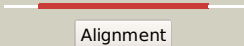

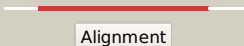

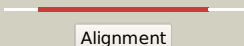







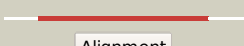











# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0525 (- )_616226_616834
Date	Fri Jul 26 01:50:07 BST 2019
Unique Job ID	90a67f3a84d4fc94

Detailed template  
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4ij5B_</a>	 Alignment		100.0	25	<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>hydrogenobacter thermophilus</i> tk-6
2	<a href="#">d1h2ea_</a>	 Alignment		100.0	23	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
3	<a href="#">c4pz9B_</a>	 Alignment		100.0	28	<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
4	<a href="#">c5zkkA_</a>	 Alignment		100.0	21	<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
5	<a href="#">c4embD_</a>	 Alignment		100.0	16	<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
6	<a href="#">c6e4bC_</a>	 Alignment		100.0	21	<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
7	<a href="#">c2yn0A_</a>	 Alignment		100.0	20	<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
8	<a href="#">d1xq9a_</a>	 Alignment		100.0	21	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
9	<a href="#">d1e58a_</a>	 Alignment		100.0	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
10	<a href="#">c1yxjD_</a>	 Alignment		100.0	18	<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
11	<a href="#">c2a6pA_</a>	 Alignment		100.0	22	<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 of2 the open reading frame rv3214 from mycobacterium tuberculosis

12	<a href="#">d1riia_</a>	Alignment		100.0	18	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
13	<a href="#">c2yn2A_</a>	Alignment		100.0	16	<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
14	<a href="#">c5vveA_</a>	Alignment		100.0	18	<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
15	<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
16	<a href="#">d1qhfa_</a>	Alignment		100.0	19	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
17	<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
18	<a href="#">d1fzta_</a>	Alignment		100.0	21	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
19	<a href="#">c3e9eB_</a>	Alignment		100.0	26	<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
20	<a href="#">c3eznB_</a>	Alignment		100.0	20	<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
21	<a href="#">c3higB_</a>	Alignment	not modelled	100.0	19	<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
22	<a href="#">c5um0A_</a>	Alignment	not modelled	100.0	17	<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
23	<a href="#">c3f3kA_</a>	Alignment	not modelled	100.0	18	<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.
24	<a href="#">d3pgma_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
25	<a href="#">c3d8hB_</a>	Alignment	not modelled	100.0	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
26	<a href="#">c2i1vB_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphate <b>PDBTitle:</b> crystal structure of pfkfb3 in complex with adp and2 fructose-2,6-bisphosphate
27	<a href="#">c1k6mA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase, hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphate 2- <b>PDBTitle:</b> crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase <b>Fold:</b> Phosphoglycerate mutase-like

28	<a href="#">d1bifa2</a>	Alignment	not modelled	100.0	20	<b>Supersfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
29	<a href="#">c3dcyA_</a>	Alignment	not modelled	100.0	24	<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.
30	<a href="#">d2hhja1</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Phosphoglycerate mutase-like <b>Supersfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
31	<a href="#">c4eo9A_</a>	Alignment	not modelled	100.0	21	<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="#">c1bifA_</a>	Alignment	not modelled	100.0	21	<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
33	<a href="#">c3d4iD_</a>	Alignment	not modelled	100.0	21	<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
34	<a href="#">d1k6ma2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Phosphoglycerate mutase-like <b>Supersfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
35	<a href="#">d1tipa_</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> Phosphoglycerate mutase-like <b>Supersfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
36	<a href="#">c2ikqA_</a>	Alignment	not modelled	100.0	21	<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
37	<a href="#">c2qniA_</a>	Alignment	not modelled	100.0	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
38	<a href="#">c3mxoB_</a>	Alignment	not modelled	100.0	17	<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)
39	<a href="#">c3c7tB_</a>	Alignment	not modelled	100.0	22	<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="#">d1v37a_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Phosphoglycerate mutase-like <b>Supersfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Cofactor-dependent phosphoglycerate mutase
41	<a href="#">c3eozB_</a>	Alignment	not modelled	100.0	18	<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="#">c5gg7A_</a>	Alignment	not modelled	100.0	23	<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)
43	<a href="#">c2rfiB_</a>	Alignment	not modelled	100.0	20	<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
44	<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
45	<a href="#">c3f2iD_</a>	Alignment	not modelled	99.9	17	<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	18	<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	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="#">c2glcA_</a>	Alignment	not modelled	98.2	18	<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
49	<a href="#">c5cdhE_</a>	Alignment	not modelled	98.1	22	<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
50	<a href="#">d1rpaA_</a>	Alignment	not modelled	98.0	22	<b>Fold:</b> Phosphoglycerate mutase-like <b>Supersfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
51	<a href="#">d1nd6a_</a>	Alignment	not modelled	98.0	19	<b>Fold:</b> Phosphoglycerate mutase-like <b>Supersfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
52	<a href="#">c4arvB_</a>	Alignment	not modelled	97.9	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> phytase; <b>PDBTitle:</b> yersinia kristensenii phytase apo form
						<b>Fold:</b> Phosphoglycerate mutase-like

