Phyre^2

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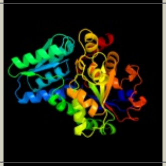
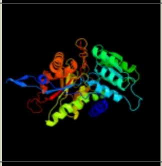
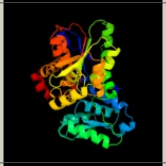
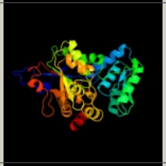
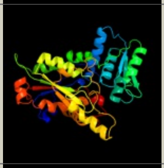
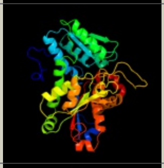
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3r0zA_	Alignment		100.0	89	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of apo d-serine deaminase from salmonella2 typhimurium
2	c1tdjA_	Alignment		100.0	21	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
3	d1pwha_	Alignment		100.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
4	c3l6cA_	Alignment		100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**serine racemase; **PDBTitle:** x-ray crystal structure of rat serine racemase in complex with2 malonate a potent inhibitor
5	c3iauA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine deaminase; **PDBTitle:** the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
6	c2gn0A_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine dehydratase catabolic; **PDBTitle:** crystal structure of dimeric biodegradative threonine deaminase (tdcb)2 from salmonella typhimurium at 1.7 a resolution (triclinic form with3 one complete subunit built in alternate conformation)
7	c1p5jA_	Alignment		100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
8	d1p5ja_	Alignment		100.0	19	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
9	d1v71a1	Alignment		100.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
10	c2rkbE_	Alignment		100.0	20	**PDB header:**lyase **Chain:** E: **PDB Molecule:**serine dehydratase-like; **PDBTitle:** serine dehydratase like-1 from human cancer cells
11	d1ve5a1	Alignment		100.0	25	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes

12	c2zsjB_	Alignment		100.0	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**threonine synthase; **PDBTitle:** crystal structure of threonine synthase from aquifex aeolicus vf5
13	c3pc3A_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cg1753, isoform a; **PDBTitle:** full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
14	d1jbqa_	Alignment		100.0	18	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
15	c2d1fA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** structure of mycobacterium tuberculosis threonine synthase
16	c1jbqD_	Alignment		100.0	18	**PDB header:**lyase **Chain:** D: **PDB Molecule:**cystathionine beta-synthase; **PDBTitle:** structure of human cystathionine beta-synthase: a unique pyridoxal 5'-2 phosphate dependent hemeprotein
17	d1tdja1	Alignment		100.0	21	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
18	d1v7ca_	Alignment		100.0	22	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
19	d1e5xa_	Alignment		100.0	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
20	d1z7wa1	Alignment		100.0	19	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
21	c1x1qA_	Alignment	not modelled	100.0	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
22	c2pqmA_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
23	d1qopb_	Alignment	not modelled	100.0	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
24	c3dwgA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase b; **PDBTitle:** crystal structure of a sulfur carrier protein complex found in the2 cysteine biosynthetic pathway of mycobacterium tuberculosis
25	d1vela1	Alignment	not modelled	100.0	23	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
26	d1v8za1	Alignment	not modelled	100.0	16	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
						Fold: Tryptophan synthase beta subunit-like PLP-dependent

27	d1y7la1	Alignment	not modelled	100.0	21	enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
28	d1wkva1	Alignment	not modelled	100.0	15	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
29	d1fcja_	Alignment	not modelled	100.0	22	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
30	d2bhsa1	Alignment	not modelled	100.0	20	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
31	c2q3bA_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase a; **PDBTitle:** 1.8 a resolution crystal structure of o-acetylserine sulfhydrylase2 (oass) holoenzyme from mycobacterium tuberculosis
32	d1o58a_	Alignment	not modelled	100.0	23	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
33	c2o2jA_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
34	c2eguA_	Alignment	not modelled	100.0	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
