

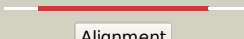

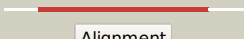












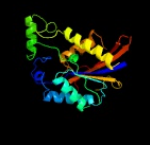






# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2419c_(-)_2717138_2717809
Date	Wed Aug 7 12:50:04 BST 2019
Unique Job ID	e1276560df48dae9

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4pz9B_</a>	 Alignment		100.0	99	<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="#">c4ij5B_</a>	 Alignment		100.0	28	<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</i> tk-6
3	<a href="#">d1h2ea_</a>	 Alignment		100.0	31	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
4	<a href="#">c2yn0A_</a>	 Alignment		100.0	18	<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
5	<a href="#">c5zkkA_</a>	 Alignment		100.0	26	<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
6	<a href="#">c4embD_</a>	 Alignment		100.0	26	<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
7	<a href="#">c3r7aA_</a>	 Alignment		100.0	23	<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 bacillus anthracis2 str. Sterne
8	<a href="#">c2yn2A_</a>	 Alignment		100.0	21	<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
9	<a href="#">c3e9eB_</a>	 Alignment		100.0	25	<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
10	<a href="#">d1xq9a_</a>	 Alignment		100.0	27	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
11	<a href="#">c2a6pA_</a>	 Alignment		100.0	32	<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 the open reading frame rv3214 from mycobacterium tuberculosis

12	<a href="#">c1yxjD_</a>	Alignment		100.0	24	<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
13	<a href="#">d1e58a_</a>	Alignment		100.0	24	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
14	<a href="#">c6e4bC_</a>	Alignment		100.0	26	<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
15	<a href="#">c5vveA_</a>	Alignment		100.0	26	<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
16	<a href="#">c3ll4B_</a>	Alignment		100.0	19	<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
17	<a href="#">c3dcyA_</a>	Alignment		100.0	28	<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="#">d1riia_</a>	Alignment		100.0	28	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
19	<a href="#">d1qhfa_</a>	Alignment		100.0	27	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
20	<a href="#">c3f3kA_</a>	Alignment		100.0	20	<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 saccharomyces2 cerevisiae.
21	<a href="#">d1fzta_</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
22	<a href="#">c3eznB_</a>	Alignment	not modelled	100.0	27	<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
23	<a href="#">c5um0A_</a>	Alignment	not modelled	100.0	25	<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
24	<a href="#">c2i1vB_</a>	Alignment	not modelled	100.0	25	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2- <b>PDBTitle:</b> crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
25	<a href="#">c1k6mA_</a>	Alignment	not modelled	100.0	25	<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
26	<a href="#">c1bifA_</a>	Alignment	not modelled	100.0	23	<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
27	<a href="#">c3d8hB_</a>	Alignment	not modelled	100.0	25	<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

28	<a href="#">d2hhja1</a>	Alignment	not modelled	100.0	26	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
29	<a href="#">c3hjbB</a>	Alignment	not modelled	100.0	23	<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
30	<a href="#">d1bifa2</a>	Alignment	not modelled	100.0	23	<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
31	<a href="#">c4eo9A</a>	Alignment	not modelled	100.0	28	<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
32	<a href="#">d3pgma</a>	Alignment	not modelled	100.0	27	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
33	<a href="#">d1k6ma2</a>	Alignment	not modelled	100.0	24	<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
34	<a href="#">c3d4iD</a>	Alignment	not modelled	100.0	22	<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
35	<a href="#">d1tipa</a>	Alignment	not modelled	100.0	26	<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
36	<a href="#">c3mxoB</a>	Alignment	not modelled	100.0	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> serine/threonine-protein phosphatase pgam5, mitochondrial; <b>PDBTitle:</b> crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
37	<a href="#">c2ikqA</a>	Alignment	not modelled	100.0	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
38	<a href="#">c2qniA</a>	Alignment	not modelled	100.0	19	<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
39	<a href="#">c3c7tB</a>	Alignment	not modelled	100.0	18	<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
40	<a href="#">c3eozB</a>	Alignment	not modelled	100.0	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
41	<a href="#">d1v37a</a>	Alignment	not modelled	100.0	31	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
42	<a href="#">c2rflB</a>	Alignment	not modelled	100.0	24	<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
43	<a href="#">c1ujcA</a>	Alignment	not modelled	100.0	20	<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	99.9	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	99.9	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	99.9	22	<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	99.9	27	<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="#">d1nd6a</a>	Alignment	not modelled	98.5	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
49	<a href="#">c4jodA</a>	Alignment	not modelled	98.5	21	<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
50	<a href="#">c5cdhE</a>	Alignment	not modelled	98.4	20	<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
51	<a href="#">d1rpaa</a>	Alignment	not modelled	98.3	17	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
52	<a href="#">c4arvB</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> yersinia kristensenii phytase apo form
						<b>PDB header:</b> hydrolase

