Phyre^2

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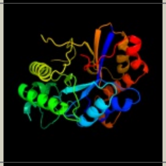
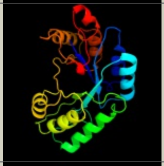
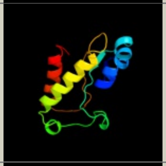
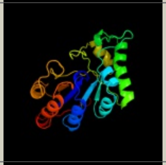
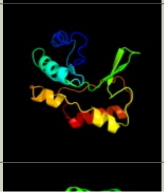
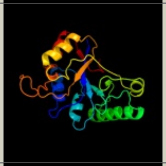
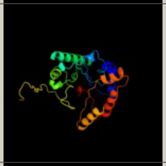
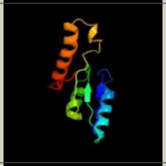
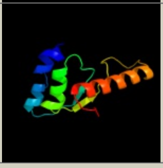
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2i5ia1	Alignment		100.0	38	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**YdjC-like
2	c2e67D_	Alignment		100.0	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein tthb029; **PDBTitle:** crystal structure of the hypothetical protein tthb029 from thermus2 thermophilus hb8
3	d2nlya1	Alignment		97.9	11	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**Divergent polysaccharide deacetylase
4	c2qv5A_	Alignment		97.4	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu2773; **PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58
5	c2vyoA_	Alignment		97.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitooligosaccharide deacetylase; **PDBTitle:** chitin deacetylase family member from encephalitozoon2 cuniculi
6	c2c1iA_	Alignment		96.7	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase; **PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant.
7	c2x5eA_	Alignment		96.7	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**upf0271 protein pa4511; **PDBTitle:** crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa
8	d2dfaa1	Alignment		96.6	24	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
9	d1ny1a_	Alignment		96.6	21	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
10	d1v6ta_	Alignment		96.6	20	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like
11	d1xw8a_	Alignment		95.7	22	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**LamB/YcsF-like

12	c1w17A_	Alignment		95.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa; **PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase.
13	c2w3zA_	Alignment		95.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deacetylase; **PDBTitle:** structure of a streptococcus mutans ce4 esterase
14	d2c71a1	Alignment		94.6	14	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
15	c3qbuD_	Alignment		86.5	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of putative peptidoglyacn deactelyase (hp0310) from2 helicobacter pylori
16	d2c1ia1	Alignment		81.9	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
17	d1z7aa1	Alignment		81.1	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**PA1517-like
18	d2cc0a1	Alignment		76.9	17	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
19	d2iw0a1	Alignment		73.3	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
20	c3s6oD_	Alignment		66.2	13	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**polysaccharide deacetylase family protein; **PDBTitle:** crystal structure of a polysaccharide deacetylase family protein from2 burkholderia pseudomallei
21	c2iw0A_	Alignment	not modelled	55.5	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitin deacetylase; **PDBTitle:** structure of the chitin deacetylase from the fungal2 pathogen colletotrichum lindemuthianum
22	c2zktB_	Alignment	not modelled	51.6	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**2,3-bisphosphoglycerate-independent phosphoglycerate **PDBTitle:** structure of ph0037 protein from pyrococcus horikoshii
23	d2j13a1	Alignment	not modelled	47.7	23	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**NodB-like polysaccharide deacetylase
24	d1k1xa3	Alignment	not modelled	47.5	16	**Fold:**7-stranded beta/alpha barrel **Superfamily:**Glycoside hydrolase/deacetylase **Family:**4-alpha-glucanotransferase, N-terminal domain
25	d1dg9a_	Alignment	not modelled	37.0	12	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**Phosphotyrosine protein phosphatases I **Family:**Low-molecular-weight phosphotyrosine protein phosphatases
26	c1i32D_	Alignment	not modelled	35.2	15	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**glyceraldehyde 3-phosphate dehydrogenase; **PDBTitle:** leishmania mexicana glyceraldehyde-3-phosphate2 dehydrogenase in complex with inhibitors
27	c3e2vA_	Alignment	not modelled	33.4	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**3'-5'-exonuclease; **PDBTitle:** crystal structure of an uncharacterized amidohydrolase from2 saccharomyces cerevisiae
28	c3gk7A_	Alignment	not modelled	32.4	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase from2 clostridium aminobutyricum
						PDB header:hydrolase

29	c3ipwA_	Alignment	not modelled	28.7	18	**Chain:** A: **PDB Molecule:**hydrolase tatd family protein; **PDBTitle:** crystal structure of hydrolase tatd family protein from entamoeba2 histolytica