35	d1f2da_	Alignment	not modelled	100.0	15	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
36	d1tyza_	Alignment	not modelled	100.0	17	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
37	d1j0aa_	Alignment	not modelled	100.0	17	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
38	d1vb3a1	Alignment	not modelled	100.0	18	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
39	c3v7nA_	Alignment	not modelled	100.0	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** crystal structure of threonine synthase (thrc) from from burkholderia2 thailandensis
40	d1kl7a_	Alignment	not modelled	100.0	13	**Fold:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Superfamily:**Tryptophan synthase beta subunit-like PLP-dependent enzymes **Family:**Tryptophan synthase beta subunit-like PLP-dependent enzymes
41	d1vp8a_	Alignment	not modelled	95.2	20	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
42	d1c1da1	Alignment	not modelled	94.2	28	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
43	d1l7da1	Alignment	not modelled	88.2	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
44	d1ml4a2	Alignment	not modelled	87.5	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
45	d1xgka_	Alignment	not modelled	87.5	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
46	d1cdoa2	Alignment	not modelled	86.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
47	d1o8ca2	Alignment	not modelled	86.1	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
						Fold: Pyruvate kinase C-terminal domain-like

48	d1t57a_	Alignment	not modelled	86.0	17	**Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
49	c3iupB_	Alignment	not modelled	84.9	12	**PDB header:**oxidoreductase **Chain: B: PDB Molecule:**putative nadph:quinone oxidoreductase; **PDBTitle:** crystal structure of putative nadph:quinone oxidoreductase2 (yp_296108.1) from ralstonia eutropha jmp134 at 1.70 a resolution
50	c1ml4A_	Alignment	not modelled	82.7	15	**PDB header:**transferase **Chain: A: PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
51	d1p0fa2	Alignment	not modelled	82.3	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
52	c3krtC_	Alignment	not modelled	80.3	18	**PDB header:**oxidoreductase **Chain: C: PDB Molecule:**crotonyl coa reductase; **PDBTitle:** crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
53	c2rgwD_	Alignment	not modelled	79.8	10	**PDB header:**transferase **Chain: D: PDB Molecule:**aspartate carbamoyltransferase; **PDBTitle:** catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
54	c3ndnC_	Alignment	not modelled	76.4	13	**PDB header:**lyase **Chain: C: PDB Molecule:**o-succinylhomoserine sulfhydrylase; **PDBTitle:** crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
55	d1o89a2	Alignment	not modelled	76.3	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
56	c3d64A_	Alignment	not modelled	74.0	15	**PDB header:**hydrolase **Chain: A: PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from2 burkholderia pseudomallei
57	c3dhyC_	Alignment	not modelled	73.3	12	**PDB header:**hydrolase **Chain: C: PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
58	c3oneA_	Alignment	not modelled	71.3	13	**PDB header:**hydrolase/hydrolase substrate **Chain: A: PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of lupinus luteus s-adenosyl-l-homocysteine2 hydrolase in complex with adenine
59	c3n58D_	Alignment	not modelled	70.7	15	**PDB header:**hydrolase **Chain: D: PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of s-adenosyl-l-homocysteine hydrolase from brucella2 melitensis in ternary complex with nad and adenosine, orthorhombic3 form
60	d1ekxa2	Alignment	not modelled	70.6	11	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
61	d1bg6a2	Alignment	not modelled	65.8	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
62	c2vhyB_	Alignment	not modelled	65.7	19	**PDB header:**oxidoreductase **Chain: B: PDB Molecule:**alanine dehydrogenase; **PDBTitle:** crystal structure of apo l-alanine dehydrogenase from2 mycobacterium tuberculosis
63	c1d4fD_	Alignment	not modelled	65.3	14	**PDB header:**hydrolase **Chain: D: PDB Molecule:**s-adenosylhomocysteine hydrolase; **PDBTitle:** crystal structure of recombinant rat-liver d244e mutant s-2 adenosylhomocysteine hydrolase
64	d1tt7a2	Alignment	not modelled	65.2	19	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
65	d1mdoa_	Alignment	not modelled	63.9	15	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
