Phyre2

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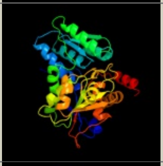
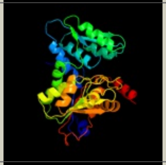
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2gn0A_	Alignment		100.0	95	**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)
2	c1tdjA_	Alignment		100.0	36	**PDB header:**allostery **Chain:** A: **PDB Molecule:**biosynthetic threonine deaminase; **PDBTitle:** threonine deaminase (biosynthetic) from e. coli
3	d1v71a1	Alignment		100.0	39	**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	33	**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	35	**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	d1tdja1	Alignment		100.0	36	**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
7	d1ve5a1	Alignment		100.0	38	**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
8	d1pwha_	Alignment		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
9	d1p5ja_	Alignment		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
10	c1p5jA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-serine dehydratase; **PDBTitle:** crystal structure analysis of human serine dehydratase
11	c2rkbE_	Alignment		100.0	23	**PDB header:**lyase **Chain:** E: **PDB Molecule:**serine dehydratase-like; **PDBTitle:** serine dehydratase like-1 from human cancer cells

12	c3r0zA_	Alignment		100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of apo d-serine deaminase from salmonella2 typhimurium
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	d1ve1a1	Alignment		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
15	c2pqmA_	Alignment		100.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
16	d1z7wa1	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
17	d1jbqa_	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
18	c1jbqD_	Alignment		100.0	22	**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
19	c2d1fA_	Alignment		100.0	23	**PDB header:**lyase **Chain:** A: **PDB Molecule:**threonine synthase; **PDBTitle:** structure of mycobacterium tuberculosis threonine synthase
20	c1x1qA_	Alignment		100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
21	d2bhsa1	Alignment	not modelled	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
22	d1v8za1	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
23	c2zsjB_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**threonine synthase; **PDBTitle:** crystal structure of threonine synthase from aquifex aeolicus vf5
24	d1wkva1	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
25	d1qopb_	Alignment	not modelled	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
26	c3dwgA_	Alignment	not modelled	100.0	15	**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
27	d1v7ca_	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
28	c2q3bA_	Alignment	not modelled	100.0	20	**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
29	d1o58a_	Alignment	not modelled	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
30	d1y7la1	Alignment	not modelled	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
31	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
32	c2eguA_	Alignment	not modelled	100.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cysteine synthase; **PDBTitle:** crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
33	d1e5xa_	Alignment	not modelled	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
34	c2o2jA_	Alignment	not modelled	100.0	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase beta chain; **PDBTitle:** mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
35	d1j0aa_	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	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
37	d1tyza_	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
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	d1kl7a_	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
40	d1vp8a_	Alignment	not modelled	94.8	19	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
41	d1t57a_	Alignment	not modelled	93.4	18	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**PK C-terminal domain-like **Family:**MTH1675-like
42	d1xgka_	Alignment	not modelled	93.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
43	c3iupB_	Alignment	not modelled	92.9	14	**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
44	d1bg6a2	Alignment	not modelled	90.8	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**6-phosphogluconate dehydrogenase-like, N-terminal domain
45	d1o8ca2	Alignment	not modelled	89.6	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
46	d1c1da1	Alignment	not modelled	86.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Aminoacid dehydrogenase-like, C-terminal domain
						Fold:ATC-like

