





























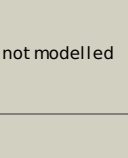


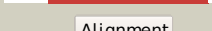


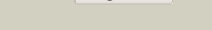








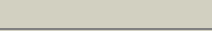
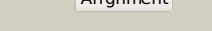
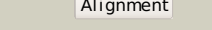


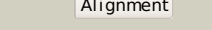


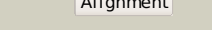
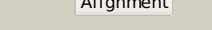
Phyre2

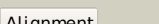

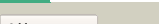
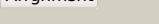
Email	I.a.kelley@imperial.ac.uk
Description	P00934
Date	Thu Jan 5 10:57:12 GMT 2012
Unique Job ID	428e7cd3fedaa765

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	dlvb3a1	 Alignment		100.0	100	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
2	d1kl7a_	 Alignment		100.0	35	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
3	c3v7nA_	 Alignment		100.0	28	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase (thrc) from from burkholderia2 thailandensis
4	d1e5xa_	 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
5	dlv8za1	 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
6	c2d1fA_	 Alignment		100.0	23	PDB header: lyase Chain: A: PDB Molecule: threonine synthase; PDBTitle: structure of mycobacterium tuberculosis threonine synthase
7	dlv7ca_	 Alignment		100.0	24	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	c2zsjB_	 Alignment		100.0	20	PDB header: lyase Chain: B: PDB Molecule: threonine synthase; PDBTitle: crystal structure of threonine synthase from aquifex aeolicus vf5
9	dlqopb_	 Alignment		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
10	dlpwha_	 Alignment		100.0	14	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
11	c1tdjA_	 Alignment		100.0	17	PDB header: allostery Chain: A: PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli

12	c2rkbE	Alignment		100.0	14 PDB header: lyase Chain: E: PDB Molecule: serine dehydratase-like; PDBTitle: serine dehydratase like-1 from human cancer cells
13	c1x1qA	Alignment		100.0	17 PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: crystal structure of tryptophan synthase beta chain from thermus2 thermophilus hb8
14	c2gn0A	Alignment		100.0	16 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)
15	c3r0zA	Alignment		100.0	16 PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of apo d-serine deaminase from salmonella2 typhimurium
16	dlv71a1	Alignment		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
17	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
18	dlp5ja	Alignment		100.0	14 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	clp5jA	Alignment		100.0	14 PDB header: lyase Chain: A: PDB Molecule: l-serine dehydratase; PDBTitle: crystal structure analysis of human serine dehydratase
20	dltdja1	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	dlv71a1	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
22	dlwkva1	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
23	dlve5a1	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	c3iauA	Alignment	not modelled	100.0	16 PDB header: lyase Chain: A: PDB Molecule: threonine deaminase; PDBTitle: the structure of the processed form of threonine deaminase isoform 22 from solanum lycopersicum
25	dlve1a1	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
26	dljbqa	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
27	c1jbqD_	 Alignment	not modelled	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
28	c3pc3A_	 Alignment	not modelled	100.0	19	PDB header: lyase Chain: A: PDB Molecule: cg1753, isoform a; PDBTitle: full length structure of cystathionine beta-synthase from drosophila2 in complex with aminoacrylate
29	d2bhsa1	 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	dlz7wa1	 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
31	d1o58a_	 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
32	c3dwgA_	 Alignment	not modelled	100.0	18	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
33	d1fcja_	 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
34	c2pqmA_	 Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of cysteine synthase (oass) from entamoeba2 histolytica at 1.86 a resolution
35	c2q3bA_	 Alignment	not modelled	100.0	16	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
36	c2o2jA_	 Alignment	not modelled	100.0	16	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase beta chain; PDBTitle: mycobacterium tuberculosis tryptophan synthase beta chain2 dimer (apoform)
37	c2eguA_	 Alignment	not modelled	100.0	21	PDB header: transferase Chain: A: PDB Molecule: cysteine synthase; PDBTitle: crystal structure of o-acetylserine sulfhydrase from geobacillus2 kaustophilus hta426
38	d1f2da_	 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
39	d1tyza_	 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
40	d1j0aa_	 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	c2qx7A_	 Alignment	not modelled	80.8	18	PDB header: plant protein Chain: A: PDB Molecule: eugenol synthase 1; PDBTitle: structure of eugenol synthase from ocimum basilicum
42	d1vp8a_	 Alignment	not modelled	80.8	17	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
43	d1xgka_	 Alignment	not modelled	79.4	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
44	d1qsga_	 Alignment	not modelled	77.8	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
45	c3s8mA_	 Alignment	not modelled	72.4	9	PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-acp reductase; PDBTitle: the crystal structure of fabv
46	d1t57a_	 Alignment	not modelled	69.0	16	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: MTH1675-like
47	c2uv8C_	 Alignment	not modelled	68.8	17	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha (fas2); PDBTitle: crystal structure of yeast fatty acid synthase with stalled2 acyl carrier protein at 3.1 angstrom resolution
48	d1o8ca2	 Alignment	not modelled	64.9	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain

49	c3imfA_	 Alignment	not modelled	63.5	18	PDB header: oxidoreductase Chain: A: PDB Molecule: short chain dehydrogenase; PDBTitle: 1.99 angstrom resolution crystal structure of a short chain2 dehydrogenase from bacillus anthracis str. 'ames ancestor'
50	d1ecfa1	 Alignment	not modelled	63.2	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
51	d1gph11	 Alignment	not modelled	61.0	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
52	c3icca_	 Alignment	not modelled	59.8	18	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 3-oxoacyl-(acyl carrier protein) reductase; PDBTitle: crystal structure of a putative 3-oxoacyl-(acyl carrier protein)2 reductase from bacillus anthracis at 1.87 a resolution
53	c2q2qG_	 Alignment	not modelled	58.5	10	PDB header: oxidoreductase Chain: G: PDB Molecule: beta-d-hydroxybutyrate dehydrogenase; PDBTitle: structure of d-3-hydroxybutyrate dehydrogenase from pseudomonas putida
54	c1m6yA_	 Alignment	not modelled	58.2	12	PDB header: transferase Chain: A: PDB Molecule: s-adenosyl-methyltransferase mraw; PDBTitle: crystal structure analysis of tm0872, a putative sam-2 dependent methyltransferase, complexed with sah
55	c3ek2D_	 Alignment	not modelled	57.8	13	PDB header: oxidoreductase Chain: D: PDB Molecule: enoyl-(acyl-carrier-protein) reductase (nadh); PDBTitle: crystal structure of enoyl-(acyl carrier protein) reductase2 from burkholderia pseudomallei 1719b
56	c2vkzC_	 Alignment	not modelled	57.7	17	PDB header: transferase Chain: C: PDB Molecule: fatty acid synthase subunit alpha; PDBTitle: structure of the cerulenin-inhibited fungal fatty acid2 synthase type i multienzyme complex
57	c2rgwD_	 Alignment	not modelled	55.8	16	PDB header: transferase Chain: D: PDB Molecule: aspartate carbamoyltransferase; PDBTitle: catalytic subunit of m. jannaschii aspartate2 transcarbamoylase
58	d1ae1a_	 Alignment	not modelled	54.7	14	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
59	d1q59a_	 Alignment	not modelled	52.9	11	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
60	c2p2qD_	 Alignment	not modelled	50.8	17	PDB header: transferase Chain: D: PDB Molecule: ornithine carbamoyltransferase; PDBTitle: crystal structure of ornithine carbamoyltransferase from mycobacterium2 tuberculosis (rv1656): orthorhombic form
61	c3qvoA_	 Alignment	not modelled	47.0	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nmra family protein; PDBTitle: structure of a rossmann-fold nad(p)-binding family protein from2 shigella flexneri.
62	c3ez1A_	 Alignment	not modelled	46.8	12	PDB header: oxidoreductase Chain: A: PDB Molecule: acetoacetyl-coa reductase; PDBTitle: crystal structure of acetyacetyl-coa reductase from2 burkholderia pseudomallei 1710b
63	c1stzB_	 Alignment	not modelled	45.4	28	PDB header: transcription Chain: B: PDB Molecule: heat-inducible transcription repressor hrca homolog; PDBTitle: crystal structure of a hypothetical protein at 2.2 a resolution
64	c1gph1_	 Alignment	not modelled	45.4	18	PDB header: transferase(glutamine amidotransferase) Chain: 1: PDB Molecule: glutamine phosphoribosyl-pyrophosphate amidotransferase; PDBTitle: structure of the allosteric regulatory enzyme of purine biosynthesis
65	d2ax3a2	 Alignment	not modelled	43.5	12	Fold: YjeF N-terminal domain-like Superfamily: YjeF N-terminal domain-like Family: YjeF N-terminal domain-like
66	c2qkmF_	 Alignment	not modelled	43.4	23	PDB header: hydrolase Chain: F: PDB Molecule: spac19a8.12 protein; PDBTitle: the crystal structure of fission yeast mrna decapping enzyme dcp1-dcp22 complex
67	d2qklb1	 Alignment	not modelled	43.3	23	Fold: Dcp2 domain-like Superfamily: Dcp2 domain-like Family: Dcp2 box A domain
68	c3kb8A_	 Alignment	not modelled	43.2	13	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
69	c3toxG_	 Alignment	not modelled	43.2	17	PDB header: oxidoreductase Chain: G: PDB Molecule: short chain dehydrogenase; PDBTitle: crystal structure of a short chain dehydrogenase in complex with2 nad(p) from sinorhizobium meliloti 1021
70	c3qp9C_	 Alignment	not modelled	43.1	15	PDB header: oxidoreductase Chain: C: PDB Molecule: type i polyketide synthase pikaii; PDBTitle: the structure of a c2-type ketoreductase from a modular polyketide2 synthase
71	d1pq1a_	 Alignment	not modelled	41.9	14	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
