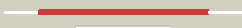























Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1276c_(-)_1425444_1425920
Date	Wed Jul 31 22:05:37 BST 2019
Unique Job ID	3b355d2fb53410cf

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4hbzA_	 Alignment		100.0	44	PDB header: hydrolase, isomerase Chain: A: PDB Molecule: putative phosphohistidine phosphatase, sixa; PDBTitle: the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartita.
2	c2rf1B_	 Alignment		100.0	32	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
3	c3f2iD_	 Alignment		100.0	20	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: alr0221 protein; PDBTitle: crystal structure of the alr0221 protein from nostoc, northeast2 structural genomics consortium target nsr422.
4	c1ujcA_	 Alignment		100.0	28	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
5	c3mxoB_	 Alignment		100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgam5, mitochondrial; PDBTitle: crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
6	c3d4iD_	 Alignment		100.0	27	PDB header: hydrolase Chain: D: PDB Molecule: sts-2 protein; PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2
7	d1e58a_	 Alignment		100.0	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
8	c3fjyB_	 Alignment		100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
9	c3c7tB_	 Alignment		100.0	23	PDB header: hydrolase Chain: B: PDB Molecule: ecdysteroid-phosphate phosphatase; PDBTitle: crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
10	c5gg7A_	 Alignment		100.0	17	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, nudix family protein; PDBTitle: crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
11	c2ikqA_	 Alignment		100.0	27	PDB header: signaling protein, immune system Chain: A: PDB Molecule: suppressor of t-cell receptor signaling 1; PDBTitle: crystal structure of mouse sts-1 pgm domain in complex with phosphate

12	c1yxjD_	Alignment		99.9	26	PDB header: isomerase Chain: D: PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
13	d2hhja1	Alignment		99.9	29	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
14	c4embD_	Alignment		99.9	26	PDB header: isomerase Chain: D: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpma from borrelia2 burgdorferi b31
15	d1riia_	Alignment		99.9	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
16	c4pz9B_	Alignment		99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: glucosyl-3-phosphoglycerate phosphatase; PDBTitle: the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c
17	c3eznB_	Alignment		99.9	25	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
18	c5um0A_	Alignment		99.9	28	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of 2,3-bisphosphoglycerate-dependent2 phosphoglycerate mutase from neisseria gonorrhoeae
19	d1qhfa_	Alignment		99.9	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
20	c2a6pA_	Alignment		99.9	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: possible phosphoglycerate mutase gpm2; PDBTitle: structure solution to 2.2 angstrom and functional characterisation of2 the open reading frame rv3214 from mycobacterium tuberculosis
21	c5vveA_	Alignment	not modelled	99.9	26	PDB header: isomerase Chain: A: PDB Molecule: phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from naegleria fowleri
22	d1xq9a_	Alignment	not modelled	99.9	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
23	c2yn0A_	Alignment	not modelled	99.9	18	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 55 kda subunit; PDBTitle: tau55 histidine phosphatase domain
24	d1fzta_	Alignment	not modelled	99.9	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
25	c2yn2A_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ynl108c; PDBTitle: huf protein - paralogue of the tau55 histidine phosphatase domain
26	c3ll4B_	Alignment	not modelled	99.9	21	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
27	c3d8hB_	Alignment	not modelled	99.9	27	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
28	c3f3kA_	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
						Fold: Phosphoglycerate mutase-like

29	d3pgma_	Alignment	not modelled	99.9	25	Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
30	c2qniA_	Alignment	not modelled	99.9	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu0299; PDBTitle: crystal structure of uncharacterized protein atu0299
31	d1bifa2	Alignment	not modelled	99.9	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
32	c5zkkA_	Alignment	not modelled	99.9	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphoglycerate mutase family protein, putative; PDBTitle: crystal structure of phosphoserine phosphatase from entamoeba2 histolytica
33	c4eo9A_	Alignment	not modelled	99.9	25	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
34	c1k6mA_	Alignment	not modelled	99.9	21	PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2- PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase
35	c2i1vB_	Alignment	not modelled	99.9	19	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6- PDBTitle: crystal structure of pkfb3 in complex with adp and2 fructose-2,6-bisphosphate
36	d1k6ma2	Alignment	not modelled	99.9	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
37	d1tipa_	Alignment	not modelled	99.9	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
38	c3dcyA_	Alignment	not modelled	99.9	21	PDB header: apoptosis regulator Chain: A: PDB Molecule: regulator protein; PDBTitle: crystal structure a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.
39	c4ij5B_	Alignment	not modelled	99.9	19	PDB header: hydrolase Chain: B: PDB Molecule: phosphoserine phosphatase 1; PDBTitle: crystal structure of a novel-type phosphoserine phosphatase from2 <i>hydrogenobacter thermophilus</i> tk-6
40	c1bifA_	Alignment	not modelled	99.9	18	PDB header: bifunctional enzyme Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; PDBTitle: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
41	c3r7aA_	Alignment	not modelled	99.9	23	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. Sterne
42	c3e9eB_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074; PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio
43	c6e4bC_	Alignment	not modelled	99.9	26	PDB header: hydrolase Chain: C: PDB Molecule: adenosylcobalamin/alpha-ribazole phosphatase; PDBTitle: the crystal structure of a putative alpha-ribazole-5'-p phosphatase2 from escherichia coli str. k-12 substr. mg1655
44	d1h2ea_	Alignment	not modelled	99.9	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
45	c3higB_	Alignment	not modelled	99.9	16	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-ribazole-5'-phosphate phosphatase cobc; PDBTitle: crystal structure of putative alpha-ribazole-5'-phosphate phosphatase2 cobc from vibrio parahaemolyticus
46	c3eozB_	Alignment	not modelled	99.9	25	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
47	d1v37a_	Alignment	not modelled	99.9	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
48	c2glcA_	Alignment	not modelled	97.3	23	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: structure of francisella tularensis histidine acid phosphatase bound2 to orthovanadate
49	c5cdhE_	Alignment	not modelled	97.0	18	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: major acid phosphatase; PDBTitle: structure of legionella pneumophila histidine acid phosphatase2 complexed with I(+)-tartrate
50	d1nd6a_	Alignment	not modelled	97.0	15	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
51	c4arvB_	Alignment	not modelled	96.7	23	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: yersinia kristensenii phytase apo form
52	c2wniC_	Alignment	not modelled	96.5	22	PDB header: hydrolase Chain: C: PDB Molecule: 3-phytase; PDBTitle: crystal structure analysis of klebsiella sp asr1 phytase
53	d1dkla_	Alignment	not modelled	96.4	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase

54	d1nt4a_	Alignment	not modelled	96.3	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
55	d1rpa_	Alignment	not modelled	96.2	11	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
56	d1ihpa_	Alignment	not modelled	96.0	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
57	c4fdtB_	Alignment	not modelled	96.0	16	PDB header: hydrolase Chain: B: PDB Molecule: putative multiple inositol polyphosphate histidine PDBTitle: crystal structure of a multiple inositol polyphosphate phosphatase
58	c4jodA_	Alignment	not modelled	95.9	16	PDB header: hydrolase Chain: A: PDB Molecule: lysophosphatidic acid phosphatase type 6; PDBTitle: crystal structure of human lysophosphatidic acid phosphatase type 62 complexed with tris
59	c3zhcB_	Alignment	not modelled	95.8	32	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: structure of the phytase from citrobacter braakii at 2.3 angstrom2 resolution.
60	d1qwoa_	Alignment	not modelled	95.8	18	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
61	c4aruA_	Alignment	not modelled	95.3	26	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: hafnia alvei phytase in complex with tartrate
62	d1qfxa_	Alignment	not modelled	95.1	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
63	c2qfiB_	Alignment	not modelled	94.0	18	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castellii at 2.3 a
64	c3zqjF_	Alignment	not modelled	52.6	17	PDB header: dna binding protein Chain: F: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
65	d1zpd2	Alignment	not modelled	40.6	9	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
66	c3rfuC_	Alignment	not modelled	31.8	9	PDB header: hydrolase, membrane protein Chain: C: PDB Molecule: copper efflux atpase; PDBTitle: crystal structure of a copper-transporting pib-type atpase
67	c1f2uD_	Alignment	not modelled	25.0	15	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
68	d1su7a_	Alignment	not modelled	22.6	20	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Carbon monoxide dehydrogenase
69	c1jqkE_	Alignment	not modelled	21.5	24	PDB header: oxidoreductase Chain: E: PDB Molecule: carbon monoxide dehydrogenase; PDBTitle: crystal structure of carbon monoxide dehydrogenase from2 rhodospirillum rubrum
70	d1jqka_	Alignment	not modelled	21.5	24	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Carbon monoxide dehydrogenase
71	c2ywtA_	Alignment	not modelled	21.0	14	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
72	d1oaoa_	Alignment	not modelled	20.5	20	Fold: Prismane protein-like Superfamily: Prismane protein-like Family: Carbon monoxide dehydrogenase
73	c5j21C_	Alignment	not modelled	19.8	17	PDB header: hydrolase Chain: C: PDB Molecule: bifunctional oligoribonuclease and pap phosphatase nrna; PDBTitle: structure of bacillus nanornase a (wt)
74	c3pihA_	Alignment	not modelled	18.2	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
75	c2w93A_	Alignment	not modelled	18.0	9	PDB header: lyase Chain: A: PDB Molecule: pyruvate decarboxylase isozyme 1; PDBTitle: crystal structure of the saccharomyces cerevisiae pyruvate2 decarboxylase variant e477q in complex with the surrogate pyruvamide
76	c3zqjC_	Alignment	not modelled	15.8	23	PDB header: dna binding protein Chain: C: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
77	c5xu1A_	Alignment	not modelled	15.2	16	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of a non-canonical abc transporter from streptococcus2 pneumoniae r6
78	d2fy8a1	Alignment	not modelled	14.0	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
79	c5xeiA_	Alignment	not modelled	13.1	12	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

