

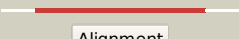

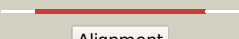











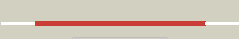







Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3837c_(-)_4311187_4311885
Date	Fri Aug 9 18:20:55 BST 2019
Unique Job ID	a84fb1c567f18069

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ij5B_	 Alignment		100.0	25	PDB header: hydrolase Chain: B; PDB Molecule: phosphoserine phosphatase 1; PDBTitle: crystal structure of a novel-type phosphoserine phosphatase from <i>hydrogenobacter thermophilus</i> tk-6
2	d1e58a_	 Alignment		100.0	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
3	c5vveA_	 Alignment		100.0	21	PDB header: isomerase Chain: A; PDB Molecule: phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from <i>naegleria fowleri</i>
4	c1k6mA_	 Alignment		100.0	20	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
5	c1bifA_	 Alignment		100.0	20	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
6	d1xq9a_	 Alignment		100.0	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
7	c3f3kA_	 Alignment		100.0	21	PDB header: structural genomics, unknown function Chain: A; PDB Molecule: uncharacterized protein ykr043c; PDBTitle: the structure of uncharacterized protein ykr043c from <i>saccharomyces2 cerevisiae</i> .
8	c4embD_	 Alignment		100.0	21	PDB header: isomerase Chain: D; PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of a phosphoglycerate mutase gpma from <i>borrelia2 burgdorferi</i> b31
9	c1vjxD_	 Alignment		100.0	26	PDB header: isomerase, hydrolase Chain: D; PDB Molecule: phosphoglycerate mutase 1; PDBTitle: crystal structure of human b type phosphoglycerate mutase
10	c4pz9B_	 Alignment		100.0	27	PDB header: hydrolase Chain: B; PDB Molecule: glucosyl-3-phosphoglycerate phosphatase; PDBTitle: the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c
11	c3ll4B_	 Alignment		100.0	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

12	d1fzta_	Alignment		100.0	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
13	d1riia_	Alignment		100.0	25	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
14	d1h2ea_	Alignment		100.0	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
15	d1bifa2	Alignment		100.0	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
16	c2i1vB_	Alignment		100.0	21	PDB header: transferase, hydrolase Chain: B: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6- PDBTitle: crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
17	d1qhfa_	Alignment		100.0	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
18	c5um0A_	Alignment		100.0	21	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	d2hhja1	Alignment		100.0	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
20	c5zkkA_	Alignment		100.0	22	PDB header: hydrolase Chain: A: PDB Molecule: phosphoglycerate mutase family protein, putative; PDBTitle: crystal structure of phosphoserine phosphatase from entamoeba2 histolytica
21	c3eznB_	Alignment	not modelled	100.0	24	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
22	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
23	d1k6ma2	Alignment	not modelled	100.0	20	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
24	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
25	c3e9eB_	Alignment	not modelled	100.0	24	PDB header: hydrolase Chain: B: PDB Molecule: zgc:56074; PDBTitle: structure of full-length h11a mutant form of tigar from danio rerio
26	c3d8hB_	Alignment	not modelled	100.0	23	PDB header: isomerase Chain: B: PDB Molecule: glycolytic phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
27	c4eo9A_	Alignment	not modelled	100.0	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
						PDB header: hydrolase

