

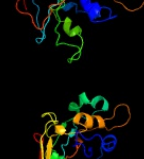
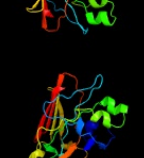

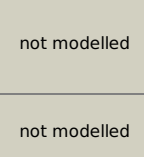


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3536c (-)_3974690_3975475
Date	Fri Aug 9 18:20:21 BST 2019
Unique Job ID	Ofd8ee3a70968cfd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5d2hA_	Alignment		100.0	34	PDB header: lyase Chain: A: PDB Molecule: 4-oxalocrotonate decarboxylase nahk; PDBTitle: 4-oxalocrotonate decarboxylase from pseudomonas putida g7 - complexed2 with magnesium and alpha-ketoglutarate
2	d1sv6a_	Alignment		100.0	42	Fold: FAH Superfamily: FAH Family: FAH
3	c2eb5D_	Alignment		100.0	43	PDB header: lyase Chain: D: PDB Molecule: 2-oxo-hept-3-ene-1,7-dioate hydratase; PDBTitle: crystal structure of hpcg complexed with oxalate
4	c3l53F_	Alignment		100.0	16	PDB header: structural genomics, unknown function Chain: F: PDB Molecule: putative fumarylacetoacetate isomerase/hydrolase; PDBTitle: crystal structure of a putative fumarylacetoacetate2 isomerase/hydrolase from oleispira antarctica
5	d1sawa_	Alignment		100.0	19	Fold: FAH Superfamily: FAH Family: FAH
6	c3qdfA_	Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from mycobacterium marinum
7	c3s52A_	Alignment		100.0	20	PDB header: hydrolase Chain: A: PDB Molecule: putative fumarylacetoacetate hydrolase family protein; PDBTitle: crystal structure of a putative fumarylacetoacetate hydrolase family2 protein from yersinia pestis co92
8	c4maqB_	Alignment		100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: putative fumarylpyruvate hydrolase; PDBTitle: crystal structure of a putative fumarylpyruvate hydrolase from2 burkholderia cenocepacia
9	d1nr9a_	Alignment		100.0	21	Fold: FAH Superfamily: FAH Family: FAH
10	d1gtta1	Alignment		100.0	15	Fold: FAH Superfamily: FAH Family: FAH
11	c1wzoC_	Alignment		100.0	20	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8

12	d1gta2	Alignment		100.0	15	Fold: FAH Superfamily: FAH Family: FAH
13	c6iybB	Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: 5-oxopent-3-ene-1,2,5-tricarboxylate decarboxylase; PDBTitle: fumarylacetoacetate hydrolase (eafah) from psychrophilic2 exiguobacterium antarcticum
14	c1i7oC	Alignment		100.0	15	PDB header: isomerase, lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate degradation bifunctional PDBTitle: crystal structure of hpce
15	c2dfuB	Alignment		100.0	17	PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
16	c3r6oA	Alignment		100.0	20	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1, 7-dioate isomerase; PDBTitle: crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioate isomerase from mycobacterium abscessus
17	c6jvwA	Alignment		100.0	15	PDB header: hydrolase Chain: A: PDB Molecule: maleylpyruvate hydrolase; PDBTitle: crystal structure of maleylpyruvate hydrolase from sphingobium sp.2 syk-6 in complex with manganese (ii) ion and pyruvate
18	c4dbbA	Alignment		100.0	13	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of cg1458 with inhibitor
19	d1nkqa	Alignment		100.0	16	Fold: FAH Superfamily: FAH Family: FAH
20	c3lzkC	Alignment		100.0	16	PDB header: hydrolase Chain: C: PDB Molecule: fumarylacetoacetate hydrolase family protein; PDBTitle: the crystal structure of a probably aromatic amino acid2 degradation protein from sinorhizobium meliloti 1021
21	c2q1dX	Alignment	not modelled	99.9	13	PDB header: lyase Chain: X: PDB Molecule: 2-keto-3-deoxy-d-arabinonate dehydratase; PDBTitle: 2-keto-3-deoxy-d-arabinonate dehydratase complexed with magnesium and 2,5-dioxopentanoate
22	d1hyoa2	Alignment	not modelled	99.9	18	Fold: FAH Superfamily: FAH Family: FAH
23	c4qkuC	Alignment	not modelled	99.9	23	PDB header: hydrolase Chain: C: PDB Molecule: hydrolase; PDBTitle: crystal structure of a putative hydrolase from burkholderia2 cenocepacia
24	c1hyoB	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: fumarylacetoacetate hydrolase; PDBTitle: crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphinoyl)-3-oxo-butanoic3 acid
25	d1t8sa	Alignment	not modelled	65.7	20	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
26	d1ybfa	Alignment	not modelled	42.9	16	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
27	c3teeA	Alignment	not modelled	38.7	20	PDB header: chaperone Chain: A: PDB Molecule: flagella basal body p-ring formation protein flga; PDBTitle: crystal structure of salmonella flga in open form
28	c3frnA	Alignment	not modelled	29.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: flagellar protein flga; PDBTitle: crystal structure of flagellar protein flga from thermotoga maritima2 msb8