66	d1otha2	Alignment	not modelled	63.0	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
67	d1fg7a_	Alignment	not modelled	62.1	13	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
68	c3jtxB_	Alignment	not modelled	58.5	13	**PDB header:**transferase **Chain: B: PDB Molecule:**aminotransferase; **PDBTitle:** crystal structure of aminotransferase (np_283882.1) from neisseria2 meningitidis z2491 at 1.91 a resolution
69	d1pvva2	Alignment	not modelled	57.5	24	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
70	c3ketA_	Alignment	not modelled	57.2	16	**PDB header:**transcription/dna **Chain: A: PDB Molecule:**redox-sensing transcriptional repressor rex; **PDBTitle:** crystal structure of a rex-family transcriptional regulatory protein2 from streptococcus agalactiae bound to a palindromic operator
71	d1u3wa2	Alignment	not modelled	57.0	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
72	c1l7eC_	Alignment	not modelled	56.8	18	**PDB header:**oxidoreductase **Chain: C: PDB Molecule:**nicotinamide nucleotide transhydrogenase, **PDBTitle:** crystal structure of r. rubrum transhydrogenase domain i2 with bound nadh

73	c2qx7A_	Alignment	not modelled	56.1	22	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
74	d1pg5a2	Alignment	not modelled	56.0	18	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
75	d1d1ta2	Alignment	not modelled	55.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
76	d1o69a_	Alignment	not modelled	55.2	9	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
77	c2c7tA_	Alignment	not modelled	55.1	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine-2-deoxy-scyllo-inosose **PDBTitle:** crystal structure of the plp-bound form of btrr,2 a dual functional aminotransferase involved in butirosin3 biosynthesis.
78	c3p2yA_	Alignment	not modelled	54.8	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alanine dehydrogenase/pyridine nucleotide transhydrogenase; **PDBTitle:** crystal structure of alanine dehydrogenase/pyridine nucleotide2 transhydrogenase from mycobacterium smegmatis
79	d2bwna1	Alignment	not modelled	53.8	8	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
80	c3c1oA_	Alignment	not modelled	53.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**eugenol synthase; **PDBTitle:** the multiple phenylpropene synthases in both clarkia2 breweri and petunia hybrida represent two distinct lineages
81	c3eywA_	Alignment	not modelled	53.6	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**c-terminal domain of glutathione-regulated potassium-efflux **PDBTitle:** crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
82	c3d4oA_	Alignment	not modelled	52.7	23	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dipicolinate synthase subunit a; **PDBTitle:** crystal structure of dipicolinate synthase subunit a (np_243269.1)2 from bacillus halodurans at 2.10 a resolution
83	c2bruB_	Alignment	not modelled	52.4	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nad(p) transhydrogenase subunit alpha; **PDBTitle:** complex of the domain i and domain iii of escherichia coli2 transhydrogenase
84	d1vpda2	Alignment	not modelled	51.7	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
85	d1trba1	Alignment	not modelled	51.5	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
86	d1u7za_	Alignment	not modelled	50.8	18	**Fold:**Ribokinase-like **Superfamily:**CoaB-like **Family:**CoaB-like
87	d1e3ia2	Alignment	not modelled	50.5	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
88	c2gk4A_	Alignment	not modelled	50.0	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** the crystal structure of the dna/pantothenate metabolism flavoprotein2 from streptococcus pneumoniae
89	c1v8bA_	Alignment	not modelled	49.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**adenosylhomocysteinase; **PDBTitle:** crystal structure of a hydrolase
90	c3q98A_	Alignment	not modelled	49.7	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
91	d1wvga1	Alignment	not modelled	49.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
92	d1b9ha_	Alignment	not modelled	48.9	10	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
93	c2gf2B_	Alignment	not modelled	48.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of human hydroxyisobutyrate dehydrogenase
94	c3k7yA_	Alignment	not modelled	48.7	4	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate aminotransferase; **PDBTitle:** aspartate aminotransferase of plasmodium falciparum
95	d1pjca1	Alignment	not modelled	47.7	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