53	<a href="#">c4fdtB</a>	Alignment	not modelled	98.3	19	<b>Chain:</b> B; <b>PDB Molecule:</b> putative multiple inositol polyphosphate histidine <b>PDBTitle:</b> crystal structure of a multiple inositol polyphosphate phosphatase
54	<a href="#">c4aruA</a>	Alignment	not modelled	98.2	13	<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
55	<a href="#">c2glcA</a>	Alignment	not modelled	98.2	26	<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
56	<a href="#">d1ihpa</a>	Alignment	not modelled	97.9	26	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
57	<a href="#">c3zhcB</a>	Alignment	not modelled	97.8	13	<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.
58	<a href="#">c2wniC</a>	Alignment	not modelled	97.8	26	<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
59	<a href="#">d1qwoa</a>	Alignment	not modelled	97.7	20	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
60	<a href="#">d1dkla</a>	Alignment	not modelled	97.7	17	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
61	<a href="#">d1nt4a</a>	Alignment	not modelled	97.6	15	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
62	<a href="#">d1qfxa</a>	Alignment	not modelled	97.5	27	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
63	<a href="#">c2gfiB</a>	Alignment	not modelled	97.3	24	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> crystal structure of the phytase from d. castellii at 2.3 a
64	<a href="#">c4r1dA</a>	Alignment	not modelled	80.8	19	<b>PDB header:</b> hydrolase/hydrolase inhibitor <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> the crystal structure of tle4-tli4 complex
65	<a href="#">d2hrca1</a>	Alignment	not modelled	45.8	7	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatase
66	<a href="#">c2jfnA</a>	Alignment	not modelled	35.5	19	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murnac-ala
67	<a href="#">c5ijwA</a>	Alignment	not modelled	30.1	15	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> glutamate racemase (muri) from mycobacterium smegmatis with bound d-2 glutamate, 1.8 angstrom resolution, x-ray diffraction
68	<a href="#">c3lfhF</a>	Alignment	not modelled	29.2	20	<b>PDB header:</b> transferase <b>Chain:</b> F; <b>PDB Molecule:</b> phosphotransferase system, mannose/fructose-specific <b>PDBTitle:</b> crystal structure of manxa from thermoanaerobacter tengcongensis
69	<a href="#">c3uuEA</a>	Alignment	not modelled	27.1	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> lip1, secretory lipase (family 3); <b>PDBTitle:</b> crystal structure of mono- and diacylglycerol lipase from malassezia2 globosa
70	<a href="#">d1tiaa</a>	Alignment	not modelled	24.7	33	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
71	<a href="#">c3o0dF</a>	Alignment	not modelled	23.4	24	<b>PDB header:</b> hydrolase <b>Chain:</b> F; <b>PDB Molecule:</b> triacylglycerol lipase; <b>PDBTitle:</b> crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution
72	<a href="#">c5gw8A</a>	Alignment	not modelled	23.4	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> hypothetical secretory lipase (family 3); <b>PDBTitle:</b> crystal structure of a putative dag-like lipase (mgmdl2) from2 malassezia globosa
73	<a href="#">c5xk2A</a>	Alignment	not modelled	21.9	36	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> diacylglycerol lipase; <b>PDBTitle:</b> crystal structure of mono- and diacylglycerol lipase from aspergillus2 oryzae
74	<a href="#">c3ngmB</a>	Alignment	not modelled	21.8	33	<b>PDB header:</b> hydrolase <b>Chain:</b> B; <b>PDB Molecule:</b> extracellular lipase; <b>PDBTitle:</b> crystal structure of lipase from gibberella zeae
75	<a href="#">d1b74a1</a>	Alignment	not modelled	20.6	17	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/glutamate racemase <b>Family:</b> Aspartate/glutamate racemase
76	<a href="#">c2wmyH</a>	Alignment	not modelled	20.4	10	<b>PDB header:</b> hydrolase <b>Chain:</b> H; <b>PDB Molecule:</b> putative acid phosphatase wzb; <b>PDBTitle:</b> crystal structure of the tyrosine phosphatase wzb from2 escherichia coli k30 in complex with sulphate.
77	<a href="#">c2jzcA</a>	Alignment	not modelled	20.3	25	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-n-acetylglucosamine transferase subunit <b>PDBTitle:</b> nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
						<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> putative phosphoenolpyruvate-dependent sugar

