




















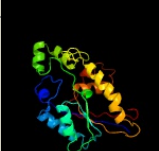








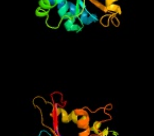


# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0754_(PE_PGRS11)_846162_847916
Date	Fri Jul 26 01:50:33 BST 2019
Unique Job ID	6e60beece722dd7f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4pz9B_</a>	 Alignment		100.0	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> glucosyl-3-phosphoglycerate phosphatase; <b>PDBTitle:</b> the native structure of mycobacterial glucosyl-3-phosphoglycerate2 phosphatase rv2419c
2	<a href="#">c3f3kA_</a>	 Alignment		100.0	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein ykr043c; <b>PDBTitle:</b> the structure of uncharacterized protein ykr043c from <i>saccharomyces2 cerevisiae</i> .
3	<a href="#">c2ikqA_</a>	 Alignment		99.9	20	<b>PDB header:</b> signaling protein, immune system <b>Chain:</b> A; <b>PDB Molecule:</b> suppressor of t-cell receptor signaling 1; <b>PDBTitle:</b> crystal structure of mouse sts-1 pgm domain in complex with phosphate
4	<a href="#">c3r7aA_</a>	 Alignment		99.9	15	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> phosphoglycerate mutase, putative; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from <i>bacillus anthracis2 str. sterne</i>
5	<a href="#">c2yn0A_</a>	 Alignment		99.9	14	<b>PDB header:</b> transcription <b>Chain:</b> A; <b>PDB Molecule:</b> transcription factor tau 55 kda subunit; <b>PDBTitle:</b> tau55 histidine phosphatase domain
6	<a href="#">c4ij5B_</a>	 Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> phosphoserine phosphatase 1; <b>PDBTitle:</b> crystal structure of a novel-type phosphoserine phosphatase from <i>2 hydrogenobacter thermophilus tk-6</i>
7	<a href="#">c3d4iD_</a>	 Alignment		99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> D; <b>PDB Molecule:</b> sts-2 protein; <b>PDBTitle:</b> crystal structure of the 2h-phosphatase domain of sts-2
8	<a href="#">c2qniA_</a>	 Alignment		99.9	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein atu0299; <b>PDBTitle:</b> crystal structure of uncharacterized protein atu0299
9	<a href="#">d1h2ea_</a>	 Alignment		99.9	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
10	<a href="#">c3ll4B_</a>	 Alignment		99.9	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> uncharacterized protein ykr043c; <b>PDBTitle:</b> structure of the h13a mutant of ykr043c in complex with fructose-1,6-2 bisphosphate
11	<a href="#">d1e58a_</a>	 Alignment		99.9	17	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase

12	<a href="#">c5zkkA</a>	Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate mutase family protein, putative; <b>PDBTitle:</b> crystal structure of phosphoserine phosphatase from entamoeba2 histolytica
13	<a href="#">c4embD</a>	Alignment		99.9	18	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of a phosphoglycerate mutase gpmA from borrelia2 burgdorferi b31
14	<a href="#">c3e9eB</a>	Alignment		99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> zgc:56074; <b>PDBTitle:</b> structure of full-length h11a mutant form of tigar from danio rerio
15	<a href="#">d1riia</a>	Alignment		99.9	19	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
16	<a href="#">c1yxjD</a>	Alignment		99.9	16	<b>PDB header:</b> isomerase, hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoglycerate mutase 1; <b>PDBTitle:</b> crystal structure of human b type phosphoglycerate mutase
17	<a href="#">c3dcyA</a>	Alignment		99.9	19	<b>PDB header:</b> apoptosis regulator <b>Chain:</b> A: <b>PDB Molecule:</b> regulator protein; <b>PDBTitle:</b> crystal structure a tp53-induced glycolysis and apoptosis regulator2 protein from homo sapiens.
18	<a href="#">c5vveA</a>	Alignment		99.9	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from naegleria fowleri
19	<a href="#">c2yn2A</a>	Alignment		99.9	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ynl108c; <b>PDBTitle:</b> huf protein - paralogue of the tau55 histidine phosphatase domain
20	<a href="#">d1xq9a</a>	Alignment		99.9	19	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
21	<a href="#">c2i1vB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase <b>PDBTitle:</b> crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
22	<a href="#">c3c7tB</a>	Alignment	not modelled	99.9	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> ecdysteroid-phosphate phosphatase; <b>PDBTitle:</b> crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
23	<a href="#">d1fzta</a>	Alignment	not modelled	99.9	16	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
24	<a href="#">c3eznB</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
25	<a href="#">d1bifa2</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
26	<a href="#">c1k6mA</a>	Alignment	not modelled	99.9	22	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2- <b>PDBTitle:</b> crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase
27	<a href="#">c3hjbB</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative alpha-ribazole-5'-phosphate phosphatase cobc; <b>PDBTitle:</b> crystal structure of putative alpha-ribazole-5'-phosphate phosphatase2 cobc from vibrio parahaemolyticus
28	<a href="#">d1qhfa</a>	Alignment	not modelled	99.9	19	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase

29	<a href="#">d2hhja1</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
30	<a href="#">c2a6pA</a>	Alignment	not modelled	99.9	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> possible phosphoglycerate mutase gpm2; <b>PDBTitle:</b> structure solution to 2.2 angstrom and functional characterisation of 2 the open reading frame rv3214 from mycobacterium tuberculosis
31	<a href="#">c1bifA</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> bifunctional enzyme <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; <b>PDBTitle:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
32	<a href="#">c3d8hB</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glycolytic phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
33	<a href="#">c4eo9A</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of a phosphoglycerate mutase gpm1 from mycobacterium2 leprae
34	<a href="#">d3pgma</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
35	<a href="#">c5um0A</a>	Alignment	not modelled	99.9	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of 2,3-bisphosphoglycerate-dependent2 phosphoglycerate mutase from neisseria gonorrhoeae
36	<a href="#">c3mxoB</a>	Alignment	not modelled	99.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein phosphatase pgam5, mitochondrial; <b>PDBTitle:</b> crystal structure of human phosphoglycerate mutase family member 52 (pgam5)
37	<a href="#">c6e4bC</a>	Alignment	not modelled	99.9	20	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> adenosylcobalamin/alpha-ribazole phosphatase; <b>PDBTitle:</b> the crystal structure of a putative alpha-ribazole-5'-p phosphatase2 from escherichia coli str. k-12 substr. mg1655
38	<a href="#">d1k6ma2</a>	Alignment	not modelled	99.9	22	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
39	<a href="#">d1tipa</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
40	<a href="#">c2rf1B</a>	Alignment	not modelled	99.8	19	<b>PDB header:</b> hydrolase, isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphohistidine phosphatase sixa; <b>PDBTitle:</b> crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
41	<a href="#">c3eozB</a>	Alignment	not modelled	99.8	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> putative phosphoglycerate mutase; <b>PDBTitle:</b> crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
42	<a href="#">d1v37a</a>	Alignment	not modelled	99.8	23	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
43	<a href="#">c1ujcA</a>	Alignment	not modelled	99.8	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphohistidine phosphatase sixa; <b>PDBTitle:</b> structure of the protein histidine phosphatase sixa2 complexed with tungstate
44	<a href="#">c5gg7A</a>	Alignment	not modelled	99.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hydrolase, nudix family protein; <b>PDBTitle:</b> crystal structure of mycobacterium smegmatis mutt1 in complex with 8-2 oxo-dgtp, 8-oxo-dgmp and pyrophosphate (i)
45	<a href="#">c3f2iD</a>	Alignment	not modelled	99.6	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> alr0221 protein; <b>PDBTitle:</b> crystal structure of the alr0221 protein from nostoc, northeast2 structural genomics consortium target nsr422.
46	<a href="#">c3fjyB</a>	Alignment	not modelled	99.6	15	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> probable mutt1 protein; <b>PDBTitle:</b> crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
47	<a href="#">c4hbzA</a>	Alignment	not modelled	99.5	21	<b>PDB header:</b> hydrolase, isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> putative phosphohistidine phosphatase, sixa; <b>PDBTitle:</b> the structure of putative phosphohistidine phosphatase sixa from2 nakamurella multipartitia.
48	<a href="#">c2zj6A</a>	Alignment	not modelled	99.3	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
49	<a href="#">c2qubG</a>	Alignment	not modelled	99.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> extracellular lipase; <b>PDBTitle:</b> crystal structure of extracellular lipase lipa from serratia2 marcescens
50	<a href="#">c1k7qA</a>	Alignment	not modelled	99.0	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> secreted protease c; <b>PDBTitle:</b> prtC from erwinia chrysanthemi: e189a mutant
51	<a href="#">c1satA</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> hydrolase (serine protease) <b>Chain:</b> A: <b>PDB Molecule:</b> serratia protease; <b>PDBTitle:</b> crystal structure of the 50 kda metallo protease from s.2 marcescens
52	<a href="#">c3p4gD</a>	Alignment	not modelled	98.5	11	<b>PDB header:</b> antifreeze protein <b>Chain:</b> D: <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> x-ray crystal structure of a hyperactive, ca2+-dependent, beta-helical2 antifreeze protein from an antarctic bacterium

53	<a href="#">d1kapp1</a>	Alignment	not modelled	98.1	17	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
54	<a href="#">c1ygvA_</a>	Alignment	not modelled	98.1	15	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> A: <b>PDB Molecule:</b> collagen i alpha 1; <b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule: rigid refinement
55	<a href="#">d1sata1</a>	Alignment	not modelled	98.0	15	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
56	<a href="#">d1g9ka1</a>	Alignment	not modelled	97.9	15	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
57	<a href="#">c1om8A_</a>	Alignment	not modelled	97.9	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> serralysin; <b>PDBTitle:</b> crystal structure of a cold adapted alkaline protease from pseudomonas2 tac ii 18, co-crystallized with 10 mm edta
58	<a href="#">d1k7ia1</a>	Alignment	not modelled	97.8	18	<b>Fold:</b> Single-stranded right-handed beta-helix <b>Superfamily:</b> beta-Roll <b>Family:</b> Serralysin-like metalloprotease, C-terminal domain
59	<a href="#">c1jiwP_</a>	Alignment	not modelled	97.7	22	<b>PDB header:</b> hydrolase/hyrolase inhibitor <b>Chain:</b> P: <b>PDB Molecule:</b> alkaline metalloproteinase; <b>PDBTitle:</b> crystal structure of the apr-aprin complex
60	<a href="#">c2ml3A_</a>	Alignment	not modelled	97.7	21	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6; <b>PDBTitle:</b> solution structure of alge6r3 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
61	<a href="#">c2ml2A_</a>	Alignment	not modelled	97.5	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 6; <b>PDBTitle:</b> solution structure of alge6r2 subunit from the azotobacter vinelandii2 mannuronan c5-epimerase
62	<a href="#">c2agmA_</a>	Alignment	not modelled	97.4	24	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> poly(beta-d-mannuronate) c5 epimerase 4; <b>PDBTitle:</b> solution structure of the r-module from alge4
63	<a href="#">c3hqvB_</a>	Alignment	not modelled	97.2	15	<b>PDB header:</b> structural protein, contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen alpha-2(i) chain; <b>PDBTitle:</b> low resolution, molecular envelope structure of type i2 collagen in situ determined by fiber diffraction. single3 type i collagen molecule, rigid body refinement
64	<a href="#">c4q1qA_</a>	Alignment	not modelled	96.6	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> adhesin/invasin tiba autotransporter; <b>PDBTitle:</b> crystal structure of tibi-catalyzed hyper-glycosylated tiba55-3502 fragment
65	<a href="#">c5xfsA_</a>	Alignment	not modelled	96.4	53	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein pe8; <b>PDBTitle:</b> crystal structure of pe8-ppe15 in complex with esp5 from m.2 tuberculosis
66	<a href="#">c2g38A_</a>	Alignment	not modelled	96.4	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> pe family protein; <b>PDBTitle:</b> a pe/pppe protein complex from mycobacterium tuberculosis
67	<a href="#">d2g38a1</a>	Alignment	not modelled	96.4	35	<b>Fold:</b> Ferritin-like <b>Superfamily:</b> PE/PPE dimer-like <b>Family:</b> PE
68	<a href="#">c1y0fB_</a>	Alignment	not modelled	96.3	16	<b>PDB header:</b> structural protein/contractile protein <b>Chain:</b> B: <b>PDB Molecule:</b> collagen i alpha 2; <b>PDBTitle:</b> the structure of collagen type i. single type i collagen2 molecule
69	<a href="#">c5cxA_</a>	Alignment	not modelled	96.2	25	<b>PDB header:</b> toxin <b>Chain:</b> A: <b>PDB Molecule:</b> bifunctional hemolysin/adenylate cyclase; <b>PDBTitle:</b> crystal structure of rtx domain block v of adenylate cyclase toxin2 from bordetella pertussis
70	<a href="#">c2g1cA_</a>	Alignment	not modelled	91.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine acid phosphatase; <b>PDBTitle:</b> structure of francisella tularensis histidine acid phosphatase bound2 to orthovanadate
71	<a href="#">c5cdhE_</a>	Alignment	not modelled	89.3	28	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> E: <b>PDB Molecule:</b> major acid phosphatase; <b>PDBTitle:</b> structure of legionella pneumophila histidine acid phosphatase2 complexed with l(+)-tartrate
72	<a href="#">c5juhA_</a>	Alignment	not modelled	81.3	11	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> antifreeze protein; <b>PDBTitle:</b> crystal structure of c-terminal domain (rv) of mpafp
73	<a href="#">c4jodA_</a>	Alignment	not modelled	80.8	25	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lysophosphatidic acid phosphatase type 6; <b>PDBTitle:</b> crystal structure of human lysophosphatidic acid phosphatase type 62 complexed with tris
74	<a href="#">d1nd6a_</a>	Alignment	not modelled	76.6	26	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
75	<a href="#">d1ihpa_</a>	Alignment	not modelled	75.0	16	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
76	<a href="#">d1rpaA_</a>	Alignment	not modelled	72.7	21	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
77	<a href="#">c4fdtB_</a>	Alignment	not modelled	71.7	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> putative multiple inositol polyphosphate histidine <b>PDBTitle:</b> crystal structure of a multiple inositol polyphosphate phosphatase
78	<a href="#">c4aruA_</a>	Alignment	not modelled	71.4	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine acid phosphatase;

