



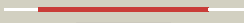




























# Phyre2

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Description	P06988
Date	Thu Jan 5 10:59:46 GMT 2012
Unique Job ID	8791e5b37cf5d74e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1k75a_</a>	 Alignment		100.0	99	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> L-histidinol dehydrogenase HisD
2	<a href="#">c2w8qA_</a>	 Alignment		99.1	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase, <b>PDBTitle:</b> the crystal structure of human ssadh in complex with ssa.
3	<a href="#">d1ky8a_</a>	 Alignment		99.0	18	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
4	<a href="#">d1euha_</a>	 Alignment		98.9	14	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
5	<a href="#">c3ek1C_</a>	 Alignment		98.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase from brucella2 melitensis biovar abortus 2308
6	<a href="#">c3k2wD_</a>	 Alignment		98.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> betaine-aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of betaine-aldehyde dehydrogenase from2 pseudoalteromonas atlantica t6c
7	<a href="#">c3efvC_</a>	 Alignment		98.8	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> putative succinate-semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of a putative succinate-semialdehyde dehydrogenase2 from salmonella typhimurium lt2 with bound nad
8	<a href="#">d1o04a_</a>	 Alignment		98.8	17	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
9	<a href="#">c3lnsD_</a>	 Alignment		98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> benzaldehyde dehydrogenase; <b>PDBTitle:</b> benzaldehyde dehydrogenase, a class 3 aldehyde dehydrogenase, with2 bound nadp+ and benzoate adduct
10	<a href="#">c2d4eB_</a>	 Alignment		98.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 5-carboxymethyl-2-hydroxymuconate semialdehyde <b>PDBTitle:</b> crystal structure of the hpcc from thermus thermophilus hb8
11	<a href="#">c3k9dD_</a>	 Alignment		98.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of probable aldehyde dehydrogenase from listeria2 monocytogenes egd-e

12	<a href="#">c3jz4C_</a>	Alignment		98.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase [nadp+]; <b>PDBTitle:</b> crystal structure of e. coli nadp dependent enzyme
13	<a href="#">d1ag8a_</a>	Alignment		98.7	18	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
14	<a href="#">c3prlD_</a>	Alignment		98.7	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> nadp-dependent glyceraldehyde-3-phosphate dehydrogenase; <b>PDBTitle:</b> crystal structure of nadp-dependent glyceraldehyde-3-phosphate2 dehydrogenase from bacillus halodurans c-125
15	<a href="#">c3rosA_</a>	Alignment		98.7	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad-dependent aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent aldehyde dehydrogenase from2 lactobacillus acidophilus
16	<a href="#">d1ad3a_</a>	Alignment		98.7	14	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
17	<a href="#">c1vluB_</a>	Alignment		98.6	11	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> gamma-glutamyl phosphate reductase; <b>PDBTitle:</b> crystal structure of gamma-glutamyl phosphate reductase (yor323c) from2 saccharomyces cerevisiae at 2.40 a resolution
18	<a href="#">c3r31A_</a>	Alignment		98.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of betaine aldehyde dehydrogenase from agrobacterium2 tumefaciens
19	<a href="#">d1a4sa_</a>	Alignment		98.6	16	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
20	<a href="#">c2hg2A_</a>	Alignment		98.6	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase a; <b>PDBTitle:</b> structure of lactaldehyde dehydrogenase
21	<a href="#">c3iwbB_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aminoaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aminoaldehyde dehydrogenase 1 from2 pisum sativum (psamadh1)
22	<a href="#">c3ed6B_</a>	Alignment	not modelled	98.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> 1.7 angstrom resolution crystal structure of betaine aldehyde2 dehydrogenase (betb) from staphylococcus aureus
23	<a href="#">d1bxsA_</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
24	<a href="#">c3ifgH_</a>	Alignment	not modelled	98.6	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of succinate-semialdehyde dehydrogenase from2 burkholderia pseudomallei, part 1 of 2
25	<a href="#">c3pqaA_</a>	Alignment	not modelled	98.5	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> lactaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of glyceraldehyde-3-phosphate dehydrogenase gapn2 from methanocaldococcus jannaschii dsm 2661
26	<a href="#">d1o20a_</a>	Alignment	not modelled	98.4	13	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
27	<a href="#">c2jg7G_</a>	Alignment	not modelled	98.4	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> antiquitin; <b>PDBTitle:</b> crystal structure of seabream antiquitin and elucidation of2 its substrate specificity
28	<a href="#">c3rh9A_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> succinate-semialdehyde dehydrogenase (nad(p)(+));

						<b>PDBTitle:</b> the crystal structure of oxidoreductase from marinobacter aquaeolei
29	<a href="#">dluzba_</a>	Alignment	not modelled	98.4	21	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
30	<a href="#">c3r64A_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nad dependent benzaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of a nad-dependent benzaldehyde dehydrogenase from2 corynebacterium glutamicum
31	<a href="#">c3v4cB_</a>	Alignment	not modelled	98.4	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase (nadh+); <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
32	<a href="#">d1o9ja_</a>	Alignment	not modelled	98.3	16	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
33	<a href="#">c2o2qA_</a>	Alignment	not modelled	98.3	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formyltetrahydrofolate dehydrogenase; <b>PDBTitle:</b> crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
34	<a href="#">c3b4wA_</a>	Alignment	not modelled	98.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis aldehyde dehydrogenase2 complexed with nad+
35	<a href="#">d1wnda_</a>	Alignment	not modelled	98.2	18	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
36	<a href="#">c3i44A_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase from bartonella2 henselae at 2.0a resolution
37	<a href="#">c3qanB_</a>	Alignment	not modelled	98.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-pyrroline-5-carboxylate dehydrogenase 1; <b>PDBTitle:</b> crystal structure of 1-pyrroline-5-carboxylate dehydrogenase from2 bacillus halodurans
38	<a href="#">c3ju8B_</a>	Alignment	not modelled	98.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> succinylglutamic semialdehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of succinylglutamic semialdehyde dehydrogenase from2 pseudomonas aeruginosa.
39	<a href="#">c1t90B_</a>	Alignment	not modelled	98.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable methylmalonate-semialdehyde dehydrogenase <b>PDBTitle:</b> crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
40	<a href="#">d1vlua_</a>	Alignment	not modelled	98.1	12	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
41	<a href="#">d1bi9a_</a>	Alignment	not modelled	98.1	15	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
42	<a href="#">c2ve5H_</a>	Alignment	not modelled	98.1	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> H: <b>PDB Molecule:</b> betaine aldehyde dehydrogenase; <b>PDBTitle:</b> crystallographic structure of betaine aldehyde2 dehydrogenase from pseudomonas aeruginosa
43	<a href="#">c3hazA_</a>	Alignment	not modelled	98.0	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> proline dehydrogenase; <b>PDBTitle:</b> crystal structure of bifunctional proline utilization a2 (puta) protein
44	<a href="#">c2h5gA_</a>	Alignment	not modelled	97.9	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> delta 1-pyrroline-5-carboxylate synthetase; <b>PDBTitle:</b> crystal structure of human pyrroline-5-carboxylate synthetase
45	<a href="#">c3my7A_</a>	Alignment	not modelled	97.8	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase/acetaldehyde dehydrogenase; <b>PDBTitle:</b> the crystal structure of the acdh domain of an alcohol dehydrogenase2 from vibrio parahaemolyticus to 2.25a
46	<a href="#">d1ez0a_</a>	Alignment	not modelled	97.5	14	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
47	<a href="#">c2vroB_</a>	Alignment	not modelled	96.2	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of aldehyde dehydrogenase from2 burkholderia xenovorans lb400
48	<a href="#">c2ax3A_</a>	Alignment	not modelled	81.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein tm0922; <b>PDBTitle:</b> crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
49	<a href="#">d2csua2</a>	Alignment	not modelled	80.3	13	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
50	<a href="#">d1jcea1</a>	Alignment	not modelled	66.0	34	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
51	<a href="#">d2e8aa1</a>	Alignment	not modelled	59.4	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
52	<a href="#">d1bupa1</a>	Alignment	not modelled	58.5	23	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
53	<a href="#">c1e1cA_</a>	Alignment	not modelled	58.5	20	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> methylmalonyl-coa mutase alpha chain; <b>PDBTitle:</b> methylmalonyl-coa mutase h244a mutant

