Phyre2

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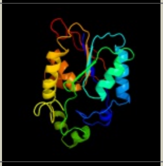
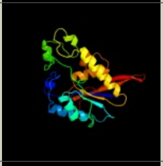
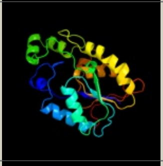
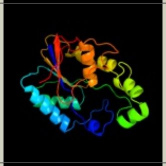
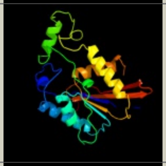
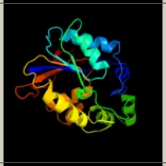
Description	P0A7A2
Date	Thu Jan 5 11:05:10 GMT 2012
Unique Job ID	c58d72c843b22ec5

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1h2ea_	Alignment		100.0	31	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
2	d1e58a_	Alignment		100.0	20	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
3	c3r7aA_	Alignment		100.0	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate mutase, putative; **PDBTitle:** crystal structure of phosphoglycerate mutase from bacillus anthracis2 str. sterne
4	c1yjxD_	Alignment		100.0	22	**PDB header:**isomerase, hydrolase **Chain:** D: **PDB Molecule:**phosphoglycerate mutase 1; **PDBTitle:** crystal structure of human b type phosphoglycerate mutase
5	c3eznB_	Alignment		100.0	23	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-dependent phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglyceromutase from burkholderia2 pseudomallei 1710b
6	c2a6pA_	Alignment		100.0	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible phosphoglycerate mutase gpm2; **PDBTitle:** structure solution to 2.2 angstrom and functional characterisation of2 the open reading frame rv3214 from mycobacterium tuberculosis
7	c3dcyA_	Alignment		100.0	31	**PDB header:**apoptosis regulator **Chain:** A: **PDB Molecule:**regulator protein; **PDBTitle:** crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
8	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
9	d1xq9a_	Alignment		100.0	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
10	d1qhfa_	Alignment		100.0	25	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
11	d1riia_	Alignment		100.0	24	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase

12	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 saccharomyces2 cerevisiae.
13	d1fzta_	Alignment		100.0	23	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
14	d1bifa2	Alignment		100.0	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
15	c3e9eB_	Alignment		100.0	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zgc:56074; **PDBTitle:** structure of full-length h11a mutant form of tigar from danio rerio
16	d2hhja1	Alignment		100.0	21	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
17	c2i1vB_	Alignment		100.0	22	**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
18	c3d8hB_	Alignment		100.0	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**glycolytic phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from cryptosporidium2 parvum, cgd7_4270
19	c1k6mA_	Alignment		100.0	23	**PDB header:**transferase, hydrolase **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/fructose-2,6- **PDBTitle:** crystal structure of human liver 6-phosphofructo-2-2 kinase/fructose-2,6-bisphosphatase
20	d3pgma_	Alignment		100.0	24	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
21	c1bifA_	Alignment	not modelled	100.0	23	**PDB header:**bifunctional enzyme **Chain:** A: **PDB Molecule:**6-phosphofructo-2-kinase/ fructose-2,6-bisphosphatase; **PDBTitle:** 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase bifunctional2 enzyme complexed with atp-g-s and phosphate
22	d1k6ma2	Alignment	not modelled	100.0	23	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
23	d1tipa_	Alignment	not modelled	100.0	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase, phosphatase domain
24	c3hjgB_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative alpha-ribazole-5'-phosphate phosphatase **PDBTitle:** crystal structure of putative alpha-ribazole-5'-phosphate2 phosphatase cobc from vibrio parahaemolyticus
25	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
26	c2qniA_	Alignment	not modelled	100.0	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu0299; **PDBTitle:** crystal structure of uncharacterized protein atu0299
27	c2ikqA_	Alignment	not modelled	100.0	19	**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
28	c3mxoB_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**serine/threonine-protein phosphatase pgam5, mitochondrial;