29	c4kmaA	Alignment	not modelled	28.9	20	PDB header: protein binding Chain: A: PDB Molecule: gm14141p; PDBTitle: crystal structure of drosophila suppressor of fused
30	d1m1la	Alignment	not modelled	25.8	30	Fold: Suppressor of Fused, N-terminal domain Superfamily: Suppressor of Fused, N-terminal domain Family: Suppressor of Fused, N-terminal domain
31	c3mb8A	Alignment	not modelled	24.9	17	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase; PDBTitle: crystal structure of purine nucleoside phosphorylase from toxoplasma2 gondii in complex with immucillin-h
32	c2zy3A	Alignment	not modelled	24.3	15	PDB header: lyase Chain: A: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
33	d2f4la1	Alignment	not modelled	24.2	21	Fold: CUB-like Superfamily: Acetamidase/Formamidase-like Family: Acetamidase/Formamidase-like
34	c4z92A	Alignment	not modelled	22.5	28	PDB header: virus Chain: A: PDB Molecule: capsid subunit vp1; PDBTitle: crystal structure of parechovirus-1 virion
35	c3qrqA	Alignment	not modelled	21.9	29	PDB header: rna binding protein/rna Chain: A: PDB Molecule: putative uncharacterized protein tthb192; PDBTitle: structure of thermus thermophilus cse3 bound to an rna representing a2 pre-cleavage complex
36	d1q1ga	Alignment	not modelled	21.1	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
37	c1nw4C	Alignment	not modelled	21.1	17	PDB header: transferase Chain: C: PDB Molecule: uridine phosphorylase, putative; PDBTitle: crystal structure of plasmodium falciparum purine nucleoside2 phosphorylase in complex with immh and sulfate
38	c3m9bK	Alignment	not modelled	21.0	23	PDB header: chaperone Chain: K: PDB Molecule: proteasome-associated atpase; PDBTitle: crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
39	c3b9tD	Alignment	not modelled	19.9	38	PDB header: hydrolase Chain: D: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of predicted acetamidase/formamidase (yp_546212.1)2 from methylobacillus flagellatus kt at 1.58 a resolution
40	c3f6tA	Alignment	not modelled	19.3	18	PDB header: transferase Chain: A: PDB Molecule: aspartate aminotransferase; PDBTitle: crystal structure of aspartate aminotransferase (e.c. 2.6.1.1)2 (yp_194538.1) from lactobacillus acidophilus ncfm at 2.15 a3 resolution
41	c2zy4F	Alignment	not modelled	19.1	13	PDB header: lyase Chain: F: PDB Molecule: l-aspartate beta-decarboxylase; PDBTitle: dodecameric l-aspartate beta-decarboxylase
42	c4r31A	Alignment	not modelled	18.2	17	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of a putative uridine phosphorylase from2 actinobacillus succinogenes 130z (target nysgrc-029667)
43	d1g7sa1	Alignment	not modelled	18.0	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Translation proteins Family: Elongation factors
44	c1yyca	Alignment	not modelled	16.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative late embryogenesis abundant protein; PDBTitle: solution structure of a putative late embryogenesis2 abundant (lea) protein at2g46140.1
45	c5l9wA	Alignment	not modelled	14.7	21	PDB header: ligase Chain: A: PDB Molecule: acetophenone carboxylase delta subunit; PDBTitle: crystal structure of the apc core complex
46	c4ldnA	Alignment	not modelled	14.5	15	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of a putative purine nucleoside phosphorylase from2 vibrio fischeri es114 (target nysgrc-029521)
47	c3mjJD	Alignment	not modelled	12.7	28	PDB header: hydrolase Chain: D: PDB Molecule: predicted acetamidase/formamidase; PDBTitle: crystal structure analysis of a recombinant predicted2 acetamidase/formamidase from the thermophile thermoanaerobacter3 tengcongensis
48	d2qamc2	Alignment	not modelled	12.7	31	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
49	c5svbD	Alignment	not modelled	12.5	12	PDB header: ligase Chain: D: PDB Molecule: acetone carboxylase alpha subunit; PDBTitle: mechanism of atp-dependent acetone carboxylation, acetone carboxylase2 amp bound structure
50	d3pnpa	Alignment	not modelled	12.0	15	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
51	d1jroa2	Alignment	not modelled	11.8	21	Fold: beta-Grasp (ubiquitin-like) Superfamily: 2Fe-2S ferredoxin-like Family: 2Fe-2S ferredoxin domains from multidomain proteins
52	d1rl2a2	Alignment	not modelled	11.5	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
53	c4lkrA	Alignment	not modelled	11.3	13	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deod-type; PDBTitle: crystal structure of deod-3 gene product from shewanella

						oneidensis2 mr-1, nysgrc target 029437
54	d1k9sa_	Alignment	not modelled	11.1	15	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
55	c3qpbB_	Alignment	not modelled	11.1	22	PDB header: transferase Chain: B: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of streptococcus pyogenes uridine phosphorylase2 reveals a subclass of the np-i superfamily
56	c5n76C_	Alignment	not modelled	11.1	26	PDB header: nickel-binding protein Chain: C: PDB Molecule: coot; PDBTitle: crystal structure of the apo-form of the co dehydrogenase accessory2 protein coot from rhodospirillum rubrum
57	c1gr3A_	Alignment	not modelled	11.1	16	PDB header: collagen Chain: A: PDB Molecule: collagen x; PDBTitle: structure of the human collagen x nc1 trimer
58	d1gr3a_	Alignment	not modelled	11.1	16	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
59	c4kmhB_	Alignment	not modelled	11.0	30	PDB header: protein binding Chain: B: PDB Molecule: suppressor of fused homolog; PDBTitle: crystal structure of suppressor of fused d20
60	d2o8ra3	Alignment	not modelled	10.8	18	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
61	d2affa1	Alignment	not modelled	10.5	17	Fold: SMAD/FHA domain Superfamily: SMAD/FHA domain Family: FHA domain
62	c4lnhA_	Alignment	not modelled	10.4	14	PDB header: transferase Chain: A: PDB Molecule: uridine phosphorylase; PDBTitle: crystal structure of uridine phosphorylase from vibrio fischeri es114.2 nysgrc target 29520.
63	c2nbgA_	Alignment	not modelled	10.3	27	PDB header: translation Chain: A: PDB Molecule: translation initiation factor if-2; PDBTitle: structure of the geobacillus stearothermophilus if2 g3-subdomain
64	c1z34A_	Alignment	not modelled	10.0	13	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
65	c4xinB_	Alignment	not modelled	9.9	15	PDB header: unknown function Chain: B: PDB Molecule: lpqh orthologue; PDBTitle: x-ray crystal structure of an lpqh orthologue from mycobacterium avium
66	c3f5tA_	Alignment	not modelled	9.7	28	PDB header: viral protein Chain: A: PDB Molecule: nonstructural protein 1; PDBTitle: x-ray structure of h5n1 ns1
67	d1xo8a_	Alignment	not modelled	9.6	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: LEA14-like Family: LEA14-like
68	c4m7wA_	Alignment	not modelled	9.2	15	PDB header: transferase Chain: A: PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of purine nucleoside phosphorylase from leptotrichia2 buccalis c-1013-b, nysgrc target 029767.
69	c3l4qA_	Alignment	not modelled	9.2	28	PDB header: viral protein/protein binding Chain: A: PDB Molecule: non-structural protein 1; PDBTitle: structural insights into phosphoinositide 3-kinase activation by the2 influenza a virus ns1 protein
70	c3pc0D_	Alignment	not modelled	9.2	15	PDB header: ligase Chain: D: PDB Molecule: phenylalanyl-trna synthetase, beta chain; PDBTitle: crystal structure of e. coli phenylalanine-trna synthetase complexed2 with phenylalanine and amp
71	d1nds2	Alignment	not modelled	9.0	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
72	d1clca2	Alignment	not modelled	8.7	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: E-set domains of sugar-utilizing enzymes
73	c4l0mA_	Alignment	not modelled	8.7	22	PDB header: hydrolase Chain: A: PDB Molecule: putative 5'-methylthioadenosine/s-adenosylhomocysteine PDBTitle: crystal structure of a putative 5'-methylthioadenosine/s-2 adenosylhomocysteine nucleosidase from borrelia burgdorferi b31 bound3 to adenine (target nysgrc-029268)
74	d2gx9a1	Alignment	not modelled	8.3	28	Fold: Ns1 effector domain-like Superfamily: Ns1 effector domain-like Family: Ns1 effector domain-like
75	c2m0nA_	Alignment	not modelled	8.2	17	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of a duf3349 annotated protein from mycobacterium2 abscessus, mab_3403c. seattle structural genomics center for3 infectious disease target myaba.17112.a.a2
76	d1c3ha_	Alignment	not modelled	8.1	22	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
77	d1vhwa_	Alignment	not modelled	8.0	17	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
78	d3bgsa1	Alignment	not modelled	7.9	19	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
						PDB header: transferase