54	<a href="#">d3bc8a1</a>	Alignment	not modelled	48.7	9	<b>Fold:</b> PLP-dependent transferase-like <b>Superfamily:</b> PLP-dependent transferases <b>Family:</b> SepSecS-like
55	<a href="#">c2q8nB</a>	Alignment	not modelled	42.2	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> crystal structure of glucose-6-phosphate isomerase (ec2 5.3.1.9) (tm1385) from thermotoga maritima at 1.82 a3 resolution
56	<a href="#">c3ljkA</a>	Alignment	not modelled	37.8	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> glucose-6-phosphate isomerase from francisella tularensis.
57	<a href="#">d1oi7a2</a>	Alignment	not modelled	37.6	15	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
58	<a href="#">c2duwA</a>	Alignment	not modelled	36.2	12	<b>PDB header:</b> ligand binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> putative coa-binding protein; <b>PDBTitle:</b> solution structure of putative coa-binding protein of2 klebsiella pneumoniae
59	<a href="#">c3ic5A</a>	Alignment	not modelled	35.6	23	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative saccharopine dehydrogenase; <b>PDBTitle:</b> n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
60	<a href="#">c2csuB</a>	Alignment	not modelled	32.5	13	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> 457aa long hypothetical protein; <b>PDBTitle:</b> crystal structure of ph0766 from pyrococcus horikoshii ot3
61	<a href="#">c2dc0A</a>	Alignment	not modelled	32.3	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable amidase; <b>PDBTitle:</b> crystal structure of amidase
62	<a href="#">d1vdra</a>	Alignment	not modelled	31.0	18	<b>Fold:</b> Dihydrofolate reductase-like <b>Superfamily:</b> Dihydrofolate reductase-like <b>Family:</b> Dihydrofolate reductases
63	<a href="#">d1mt5a</a>	Alignment	not modelled	30.9	13	<b>Fold:</b> Amidase signature (AS) enzymes <b>Superfamily:</b> Amidase signature (AS) enzymes <b>Family:</b> Amidase signature (AS) enzymes
64	<a href="#">c3ketA</a>	Alignment	not modelled	30.8	17	<b>PDB header:</b> transcription/dna <b>Chain:</b> A: <b>PDB Molecule:</b> redox-sensing transcriptional repressor rex; <b>PDBTitle:</b> crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
65	<a href="#">d2dt5a2</a>	Alignment	not modelled	29.2	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> Transcriptional repressor Rex, C-terminal domain
66	<a href="#">c3jstA</a>	Alignment	not modelled	27.9	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative pterin-4-alpha-carbinolamine dehydratase; <b>PDBTitle:</b> crystal structure of transcriptional coactivator/pterin dehydratase2 from brucella melitensis
67	<a href="#">d1ulza2</a>	Alignment	not modelled	27.3	27	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
68	<a href="#">d1dkgd1</a>	Alignment	not modelled	26.9	25	<b>Fold:</b> Ribonuclease H-like motif <b>Superfamily:</b> Actin-like ATPase domain <b>Family:</b> Actin/HSP70
69	<a href="#">d1xpmal</a>	Alignment	not modelled	25.1	13	<b>Fold:</b> Thiolase-like <b>Superfamily:</b> Thiolase-like <b>Family:</b> Chalcone synthase-like
70	<a href="#">c2khoA</a>	Alignment	not modelled	24.7	25	<b>PDB header:</b> chaperone <b>Chain:</b> A: <b>PDB Molecule:</b> heat shock protein 70; <b>PDBTitle:</b> nmr-rdc / xray structure of e. coli hsp70 (dnak) chaperone2 (1-605) complexed with adp and substrate
71	<a href="#">c3lehA</a>	Alignment	not modelled	24.7	13	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> putative hydroxymethylglutaryl-coa synthase; <b>PDBTitle:</b> the crystal structure of smu.943c from streptococcus mutans ua159
72	<a href="#">c1x9eB</a>	Alignment	not modelled	24.4	14	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> hmg-coa synthase; <b>PDBTitle:</b> crystal structure of hmg-coa synthase from enterococcus2 faecalis
73	<a href="#">d2ielal</a>	Alignment	not modelled	24.1	29	<b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> Adenine nucleotide alpha hydrolases-like <b>Family:</b> Universal stress protein-like
74	<a href="#">d1sp8a1</a>	Alignment	not modelled	23.7	16	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
75	<a href="#">c3ilmD</a>	Alignment	not modelled	23.7	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> alr3790 protein; <b>PDBTitle:</b> crystal structure of the alr3790 protein from anabaena sp. northeast2 structural genomics consortium target nsr437h
76	<a href="#">c2vyaB</a>	Alignment	not modelled	21.9	13	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> fatty-acid amide hydrolase 1; <b>PDBTitle:</b> crystal structure of fatty acid amide hydrolase conjugated2 with the drug-like inhibitor pf-750
77	<a href="#">d1k1va</a>	Alignment	not modelled	21.2	11	<b>Fold:</b> A DNA-binding domain in eukaryotic transcription factors <b>Superfamily:</b> A DNA-binding domain in eukaryotic transcription factors <b>Family:</b> A DNA-binding domain in eukaryotic transcription factors
78	<a href="#">d1oi7a1</a>	Alignment	not modelled	20.1	17	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
						<b>Fold:</b> PreATP-grasp domain