72	c3d3jA_	 Alignment	not modelled	41.5	20	PDB header: protein binding Chain: A: PDB Molecule: enhancer of mrna-decapping protein 3; PDBTitle: crystal structure of human edc3p
73	c3grkE_	 Alignment	not modelled	41.2	13	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
74	c2vzkD_	Alignment	not modelled	40.9	20 PDB header: transferase Chain: D: PDB Molecule: glutamate n-acetyltransferase 2 beta chain; PDBTitle: structure of the acyl-enzyme complex of an n-terminal2 nucleophile (ntn) hydrolase, oat2
75	d1qyda_	Alignment	not modelled	39.5	16 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
76	c3ijrF_	Alignment	not modelled	37.8	16 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+
77	c2vofA_	Alignment	not modelled	37.6	25 PDB header: apoptosis Chain: A: PDB Molecule: bcl-2-related protein a1; PDBTitle: structure of mouse a1 bound to the puma bh3-domain
78	c3i5mA_	Alignment	not modelled	37.5	24 PDB header: oxidoreductase Chain: A: PDB Molecule: putative leucoanthocyanidin reductase 1; PDBTitle: structure of the apo form of leucoanthocyanidin reductase from vitis2 vinifera
79	d1yfza1	Alignment	not modelled	36.9	13 Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
80	c1yfaA_	Alignment	not modelled	36.9	13 PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
81	d1a1va1	Alignment	not modelled	36.7	15 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: RNA helicase
82	c3e59A_	Alignment	not modelled	36.5	24 PDB header: transferase Chain: A: PDB Molecule: pyoverdine biosynthesis protein pvca; PDBTitle: crystal structure of the pvca (pa2254) protein from pseudomonas2 aeruginosa
83	d1fw8a_	Alignment	not modelled	36.0	19 Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
84	c3gdfA_	Alignment	not modelled	35.8	21 PDB header: oxidoreductase Chain: A: PDB Molecule: probable nadp-dependent mannitol dehydrogenase; PDBTitle: crystal structure of the nadp-dependent mannitol dehydrogenase from2 cladospirum herbarum.
85	c1vraB_	Alignment	not modelled	35.1	22 PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj; PDBTitle: crystal structure of arginine biosynthesis bifunctional protein argj2 (10175521) from bacillus halodurans at 2.00 a resolution
86	c3v8bC_	Alignment	not modelled	34.8	15 PDB header: oxidoreductase Chain: C: PDB Molecule: putative dehydrogenase, possibly 3-oxoacyl-[acyl-carrier PDBTitle: crystal structure of a 3-ketoacyl-acp reductase from sinorhizobium2 meliloti 1021
87	c3ppiA_	Alignment	not modelled	34.7	20 PDB header: oxidoreductase Chain: A: PDB Molecule: 3-hydroxyacyl-coa dehydrogenase type-2; PDBTitle: crystal structure of 3-hydroxyacyl-coa dehydrogenase type-2 from2 mycobacterium avium
88	c1oi7A_	Alignment	not modelled	34.5	12 PDB header: synthetase Chain: A: PDB Molecule: succinyl-coa synthetase alpha chain; PDBTitle: the crystal structure of succinyl-coa synthetase alpha2 subunit from thermus thermophilus
89	c3oidA_	Alignment	not modelled	34.5	18 PDB header: oxidoreductase Chain: A: PDB Molecule: enoyl-[acyl-carrier-protein] reductase [nadph]; PDBTitle: crystal structure of enoyl-acp reductases iii (fabl) from b. subtilis2 (complex with nadp and tcl)
90	d1p9oa_	Alignment	not modelled	34.3	35 Fold: Ribokinase-like Superfamily: CoaB-like Family: CoaB-like
91	d2rhca1	Alignment	not modelled	33.7	13 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
92	c2qn9B_	Alignment	not modelled	33.3	11 PDB header: lyase Chain: B: PDB Molecule: udp-glcnac c6 dehydratase; PDBTitle: crystal structure of udp-glcnac inverting 4,6-dehydratase in complex2 with nadp and udp-glc
93	c3it4B_	Alignment	not modelled	33.3	32 PDB header: transferase Chain: B: PDB Molecule: arginine biosynthesis bifunctional protein argj PDBTitle: the crystal structure of ornithine acetyltransferase from2 mycobacterium tuberculosis (rv1653) at 1.7 a
94	d1trba1	Alignment	not modelled	32.8	26 Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
95	c3cxtA_	Alignment	not modelled	32.7	15 PDB header: oxidoreductase Chain: A: PDB Molecule: dehydrogenase with different specificities; PDBTitle: quaternary complex structure of gluconate 5-dehydrogenase from2 streptococcus suis type 2
96	c2zafC_	Alignment	not modelled	32.5	12 PDB header: oxidoreductase Chain: C: PDB Molecule: dehydrogenase/reductase sdr family