80	c3lkIB_	Alignment	not modelled	13.1	12	PDB header: transport protein Chain: B: PDB Molecule: antisigma-factor antagonist stas; PDBTitle: crystal structure of the c-terminal domain of anti-sigma factor2 antagonist stas from rhodobacter sphaeroides
81	c2pcjB_	Alignment	not modelled	12.7	16	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein Iold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
82	c3ux8A_	Alignment	not modelled	12.4	32	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc, a subunit; PDBTitle: crystal structure of uvra
83	c6b6xA_	Alignment	not modelled	11.5	23	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase; PDBTitle: crystal structure of desulfovibrio vulgaris carbon monoxide2 dehydrogenase, dithionite-reduced (protein batch 2), canonical c-3 cluster
84	c5mrwF_	Alignment	not modelled	11.3	16	PDB header: hydrolase Chain: F: PDB Molecule: potassium-transporting atpase atp-binding subunit; PDBTitle: structure of the kdpfabc complex
85	d1we3a2	Alignment	not modelled	11.2	11	Fold: The "swivelling" beta/beta/alpha domain Superfamily: GroEL apical domain-like Family: GroEL-like chaperone, apical domain
86	d1chda_	Alignment	not modelled	11.1	17	Fold: Methylesterase CheB, C-terminal domain Superfamily: Methylesterase CheB, C-terminal domain Family: Methylesterase CheB, C-terminal domain
87	c3cf4A_	Alignment	not modelled	11.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
88	c2vbiF_	Alignment	not modelled	10.8	11	PDB header: lyase Chain: F: PDB Molecule: pyruvate decarboxylase; PDBTitle: holostructure of pyruvate decarboxylase from acetobacter pasteurianus
89	d3b48a1	Alignment	not modelled	10.6	17	Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: DhaM-like
90	d1ovma2	Alignment	not modelled	10.4	11	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase Pyr module
91	d1b0ua_	Alignment	not modelled	10.3	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
92	c1ovmC_	Alignment	not modelled	9.8	11	PDB header: lyase Chain: C: PDB Molecule: indole-3-pyruvate decarboxylase; PDBTitle: crystal structure of indolepyruvate decarboxylase from2 enterobacter cloacae
93	c6n9IA_	Alignment	not modelled	9.8	23	PDB header: dna binding protein Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: crystal structure of t. maritima uvra d117-399 with adp
94	c3gdwA_	Alignment	not modelled	9.4	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sigma-54 interaction domain protein; PDBTitle: crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
95	c4miyB_	Alignment	not modelled	9.2	10	PDB header: oxidoreductase Chain: B: PDB Molecule: inositol 2-dehydrogenase/d-chiro-inositol 3-dehydrogenase; PDBTitle: crystal structure of myo-inositol dehydrogenase from lactobacillus2 casei in complex with nad and myo-inositol
96	c6elqA_	Alignment	not modelled	9.1	20	PDB header: oxidoreductase Chain: A: PDB Molecule: carbon monoxide dehydrogenase; PDBTitle: carbon monoxide dehydrogenase iv from carboxydotherrmus2 hydrogenoformans
97	c5cviB_	Alignment	not modelled	9.0	20	PDB header: transcription regulator Chain: B: PDB Molecule: slor; PDBTitle: structure of the manganese regulator slor
98	c5tf3A_	Alignment	not modelled	9.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: putative membrane protein; PDBTitle: crystal structure of protein of unknown function ypo2564 from yersinia2 pestis
99	c5e68A_	Alignment	not modelled	8.9	26	PDB header: lyase Chain: A: PDB Molecule: s-ribosylhomocysteine lyase; PDBTitle: high resolution crystal structure of luxs - quorum sensor molecular2 complex from salmonella typhi at 1.58 angstroms