79	<a href="#">d2j9ga2</a>	Alignment	not modelled	19.3	19	<b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
80	<a href="#">c3ff1B</a>	Alignment	not modelled	19.2	24	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glucose-6-phosphate isomerase; <b>PDBTitle:</b> structure of glucose 6-phosphate isomerase from staphylococcus aureus
81	<a href="#">d1iuka</a>	Alignment	not modelled	18.5	15	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
82	<a href="#">c3mogA</a>	Alignment	not modelled	18.2	13	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 3-hydroxybutyryl-coa dehydrogenase; <b>PDBTitle:</b> crystal structure of 3-hydroxybutyryl-coa dehydrogenase from2 escherichia coli k12 substr. mg1655
83	<a href="#">c2ebbA</a>	Alignment	not modelled	18.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine2 dehydratase (pterin carbinolamine dehydratase) from3 geobacillus kaustophilus hta426
84	<a href="#">d1y81a1</a>	Alignment	not modelled	17.7	16	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
85	<a href="#">c3h0rP</a>	Alignment	not modelled	17.6	11	<b>PDB header:</b> ligase <b>Chain:</b> P: <b>PDB Molecule:</b> glutamyl-trna(gln) amidotransferase subunit a; <b>PDBTitle:</b> structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
86	<a href="#">c2dt5A</a>	Alignment	not modelled	17.5	13	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> at-rich dna-binding protein; <b>PDBTitle:</b> crystal structure of tha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
87	<a href="#">c1xtB</a>	Alignment	not modelled	17.1	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-hydroxy-3-methylglutaryl-coa synthase; <b>PDBTitle:</b> staphylococcus aureus 3-hydroxy-3-methylglutaryl-coa2 synthase
88	<a href="#">c1zczA</a>	Alignment	not modelled	17.1	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> peroxisomal bifunctional enzyme; <b>PDBTitle:</b> crystal structure of 3-hydroxyacyl-coa dehydrogenase
89	<a href="#">c3hl2D</a>	Alignment	not modelled	17.0	11	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> o-phosphoseryl-trna(sec) selenium transferase; <b>PDBTitle:</b> the crystal structure of the human sepsecs-trnasec complex
90	<a href="#">d1sqda1</a>	Alignment	not modelled	16.8	13	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
91	<a href="#">c3k2gA</a>	Alignment	not modelled	16.2	22	<b>PDB header:</b> resiniferatoxin binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> resiniferatoxin-binding, phosphotriesterase- <b>PDBTitle:</b> crystal structure of a resiniferatoxin-binding protein from2 rhodobacter sphaeroides
92	<a href="#">d1sqia1</a>	Alignment	not modelled	16.1	7	<b>Fold:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Superfamily:</b> Glyoxalase/Bleomycin resistance protein/Dihydroxybiphenyl dioxygenase <b>Family:</b> Extradiol dioxygenases
93	<a href="#">d1euca1</a>	Alignment	not modelled	15.9	31	<b>Fold:</b> NAD(P)-binding Rossmann-fold domains <b>Superfamily:</b> NAD(P)-binding Rossmann-fold domains <b>Family:</b> CoA-binding domain
94	<a href="#">c2kw3A</a>	Alignment	not modelled	15.8	31	<b>PDB header:</b> dna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> dna-binding protein rfx5; <b>PDBTitle:</b> heterotrimeric interaction between rfx5 and rfxap
95	<a href="#">c3nkgA</a>	Alignment	not modelled	15.4	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein geba250068378; <b>PDBTitle:</b> crystal structure of geba250068378 from sulfurospirillum deleyianum
96	<a href="#">c3en0A</a>	Alignment	not modelled	14.9	15	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> cyanophycinase; <b>PDBTitle:</b> the structure of cyanophycinase
97	<a href="#">c3tl8K</a>	Alignment	not modelled	14.8	18	<b>PDB header:</b> transferase/ligase <b>Chain:</b> K: <b>PDB Molecule:</b> effector protein hopab2; <b>PDBTitle:</b> the avrptob-bak1 complex reveals two structurally similar2 kinaseinteracting domains in a single type iii effector
98	<a href="#">d2gi3a1</a>	Alignment	not modelled	14.8	17	<b>Fold:</b> Amidase signature (AS) enzymes <b>Superfamily:</b> Amidase signature (AS) enzymes <b>Family:</b> Amidase signature (AS) enzymes
99	<a href="#">c2v6uB</a>	Alignment	not modelled	14.6	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> pterin-4a-carbinolamine dehydratase; <b>PDBTitle:</b> high resolution crystal structure of pterin-4a-2 carbinolamine dehydratase from toxoplasma gondii