96	c1vpdA_	Alignment	not modelled	47.1	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**tartronate semialdehyde reductase; **PDBTitle:** x-ray crystal structure of tartronate semialdehyde reductase2 [salmonella typhimurium lt2]
97	c3ffrA_	Alignment	not modelled	47.1	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoserine aminotransferase serc; **PDBTitle:** crystal structure of a phosphoserine aminotransferase serc (chu_0995)2 from cytophaga hutchinsonii atcc 33406 at 1.75 a resolution
98	c3pduF_	Alignment	not modelled	47.1	26	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**3-hydroxyisobutyrate dehydrogenase family protein; **PDBTitle:** crystal structure of gamma-hydroxybutyrate

						dehydrogenase from2 geobacter sulfurreducens in complex with nadp+
99	d2jhfa2	Alignment	not modelled	46.9	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
100	c3cumA_	Alignment	not modelled	46.3	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable 3-hydroxyisobutyrate dehydrogenase; **PDBTitle:** crystal structure of a possible 3-hydroxyisobutyrate dehydrogenase2 from pseudomonas aeruginosa pao1
101	d1tuga1	Alignment	not modelled	46.3	13	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
102	c4a10A_	Alignment	not modelled	46.3	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**octenoyl-coa reductase/carboxylase; **PDBTitle:** apo-structure of 2-octenoyl-coa carboxylase reductase cinf from2 streptomyces sp.
103	c1gthD_	Alignment	not modelled	46.3	18	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**dihydropyrimidine dehydrogenase; **PDBTitle:** dihydropyrimidine dehydrogenase (dpd) from pig, ternary2 complex with nadph and 5-iodouracil
104	d2ay1a_	Alignment	not modelled	45.9	12	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**AAT-like
105	c2dt5A_	Alignment	not modelled	45.5	25	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**at-rich dna-binding protein; **PDBTitle:** crystal structure of ttha1657 (at-rich dna-binding protein) from2 thermus thermophilus hb8
106	d1hyua1	Alignment	not modelled	45.0	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
107	c2o0rA_	Alignment	not modelled	44.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rv0858c (n-succinyldiaminopimelate aminotransferase); **PDBTitle:** the three-dimensional structure of n-succinyldiaminopimelate2 aminotransferase from mycobacterium tuberculosis
108	d1llua2	Alignment	not modelled	43.9	17	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
109	c3bcxA_	Alignment	not modelled	43.6	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cdp-6-deoxy-l-threo-d-glycero-4-hexulose-3- **PDBTitle:** e1 dehydrase
110	c3gvpB_	Alignment	not modelled	43.2	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**adenosylhomocysteinase 3; **PDBTitle:** human sahh-like domain of human adenosylhomocysteinase 3
111	d1kola2	Alignment	not modelled	43.1	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
112	d1xa0a2	Alignment	not modelled	42.7	24	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
113	c3qhaB_	Alignment	not modelled	42.6	26	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** crystal structure of a putative oxidoreductase from mycobacterium2 avium 104
114	c3fwzA_	Alignment	not modelled	42.2	18	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**inner membrane protein ybal; **PDBTitle:** crystal structure of trka-n domain of inner membrane protein ybal from2 escherichia coli
115	c2po3B_	Alignment	not modelled	41.5	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-dehydrase; **PDBTitle:** crystal structure analysis of desi in the presence of its2 tdp-sugar product
116	c3pefA_	Alignment	not modelled	41.3	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**6-phosphogluconate dehydrogenase, nad-binding; **PDBTitle:** crystal structure of gamma-hydroxybutyrate dehydrogenase from2 geobacter metallireducens in complex with nadp+
117	d1vdca1	Alignment	not modelled	41.2	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
118	c3s8mA_	Alignment	not modelled	41.0	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acp reductase; **PDBTitle:** the crystal structure of fabv
119	c1ortD_	Alignment	not modelled	40.7	22	**PDB header:**transferase **Chain:** D: **PDB Molecule:**ornithine transcarbamoylase; **PDBTitle:** ornithine transcarbamoylase from pseudomonas aeruginosa
120	d2hmva1	Alignment	not modelled	39.3	22	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain