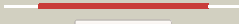



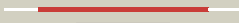




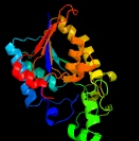














Phyre2

Email mdejesus@rockefeller.edu
 Description RVBD0489 (gpm1)_578429_579178
 Date Fri Jul 26 01:50:03 BST 2019
 Unique Job ID 9ec909f54ecb32b8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1riia_	 Alignment		100.0	100	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
2	d1e58a_	 Alignment		100.0	48	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
3	d2hhja1	 Alignment		100.0	42	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
4	c1yxjD_	 Alignment		100.0	46	PDB header: isomerase, hydrolase Chain: D: PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
5	c5vveA_	 Alignment		100.0	49	PDB header: isomerase Chain: A: PDB Molecule: phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from naegleria fowleri
6	c4eo9A_	 Alignment		100.0	88	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
7	d1qhfA_	 Alignment		100.0	64	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
8	d1xq9a_	 Alignment		100.0	50	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
9	c4embD_	 Alignment		100.0	48	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
10	c5um0A_	 Alignment		100.0	48	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
11	c3eznB_	 Alignment		100.0	57	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b

12	c3d8hB_	Alignment		100.0	46	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
13	d3pgma_	Alignment		100.0	61	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
14	d1fzta_	Alignment		100.0	44	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
15	c2i1vB_	Alignment		100.0	28	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
16	c1k6mA_	Alignment		100.0	28	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
17	c3ll4B_	Alignment		100.0	23	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
18	c1bifA_	Alignment		100.0	25	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
19	c3f3kA_	Alignment		100.0	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
20	d1bifa2	Alignment		100.0	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
21	d1k6ma2	Alignment	not modelled	100.0	28	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
22	c3r7aA_	Alignment	not modelled	100.0	22	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. Sterne
23	c3dcyA_	Alignment	not modelled	100.0	27	PDB header: apoptosis regulator Chain: A: PDB Molecule: regulator protein; PDBTitle: crystal structure a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.
24	c4ij5B_	Alignment	not modelled	100.0	23	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
25	c2a6pA_	Alignment	not modelled	100.0	28	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
26	c6e4bC_	Alignment	not modelled	100.0	22	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
27	c2ikqA_	Alignment	not modelled	100.0	21	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
28	c1n7pB_	Alignment	not modelled	100.0	29	PDB header: hydrolase Chain: B: PDB Molecule: glucosyl-3-phosphoglycerate phosphatase;

28	c4p2zB	Alignment	not modelled	100.0	29	PDBTitle: the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c
29	c3d4iD	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: D: PDB Molecule: sts-2 protein; PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2
30	c2yn0A	Alignment	not modelled	100.0	18	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 55 kda subunit; PDBTitle: tau55 histidine phosphatase domain
31	c5zkA	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: phosphoglycerate mutase family protein, putative; PDBTitle: crystal structure of phosphoserine phosphatase from entamoeba2 histolytica
32	d1h2ea	Alignment	not modelled	100.0	29	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
33	c2yn2A	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ynl108c; PDBTitle: huf protein - paralogue of the tau55 histidine phosphatase domain
34	d1tipa	Alignment	not modelled	100.0	28	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
35	c3e9eB	Alignment	not modelled	100.0	27	PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074; PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio
36	c3c7tB	Alignment	not modelled	100.0	22	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
37	c3h9gB	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: B: PDB Molecule: putative alpha-ribose-5'-phosphate phosphatase cobc; PDBTitle: crystal structure of putative alpha-ribose-5'-phosphate phosphatase2 cobc from vibrio parahaemolyticus
38	c2qniA	Alignment	not modelled	100.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu0299; PDBTitle: crystal structure of uncharacterized protein atu0299
39	c3mxoB	Alignment	not modelled	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)
40	d1v37a	Alignment	not modelled	100.0	35	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
41	c3eozB	Alignment	not modelled	100.0	22	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
42	c1ujcA	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
43	c2rf1B	Alignment	not modelled	100.0	23	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
44	c3f2iD	Alignment	not modelled	99.9	26	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.
45	c5gg7A	Alignment	not modelled	99.9	14	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)
46	c4hbzA	Alignment	not modelled	99.9	25	PDB header: hydrolase, isomerase Chain: A: PDB Molecule: putative phosphohistidine phosphatase, sixa; PDBTitle: the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartita.
47	c3fjyB	Alignment	not modelled	99.9	25	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
48	c2glcA	Alignment	not modelled	98.6	16	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: structure of francisella tularensis histidine acid phosphatase bound2 to orthovanadate
49	d1nd6a	Alignment	not modelled	98.5	16	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
50	c5cdhE	Alignment	not modelled	98.3	15	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: major acid phosphatase; PDBTitle: structure of legionella pneumophila histidine acid phosphatase2 complexed with l(+)-tartrate
51	c4jodA	Alignment	not modelled	98.3	20	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
52	d1rpaA	Alignment	not modelled	98.0	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
53	c2wniC	Alignment	not modelled	97.7	26	PDB header: hydrolase Chain: C: PDB Molecule: 3-phytase;