96	c2zdc_	Alignment	not modelled	32.3	12	member 4; PDBTitle: crystal structure of a mammalian reductase
97	d1uana_	Alignment	not modelled	32.3	23	Fold: LmbE-like Superfamily: LmbE-like Family: LmbE-like
98	c3bmrA_	Alignment	not modelled	32.0	17	PDB header: oxidoreductase Chain: A: PDB Molecule: pteridine reductase; PDBTitle: structure of pteridine reductase 1 (ptr1) from trypanosoma2 brucei in ternary complex with cofactor (nadp+) and3 inhibitor (compound ax6)
99	d1f16a_	Alignment	not modelled	32.0	15	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
100	c2gk4A_	Alignment	not modelled	31.9	11	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
101	c2yv6A_	Alignment	not modelled	31.2	17	PDB header: apoptosis Chain: A: PDB Molecule: bcl-2 homologous antagonist/killer; PDBTitle: crystal structure of human bcl-2 family protein bak
102	d2gnoa2	Alignment	not modelled	30.8	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
103	d2gdza1	Alignment	not modelled	30.2	16	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
104	d1bxla_	Alignment	not modelled	30.0	15	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
105	d1xdpa3	Alignment	not modelled	29.8	14	Fold: Phospholipase D/nuclease Superfamily: Phospholipase D/nuclease Family: Polyphosphate kinase C-terminal domain
106	c3ioyB_	Alignment	not modelled	29.4	13	PDB header: oxidoreductase Chain: B: PDB Molecule: short-chain dehydrogenase/reductase sdr; PDBTitle: structure of putative short-chain dehydrogenase (saro_0793)2 from novosphingobium aromaticivorans
107	c3dfmA_	Alignment	not modelled	29.2	19	PDB header: hydrolase Chain: A: PDB Molecule: teicoplanin pseudoaglycone deacetylase orf2; PDBTitle: the crystal structure of the zinc inhibited form of2 teicoplanin deacetylase orf2
108	d1hgxa_	Alignment	not modelled	29.0	18	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
109	c1n7gB_	Alignment	not modelled	28.9	12	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.
110	d1hdia_	Alignment	not modelled	28.9	21	Fold: Phosphoglycerate kinase Superfamily: Phosphoglycerate kinase Family: Phosphoglycerate kinase
111	c1w4zA_	Alignment	not modelled	28.8	14	PDB header: antibiotic biosynthesis Chain: A: PDB Molecule: ketoacyl reductase; PDBTitle: structure of actinorhodin polyketide (actiii) reductase
112	c2qioA_	Alignment	not modelled	28.6	13	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
113	d1vz6a_	Alignment	not modelled	28.2	20	Fold: DmpA/ArgJ-like Superfamily: DmpA/ArgJ-like Family: ArgJ-like
114	c3c7cB_	Alignment	not modelled	27.9	13	PDB header: oxidoreductase Chain: B: PDB Molecule: octopine dehydrogenase; PDBTitle: a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
115	c3dfiA_	Alignment	not modelled	27.8	19	PDB header: hydrolase Chain: A: PDB Molecule: pseudoaglycone deacetylase dbv21; PDBTitle: the crystal structure of antimicrobial reagent a40926 pseudoaglycone2 deacetylase dbv21
116	c3lxmC_	Alignment	not modelled	27.6	13	PDB header: transferase Chain: C: PDB Molecule: aspartate carbamoyltransferase; PDBTitle: 2.00 angstrom resolution crystal structure of a catalytic2 subunit of an aspartate carbamoyltransferase (pyrb) from3 yersinia pestis co92
117	c3r3sD_	Alignment	not modelled	27.6	15	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase; PDBTitle: structure of the ygha oxidoreductase from salmonella enterica
118	d1mxha_	Alignment	not modelled	27.1	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
119	d1ysga1	Alignment	not modelled	26.9	14	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
120	d1k3ka_	Alignment	not modelled	26.8	24	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death