30	c2i09A_	Alignment	not modelled	28.4	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**phosphopentomutase; **PDBTitle:** crystal structure of putative phosphopentomutase from streptococcus2 mutans
31	c3dnfB_	Alignment	not modelled	22.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate reductase; **PDBTitle:** structure of (e)-4-hydroxy-3-methyl-but-2-enyl diphosphate reductase,2 the terminal enzyme of the non-mevalonate pathway
32	c1tx2A_	Alignment	not modelled	21.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhps, dihydropteroate synthase; **PDBTitle:** dihydropteroate synthetase, with bound inhibitor manic, from bacillus2 anthracis
33	d1tx2a_	Alignment	not modelled	21.4	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**Dihydropteroate synthetase-like **Family:**Dihydropteroate synthetase
34	d3eeqa1	Alignment	not modelled	19.9	18	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
35	c2p90B_	Alignment	not modelled	19.5	13	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hypothetical protein cgl1923; **PDBTitle:** the crystal structure of a protein of unknown function from2 corynebacterium glutamicum atcc 13032
36	d2pw9a1	Alignment	not modelled	17.7	12	**Fold:**Cytidine deaminase-like **Superfamily:**Cytidine deaminase-like **Family:**FdhD/NarQ
37	c3rxzA_	Alignment	not modelled	17.5	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**polysaccharide deacetylase; **PDBTitle:** crystal structure of putative polysaccharide deacetylase from2 mycobacterium smegmatis
38	c2kl8A_	Alignment	not modelled	16.5	33	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
39	c2b4rQ_	Alignment	not modelled	16.4	19	**PDB header:**oxidoreductase **Chain:** Q: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde-3-phosphate dehydrogenase from2 plasmodium falciparum at 2.25 angstrom resolution reveals intriguing3 extra electron density in the active site
40	d1ggaa1	Alignment	not modelled	16.1	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
41	c3eh7A_	Alignment	not modelled	14.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** the structure of a putative 4-hydroxybutyrate coa-transferase from2 porphyromonas gingivalis w83
42	c2oasA_	Alignment	not modelled	13.9	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coenzyme a transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coenzyme a transferase (atoa)2 in complex with coa from shewanella oneidensis, northeast structural3 genomics target sor119.
43	c3k2gA_	Alignment	not modelled	13.3	14	**PDB header:**resiniferatoxin binding protein **Chain:** A: **PDB Molecule:**resiniferatoxin-binding, phosphotriesterase- **PDBTitle:** crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
44	c3ke8A_	Alignment	not modelled	13.1	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-enyl diphosphate **PDBTitle:** crystal structure of isph:hmbpp-complex
45	c2xioA_	Alignment	not modelled	13.0	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
46	d1ee0a2	Alignment	not modelled	12.9	6	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
47	d1y74b1	Alignment	not modelled	12.4	19	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
48	c1cerC_	Alignment	not modelled	12.3	24	**PDB header:**oxidoreductase (aldehyde(d)-nad(a)) **Chain:** C: **PDB Molecule:**holo-d-glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** determinants of enzyme thermostability observed in the2 molecular structure of thermus aquaticus d-glyceraldehyde-3 3-phosphate dehydrogenase at 2.5 angstroms resolution
49	c3m8yC_	Alignment	not modelled	12.2	29	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**phosphopentomutase; **PDBTitle:** phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
50	c3eeqB_	Alignment	not modelled	12.1	18	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative cobalamin biosynthesis protein g **PDBTitle:** crystal structure of a putative cobalamin biosynthesis2 protein g homolog from sulfolobus solfataricus
51	d1e6va2	Alignment	not modelled	12.0	20	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
						PDB header:oxidoreductase **Chain:** C: **PDB Molecule:**pyruvate dehydrogenase complex,

52	c2eq9C_	Alignment	not modelled	11.8	11	dihydrolipoamide **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
53	c2l09A_	Alignment	not modelled	11.7	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**asr4154 protein; **PDBTitle:** solution nmr structure of protein asr4154 from nostoc sp. pcc71202 northeast structural genomics consortium target id nsr143
54	c3tqnC_	Alignment	not modelled	11.6	7	**PDB header:**transcription **Chain:** C: **PDB Molecule:**transcriptional regulator, gntr family; **PDBTitle:** structure of the transcriptional regulator of the gntr family, from2 coxiella burnetii.