						PDBTitle: crystal structure analysis of klebsiella sp asr1 phytase
54	c3zhcB	Alignment	not modelled	97.6	17	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: structure of the phytase from citrobacter braakii at 2.3 angstrom2 resolution.
55	c4arvB	Alignment	not modelled	97.6	20	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: yersinia kristensenii phytase apo form
56	d1qwoa	Alignment	not modelled	97.6	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
57	d1dkla	Alignment	not modelled	97.6	14	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
58	d1ihpa	Alignment	not modelled	97.6	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
59	d1qfxa	Alignment	not modelled	97.5	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
60	c4aruA	Alignment	not modelled	97.5	17	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: hafnia alvei phytase in complex with tartrate
61	d1nt4a	Alignment	not modelled	97.5	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
62	c2gfiB	Alignment	not modelled	97.4	12	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castelli at 2.3 a
63	c4fdtB	Alignment	not modelled	96.7	13	PDB header: hydrolase Chain: B: PDB Molecule: putative multiple inositol polyphosphate histidine PDBTitle: crystal structure of a multiple inositol polyphosphate phosphatase
64	c5oltA	Alignment	not modelled	29.3	30	PDB header: transferase Chain: A: PDB Molecule: cellulose biosynthesis protein bcsg; PDBTitle: crystal structure of the extramembrane domain of the cellulose2 biosynthetic protein bcsg from salmonella typhimurium
65	c2olkD	Alignment	not modelled	29.3	18	PDB header: hydrolase Chain: D: PDB Molecule: amino acid abc transporter; PDBTitle: abc protein artp in complex with adp-beta-s
66	c4hluC	Alignment	not modelled	27.9	18	PDB header: hydrolase Chain: C: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: structure of the ecfa-a' heterodimer bound to adp
67	c3zqiC	Alignment	not modelled	26.9	18	PDB header: dna binding protein Chain: C: PDB Molecule: uvrabc system protein a; PDBTitle: mycobacterium tuberculosis uvra
68	c4rkkA	Alignment	not modelled	25.7	12	PDB header: hydrolase Chain: A: PDB Molecule: laforin; PDBTitle: structure of a product bound phosphatase
69	c5x40A	Alignment	not modelled	24.2	15	PDB header: transport protein Chain: A: PDB Molecule: cobalt abc transporter atp-binding protein; PDBTitle: structure of a cbio dimer bound with amppcp
70	c5d3mF	Alignment	not modelled	23.4	21	PDB header: transport protein Chain: F: PDB Molecule: energy-coupling factor transporter atp-binding protein PDBTitle: folate ecf transporter: amppnp bound state
71	c3uuuA	Alignment	not modelled	23.3	14	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
72	c5gw8A	Alignment	not modelled	22.9	14	PDB header: hydrolase Chain: A: PDB Molecule: hypothetical secretory lipase (family 3); PDBTitle: crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
73	c4d7aA	Alignment	not modelled	22.7	9	PDB header: ligase Chain: A: PDB Molecule: trna threonylcarbamoyladenine dehydratase; PDBTitle: crystal structure of e. coli trna n6-threonylcarbamoyladenine2 dehydratase, tcda, in complex with amp at 1.801 angstroem3 resolution
74	d1ji0a	Alignment	not modelled	22.0	21	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
75	c2yz2B	Alignment	not modelled	21.9	21	PDB header: hydrolase Chain: B: PDB Molecule: putative abc transporter atp-binding protein tm_0222; PDBTitle: crystal structure of the abc transporter in the cobalt transport2 system
76	c3j16B	Alignment	not modelled	21.3	21	PDB header: ribosome Chain: B: PDB Molecule: rli1p; PDBTitle: models of ribosome-bound dom34p and rli1p and their ribosomal binding2 partners
77	c5x7kB	Alignment	not modelled	21.2	18	PDB header: transport protein Chain: B: PDB Molecule: lipase b; PDBTitle: crystal structure of the nucleotide-binding domain (nbd) of lipb, a2 abc transporter subunit of a type i secretion system
78	c2d2fA	Alignment	not modelled	20.8	12	PDB header: protein binding Chain: A: PDB Molecule: sufc protein; PDBTitle: crystal structure of atypical cytoplasmic abc-atpase sufcd from thermus2 thermophilus hb8
						PDB header: hydrolase/dna

79	c3pihA_	Alignment	not modelled	20.8	21	Chain: A: PDB Molecule: uvrabc system protein a; PDBTitle: t. maritima uvra in complex with fluorescein-modified dna
80	d1vp1a_	Alignment	not modelled	20.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
81	c2pcjB_	Alignment	not modelled	20.7	15	PDB header: hydrolase Chain: B: PDB Molecule: lipoprotein-releasing system atp-binding protein lold; PDBTitle: crystal structure of abc transporter (aq_297) from aquifex aeolicus2 vf5
82	c5xu1A_	Alignment	not modelled	20.6	21	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
83	c3bk7A_	Alignment	not modelled	20.4	30	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
84	c1yqtA_	Alignment	not modelled	20.1	29	PDB header: hydrolyase/translation Chain: A: PDB Molecule: rnase I inhibitor; PDBTitle: rnase-I inhibitor
85	c4rvca_	Alignment	not modelled	19.9	12	PDB header: transport protein Chain: A: PDB Molecule: abc transporter atp-binding protein; PDBTitle: structure of atp binding subunit of abc transporter
86	c4p31B_	Alignment	not modelled	19.7	27	PDB header: hydrolase Chain: B: PDB Molecule: lipopolysaccharide export system atp-binding protein lptb; PDBTitle: crystal structure of a selenomethionine derivative of e. coli lptb in2 complex with adp-magnesium
87	c6dc6A_	Alignment	not modelled	19.6	17	PDB header: signaling protein/ligase Chain: A: PDB Molecule: ubiquitin-like modifier-activating enzyme 1; PDBTitle: crystal structure of human ubiquitin activating enzyme e1 (uba1) in2 complex with ubiquitin
88	d1b0ua_	Alignment	not modelled	19.5	18	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
89	c1f2uD_	Alignment	not modelled	18.8	15	PDB header: replication Chain: D: PDB Molecule: rad50 abc-atpase; PDBTitle: crystal structure of rad50 abc-atpase
90	c3ux8A_	Alignment	not modelled	18.6	28	PDB header: dna binding protein Chain: A: PDB Molecule: excinuclease abc, a subunit; PDBTitle: crystal structure of uvra
91	d1tiaa_	Alignment	not modelled	17.8	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
92	d1vjea_	Alignment	not modelled	17.7	14	Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
93	c5xk2A_	Alignment	not modelled	17.4	14	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
94	c5e68A_	Alignment	not modelled	16.9	19	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
95	c3dhwC_	Alignment	not modelled	16.6	18	PDB header: membrane protein/hydrolase Chain: C: PDB Molecule: methionine import atp-binding protein metn; PDBTitle: crystal structure of methionine importer metni
96	c5ws4A_	Alignment	not modelled	16.4	15	PDB header: membrane protein Chain: A: PDB Molecule: macrolide export atp-binding/permease protein macb; PDBTitle: crystal structure of tripartite-type abc transporter macb from2 acinetobacter baumannii
97	d1p9oa_	Alignment	not modelled	16.1	18	Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
98	c3nzeB_	Alignment	not modelled	15.9	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 aureusens tc1.
99	d1m3ga_	Alignment	not modelled	15.7	13	Fold: (Phosphotyrosine protein) phosphatases II Superfamily: (Phosphotyrosine protein) phosphatases II Family: Dual specificity phosphatase-like