78	<a href="#">c3mtgA_</a>	Alignment	not modelled	20.0	17	<b>PDBTitle:</b> 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
79	<a href="#">d1dg9a_</a>	Alignment	not modelled	19.3	17	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
80	<a href="#">d2vcha1</a>	Alignment	not modelled	19.1	20	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
81	<a href="#">d1jl3a_</a>	Alignment	not modelled	19.0	10	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
82	<a href="#">d2acva1</a>	Alignment	not modelled	16.8	25	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
83	<a href="#">d1tiba_</a>	Alignment	not modelled	16.0	36	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
84	<a href="#">d3tgla_</a>	Alignment	not modelled	15.6	24	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
85	<a href="#">c2fekA_</a>	Alignment	not modelled	15.4	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> low molecular weight protein-tyrosine- <b>PDBTitle:</b> structure of a protein tyrosine phosphatase
86	<a href="#">c5gotA_</a>	Alignment	not modelled	14.2	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> low molecular weight phosphotyrosine phosphatase family <b>PDBTitle:</b> crystal structure of sp-ptp, low molecular weight protein tyrosine2 phosphatase from streptococcus pyogenes
87	<a href="#">c4d74A_</a>	Alignment	not modelled	14.1	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> protein-tyrosine-phosphatase amsi; <b>PDBTitle:</b> 1.57 a crystal structure of erwinia amylovora tyrosine phosphatase2 amsi
88	<a href="#">c6o86A_</a>	Alignment	not modelled	13.9	20	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-glycosyltransferase 76g1; <b>PDBTitle:</b> crystal structure of semet udp-dependent glucosyltransferases (ugt)2 from stevia rebaudiana in complex with udp
89	<a href="#">c1u2pA_</a>	Alignment	not modelled	13.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> low molecular weight protein-tyrosine- <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis low2 molecular protein tyrosine phosphatase (mptpa) at 1.9a3 resolution
90	<a href="#">c2qi4A_</a>	Alignment	not modelled	13.8	10	<b>PDB header:</b> hydrolase <b>Chain:</b> A; <b>PDB Molecule:</b> possible phosphotyrosine protein phosphatase; <b>PDBTitle:</b> solution structure of the low molecular weight protein2 tyrosine phosphatase from campylobacter jejuni.
91	<a href="#">c2o61A_</a>	Alignment	not modelled	13.6	21	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-glucuronosyltransferase 2b7; <b>PDBTitle:</b> crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
92	<a href="#">d3beda1</a>	Alignment	not modelled	13.3	24	<b>Fold:</b> PTS system fructose IIA component-like <b>Superfamily:</b> PTS system fructose IIA component-like <b>Family:</b> EIIA-man component-like
93	<a href="#">c2l18A_</a>	Alignment	not modelled	13.3	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A; <b>PDB Molecule:</b> arsenate reductase; <b>PDBTitle:</b> an arsenate reductase in the phosphate binding state
94	<a href="#">c3wc4A_</a>	Alignment	not modelled	13.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-glucose:anthocyanidin 3-o-glucosyltransferase; <b>PDBTitle:</b> crystal structure of udp-glucose: anthocyanidin 3-o-2 glucosyltransferase from clitoria ternatea
95	<a href="#">c3hbjA_</a>	Alignment	not modelled	13.1	22	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> flavonoid 3-o-glucosyltransferase; <b>PDBTitle:</b> structure of ugt78g1 complexed with udp
96	<a href="#">d1d1qa_</a>	Alignment	not modelled	13.0	21	<b>Fold:</b> Phosphotyrosine protein phosphatases I-like <b>Superfamily:</b> Phosphotyrosine protein phosphatases I <b>Family:</b> Low-molecular-weight phosphotyrosine protein phosphatases
97	<a href="#">c3gx1A_</a>	Alignment	not modelled	12.7	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> lin1832 protein; <b>PDBTitle:</b> crystal structure of a domain of lin1832 from listeria innocua
98	<a href="#">c3hfrA_</a>	Alignment	not modelled	12.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from listeria monocytogenes
99	<a href="#">c5v2kA_</a>	Alignment	not modelled	12.3	17	<b>PDB header:</b> transferase <b>Chain:</b> A; <b>PDB Molecule:</b> udp-glycosyltransferase 74f2; <b>PDBTitle:</b> crystal structure of udp-glucosyltransferase, ugt74f2 (t15a), with udp2 and 2-bromobenzoic acid