55	c3k13A_	Alignment	not modelled	11.4	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
56	c2l82A_	Alignment	not modelled	11.4	44	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**designed protein or32; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
57	c3dqqB_	Alignment	not modelled	11.2	28	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative trna synthase; **PDBTitle:** the crystal structure of the putative trna synthase from salmonella2 typhimurium lt2
58	d1k1da2	Alignment	not modelled	11.2	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**Hydantoinase (dihydropyrimidinase), catalytic domain
59	d2g39a2	Alignment	not modelled	11.1	6	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**CoA transferase alpha subunit-like
60	c2wmyH_	Alignment	not modelled	11.0	17	**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.
61	c3d3uA_	Alignment	not modelled	11.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**4-hydroxybutyrate coa-transferase; **PDBTitle:** crystal structure of 4-hydroxybutyrate coa-transferase (abft-2) from2 porphyromonas gingivalis. northeast structural genomics consortium3 target pgr26
62	c2fekA_	Alignment	not modelled	10.7	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**low molecular weight protein-tyrosine- **PDBTitle:** structure of a protein tyrosine phosphatase
63	c1vbiA_	Alignment	not modelled	10.7	4	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**type 2 malate/lactate dehydrogenase; **PDBTitle:** crystal structure of type 2 malate/lactate dehydrogenase from thermus2 thermophilus hb8
64	c2nvvF_	Alignment	not modelled	10.5	9	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**acetyl-coa hydrolase/transferase family protein; **PDBTitle:** crystal structure of the putative acetyl-coa hydrolase/transferase2 pg1013 from porphyromonas gingivalis, northeast structural genomics3 target pgr16.
65	d1u0ua2	Alignment	not modelled	10.5	12	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
66	c3dxiB_	Alignment	not modelled	10.4	16	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of the n-terminal domain of a putative2 aldolase (bvu_2661) from bacteroides vulgatus
67	d1s7ia_	Alignment	not modelled	10.4	22	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**DGPF domain (Pfam 04946)
68	d1k3ta1	Alignment	not modelled	10.3	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
69	c3dv0I_	Alignment	not modelled	10.2	17	**PDB header:**oxidoreductase/transferase **Chain:** I: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
70	d2p90a1	Alignment	not modelled	10.0	13	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Cgl1923-like **Family:**Cgl1923-like
71	d2w6ka1	Alignment	not modelled	9.8	16	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
72	c3kltB_	Alignment	not modelled	9.6	17	**PDB header:**structural protein **Chain:** B: **PDB Molecule:**vimentin; **PDBTitle:** crystal structure of a vimentin fragment
73	c2zxqA_	Alignment	not modelled	9.6	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** crystal structure of endo-alpha-n-acetylgalactosaminidase2 from bifidobacterium longum (engbf)
74	c2eq7C_	Alignment	not modelled	9.6	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**2-oxoglutarate dehydrogenase e2 component; **PDBTitle:** crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
75	d1e6ya2	Alignment	not modelled	9.2	25	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain
						PDB header:biosynthetic protein

76	c3by5A_	Alignment	not modelled	9.2	13	**Chain:** A: **PDB Molecule:**cobalamin biosynthesis protein; **PDBTitle:** crystal structure of cobalamin biosynthesis protein chig from2 agrobacterium tumefaciens str. c58