28	c2yn2A_	Alignment	not modelled	100.0	16	Chain: A: PDB Molecule: uncharacterized protein ynl108c; PDBTitle: huf protein - paralogue of the tau55 histidine phosphatase domain
29	c2a6pA_	Alignment	not modelled	100.0	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: possible phosphoglycerate mutase gpm2; PDBTitle: structure solution to 2.2 angstrom and functional characterisation of 2 the open reading frame rv3214 from mycobacterium tuberculosis
30	c3dcyA_	Alignment	not modelled	100.0	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.
31	d3pgma_	Alignment	not modelled	100.0	22	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
32	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
33	c3r7aA_	Alignment	not modelled	100.0	20	PDB header: transferase Chain: A: PDB Molecule: phosphoglycerate mutase, putative; PDBTitle: crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
34	c2ikqA_	Alignment	not modelled	100.0	16	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
35	d1tipa_	Alignment	not modelled	100.0	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
36	c3higB_	Alignment	not modelled	100.0	15	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
37	c3c7tB_	Alignment	not modelled	100.0	17	PDB header: hydrolase Chain: B: PDB Molecule: ecdysteroid-phosphate phosphatase; PDBTitle: crystal structure of the ecdysone phosphate phosphatase, eppase, from 2 bombyx mori in complex with tungstate
38	c2qniA_	Alignment	not modelled	100.0	16	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	21	PDB header: hydrolase Chain: B: PDB Molecule: serine/threonine-protein phosphatase pgam5, mitochondrial; PDBTitle: crystal structure of human phosphoglycerate mutase family member 52 (pgam5)
40	d1v37a_	Alignment	not modelled	100.0	26	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Cofactor-dependent phosphoglycerate mutase
41	c3eozB_	Alignment	not modelled	100.0	20	PDB header: isomerase Chain: B: PDB Molecule: putative phosphoglycerate mutase; PDBTitle: crystal structure of phosphoglycerate mutase from plasmodium 2 falciparum, pfd0660w
42	c2rfiB_	Alignment	not modelled	100.0	21	PDB header: hydrolase, isomerase Chain: B: PDB Molecule: putative phosphohistidine phosphatase sixa; PDBTitle: crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
43	c1ujcA_	Alignment	not modelled	100.0	18	PDB header: hydrolase Chain: A: PDB Molecule: phosphohistidine phosphatase sixa; PDBTitle: structure of the protein histidine phosphatase sixa2 complexed with tungstate
44	c5gg7A_	Alignment	not modelled	99.9	18	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)
45	c3f2iD_	Alignment	not modelled	99.9	22	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.
46	c4hzbA_	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 from 2 nakamurella multipartita.
47	c3fjyB_	Alignment	not modelled	99.9	18	PDB header: hydrolase Chain: B: PDB Molecule: probable mutt1 protein; PDBTitle: crystal structure of a probable mutt1 protein from bifidobacterium 2 adoloescentis
48	c2gicA_	Alignment	not modelled	97.8	19	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: structure of francisella tularensis histidine acid phosphatase bound 2 to orthovanadate
49	c4aruA_	Alignment	not modelled	97.8	17	PDB header: hydrolase Chain: A: PDB Molecule: histidine acid phosphatase; PDBTitle: hafnia alvei phytase in complex with tartrate
50	c4arvB_	Alignment	not modelled	97.8	14	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: yersinia kristensenii phytase apo form
51	d1rpaa_	Alignment	not modelled	97.8	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
52	d1ihpa_	Alignment	not modelled	97.7	24	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
53	c5cshE_	Alignment	not modelled	97.7	15	PDB header: hydrolase/hydrolase inhibitor Chain: E: PDB Molecule: major acid phosphatase;

53	c3c0nE_	Alignment	not modelled	97.7	19	PDBTitle: structure of legionella pneumophila histidine acid phosphatase2 complexed with l(+)-tartrate
54	d1nd6a_	Alignment	not modelled	97.6	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
55	c2wniC_	Alignment	not modelled	97.6	18	PDB header: hydrolase Chain: C: PDB Molecule: 3-phytase; PDBTitle: crystal structure analysis of klebsiella sp asr1 phytase
56	c4jodA_	Alignment	not modelled	97.5	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
57	d1qwoa_	Alignment	not modelled	97.4	16	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
58	c3zhcB_	Alignment	not modelled	97.4	21	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: structure of the phytase from citrobacter braakii at 2.3 angstrom2 resolution.
59	d1nt4a_	Alignment	not modelled	97.4	19	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
60	d1dkla_	Alignment	not modelled	97.3	21	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
61	d1qfxa_	Alignment	not modelled	97.1	23	Fold: Phosphoglycerate mutase-like Superfamily: Phosphoglycerate mutase-like Family: Histidine acid phosphatase
62	c4fdtB_	Alignment	not modelled	97.1	20	PDB header: hydrolase Chain: B: PDB Molecule: putative multiple inositol polyphosphate histidine PDBTitle: crystal structure of a multiple inositol polyphosphate phosphatase
63	c2gfiB_	Alignment	not modelled	96.7	21	PDB header: hydrolase Chain: B: PDB Molecule: phytase; PDBTitle: crystal structure of the phytase from d. castellii at 2.3 a
64	c4r1dA_	Alignment	not modelled	66.4	15	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the crystal structure of tie4-tii4 complex
65	c3uuuA_	Alignment	not modelled	66.1	21	PDB header: hydrolase Chain: A: PDB Molecule: lip1, secretory lipase (family 3); PDBTitle: crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
66	c5gw8A_	Alignment	not modelled	59.1	21	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
67	c5xk2A_	Alignment	not modelled	59.0	37	PDB header: hydrolase Chain: A: PDB Molecule: diacylglycerol lipase; PDBTitle: crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
68	d3tgla_	Alignment	not modelled	56.5	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
69	d1tiaa_	Alignment	not modelled	54.0	26	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
70	c3o0dF_	Alignment	not modelled	54.0	24	PDB header: hydrolase Chain: F: PDB Molecule: triacylglycerol lipase; PDBTitle: crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
71	d1tiba_	Alignment	not modelled	50.2	17	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
72	c3ngmB_	Alignment	not modelled	48.7	19	PDB header: hydrolase Chain: B: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of lipase from gibberella zeae
73	c3g7nA_	Alignment	not modelled	41.6	23	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
74	c3ecsD_	Alignment	not modelled	37.5	9	PDB header: translation Chain: D: PDB Molecule: translation initiation factor eif-2b subunit alpha; PDBTitle: crystal structure of human eif2b alpha
75	c4zemB_	Alignment	not modelled	36.5	6	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif2b-like protein, PDBTitle: crystal structure of eif2b beta from chaetomium thermophilum
76	c6ezoD_	Alignment	not modelled	36.3	13	PDB header: membrane protein Chain: D: PDB Molecule: translation initiation factor eif-2b subunit beta; PDBTitle: eukaryotic initiation factor eif2b in complex with isrib
77	c6qppA_	Alignment	not modelled	34.9	19	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: rhizomucor miehei lipase propeptide complex, native
78	d1uwca_	Alignment	not modelled	33.0	19	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
79	c5b04B_	Alignment	not modelled	32.2	9	PDB header: translation Chain: B: PDB Molecule: translation initiation factor eif-2b subunit alpha;