79	c3ggsA_	Alignment	not modelled	7.8	19	Chain: A; PDB Molecule: purine nucleoside phosphorylase; PDBTitle: human purine nucleoside phosphorylase double mutant e201q,n243d2 complexed with 2-fluoro-2'-deoxyadenosine
80	c3d6rA_	Alignment	not modelled	7.5	29	PDB header: viral protein Chain: A; PDB Molecule: non-structural protein 1; PDBTitle: structure of an avian influenza a virus ns1 protein2 effector domain
81	d2v4ja2	Alignment	not modelled	6.9	34	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: DsrA/DsrB N-terminal-domain-like
82	c4d98A_	Alignment	not modelled	6.9	17	PDB header: transferase Chain: A; PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of the hexameric purine nucleoside phosphorylase2 from bacillus subtilis in space group h32 at ph 7.5
83	d2j5wa4	Alignment	not modelled	6.9	25	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
84	c2csdB_	Alignment	not modelled	6.8	19	PDB header: isomerase Chain: B; PDB Molecule: topoisomerase v; PDBTitle: crystal structure of topoisomerase v (61 kda fragment)
85	c2mpvA_	Alignment	not modelled	6.6	26	PDB header: protein binding Chain: A; PDB Molecule: major fimbrial subunit of aggregative adherence fimbria ii PDBTitle: structural insight into host recognition and biofilm formation by2 aggregative adherence fimbriae of enteroaggregative esherichia coli
86	d1pk6c_	Alignment	not modelled	6.4	21	Fold: TNF-like Superfamily: TNF-like Family: TNF-like
87	c1r21A_	Alignment	not modelled	6.4	17	PDB header: cell cycle Chain: A; PDB Molecule: antigen ki-67; PDBTitle: solution structure of human ki67 fha domain
88	c3bsfB_	Alignment	not modelled	6.3	13	PDB header: hydrolase Chain: B; PDB Molecule: at4g34840; PDBTitle: crystal structure of the mta/sah nucleosidase
89	c4l8jA_	Alignment	not modelled	6.3	17	PDB header: transport protein Chain: A; PDB Molecule: putative efflux transporter; PDBTitle: crystal structure of a putative efflux transporter (bacegg_01895) from2 bacteroides eggerthii dsm 20697 at 2.06 a resolution
90	d2j5wa3	Alignment	not modelled	6.3	25	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
91	d1odka_	Alignment	not modelled	6.2	24	Fold: Phosphorylase/hydrolase-like Superfamily: Purine and uridine phosphorylases Family: Purine and uridine phosphorylases
92	c3pbiA_	Alignment	not modelled	6.1	22	PDB header: hydrolase Chain: A; PDB Molecule: invasion protein; PDBTitle: structure of the peptidoglycan hydrolase ripb (rv1478) from2 mycobacterium tuberculosis at 1.6 resolution
93	d2f9ha1	Alignment	not modelled	6.1	18	Fold: PTSIIA/GutA-like Superfamily: PTSIIA/GutA-like Family: PTSIIA/GutA-like
94	c4kdwA_	Alignment	not modelled	6.1	22	PDB header: cell adhesion Chain: A; PDB Molecule: antifreeze protein; PDBTitle: crystal structure of a bacterial immunoglobulin-like domain from the2 m. primoryensis ice-binding adhesin
95	d2j5wa1	Alignment	not modelled	6.1	20	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
96	c4kn5A_	Alignment	not modelled	6.0	19	PDB header: hydrolase Chain: A; PDB Molecule: methylthioadenosine nucleosidase; PDBTitle: crystal structure of a putative methylthioadenosine nucleosidase from2 weissella paramesenteroides atcc 33313 (target nysgrc-029342)
97	d1sdda1	Alignment	not modelled	6.0	26	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
98	d2j01h2	Alignment	not modelled	5.9	14	Fold: Ribosomal protein L6 Superfamily: Ribosomal protein L6 Family: Ribosomal protein L6
99	c5mx6C_	Alignment	not modelled	5.8	12	PDB header: transferase Chain: C; PDB Molecule: purine nucleoside phosphorylase deo-type; PDBTitle: crystal structure of h. pylori purine nucleoside phosphorylase from2 clinical isolate hppnp-2