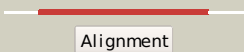

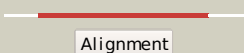

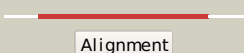

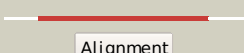



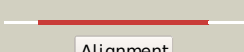

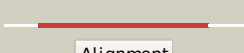

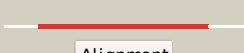









#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1onra_</a>	 Alignment		100.0	64	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
2	<a href="#">d2e1da1</a>	 Alignment		100.0	60	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
3	<a href="#">d1f05a_</a>	 Alignment		100.0	60	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
4	<a href="#">c3m16A_</a>	 Alignment		100.0	57	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transaldolase; <b>PDBTitle:</b> structure of a transaldolase from oleispira antarctica
5	<a href="#">c3igxA_</a>	 Alignment		100.0	48	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transaldolase; <b>PDBTitle:</b> 1.85 angstrom resolution crystal structure of transaldolase b (tala)2 from francisella tularensis.
6	<a href="#">c3hjzA_</a>	 Alignment		100.0	51	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> transaldolase b; <b>PDBTitle:</b> the structure of an aldolase from prochlorococcus marinus
7	<a href="#">c3cq0B_</a>	 Alignment		100.0	55	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> putative transaldolase ygr043c; <b>PDBTitle:</b> crystal structure of tal2_yeast
8	<a href="#">c3clmA_</a>	 Alignment		100.0	26	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> transaldolase; <b>PDBTitle:</b> crystal structure of transaldolase (yp_208650.1) from neisseria2 gonorrhoeae fa 1090 at 1.14 a resolution
9	<a href="#">c3s1vD_</a>	 Alignment		100.0	40	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> probable transaldolase; <b>PDBTitle:</b> transaldolase from thermoplasma acidophilum in complex with d-fructose2 6-phosphate schiff-base intermediate
10	<a href="#">d1vpxA_</a>	 Alignment		100.0	37	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
11	<a href="#">d1l6wa_</a>	 Alignment		100.0	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase

12	<a href="#">d1wx0a1</a>		Alignment		100.0	34	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
13	<a href="#">d1xm3a_</a>		Alignment		94.6	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
14	<a href="#">c2htmB_</a>		Alignment		90.9	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> B: <b>PDB Molecule:</b> thiazole biosynthesis protein thig; <b>PDBTitle:</b> crystal structure of ttha0676 from thermus thermophilus hb8
15	<a href="#">c2p10D_</a>		Alignment		87.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> D: <b>PDB Molecule:</b> ml19387 protein; <b>PDBTitle:</b> crystal structure of a putative phosphonopyruvate hydrolase (ml19387)2 from mesorhizobium loti maff303099 at 2.15 a resolution
16	<a href="#">c1o4uA_</a>		Alignment		83.2	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii quinolic acid phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
17	<a href="#">d2p10a1</a>		Alignment		82.6	25	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Mil19387-like
18	<a href="#">d1o4ua1</a>		Alignment		77.1	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
19	<a href="#">c2jbmA_</a>		Alignment		76.8	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> qprtase structure from human
20	<a href="#">c1ofaB_</a>		Alignment		74.3	24	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> phospho-2-dehydro-3-deoxyheptonate aldolase; <b>PDBTitle:</b> crystal structure of the tyrosine-regulated2 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase3 from saccharomyces cerevisiae in complex with4 phosphoenolpyruvate and cobalt(ii)
21	<a href="#">d1cjca2</a>		Alignment	not modelled	67.2	19	<b>Fold:</b> Nucleotide-binding domain <b>Superfamily:</b> Nucleotide-binding domain <b>Family:</b> N-terminal domain of adrenodoxin reductase-like
22	<a href="#">d1wa3a1</a>		Alignment	not modelled	62.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
23	<a href="#">d1of8a_</a>		Alignment	not modelled	61.6	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
24	<a href="#">d1m5wa_</a>		Alignment	not modelled	60.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Pyridoxine 5'-phosphate synthase <b>Family:</b> Pyridoxine 5'-phosphate synthase
25	<a href="#">c3labA_</a>		Alignment	not modelled	58.0	22	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> putative kdp (2-keto-3-deoxy-6-phosphogluconate) <b>PDBTitle:</b> crystal structure of a putative kdp (2-keto-3-deoxy-6-2 phosphogluconate) aldolase from oleispira antarctica
26	<a href="#">c3o6cA_</a>		Alignment	not modelled	57.0	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> pyridoxal phosphate biosynthetic protein pdxj from campylobacter2 jejuni
27	<a href="#">c2yw3E_</a>		Alignment	not modelled	54.0	30	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-oxoglutarate aldolase/2-2 dehydro-3-deoxyphosphogluconate aldolase from tthb1
28	<a href="#">d1vc4a_</a>		Alignment	not modelled	51.6	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel

					<b>Family:</b> Tryptophan biosynthesis enzymes
29	<a href="#">c3gk0H_</a>	Alignment	not modelled	50.3	19 <b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> pyridoxine 5'-phosphate synthase; <b>PDBTitle:</b> crystal structure of pyridoxal phosphate biosynthetic2 protein from burkholderia pseudomallei
30	<a href="#">dl066a_</a>	Alignment	not modelled	49.1	22 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
31	<a href="#">clqpoA_</a>	Alignment	not modelled	48.2	13 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate acid phosphoribosyl transferase; <b>PDBTitle:</b> quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
32	<a href="#">clcjcA_</a>	Alignment	not modelled	48.0	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> protein (adrenodoxin reductase); <b>PDBTitle:</b> structure of adrenodoxin reductase of mitochondrial p4502 systems
33	<a href="#">clx1oC_</a>	Alignment	not modelled	46.3	17 <b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0268 from thermus thermophilus hb8
34	<a href="#">c3sz8D_</a>	Alignment	not modelled	44.5	13 <b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 2; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia pseudomallei
35	<a href="#">dlnkua_</a>	Alignment	not modelled	44.1	25 <b>Fold:</b> DNA-glycosylase <b>Superfamily:</b> DNA-glycosylase <b>Family:</b> 3-Methyladenine DNA glycosylase I (Tag)
36	<a href="#">clps9A_</a>	Alignment	not modelled	43.6	26 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,4-dienoyl-coa reductase; <b>PDBTitle:</b> the crystal structure and reaction mechanism of e. coli 2,4-2 dienoyl coa reductase
37	<a href="#">c3ez4B_</a>	Alignment	not modelled	43.0	19 <b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> 3-methyl-2-oxobutanoate hydroxymethyltransferase; <b>PDBTitle:</b> crystal structure of 3-methyl-2-oxobutanoate2 hydroxymethyltransferase from burkholderia pseudomallei
38	<a href="#">c2b7pA_</a>	Alignment	not modelled	40.3	18 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
39	<a href="#">c3paiA_</a>	Alignment	not modelled	39.6	15 <b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase, carboxylating; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
40	<a href="#">dlvhca_</a>	Alignment	not modelled	39.5	9 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
41	<a href="#">dlmxsa_</a>	Alignment	not modelled	39.3	15 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
42	<a href="#">c3ef6A_</a>	Alignment	not modelled	39.1	23 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> toluene 1,2-dioxygenase system ferredoxin--nad(+) <b>PDBTitle:</b> crystal structure of toluene 2,3-dioxygenase reductase
43	<a href="#">c2v3aA_</a>	Alignment	not modelled	38.6	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> rubredoxin reductase; <b>PDBTitle:</b> crystal structure of rubredoxin reductase from pseudomonas2 aeruginosa.
44	<a href="#">dlqpoa1</a>	Alignment	not modelled	37.8	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
45	<a href="#">dlwbha1</a>	Alignment	not modelled	37.1	19 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
46	<a href="#">c3llvA_</a>	Alignment	not modelled	36.0	10 <b>PDB header:</b> nad(p) binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exopolyposphatase-related protein; <b>PDBTitle:</b> the crystal structure of the nad(p)-binding domain of an2 exopolyposphatase-related protein from archaeoglobus fulgidus to3 1.7a
47	<a href="#">c3ffsC_</a>	Alignment	not modelled	33.9	16 <b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> inosine-5-monophosphate dehydrogenase; <b>PDBTitle:</b> the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
48	<a href="#">dlf61a_</a>	Alignment	not modelled	33.9	17 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
49	<a href="#">c2gr2A_</a>	Alignment	not modelled	32.7	19 <b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> ferredoxin reductase; <b>PDBTitle:</b> crystal structure of ferredoxin reductase, bpha4 (oxidized form)
50	<a href="#">dlitza3</a>	Alignment	not modelled	30.9	30 <b>Fold:</b> TK C-terminal domain-like <b>Superfamily:</b> TK C-terminal domain-like <b>Family:</b> Transketolase C-terminal domain-like
51	<a href="#">c2jg6A_</a>	Alignment	not modelled	30.8	18 <b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-3-methyladenine glycosidase; <b>PDBTitle:</b> crystal structure of a 3-methyladenine dna glycosylase i2 from staphylococcus aureus
52	<a href="#">dlbd3a_</a>	Alignment	not modelled	29.4	12 <b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like

