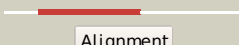



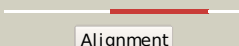



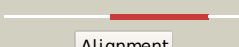

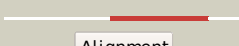













# Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A9Q7
Date	Thu Jan 5 11:11:00 GMT 2012
Unique Job ID	7bdde0d10c8225b4

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3k9dD_</a>	 Alignment		100.0	46	<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
2	<a href="#">c3my7A_</a>	 Alignment		100.0	75	<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
3	<a href="#">c3bfjK_</a>	 Alignment		100.0	34	<b>PDB header:</b> oxidoreductase <b>Chain:</b> K; <b>PDB Molecule:</b> 1,3-propanediol oxidoreductase; <b>PDBTitle:</b> crystal structure analysis of 1,3-propanediol oxidoreductase
4	<a href="#">c3ox4D_</a>	 Alignment		100.0	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D; <b>PDB Molecule:</b> alcohol dehydrogenase 2; <b>PDBTitle:</b> structures of iron-dependent alcohol dehydrogenase 2 from zymomonas2 mobilis zm4 complexed with nad cofactor
5	<a href="#">d1rrma_</a>	 Alignment		100.0	32	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
6	<a href="#">d1vlja_</a>	 Alignment		100.0	25	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
7	<a href="#">d1oj7a_</a>	 Alignment		100.0	22	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
8	<a href="#">c3hazA_</a>	 Alignment		100.0	18	<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
9	<a href="#">d1uzba_</a>	 Alignment		100.0	23	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
10	<a href="#">c2jg7G_</a>	 Alignment		100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G; <b>PDB Molecule:</b> antiquitin; <b>PDBTitle:</b> crystal structure of seabream antiquitin and elucidation of its substrate specificity
11	<a href="#">c3qanB_</a>	 Alignment		100.0	20	<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



28	<a href="#">d1euha_</a>	Alignment	not modelled	100.0	21	<b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
29	<a href="#">d1wnda_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
30	<a href="#">d1ez0a_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
31	<a href="#">c2o2qA_</a>	Alignment	not modelled	100.0	19	<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
32	<a href="#">c1t90B_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> probable methylmalonate-semialdehyde <b>PDBTitle:</b> crystal structure of methylmalonate semialdehyde2 dehydrogenase from bacillus subtilis
33	<a href="#">c3iv7B_</a>	Alignment	not modelled	100.0	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase iv; <b>PDBTitle:</b> crystal structure of iron-containing alcohol dehydrogenase2 (np_602249.1) from corynebacterium glutamicum atcc 13032 kitasato at3 2.07 a resolution
34	<a href="#">c3rosA_</a>	Alignment	not modelled	100.0	19	<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
35	<a href="#">d1ag8a_</a>	Alignment	not modelled	100.0	19	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
36	<a href="#">d1ky8a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
37	<a href="#">c3pqaA_</a>	Alignment	not modelled	100.0	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
38	<a href="#">c3r31A_</a>	Alignment	not modelled	100.0	21	<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
39	<a href="#">c3rh9A_</a>	Alignment	not modelled	100.0	17	<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
40	<a href="#">c3i44A_</a>	Alignment	not modelled	100.0	19	<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
41	<a href="#">c3jz4C_</a>	Alignment	not modelled	100.0	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
42	<a href="#">c3b4wA_</a>	Alignment	not modelled	100.0	20	<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+
43	<a href="#">d1bi9a_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
44	<a href="#">c2hg2A_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> aldehyde dehydrogenase a; <b>PDBTitle:</b> structure of lactaldehyde dehydrogenase
45	<a href="#">c3k2wD_</a>	Alignment	not modelled	100.0	21	<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
46	<a href="#">c3v4cB_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> aldehyde dehydrogenase (nadp+); <b>PDBTitle:</b> crystal structure of a semialdehyde dehydrogenase from sinorhizobium2 meliloti 1021
47	<a href="#">c3efvC_</a>	Alignment	not modelled	100.0	19	<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
48	<a href="#">c3ju8B_</a>	Alignment	not modelled	100.0	18	<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.
49	<a href="#">d1o20a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
50	<a href="#">c3jzdA_</a>	Alignment	not modelled	100.0	26	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> iron-containing alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of putative alcohol dehydrogenase (yp_298327.1) from2 ralstonia eutropha jmp134 at 2.10 a resolution
51	<a href="#">c3r64A_</a>	Alignment	not modelled	100.0	21	<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
52	<a href="#">c2vroB_</a>	Alignment	not modelled	100.0	14	<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

