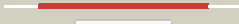



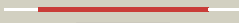





















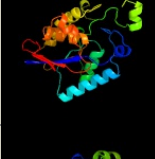
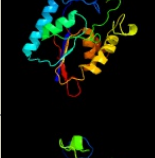
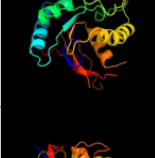

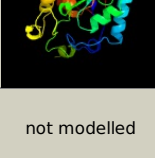


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3214_(gpm2)_3591643_3592254
Date	Thu Aug 8 16:20:41 BST 2019
Unique Job ID	dc00c72006735fa4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2a6pA_	 Alignment		100.0	100	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
2	c4ij5B_	 Alignment		100.0	26	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
3	c5zkKA_	 Alignment		100.0	25	PDB header: hydrolase Chain: A: PDB Molecule: phosphoglycerate mutase family protein, putative; PDBTitle: crystal structure of phosphoserine phosphatase from entamoeba2 histolytica
4	c4embD_	 Alignment		100.0	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
5	d1h2ea_	 Alignment		100.0	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
6	d1e58a_	 Alignment		100.0	27	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
7	d1xq9a_	 Alignment		100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
8	c1vjxD_	 Alignment		100.0	23	PDB header: isomerase, hydrolase Chain: D: PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
9	c6e4bC_	 Alignment		100.0	23	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
10	d1riia_	 Alignment		100.0	31	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
11	c3r7aA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. Sterne

12	c5vveA_	Alignment		100.0	24	PDB header: isomerase Chain: A: PDB Molecule: phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from naegleria fowleri
13	d1qhfa_	Alignment		100.0	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
14	c4pz9B_	Alignment		100.0	32	PDB header: hydrolase Chain: B: PDB Molecule: glucosyl-3-phosphoglycerate phosphatase; PDBTitle: the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c
15	c3eznB_	Alignment		100.0	25	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
16	c3d8hB_	Alignment		100.0	24	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
17	c5um0A_	Alignment		100.0	25	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
18	c2yn0A_	Alignment		100.0	18	PDB header: transcription Chain: A: PDB Molecule: transcription factor tau 55 kda subunit; PDBTitle: tau55 histidine phosphatase domain
19	d1fzta_	Alignment		100.0	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
20	d2hhja1	Alignment		100.0	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
21	c2ilvB_	Alignment	not modelled	100.0	23	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-fructose-2,6-bisphosphate PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
22	c3dcyA_	Alignment	not modelled	100.0	28	PDB header: apoptosis regulator Chain: A: PDB Molecule: regulator protein; PDBTitle: crystal structure a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.
23	c4eo9A_	Alignment	not modelled	100.0	31	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
24	c2yn2A_	Alignment	not modelled	100.0	19	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ynl108c; PDBTitle: huf protein - paralogue of the tau55 histidine phosphatase domain
25	c3f3ka_	Alignment	not modelled	100.0	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from saccharomyces2 cerevisiae.
26	c1k6mA_	Alignment	not modelled	100.0	22	PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphate 2- PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphate
27	c3ll4B_	Alignment	not modelled	100.0	28	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
28	c3e0eB_	Alignment	not modelled	100.0	26	PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074;

28	c3e9eB	Alignment	not modelled	100.0	20	PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
29	d1tipa	Alignment	not modelled	100.0	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
30	d1bifa2	Alignment	not modelled	100.0	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
31	d3pgma	Alignment	not modelled	100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
32	c1bifA	Alignment	not modelled	100.0	23	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
33	c3higB	Alignment	not modelled	100.0	20	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
34	d1k6ma2	Alignment	not modelled	100.0	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
35	c3mxB	Alignment	not modelled	100.0	21	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgam5, mitochondrial; PDBTitle: crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
36	c3d4iD	Alignment	not modelled	100.0	23	PDB header: hydrolase Chain: D: PDB Molecule: sts-2 protein; PDBTitle: crystal structure of the 2h-phosphatase domain of sts-2
37	c2ikqA	Alignment	not modelled	100.0	23	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
38	c2qniA	Alignment	not modelled	100.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein atu0299; PDBTitle: crystal structure of uncharacterized protein atu0299
39	d1v37a	Alignment	not modelled	100.0	28	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
40	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
41	c3eozB	Alignment	not modelled	100.0	19	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	17	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
43	c2rfiB	Alignment	not modelled	100.0	20	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	100.0	15	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	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)
46	c4hbzA	Alignment	not modelled	99.9	24	PDB header: hydrolase, isomerase Chain: A: PDB Molecule: putative phosphohistidine phosphatase, sixa; PDBTitle: the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartitia.
47	c3fjyB	Alignment	not modelled	99.9	12	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	98.2	25	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	98.1	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
50	c5cdhE	Alignment	not modelled	98.1	27	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	d1rpaA	Alignment	not modelled	98.1	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
52	c4jodA	Alignment	not modelled	98.0	25	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
						PDB header: hydrolase

53	c4arvB_	Alignment	not modelled	98.0	24	Chain: B; PDB Molecule: phytase; PDBTitle: yersinia kristensenii phytase apo form
54	d1ihpa_	Alignment	not modelled	97.9	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
55	c3zhcB_	Alignment	not modelled	97.9	24	PDB header: hydrolase Chain: B; PDB Molecule: phytase; PDBTitle: structure of the phytase from citrobacter braakii at 2.3 angstrom2 resolution.
56	c2wniC_	Alignment	not modelled	97.9	23	PDB header: hydrolase Chain: C; PDB Molecule: 3-phytase; PDBTitle: crystal structure analysis of klebsiella sp asr1 phytase
57	d1qwoa_	Alignment	not modelled	97.9	14	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
58	c4aruA_	Alignment	not modelled	97.8	25	PDB header: hydrolase Chain: A; PDB Molecule: histidine acid phosphatase; PDBTitle: hafnia alvei phytase in complex with tartrate
59	d1dkla_	Alignment	not modelled	97.8	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
60	d1nt4a_	Alignment	not modelled	97.8	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
61	c4fdtB_	Alignment	not modelled	97.7	21	PDB header: hydrolase Chain: B; PDB Molecule: putative multiple inositol polyphosphate histidine PDBTitle: crystal structure of a multiple inositol polyphosphate phosphatase
62	d1qfxa_	Alignment	not modelled	97.6	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
63	c2gfiB_	Alignment	not modelled	97.4	29	PDB header: hydrolase Chain: B; PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castellii at 2.3 a
64	c3uuuA_	Alignment	not modelled	71.6	14	PDB header: hydrolase Chain: A; PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
65	c5gw8A_	Alignment	not modelled	64.8	12	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
66	d1tiaa_	Alignment	not modelled	61.9	14	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
67	c5xk2A_	Alignment	not modelled	59.3	16	PDB header: hydrolase Chain: A; PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
68	d1tiba_	Alignment	not modelled	57.3	22	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
69	c3o0dF_	Alignment	not modelled	53.4	7	PDB header: hydrolase Chain: F; PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
70	c3ngmB_	Alignment	not modelled	52.0	24	PDB header: hydrolase Chain: B; PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
71	d3tgla_	Alignment	not modelled	42.6	15	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
72	c2jfnA_	Alignment	not modelled	38.0	16	PDB header: isomerase Chain: A; PDB Molecule: glutamate racemase; PDBTitle: crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
73	c3g7nA_	Alignment	not modelled	34.5	15	PDB header: hydrolase Chain: A; PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
74	d1uwca_	Alignment	not modelled	33.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
75	c3ds8A_	Alignment	not modelled	30.6	8	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: lin2722 protein; PDBTitle: the crysatl structure of the gene lin2722 products from listeria2 innocua
76	d1l1sa_	Alignment	not modelled	30.4	12	Fold: DsrEFH-like Superfamily: DsrEFH-like Family: DsrEF-like
77	c3lp5A_	Alignment	not modelled	28.4	4	PDB header: hydrolase Chain: A; PDB Molecule: putative cell surface hydrolase; PDBTitle: the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
78	c5e68A_	Alignment	not modelled	27.1	24	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
79	c3lfhF_	Alignment	not modelled	26.4	25	PDB header: transferase Chain: F; PDB Molecule: phosphotransferase system, mannose/fructose-specific PDBTitle: crystal structure of manxa from thermoanaerobacter

					tengcongensis
80	d1lgva_	Alignment	not modelled	25.9	17 Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
81	c2pd2A_	Alignment	not modelled	24.8	16 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein st0148; PDBTitle: crystal structure of (st0148) conserved hypothetical from sulfobolus2 tokodaii strain7
82	c6qppA_	Alignment	not modelled	20.9	15 PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
83	d1j3wa_	Alignment	not modelled	20.7	11 Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
84	d1j98a_	Alignment	not modelled	20.0	24 Fold: LuxS/MPP-like metallohydrolase Superfamily: LuxS/MPP-like metallohydrolase Family: Autoinducer-2 production protein LuxS
85	c2zyiB_	Alignment	not modelled	19.2	18 PDB header: hydrolase Chain: B: PDB Molecule: lipase, putative; PDBTitle: a. fulgidus lipase with fatty acid fragment and calcium
86	c4r1dA_	Alignment	not modelled	18.1	16 PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tie4-tli4 complex
87	c1zuwA_	Alignment	not modelled	17.7	8 PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase 1; PDBTitle: crystal structure of b.subtilis glutamate racemase (race) with d-glu
88	c3mtqA_	Alignment	not modelled	16.7	26 PDB header: transferase Chain: A: PDB Molecule: putative phosphoenolpyruvate-dependent sugar PDBTitle: crystal structure of a putative phosphoenolpyruvate-dependent sugar2 phosphotransferase system (pts) permease (kpn_04802) from klebsiella3 pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a resolution
89	c3fleB_	Alignment	not modelled	15.4	6 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: se_1780 protein; PDBTitle: se_1780 protein of unknown function from staphylococcus epidermidis.
90	c5ijwA_	Alignment	not modelled	13.4	13 PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction
91	c2oryA_	Alignment	not modelled	13.1	9 PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of m37 lipase
92	d1qgoa_	Alignment	not modelled	12.4	16 Fold: Chelatase-like Superfamily: Chelatase Family: Cobalt chelatase CbiK
93	c2o6lA_	Alignment	not modelled	11.9	20 PDB header: transferase Chain: A: PDB Molecule: udp-glucuronosyltransferase 2b7; PDBTitle: crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
94	c3fiuD_	Alignment	not modelled	11.5	10 PDB header: ligase Chain: D: PDB Molecule: nh(3)-dependent nad(+) synthetase; PDBTitle: structure of nmh synthetase from francisella tularensis
95	c3hbjA_	Alignment	not modelled	11.1	15 PDB header: transferase Chain: A: PDB Molecule: flavonoid 3-o-glucosyltransferase; PDBTitle: structure of ugt78g1 complexed with udp
96	d2vcha1	Alignment	not modelled	11.1	15 Fold: UDP-Glycosyltransferase/glycogen phosphorylase Superfamily: UDP-Glycosyltransferase/glycogen phosphorylase Family: UDPGT-like
97	c4nfbB_	Alignment	not modelled	10.6	15 PDB header: signaling protein Chain: B: PDB Molecule: senescence-associated carboxylesterase 101; PDBTitle: structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
98	d3beda1	Alignment	not modelled	10.0	18 Fold: PTS system fructose IIA component-like Superfamily: PTS system fructose IIA component-like Family: EIIA-man component-like
99	c1j3wb_	Alignment	not modelled	9.8	12 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: giding protein-mglb; PDBTitle: structure of gliding protein-mglb from thermus thermophilus hb8