						<b>Family:</b> Phosphoribosyltransferases (PRTases)
53	<a href="#">c3lxdA_</a>	Alignment	not modelled	28.9	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> fad-dependent pyridine nucleotide-disulphide <b>PDBTitle:</b> crystal structure of ferredoxin reductase arr from novosphingobium2 aromaticivorans
54	<a href="#">d1pv8a_</a>	Alignment	not modelled	27.7	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> 5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
55	<a href="#">c1yqzA_</a>	Alignment	not modelled	27.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> coenzyme a disulfide reductase; <b>PDBTitle:</b> structure of coenzyme a-disulfide reductase from2 staphylococcus aureus refined at 1.54 angstrom resolution
56	<a href="#">c3t4cD_</a>	Alignment	not modelled	26.0	18	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphooctonate aldolase 1; <b>PDBTitle:</b> crystal structure of 2-dehydro-3-deoxyphosphooctonate aldolase from2 burkholderia ambifaria
57	<a href="#">c1kbiB_</a>	Alignment	not modelled	25.6	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome b2; <b>PDBTitle:</b> crystallographic study of the recombinant flavin-binding domain of2 baker's yeast flavocytochrome b2: comparison with the intact wild-3 type enzyme
58	<a href="#">d1j5ta_</a>	Alignment	not modelled	25.3	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> Tryptophan biosynthesis enzymes
59	<a href="#">c3l0gD_</a>	Alignment	not modelled	25.3	19	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
60	<a href="#">d1wv2a_</a>	Alignment	not modelled	24.8	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> ThiG-like <b>Family:</b> ThiG-like
61	<a href="#">d1kbia1</a>	Alignment	not modelled	24.5	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> FMN-linked oxidoreductases <b>Family:</b> FMN-linked oxidoreductases
62	<a href="#">c1q1wA_</a>	Alignment	not modelled	24.0	22	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> putidaredoxin reductase; <b>PDBTitle:</b> crystal structure of putidaredoxin reductase from2 pseudomonas putida
63	<a href="#">d1n8fa_</a>	Alignment	not modelled	23.9	22	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
64	<a href="#">c2p0iA_</a>	Alignment	not modelled	23.3	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-rhamnonate dehydratase; <b>PDBTitle:</b> crystal structure of l-rhamnonate dehydratase from gibberella zeae
65	<a href="#">c1zcoA_</a>	Alignment	not modelled	22.9	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxyphosphoheptonate aldolase; <b>PDBTitle:</b> crystal structure of pyrococcus furiosus 3-deoxy-d-arabino-2 heptulosonate 7-phosphate synthase
66	<a href="#">c3hyxC_</a>	Alignment	not modelled	22.9	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> sulfide-quinone reductase; <b>PDBTitle:</b> 3-d x-ray structure of the sulfide:quinone oxidoreductase from aquifex2 aeolicus in complex with aurachin c
67	<a href="#">d1d9ea_</a>	Alignment	not modelled	22.1	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
68	<a href="#">c3fg2P_</a>	Alignment	not modelled	22.1	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> P: <b>PDB Molecule:</b> putative rubredoxin reductase; <b>PDBTitle:</b> crystal structure of ferredoxin reductase for the cyp199a2 system from2 rhodospseudomonas palustris
69	<a href="#">d2dw4a2</a>	Alignment	not modelled	21.6	27	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
70	<a href="#">d1b5qa1</a>	Alignment	not modelled	21.3	29	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD-linked reductases, N-terminal domain
71	<a href="#">d1nu5a1</a>	Alignment	not modelled	20.8	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Enolase C-terminal domain-like <b>Family:</b> D-glucarate dehydratase-like
72	<a href="#">c2hxtA_</a>	Alignment	not modelled	20.4	15	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> l-fuconate dehydratase; <b>PDBTitle:</b> crystal structure of l-fuconate dehydratase from xanthomonas2 campestris liganded with mg++ and d-erythronohydroxamate
73	<a href="#">d1iyna_</a>	Alignment	not modelled	20.4	20	<b>Fold:</b> Heme-dependent peroxidases <b>Superfamily:</b> Heme-dependent peroxidases <b>Family:</b> CCP-like
74	<a href="#">c2h2wA_</a>	Alignment	not modelled	19.6	38	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> homoserine o-succinyltransferase; <b>PDBTitle:</b> crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
75	<a href="#">c3tqkA_</a>	Alignment	not modelled	19.6	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> phospho-2-dehydro-3-deoxyheptonate aldolase; <b>PDBTitle:</b> structure of phospho-2-dehydro-3-deoxyheptonate aldolase from2 francisella tularensis schu s4
76	<a href="#">d1nhpa2</a>	Alignment	not modelled	19.5	24	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains

77	<a href="#">c3bw2A_</a>	Alignment	not modelled	19.5	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-nitropropane dioxygenase; <b>PDBTitle:</b> crystal structures and site-directed mutagenesis study of nitroalkane2 oxidase from streptomyces ansochromogenes
78	<a href="#">d1eepa_</a>	Alignment	not modelled	19.0	10	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Inosine monophosphate dehydrogenase (IMPDH) <b>Family:</b> Inosine monophosphate dehydrogenase (IMPDH)
79	<a href="#">d1oy0a_</a>	Alignment	not modelled	18.8	24	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Ketopantoate hydroxymethyltransferase PanB
80	<a href="#">d1d7ya2</a>	Alignment	not modelled	18.7	26	<b>Fold:</b> FAD/NAD(P)-binding domain <b>Superfamily:</b> FAD/NAD(P)-binding domain <b>Family:</b> FAD/NAD-linked reductases, N-terminal and central domains
81	<a href="#">c3dmpD_</a>	Alignment	not modelled	18.3	14	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> uracil phosphoribosyltransferase; <b>PDBTitle:</b> 2.6 a crystal structure of uracil phosphoribosyltransferase2 from burkholderia pseudomallei
82	<a href="#">c3ktcB_</a>	Alignment	not modelled	17.9	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> xylose isomerase; <b>PDBTitle:</b> crystal structure of putative sugar isomerase (yp_050048.1) from2 erwinia carotovora atroseptica scri1043 at 1.54 a resolution
83	<a href="#">c3gnnA_</a>	Alignment	not modelled	17.3	14	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
84	<a href="#">d2flia1</a>	Alignment	not modelled	17.2	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Ribulose-phosphate binding barrel <b>Family:</b> D-ribulose-5-phosphate 3-epimerase
85	<a href="#">c3noyA_</a>	Alignment	not modelled	16.4	14	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; <b>PDBTitle:</b> crystal structure of ispg (gcpe)
86	<a href="#">c2bt7A_</a>	Alignment	not modelled	16.1	29	<b>PDB header:</b> viral protein <b>Chain:</b> A: <b>PDB Molecule:</b> sigma c; <b>PDBTitle:</b> structure of the c-terminal receptor-binding domain of2 avian reovirus fibre sigma c, cd crystal form
87	<a href="#">d1qapa1</a>	Alignment	not modelled	16.1	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Nicotinate/Quinolinate PRTase C-terminal domain-like <b>Family:</b> NadC C-terminal domain-like
88	<a href="#">c3dg7B_</a>	Alignment	not modelled	15.7	10	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> muconate cycloisomerase; <b>PDBTitle:</b> crystal structure of muconate lactonizing enzyme from mucobacterium2 smegmatis complexed with muconolactone
89	<a href="#">c3rcyC_</a>	Alignment	not modelled	15.6	14	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme-like <b>PDBTitle:</b> crystal structure of mandelate racemase/muconate lactonizing enzyme-2 like protein from roseovarius sp. tm1035
90	<a href="#">c2v82A_</a>	Alignment	not modelled	15.1	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-6-phosphogalactonate aldolase; <b>PDBTitle:</b> kdpgal complexed to kdpgal
91	<a href="#">d1o5oa_</a>	Alignment	not modelled	15.1	16	<b>Fold:</b> PRTase-like <b>Superfamily:</b> PRTase-like <b>Family:</b> Phosphoribosyltransferases (PRTases)
92	<a href="#">c2v5jB_</a>	Alignment	not modelled	14.7	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; <b>PDBTitle:</b> apo class ii aldolase hpch
93	<a href="#">d2csua3</a>	Alignment	not modelled	14.5	20	<b>Fold:</b> Flavodoxin-like <b>Superfamily:</b> Succinyl-CoA synthetase domains <b>Family:</b> Succinyl-CoA synthetase domains
94	<a href="#">c2oz3F_</a>	Alignment	not modelled	14.5	21	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> mandelate racemase/muconate lactonizing enzyme; <b>PDBTitle:</b> crystal structure of l-rhamnonate dehydratase from azotobacter2 vinelandii
95	<a href="#">d1o60a_</a>	Alignment	not modelled	14.4	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I DAHP synthetase
96	<a href="#">c2zv3E_</a>	Alignment	not modelled	14.4	18	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> peptidyl-trna hydrolase; <b>PDBTitle:</b> crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
97	<a href="#">c1zfjA_</a>	Alignment	not modelled	14.3	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> inosine monophosphate dehydrogenase; <b>PDBTitle:</b> inosine monophosphate dehydrogenase (impdh; ec 1.1.1.205) from2 streptococcus pyogenes
98	<a href="#">d1a9xa3</a>	Alignment	not modelled	14.3	29	<b>Fold:</b> PreATP-grasp domain <b>Superfamily:</b> PreATP-grasp domain <b>Family:</b> BC N-terminal domain-like
99	<a href="#">d1vkfa_</a>	Alignment	not modelled	14.3	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> GlpP-like <b>Family:</b> GlpP-like