53	<a href="#">dljq5a_</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
54	<a href="#">c3lnsD_</a>	Alignment	not modelled	100.0	16	<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
55	<a href="#">d1vlua_</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> ALDH-like
56	<a href="#">c2h5gA_</a>	Alignment	not modelled	100.0	19	<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
57	<a href="#">c1vlub_</a>	Alignment	not modelled	100.0	17	<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
58	<a href="#">c3uhjE_</a>	Alignment	not modelled	100.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> E: <b>PDB Molecule:</b> probable glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of a probable glycerol dehydrogenase from2 sinorhizobium meliloti 1021
59	<a href="#">d1kq3a_</a>	Alignment	not modelled	100.0	24	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Iron-containing alcohol dehydrogenase
60	<a href="#">c1ta9A_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol dehydrogenase from schizosaccharomyces2 pombe
61	<a href="#">c3ce9A_</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycerol dehydrogenase; <b>PDBTitle:</b> crystal structure of glycerol dehydrogenase (np_348253.1) from2 clostridium acetobutylicum at 2.37 a resolution
62	<a href="#">c3okfA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinase synthase; <b>PDBTitle:</b> 2.5 angstrom resolution crystal structure of 3-dehydroquinase synthase2 (arob) from vibrio cholerae
63	<a href="#">c1xahA_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinase synthase; <b>PDBTitle:</b> crystal structure of staphylococcus aureus 3-dehydroquinase2 synthase (dhqs) in complex with zn2+ and nad+
64	<a href="#">d1sg6a_</a>	Alignment	not modelled	100.0	18	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Dehydroquinase synthase, DHQS
65	<a href="#">c2gruB_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-deoxy-scylo-inosose synthase; <b>PDBTitle:</b> crystal structure of 2-deoxy-scylo-inosose synthase2 complexed with carbagluco-6-phosphate, nad+ and co2+
66	<a href="#">c3clhA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinase synthase; <b>PDBTitle:</b> crystal structure of 3-dehydroquinase synthase (dhqs)from2 helicobacter pylori
67	<a href="#">d1ujna_</a>	Alignment	not modelled	100.0	17	<b>Fold:</b> Dehydroquinase synthase-like <b>Superfamily:</b> Dehydroquinase synthase-like <b>Family:</b> Dehydroquinase synthase, DHQS
68	<a href="#">d2jgra1</a>	Alignment	not modelled	96.8	17	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
69	<a href="#">d2bona1</a>	Alignment	not modelled	96.7	18	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
70	<a href="#">c3orsD_</a>	Alignment	not modelled	96.6	18	<b>PDB header:</b> isomerase,biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> crystal structure of n5-carboxyaminoimidazole ribonucleotide mutase2 from staphylococcus aureus
71	<a href="#">d1o4va_</a>	Alignment	not modelled	96.4	24	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
72	<a href="#">d1qcza_</a>	Alignment	not modelled	96.4	26	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
73	<a href="#">d1u11a_</a>	Alignment	not modelled	96.4	18	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
74	<a href="#">c2fw9A_</a>	Alignment	not modelled	96.4	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n5-carboxyaminoimidazole ribonucleotide mutase; <b>PDBTitle:</b> structure of pure (n5-carboxyaminoimidazole ribonucleotide mutase)2 h59f from the acidophilic bacterium acetobacter aceti, at ph 8
75	<a href="#">c3lp6D_</a>	Alignment	not modelled	96.4	21	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of rv3275c-e60a from mycobacterium tuberculosis at2 1.7a resolution
76	<a href="#">d2p1ra1</a>	Alignment	not modelled	96.3	17	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like