47	d1ml4a2	Alignment	not modelled	86.0	15	**Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
48	d1cdoa2	Alignment	not modelled	85.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
49	d1o89a2	Alignment	not modelled	84.4	23	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
50	c3eywA_	Alignment	not modelled	80.3	13	**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
51	c2p4hX_	Alignment	not modelled	79.3	9	**PDB header:**plant protein **Chain:** X: **PDB Molecule:**vestitone reductase; **PDBTitle:** crystal structure of vestitone reductase from alfalfa2 (medicago sativa l.)
52	d1l7da1	Alignment	not modelled	78.8	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Formate/glycerate dehydrogenases, NAD-domain
53	d1wvga1	Alignment	not modelled	78.2	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
54	c3s8mA_	Alignment	not modelled	77.5	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**enoyl-acp reductase; **PDBTitle:** the crystal structure of fabv
55	c3c1oA_	Alignment	not modelled	74.5	8	**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
56	d1p0fa2	Alignment	not modelled	73.7	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
57	d1ekxa2	Alignment	not modelled	73.3	15	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
58	c3ezlA_	Alignment	not modelled	73.0	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**acetoacetyl-coa reductase; **PDBTitle:** crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
59	c1ml4A_	Alignment	not modelled	70.4	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aspartate transcarbamoylase; **PDBTitle:** the pala-liganded aspartate transcarbamoylase catalytic subunit from2 pyrococcus abyssi
60	c2qx7A_	Alignment	not modelled	70.3	13	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**eugenol synthase 1; **PDBTitle:** structure of eugenol synthase from ocimum basilicum
61	c3krtC_	Alignment	not modelled	70.3	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**crotonyl coa reductase; **PDBTitle:** crystal structure of putative crotonyl coa reductase from streptomyces2 coelicolor a3(2)
62	d1fl2a1	Alignment	not modelled	69.7	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
63	c3grkE_	Alignment	not modelled	68.8	16	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase (nadh); **PDBTitle:** crystal structure of short chain dehydrogenase reductase2 sdr glucose-ribitol dehydrogenase from brucella melitensis
64	d1hyua1	Alignment	not modelled	68.6	13	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
65	d1tt7a2	Alignment	not modelled	65.7	16	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
66	d1pvva2	Alignment	not modelled	65.5	22	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
67	c3uf0A_	Alignment	not modelled	65.2	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**short-chain dehydrogenase/reductase sdr; **PDBTitle:** crystal structure of a putative nad(p) dependent gluconate 5-2 dehydrogenase from beutenbergia cavernae(efi target efi-502044) with3 bound nadp (low occupancy)
68	d1otha2	Alignment	not modelled	64.1	17	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
69	c2xecD_	Alignment	not modelled	63.5	20	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**putative maleate isomerase; **PDBTitle:** nocardia farcinica maleate cis-trans isomerase bound to2 tris
70	d1vdca1	Alignment	not modelled	63.3	11	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
71	c1n7gB_	Alignment	not modelled	63.2	9	**PDB header:**lyase **Chain:** B: **PDB Molecule:**gdp-d-mannose-4,6-dehydratase; **PDBTitle:** crystal structure of the gdp-mannose 4,6-dehydratase2 ternary complex with nadph and gdp-rhamnose.
72	d1d1ta2	Alignment	not modelled	62.2	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain

73	d1rkxa_	Alignment	not modelled	61.6	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
74	d1trba1	Alignment	not modelled	61.5	6	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
75	d1qyda_	Alignment	not modelled	61.3	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
76	c3i5mA_	Alignment	not modelled	60.8	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative leucoanthocyanidin reductase 1; **PDBTitle:** structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
77	d1nhpa2	Alignment	not modelled	59.6	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
78	c3i4fD_	Alignment	not modelled	58.9	10	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**3-oxoacyl-[acyl-carrier protein] reductase; **PDBTitle:** structure of putative 3-oxoacyl-reductase from bacillus thuringiensis
79	c2q2qG_	Alignment	not modelled	58.8	18	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**beta-d-hydroxybutyrate dehydrogenase; **PDBTitle:** structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
80	c1pjtB_	Alignment	not modelled	57.4	12	**PDB header:**transferase/oxidoreductase/lyase **Chain:** B: **PDB Molecule:**siroheme synthase; **PDBTitle:** the structure of the ser128ala point-mutant variant of cysg,2 the multifunctional3 methyltransferase/dehydrogenase/ferrochelatase for4 siroheme synthesis
81	d3lada1	Alignment	not modelled	56.9	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
82	d2hmva1	Alignment	not modelled	55.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
83	d1e3ia2	Alignment	not modelled	54.7	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
84	d1n7ha_	Alignment	not modelled	54.5	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
85	c2rghA_	Alignment	not modelled	54.5	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**alpha-glycerophosphate oxidase; **PDBTitle:** structure of alpha-glycerophosphate oxidase from2 streptococcus sp.: a template for the mitochondrial alpha-3 glycerophosphate dehydrogenase
86	c2g1uA_	Alignment	not modelled	53.8	19	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**hypothetical protein tm1088a; **PDBTitle:** crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
87	d1xa0a2	Alignment	not modelled	53.7	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
88	d2i0za1	Alignment	not modelled	53.7	15	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**HI0933 N-terminal domain-like
89	c2qioA_	Alignment	not modelled	53.6	12	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**enoyl-(acyl-carrier-protein) reductase; **PDBTitle:** x-ray structure of enoyl-acyl carrier protein reductase from bacillus2 anthracis with triclosan
90	d2jhfa2	Alignment	not modelled	53.5	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
91	c3r3sD_	Alignment	not modelled	53.5	16	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**oxidoreductase; **PDBTitle:** structure of the ygha oxidoreductase from salmonella enterica
92	c1boiA_	Alignment	not modelled	53.4	16	**PDB header:**transferase **Chain:** A: **PDB Molecule:**rhodanese; **PDBTitle:** n-terminally truncated rhodanese
93	d1llua2	Alignment	not modelled	53.3	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
94	c2exxB_	Alignment	not modelled	53.2	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**hscarg protein; **PDBTitle:** crystal structure of hscarg from homo sapiens in complex with nadp
95	c3allA_	Alignment	not modelled	52.8	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**2-methyl-3-hydroxypyridine-5-carboxylic acid oxygenase; **PDBTitle:** crystal structure of 2-methyl-3-hydroxypyridine-5-carboxylic acid2 oxygenase, mutant y270a
96	d1lvla1	Alignment	not modelled	52.4	19	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
97	c2hk8B_	Alignment	not modelled	52.1	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**shikimate dehydrogenase; **PDBTitle:** crystal structure of shikimate dehydrogenase from aquifex2 aeolicus at 2.35 angstrom resolution

98	d1u3wa2	Alignment	not modelled	51.5	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
99	d1dxla1	Alignment	not modelled	51.4	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
100	c3d3kD_	Alignment	not modelled	51.2	13	**PDB header:**protein binding **Chain:** D: **PDB Molecule:**enhancer of mrna-decapping protein 3; **PDBTitle:** crystal structure of human edc3p
101	c1ulzA_	Alignment	not modelled	51.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase n-terminal domain; **PDBTitle:** crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
102	c3q98A_	Alignment	not modelled	49.5	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**transcarbamylase; **PDBTitle:** structure of ygew encoded protein from e. coli
103	c3orqA_	Alignment	not modelled	49.2	13	**PDB header:**ligase,biosynthetic protein **Chain:** A: **PDB Molecule:**n5-carboxyaminoimidazole ribonucleotide synthetase; **PDBTitle:** crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
104	c3kzvA_	Alignment	not modelled	48.8	7	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**uncharacterized oxidoreductase yir035c; **PDBTitle:** the crystal structure of a cytoplasmic protein with unknown function2 from saccharomyces cerevisiae
105	d1ebda1	Alignment	not modelled	48.7	22	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
106	c3d4oA_	Alignment	not modelled	48.5	19	**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
107	d1pg5a2	Alignment	not modelled	47.9	2	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
108	d1kola2	Alignment	not modelled	47.6	12	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Alcohol dehydrogenase-like, C-terminal domain
109	d1ulua_	Alignment	not modelled	47.3	9	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
110	c3ijrF_	Alignment	not modelled	47.0	12	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**oxidoreductase, short chain dehydrogenase/reductase family; **PDBTitle:** 2.05 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor' in complex3 with nad+
111	d1rpna_	Alignment	not modelled	47.0	6	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
112	d1lpfa1	Alignment	not modelled	46.8	26	**Fold:**FAD/NAD(P)-binding domain **Superfamily:**FAD/NAD(P)-binding domain **Family:**FAD/NAD-linked reductases, N-terminal and central domains
113	d1vlva2	Alignment	not modelled	46.8	10	**Fold:**ATC-like **Superfamily:**Aspartate/ornithine carbamoyltransferase **Family:**Aspartate/ornithine carbamoyltransferase
114	c2ax3A_	Alignment	not modelled	46.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hypothetical protein tm0922; **PDBTitle:** crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
115	d1im5a_	Alignment	not modelled	46.5	10	**Fold:**Isochorismatase-like hydrolases **Superfamily:**Isochorismatase-like hydrolases **Family:**Isochorismatase-like hydrolases
116	d1gega_	Alignment	not modelled	46.1	10	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
117	d1ae1a_	Alignment	not modelled	45.6	7	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
118	d1ja9a_	Alignment	not modelled	45.4	13	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
119	c2bryA_	Alignment	not modelled	45.3	21	**PDB header:**transport **Chain:** A: **PDB Molecule:**nedd9 interacting protein with calponin homology **PDBTitle:** crystal structure of the native monooxygenase domain of2 mical at 1.45 a resolution
120	c3o93A_	Alignment	not modelled	44.9	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**nicotinamidase; **PDBTitle:** high resolution crystal structures of streptococcus pneumoniae2 nicotinamidase with trapped intermediates provide insights into3 catalytic mechanism and inhibition by aldehydes