						PDBTitle: crystal structure of the eukaryotic translation initiation factor 2b2 from schizosaccharomyces pombe
80	d1gya_	Alignment	not modelled	31.1	21	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Fungal lipases
81	d1jl3a_	Alignment	not modelled	30.1	14	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
82	d2hk6a1	Alignment	not modelled	28.4	10	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase
83	d1dg9a_	Alignment	not modelled	28.3	15	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
84	c4x96B_	Alignment	not modelled	27.6	10	PDB header: transferase Chain: B: PDB Molecule: phosphatidylcholine-sterol acyltransferase; PDBTitle: low resolution crystal structure of lecithin:cholesterol2 acyltransferase (lcat; residues 21-397)
85	c2wmyH_	Alignment	not modelled	24.5	15	PDB header: hydrolase Chain: H: PDB Molecule: putative acid phosphatase wzb; PDBTitle: crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
86	d1vb5a_	Alignment	not modelled	20.7	17	Fold: NagB/RpiA/CoA transferase-like Superfamily: NagB/RpiA/CoA transferase-like Family: lIF2B-like
87	c3a11D_	Alignment	not modelled	19.5	13	PDB header: isomerase Chain: D: PDB Molecule: translation initiation factor eif-2b, delta subunit; PDBTitle: crystal structure of ribose-1,5-bisphosphate isomerase from2 thermococcus kodakaraensis kod1
88	c2fekA_	Alignment	not modelled	19.3	25	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: structure of a protein tyrosine phosphatase
89	d1d1qa_	Alignment	not modelled	18.8	11	Fold: Phosphotyrosine protein phosphatases I-like Superfamily: Phosphotyrosine protein phosphatases I Family: Low-molecular-weight phosphotyrosine protein phosphatases
90	c1u2pA_	Alignment	not modelled	18.6	16	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight protein-tyrosine- PDBTitle: crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
91	c4nfuB_	Alignment	not modelled	18.4	9	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
92	c5z3mB_	Alignment	not modelled	17.8	19	PDB header: hydrolase Chain: B: PDB Molecule: phosphotyrosine protein phosphatase; PDBTitle: crystal structure of low molecular weight phosphotyrosine phosphatase2 (vclmwptp-2) from vibrio choleraeo395
93	c2gi4A_	Alignment	not modelled	17.3	15	PDB header: hydrolase Chain: A: PDB Molecule: possible phosphotyrosine protein phosphatase; PDBTitle: solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
94	c5gotA_	Alignment	not modelled	17.1	15	PDB header: hydrolase Chain: A: PDB Molecule: low molecular weight phosphotyrosine phosphatase family PDBTitle: crystal structure of sp-ptp, low molecular weight protein tyrosine2 phosphatase from streptococcus pyogenes
95	c3nzeB_	Alignment	not modelled	16.9	16	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.
96	c4d74A_	Alignment	not modelled	16.8	20	PDB header: hydrolase Chain: A: PDB Molecule: protein-tyrosine-phosphatase amsi; PDBTitle: 1.57 a crystal structure of erwinia amylovora tyrosine phosphatase2 amsi
97	c4picA_	Alignment	not modelled	16.8	21	PDB header: hydrolase Chain: A: PDB Molecule: arginine phosphatase ywle; PDBTitle: ywle arginine phosphatase from geobacillus stearothermophilus
98	c3mtqA_	Alignment	not modelled	15.8	9	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
99	d2hrca1	Alignment	not modelled	15.6	7	Fold: Chelatase-like Superfamily: Chelatase Family: Ferrochelatase