77	d3by5a1	Alignment	not modelled	9.2	13	**Fold:**CobE/GbiG C-terminal domain-like **Superfamily:**CobE/GbiG C-terminal domain-like **Family:**CobE/GbiG C-terminal domain-like
78	d1uxda_	Alignment	not modelled	9.1	5	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**GalR/LacI-like bacterial regulator
79	c2pijB_	Alignment	not modelled	9.0	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**prophage pfl 6 cro; **PDBTitle:** structure of the cro protein from prophage pfl 6 in pseudomonas2 fluorescens pf-5
80	c2k29A_	Alignment	not modelled	8.9	19	**PDB header:**transcription **Chain:** A: **PDB Molecule:**antitoxin relb; **PDBTitle:** structure of the dbd domain of e. coli antitoxin relb
81	d1w85i_	Alignment	not modelled	8.9	17	**Fold:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Superfamily:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex **Family:**Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
82	d2axoa1	Alignment	not modelled	8.2	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Atu2684-like
83	d1d1la_	Alignment	not modelled	8.2	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
84	c3ecqA_	Alignment	not modelled	8.1	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endo-alpha-n-acetylgalactosaminidase; **PDBTitle:** endo-alpha-n-acetylgalactosaminidase from streptococcus pneumoniae:2 semet structure
85	c3fcrA_	Alignment	not modelled	8.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative aminotransferase; **PDBTitle:** crystal structure of putative aminotransferase (yp_614685.1) from2 silicibacter sp. tm1040 at 1.80 a resolution
86	c3ggmB_	Alignment	not modelled	7.9	50	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein bt9727_2919; **PDBTitle:** crystal structure of bt9727_2919 from bacillus2 thuringiensis subsp. northeast structural genomics target3 bur228b
87	c3nuiA_	Alignment	not modelled	7.9	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**pyruvate transaminase; **PDBTitle:** crystal structure of omega-transferase from vibrio fluvialis js17
88	c3n2lA_	Alignment	not modelled	7.9	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**orotate phosphoribosyltransferase; **PDBTitle:** 2.1 angstrom resolution crystal structure of an orotate2 phosphoribosyltransferase (pyre) from vibrio cholerae o1 biovar eltor3 str. n16961
89	c1w3dA_	Alignment	not modelled	7.8	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dihydrolipoyllysine-residue acetyltransferase **PDBTitle:** nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
90	d3buxb3	Alignment	not modelled	7.7	32	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
91	c3cieC_	Alignment	not modelled	7.6	11	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**glyceraldehyde-3-phosphate dehydrogenase; **PDBTitle:** crystal structure of glyceraldehyde 3-phosphate2 dehydrogenase from cryptosporidium parvum
92	d1bi5a2	Alignment	not modelled	7.5	8	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
93	d1vefa1	Alignment	not modelled	7.5	7	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
94	c2gi4A_	Alignment	not modelled	7.3	7	**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.
95	d2imla1	Alignment	not modelled	7.1	23	**Fold:**Split barrel-like **Superfamily:**FMN-binding split barrel **Family:**MTH863-like
96	d4croa_	Alignment	not modelled	7.0	28	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**Phage repressors
97	d1u0ma2	Alignment	not modelled	6.9	11	**Fold:**Thiolase-like **Superfamily:**Thiolase-like **Family:**Chalcone synthase-like
98	d1xg8a_	Alignment	not modelled	6.9	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**YuzD-like
99	d1hbna2	Alignment	not modelled	6.8	26	**Fold:**Ferredoxin-like **Superfamily:**Methyl-coenzyme M reductase subunits **Family:**Methyl-coenzyme M reductase alpha and beta chain N-terminal domain