						<b>PDBTitle:</b> hafnia alvei phytase in complex with tartrate
79	<a href="#">d1qfxa_</a>	Alignment	not modelled	67.7	23	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
80	<a href="#">c3zhcB_</a>	Alignment	not modelled	67.3	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> structure of the phytase from citrobacter braakii at 2.3 angstrom2 resolution.
81	<a href="#">c4arvB_</a>	Alignment	not modelled	66.0	22	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> yersinia kristensenii phytase apo form
82	<a href="#">c2pneA_</a>	Alignment	not modelled	60.7	36	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> crystal structure of the snow flea antifreeze protein
83	<a href="#">c3boiA_</a>	Alignment	not modelled	60.7	36	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein racemate
84	<a href="#">c3boiB_</a>	Alignment	not modelled	60.7	36	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein racemate
85	<a href="#">c3bogA_</a>	Alignment	not modelled	57.2	45	<b>PDB header:</b> antifreeze protein <b>Chain:</b> A: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate
86	<a href="#">c3bogB_</a>	Alignment	not modelled	57.2	45	<b>PDB header:</b> antifreeze protein <b>Chain:</b> B: <b>PDB Molecule:</b> 6.5 kda glycine-rich antifreeze protein; <b>PDBTitle:</b> snow flea antifreeze protein quasi-racemate
87	<a href="#">d1nt4a_</a>	Alignment	not modelled	55.3	20	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
88	<a href="#">c2qfiB_</a>	Alignment	not modelled	55.1	23	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> crystal structure of the phytase from d. castelli at 2.3 a
89	<a href="#">d1qwoa_</a>	Alignment	not modelled	52.8	20	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
90	<a href="#">c2wniC_</a>	Alignment	not modelled	47.9	24	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> 3-phytase; <b>PDBTitle:</b> crystal structure analysis of klebsiella sp asr1 phytase
91	<a href="#">d1dkla_</a>	Alignment	not modelled	42.9	26	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
92	<a href="#">c3m4xA_</a>	Alignment	not modelled	42.9	43	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> no11/hop2/sun family protein; <b>PDBTitle:</b> structure of a ribosomal methyltransferase
93	<a href="#">c3gzrA_</a>	Alignment	not modelled	33.7	28	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein with a ntf2-like fold; <b>PDBTitle:</b> crystal structure of an uncharacterized protein with a cystatin-like2 fold (cc_2572) from caulobacter vibrioides at 1.40 a resolution
94	<a href="#">c2frxD_</a>	Alignment	not modelled	32.2	32	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> hypothetical protein yebu; <b>PDBTitle:</b> crystal structure of yebu, a m5c rna methyltransferase from e.coli
95	<a href="#">c2eqoA_</a>	Alignment	not modelled	24.2	24	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tnf receptor-associated factor 3-interacting <b>PDBTitle:</b> solution structure of the stn_traf3ip1_nd domain of2 interleukin 13 receptor alpha 1-binding protein-1 [homo3 sapiens]
96	<a href="#">c5fmtB_</a>	Alignment	not modelled	24.1	33	<b>PDB header:</b> protein transport <b>Chain:</b> B: <b>PDB Molecule:</b> flagellar associated protein; <b>PDBTitle:</b> crift54 ch-domain
97	<a href="#">d2qn6a2</a>	Alignment	not modelled	19.1	22	<b>Fold:</b> Elongation factor/aminomethyltransferase common domain <b>Superfamily:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain <b>Family:</b> EF-Tu/eEF-1alpha/eIF2-gamma C-terminal domain
98	<a href="#">c2l3aA_</a>	Alignment	not modelled	18.5	40	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution nmr structure of homodimer protein sp_0782 (7-79) from2 streptococcus pneumoniae northeast structural genomics consortium3 target spr104 .
99	<a href="#">c2ltdA_</a>	Alignment	not modelled	18.2	35	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein ydbc; <b>PDBTitle:</b> solution nmr structure of apo ydbc from lactococcus lactis, northeast2 structural genomics consortium (nesg) target kr150