						PDBTitle: crystal structure oh human phosphoglycerate mutase family member 52 (pgam5)
29	d1v37a_	Alignment	not modelled	100.0	35	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Cofactor-dependent phosphoglycerate mutase
30	c3c7tB_	Alignment	not modelled	100.0	20	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ecdysteroid-phosphate phosphatase; **PDBTitle:** crystal structure of the ecdysone phosphate phosphatase, eppase, from2 bombix mori in complex with tungstate
31	c3eozB_	Alignment	not modelled	100.0	30	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoglycerate mutase; **PDBTitle:** crystal structure of phosphoglycerate mutase from plasmodium2 falciparum, pfd0660w
32	c1ujcA_	Alignment	not modelled	100.0	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**phosphohistidine phosphatase sixa; **PDBTitle:** structure of the protein histidine phosphatase sixa2 complexed with tungstate
33	c2rflB_	Alignment	not modelled	100.0	27	**PDB header:**hydrolase, isomerase **Chain:** B: **PDB Molecule:**putative phosphohistidine phosphatase sixa; **PDBTitle:** crystal structure of the putative phosphohistidine phosphatase sixa2 from agrobacterium tumefaciens
34	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.
35	c3fjyB_	Alignment	not modelled	99.9	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable mutt1 protein; **PDBTitle:** crystal structure of a probable mutt1 protein from bifidobacterium2 adolescentis
36	c2glcA_	Alignment	not modelled	98.1	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**histidine acid phosphatase; **PDBTitle:** structure of francisella tularensis histidine acid2 phosphatase bound to orthovanadate
37	d1nd6a_	Alignment	not modelled	98.0	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
38	d1rpaa_	Alignment	not modelled	97.9	25	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
39	d1ihpa_	Alignment	not modelled	97.8	22	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
40	d1dkla_	Alignment	not modelled	97.7	24	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
41	c2wniC_	Alignment	not modelled	97.7	25	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**3-phytase; **PDBTitle:** crystal structure analysis of klebsiella sp asr1 phytase
42	d1qwoa_	Alignment	not modelled	97.6	17	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
43	d1nt4a_	Alignment	not modelled	97.5	16	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
44	d1qfxa_	Alignment	not modelled	97.4	26	**Fold:**Phosphoglycerate mutase-like **Superfamily:**Phosphoglycerate mutase-like **Family:**Histidine acid phosphatase
45	c2gfiB_	Alignment	not modelled	97.2	29	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phytase; **PDBTitle:** crystal structure of the phytase from d. castellii at 2.3 a
46	c3lfhF_	Alignment	not modelled	35.5	25	**PDB header:**transferase **Chain:** F: **PDB Molecule:**phosphotransferase system, mannose/fructose-specific **PDBTitle:** crystal structure of manxa from thermoanaerobacter tengcongensis
47	d1qgoa_	Alignment	not modelled	34.7	15	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Cobalt chelatase CbiK
48	d2hk6a1	Alignment	not modelled	33.3	15	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
49	c3mtqA_	Alignment	not modelled	28.7	17	**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
50	c3ngmB_	Alignment	not modelled	26.6	26	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**extracellular lipase; **PDBTitle:** crystal structure of lipase from gibberella zeae
51	d1jl3a_	Alignment	not modelled	24.4	5	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
52	d1tiaa_	Alignment	not modelled	24.2	22	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
53	c3o0dF_	Alignment	not modelled	24.0	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**triacylglycerol lipase; **PDBTitle:** crystal structure of lip2 lipase from yarrowia lipolytica at 1.7 a2 resolution

54	d1dg9a_	Alignment	not modelled	22.6	15	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
55	d1tiba_	Alignment	not modelled	22.3	21	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
56	c2wmyH_	Alignment	not modelled	19.5	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.
57	c3lp5A_	Alignment	not modelled	19.2	6	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative cell surface hydrolase; **PDBTitle:** the crystal structure of the putative cell surface hydrolase from2 lactobacillus plantarum wcfs1
58	d3tgla_	Alignment	not modelled	18.3	17	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
59	c2jzcA_	Alignment	not modelled	18.0	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-n-acetylglucosamine transferase subunit **PDBTitle:** nmr solution structure of alg13: the sugar donor subunit of2 a yeast n-acetylglucosamine transferase. northeast3 structural genomics consortium target yg1
60	d3beda1	Alignment	not modelled	16.8	24	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
61	c2fekA_	Alignment	not modelled	15.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
62	c1u2pA_	Alignment	not modelled	15.2	11	**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
63	d1pdoa_	Alignment	not modelled	15.1	29	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**EIIA-man component-like
64	c2o6lA_	Alignment	not modelled	15.1	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**udp-glucuronosyltransferase 2b7; **PDBTitle:** crystal structure of the udp-glucuronic acid binding domain2 of the human drug metabolizing udp-glucuronosyltransferase3 2b7
65	c3g7nA_	Alignment	not modelled	15.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lipase; **PDBTitle:** crystal structure of a triacylglycerol lipase from2 penicillium expansum at 1.3
66	d1l1sa_	Alignment	not modelled	14.9	9	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
67	d2ejna1	Alignment	not modelled	14.8	29	**Fold:**Uteroglobin-like **Superfamily:**Uteroglobin-like **Family:**Uteroglobin-like
68	d1d1qa_	Alignment	not modelled	14.7	5	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
69	d2vcha1	Alignment	not modelled	14.6	25	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
70	c3gx1A_	Alignment	not modelled	14.3	24	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin1832 protein; **PDBTitle:** crystal structure of a domain of lin1832 from listeria innocua
71	c2gi4A_	Alignment	not modelled	13.9	10	**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.
72	d2acva1	Alignment	not modelled	13.3	35	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
73	d1vjea_	Alignment	not modelled	13.1	13	**Fold:**LuxS/MPP-like metallohydrolase **Superfamily:**LuxS/MPP-like metallohydrolase **Family:**Autoinducer-2 production protein LuxS
74	c2l18A_	Alignment	not modelled	12.8	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**arsenate reductase; **PDBTitle:** an arsenate reductase in the phosphate binding state
75	c3hbjA_	Alignment	not modelled	12.3	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**flavonoid 3-o-glucosyltransferase; **PDBTitle:** structure of ugt78g1 complexed with udp
76	d1uwca_	Alignment	not modelled	11.9	14	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
77	c3iprC_	Alignment	not modelled	11.8	12	**PDB header:**transferase **Chain:** C: **PDB Molecule:**pts system, iia component; **PDBTitle:** crystal structure of the enterococcus faecalis gluconate2 specific eiia phosphotransferase system component
78	c3e90C_	Alignment	not modelled	11.5	23	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**ns2b cofactor; **PDBTitle:** west nile vi rus ns2b-ns3protease in complexed with2 inhibitor naph-kkr-h
79	c3ds8A_	Alignment	not modelled	11.1	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2722 protein; **PDBTitle:** the crysatl structure of the gene lin2722 products from

						listeria2 innocua
80	d1y1la_	Alignment	not modelled	11.0	16	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
81	d1nvta1	Alignment	not modelled	10.7	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
82	c2ijoA_	Alignment	not modelled	10.5	23	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**polyprotein; **PDBTitle:** crystal structure of the west nile virus ns2b-ns3 protease2 complexed with bovine pancreatic trypsin inhibitor
83	c2pd2A_	Alignment	not modelled	10.5	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st0148; **PDBTitle:** crystal structure of (st0148) conserved hypothetical from sulfolobus2 tokodaii strain7
84	d2pq6a1	Alignment	not modelled	10.0	21	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
85	c3lfjB_	Alignment	not modelled	9.9	45	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotransferase system, mannose/fructose/n- **PDBTitle:** crystal structure of manxb from thermoanaerobacter tengcongensis
86	c3jviA_	Alignment	not modelled	9.8	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein tyrosine phosphatase; **PDBTitle:** product state mimic crystal structure of protein tyrosine phosphatase2 from entamoeba histolytica
87	c2zyiB_	Alignment	not modelled	9.6	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lipase, putative; **PDBTitle:** a. fulgidus lipase with fatty acid fragment and calcium
88	d1jf8a_	Alignment	not modelled	9.5	9	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
89	c1zggA_	Alignment	not modelled	9.1	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative low molecular weight protein-tyrosine- **PDBTitle:** solution structure of a low molecular weight protein2 tyrosine phosphatase from bacillus subtilis
90	d3b48a1	Alignment	not modelled	8.9	25	**Fold:**PTS system fructose IIA component-like **Superfamily:**PTS system fructose IIA component-like **Family:**DhaM-like
91	d1lgya_	Alignment	not modelled	8.4	12	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases
92	d1lbqa_	Alignment	not modelled	7.3	15	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
93	c3rofA_	Alignment	not modelled	7.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine-phosphatase ptpa; **PDBTitle:** crystal structure of the s. aureus protein tyrosine phosphatase ptpa
94	d1nyta1	Alignment	not modelled	7.2	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
95	d2hrca1	Alignment	not modelled	7.2	10	**Fold:**Chelatase-like **Superfamily:**Chelatase **Family:**Ferrochelatase
96	c2xvzA_	Alignment	not modelled	7.1	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**chelatase, putative; **PDBTitle:** cobalt chelatase cbik (periplasmatic) from desulvobrio2 vulgaris hildenborough (co-crystallized with cobalt)
97	c2p10D_	Alignment	not modelled	7.1	23	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**mll9387 protein; **PDBTitle:** crystal structure of a putative phosphonopyruvate hydrolase (mll9387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
98	d2c1xa1	Alignment	not modelled	7.0	21	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDPGT-like
99	c3fiuD_	Alignment	not modelled	6.9	12	**PDB header:**ligase **Chain:** D: **PDB Molecule:**nh(3)-dependent nad(+) synthetase; **PDBTitle:** structure of nmn synthetase from francisella tularensis