53	<a href="#">d1ihpa_</a>	Alignment	not modelled	97.9	18	<b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
54	<a href="#">c4jodA_</a>	Alignment	not modelled	97.8	27	<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
55	<a href="#">c4aruA_</a>	Alignment	not modelled	97.7	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
56	<a href="#">c2wniC_</a>	Alignment	not modelled	97.7	22	<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
57	<a href="#">c3zhcB_</a>	Alignment	not modelled	97.7	27	<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="#">d1dkla_</a>	Alignment	not modelled	97.6	27	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
59	<a href="#">d1nt4a_</a>	Alignment	not modelled	97.6	21	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
60	<a href="#">d1qwoa_</a>	Alignment	not modelled	97.6	22	<b>Fold:</b> Phosphoglycerate mutase-like <b>Superfamily:</b> Phosphoglycerate mutase-like <b>Family:</b> Histidine acid phosphatase
61	<a href="#">c4fdtB_</a>	Alignment	not modelled	97.6	23	<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
62	<a href="#">d1qfxa_</a>	Alignment	not modelled	97.3	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	96.8	21	<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	69.1	13	<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="#">c3uuuA_</a>	Alignment	not modelled	66.7	21	<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
66	<a href="#">c5gw8A_</a>	Alignment	not modelled	64.8	16	<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
67	<a href="#">c5xk2A_</a>	Alignment	not modelled	58.4	14	<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
68	<a href="#">c3o0dF_</a>	Alignment	not modelled	56.1	10	<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
69	<a href="#">c5ijwA_</a>	Alignment	not modelled	55.6	13	<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
70	<a href="#">d1tiba_</a>	Alignment	not modelled	48.9	15	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
71	<a href="#">c3ngmB_</a>	Alignment	not modelled	47.4	36	<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
72	<a href="#">d3t gla_</a>	Alignment	not modelled	46.9	12	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
73	<a href="#">c2yjiA_</a>	Alignment	not modelled	41.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> phospholipase a1-iigamma; <b>PDBTitle:</b> crystal structure of phospholipase a1
74	<a href="#">d1tiaa_</a>	Alignment	not modelled	39.6	18	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
75	<a href="#">c6qppA_</a>	Alignment	not modelled	37.0	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> rhizomucor miehei lipase propeptide complex, native
76	<a href="#">c3g7nA_</a>	Alignment	not modelled	34.6	12	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of a triacylglycerol lipase from penicillium2 expansum at 1.3
77	<a href="#">d2hk6a1</a>	Alignment	not modelled	33.7	7	<b>Fold:</b> Chelatase-like <b>Superfamily:</b> Chelatase <b>Family:</b> Ferrochelatae
78	<a href="#">c3ds8A_</a>	Alignment	not modelled	32.6	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> lin2722 protein; <b>PDBTitle:</b> the crysatl structure of the gene lin2722 products from listeria2 innocua
79	<a href="#">c3lp5A_</a>	Alignment	not modelled	30.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell surface hydrolase; <b>PDBTitle:</b> the crystal structure of the putative cell surface hydrolase

						from2 lactobacillus plantarum wcfs1
80	<a href="#">d1uwca_</a>	Alignment	not modelled	28.6	7	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
81	<a href="#">d1lgya_</a>	Alignment	not modelled	23.0	14	<b>Fold:</b> alpha/beta-Hydrolases <b>Superfamily:</b> alpha/beta-Hydrolases <b>Family:</b> Fungal lipases
82	<a href="#">c3hfrA_</a>	Alignment	not modelled	21.5	11	<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
83	<a href="#">c2jfnA_</a>	Alignment	not modelled	21.4	15	<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
84	<a href="#">c2zyiB_</a>	Alignment	not modelled	20.0	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> lipase, putative; <b>PDBTitle:</b> a. fulgidus lipase with fatty acid fragment and calcium
85	<a href="#">c4nfbB_</a>	Alignment	not modelled	18.8	10	<b>PDB header:</b> signaling protein <b>Chain:</b> B: <b>PDB Molecule:</b> senescence-associated carboxylesterase 101; <b>PDBTitle:</b> structure of the central plant immunity signaling node eds1 in complex2 with its interaction partner sag101
86	<a href="#">c3hbjA_</a>	Alignment	not modelled	18.1	21	<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
87	<a href="#">c2jzcA_</a>	Alignment	not modelled	17.9	16	<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
88	<a href="#">d2vcha1</a>	Alignment	not modelled	17.5	24	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
89	<a href="#">c2oryA_</a>	Alignment	not modelled	16.9	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lipase; <b>PDBTitle:</b> crystal structure of m37 lipase
90	<a href="#">c5v2kA_</a>	Alignment	not modelled	16.7	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
91	<a href="#">c3wc4A_</a>	Alignment	not modelled	16.6	21	<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
92	<a href="#">c3fleB_</a>	Alignment	not modelled	16.3	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> se_1780 protein; <b>PDBTitle:</b> se_1780 protein of unknown function from staphylococcus epidermidis.
93	<a href="#">d1l1sa_</a>	Alignment	not modelled	16.1	12	<b>Fold:</b> DsrEFH-like <b>Superfamily:</b> DsrEFH-like <b>Family:</b> DsrEF-like
94	<a href="#">c2o6IA_</a>	Alignment	not modelled	15.9	10	<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
95	<a href="#">d2pq6a1</a>	Alignment	not modelled	15.6	17	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
96	<a href="#">d2ejna1</a>	Alignment	not modelled	15.4	21	<b>Fold:</b> Uteroglobin-like <b>Superfamily:</b> Uteroglobin-like <b>Family:</b> Uteroglobin-like
97	<a href="#">c3outC_</a>	Alignment	not modelled	15.3	3	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of glutamate racemase from francisella tularensis2 subsp. tularensis schu s4 in complex with d-glutamate.
98	<a href="#">d2acva1</a>	Alignment	not modelled	14.5	24	<b>Fold:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Superfamily:</b> UDP-Glycosyltransferase/glycogen phosphorylase <b>Family:</b> UDPGT-like
99	<a href="#">c6o86A_</a>	Alignment	not modelled	14.4	19	<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