77	<a href="#">c3rggD_</a>	Alignment	not modelled	96.1	24	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase, pure protein; <b>PDBTitle:</b> crystal structure of treponema denticola pure bound to air
78	<a href="#">d1k75a_</a>	Alignment	not modelled	95.9	16	<b>Fold:</b> ALDH-like <b>Superfamily:</b> ALDH-like <b>Family:</b> L-histidinol dehydrogenase HisD
79	<a href="#">c2bonB_</a>	Alignment	not modelled	95.8	18	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> lipid kinase; <b>PDBTitle:</b> structure of an escherichia coli lipid kinase (yegs)
80	<a href="#">d1u0ta_</a>	Alignment	not modelled	95.8	27	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> NAD kinase-like
81	<a href="#">d1ewka_</a>	Alignment	not modelled	95.8	10	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
82	<a href="#">c3trhl_</a>	Alignment	not modelled	95.8	22	<b>PDB header:</b> lyase <b>Chain:</b> I: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase <b>PDBTitle:</b> structure of a phosphoribosylaminoimidazole carboxylase catalytic2 subunit (pure) from coxiella burnetii
83	<a href="#">d1xmpa_</a>	Alignment	not modelled	95.7	22	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE) <b>Family:</b> N5-CAIR mutase (phosphoribosylaminoimidazole carboxylase, PurE)
84	<a href="#">c2qv7A_</a>	Alignment	not modelled	95.5	27	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> diacylglycerol kinase dgkb; <b>PDBTitle:</b> crystal structure of diacylglycerol kinase dgkb in complex with adp2 and mg
85	<a href="#">d1qo0a_</a>	Alignment	not modelled	95.2	10	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
86	<a href="#">c3s40C_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> diacylglycerol kinase; <b>PDBTitle:</b> the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. Sterne
87	<a href="#">c3h5lB_</a>	Alignment	not modelled	94.7	19	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> putative branched-chain amino acid abc <b>PDBTitle:</b> crystal structure of a putative branched-chain amino acid2 abc transporter from silicibacter pomeroyi
88	<a href="#">c2h31A_</a>	Alignment	not modelled	94.7	13	<b>PDB header:</b> ligase, lyase <b>Chain:</b> A: <b>PDB Molecule:</b> multifunctional protein ade2; <b>PDBTitle:</b> crystal structure of human paics, a bifunctional carboxylase and2 synthetase in purine biosynthesis
89	<a href="#">c3q41B_</a>	Alignment	not modelled	93.9	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate [nmda] receptor subunit zeta-1; <b>PDBTitle:</b> crystal structure of the glun1 n-terminal domain (ntd)
90	<a href="#">c3i45A_</a>	Alignment	not modelled	93.6	13	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> twin-arginine translocation pathway signal protein; <b>PDBTitle:</b> crystal structure of putative twin-arginine translocation pathway2 signal protein from rhodospirillum rubrum atcc 11170
91	<a href="#">d2qv7a1</a>	Alignment	not modelled	93.4	29	<b>Fold:</b> NAD kinase/diacylglycerol kinase-like <b>Superfamily:</b> NAD kinase/diacylglycerol kinase-like <b>Family:</b> Diacylglycerol kinase-like
92	<a href="#">c2j37W_</a>	Alignment	not modelled	93.3	21	<b>PDB header:</b> ribosome <b>Chain:</b> W: <b>PDB Molecule:</b> signal recognition particle 54 kda protein <b>PDBTitle:</b> model of mammalian srp bound to 80s rncs
93	<a href="#">d1gvea_</a>	Alignment	not modelled	93.3	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> NAD(P)-linked oxidoreductase <b>Family:</b> Aldo-keto reductases (NADP)
94	<a href="#">d1vh3a_</a>	Alignment	not modelled	93.2	19	<b>Fold:</b> Nucleotide-diphospho-sugar transferases <b>Superfamily:</b> Nucleotide-diphospho-sugar transferases <b>Family:</b> Cytidylyltransferase
95	<a href="#">c2j289_</a>	Alignment	not modelled	92.8	19	<b>PDB header:</b> ribosome <b>Chain:</b> 9: <b>PDB Molecule:</b> signal recognition particle 54; <b>PDBTitle:</b> model of e. coli srp bound to 70s rncs
96	<a href="#">c2ywxA_</a>	Alignment	not modelled	92.8	27	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylaminoimidazole carboxylase catalytic subunit; <b>PDBTitle:</b> crystal structure of phosphoribosylaminoimidazole carboxylase2 catalytic subunit from methanocaldococcus jannaschii
97	<a href="#">c3snrA_</a>	Alignment	not modelled	92.6	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular ligand-binding receptor; <b>PDBTitle:</b> rpd_1889 protein, an extracellular ligand-binding receptor from2 rhodopseudomonas palustris.
98	<a href="#">c2iy3A_</a>	Alignment	not modelled	92.1	19	<b>PDB header:</b> rna-binding <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition particle protein ffh; <b>PDBTitle:</b> structure of the e. coli signal recognition particle2 bound to a translating ribosome
99	<a href="#">c2an1D_</a>	Alignment	not modelled	92.0	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> putative kinase; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
100	<a href="#">c3ip5A_</a>	Alignment	not modelled	91.7	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein (amino acid); <b>PDBTitle:</b> structure of atu2422-gaba receptor in complex with alanine
101	<a href="#">c3dm5A_</a>	Alignment	not modelled	91.7	19	<b>PDB header:</b> rna binding protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> structures of srp54 and srp19, the two proteins



						assembling2 the ribonucleic core of the signal recognition particle3 from the archaeon pyrococcus furiosus.
102	<a href="#">c2e4wA</a>	Alignment	not modelled	91.6	4	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> metabotropic glutamate receptor 3; <b>PDBTitle:</b> crystal structure of the extracellular region of the group ii2 metabotropic glutamate receptor complexed with 1s,3s-acpd
103	<a href="#">c3i09A</a>	Alignment	not modelled	91.4	18	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> periplasmic branched-chain amino acid-binding protein; <b>PDBTitle:</b> crystal structure of a periplasmic binding protein (bma2936) from2 burkholderia mallei at 1.80 a resolution
104	<a href="#">c3cf4G</a>	Alignment	not modelled	91.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> G: <b>PDB Molecule:</b> acetyl-coa decarboxylase/synthase epsilon subunit; <b>PDBTitle:</b> structure of the codh component of the m. barkeri acds complex
105	<a href="#">c3dcjA</a>	Alignment	not modelled	91.1	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable 5'-phosphoribosylglycinamide <b>PDBTitle:</b> crystal structure of glycinamide formyltransferase (purn)2 from mycobacterium tuberculosis in complex with 5-methyl-5,3 6,7,8-tetrahydrofolic acid derivative
106	<a href="#">c3sg0A</a>	Alignment	not modelled	90.9	14	<b>PDB header:</b> signaling protein <b>Chain:</b> A: <b>PDB Molecule:</b> extracellular ligand-binding receptor; <b>PDBTitle:</b> the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2
107	<a href="#">c3eafA</a>	Alignment	not modelled	90.8	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, substrate binding protein; <b>PDBTitle:</b> crystal structure of abc transporter, substrate binding protein2 aeropyrum pernix
108	<a href="#">c3tqrA</a>	Alignment	not modelled	90.2	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phosphoribosylglycinamide formyltransferase; <b>PDBTitle:</b> structure of the phosphoribosylglycinamide formyltransferase (purn) in2 complex with ches from coxiella burnetii
109	<a href="#">d1pyfa</a>	Alignment	not modelled	90.2	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> NAD(P)-linked oxidoreductase <b>Family:</b> Aldo-keto reductases (NADP)
110	<a href="#">d1ovma1</a>	Alignment	not modelled	90.0	18	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
111	<a href="#">c3n0wA</a>	Alignment	not modelled	89.9	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc branched chain amino acid family transporter, <b>PDBTitle:</b> crystal structure of a branched chain amino acid abc transporter2 periplasmic ligand-binding protein (bx_e_c0949) from burkholderia3 xenovorans lb400 at 1.88 a resolution
112	<a href="#">d1a9xa4</a>	Alignment	not modelled	89.9	23	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
113	<a href="#">c1qzwC</a>	Alignment	not modelled	89.6	24	<b>PDB header:</b> signaling protein/rna <b>Chain:</b> C: <b>PDB Molecule:</b> signal recognition 54 kda protein; <b>PDBTitle:</b> crystal structure of the complete core of archaeal srp and2 implications for inter-domain communication
114	<a href="#">d1usga</a>	Alignment	not modelled	89.3	14	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
115	<a href="#">d1pfka</a>	Alignment	not modelled	89.3	19	<b>Fold:</b> Phosphofructokinase <b>Superfamily:</b> Phosphofructokinase <b>Family:</b> Phosphofructokinase
116	<a href="#">c2q5cA</a>	Alignment	not modelled	89.2	14	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> ntrc family transcriptional regulator; <b>PDBTitle:</b> crystal structure of ntrc family transcriptional regulator from2 clostridium acetobutylicum
117	<a href="#">d2ji7a1</a>	Alignment	not modelled	89.2	17	<b>Fold:</b> DHS-like NAD/FAD-binding domain <b>Superfamily:</b> DHS-like NAD/FAD-binding domain <b>Family:</b> Pyruvate oxidase and decarboxylase, middle domain
118	<a href="#">c3rfqC</a>	Alignment	not modelled	88.6	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> pterin-4-alpha-carbinolamine dehydratase moab2; <b>PDBTitle:</b> crystal structure of pterin-4-alpha-carbinolamine dehydratase moab22 from mycobacterium marinum
119	<a href="#">d2liva</a>	Alignment	not modelled	88.6	14	<b>Fold:</b> Periplasmic binding protein-like I <b>Superfamily:</b> Periplasmic binding protein-like I <b>Family:</b> L-arabinose binding protein-like
120	<a href="#">d1y5ea1</a>	Alignment	not modelled	88.4	21	<b>Fold:</b> Molybdenum cofactor biosynthesis proteins <b>Superfamily:</b> Molybdenum cofactor biosynthesis proteins <b>Family:</b> MogA-like