the pvca (pa2254) protein from pseudomonas2 aeruginosa
85	c5zi9B	Alignment	not modelled	19.3	20	PDB header: hydrolase Chain: B: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal strcuture of type-ii log from streptomyces coelicolor a3
86	d1dbfa	Alignment	not modelled	18.6	12	Fold: Bacillus chorismate mutase-like Superfamily: YjgF-like Family: Chorismate mutase
87	c2f8mB	Alignment	not modelled	18.6	18	PDB header: isomerase Chain: B: PDB Molecule: ribose 5-phosphate isomerase; PDBTitle: ribose 5-phosphate isomerase from plasmodium falciparum
88	c2gaaA	Alignment	not modelled	18.2	9	PDB header: unknown function Chain: A: PDB Molecule: hypothetical 39.9 kda protein; PDBTitle: crystal structure of yfh7 from saccharomyces cerevisiae: a2 putative p-loop containing kinase with a circular3 permutation.
89	c3l7oB	Alignment	not modelled	17.8	17	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
90	c3fiuD	Alignment	not modelled	17.5	9	PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
91	c6gwjK	Alignment	not modelled	16.6	21	PDB header: rna binding protein Chain: K: PDB Molecule: probable trna n6-adenosine threonylcarbamoyltransferase; PDBTitle: protein complex
92	c1y8qA	Alignment	not modelled	16.5	16	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like 1 activating enzyme e1a; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
93	d2a7ya1	Alignment	not modelled	16.4	32	Fold: SH3-like barrel Superfamily: Cell growth inhibitor/plasmid maintenance toxic component Family: Rv2302-like
94	c2a7yA	Alignment	not modelled	16.4	32	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rv2302/mt2359; PDBTitle: solution structure of the conserved hypothetical protein2 rv2302 from the bacterium mycobacterium tuberculosis
95	c1lk5C	Alignment	not modelled	16.3	17	PDB header: isomerase Chain: C: PDB Molecule: d-ribose-5-phosphate isomerase; PDBTitle: structure of the d-ribose-5-phosphate isomerase from2 pyrococcus horikoshii
96	c4xfrB	Alignment	not modelled	15.5	33	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a domain of unknown function (duf1537) from2 bordetella bronchiseptica (bb3215), target efi-511620, with bound3 citrate, domain swapped dimer, space group p6522
97	c5ghaC	Alignment	not modelled	15.3	18	PDB header: transferase/transport protein Chain: C: PDB Molecule: sulfur transferase ttua; PDBTitle: sulfur transferase ttua in complex with sulfur carrier ttub
98	c5wq3A	Alignment	not modelled	15.2	24	PDB header: hydrolase Chain: A: PDB Molecule: cytokinin riboside 5'-monophosphate phosphoribohydrolase; PDBTitle: crystal strcuture of type-ii log from corynebacterium glutamicum
99	d2b8na1	Alignment	not modelled	15.1	22	Fold: GckA/TtuD-like Superfamily: GckA/TtuD-like Family: GckA/TtuD-like