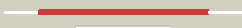































# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1769_(-)_2002633_2003877
Date	Fri Aug 2 13:30:37 BST 2019
Unique Job ID	c53e4ea216c6c1e1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3gwqB_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> d-serine deaminase; <b>PDBTitle:</b> crystal structure of a putative d-serine deaminase (bx_e_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
2	<a href="#">c3wqgB_</a>	 Alignment		100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> d-threo-3-hydroxyaspartate dehydratase; <b>PDBTitle:</b> d-threo-3-hydroxyaspartate dehydratase c353a mutant in the metal-free2 form
3	<a href="#">c3llxA_</a>	 Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> predicted amino acid aldolase or racemase; <b>PDBTitle:</b> crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
4	<a href="#">c4v15B_</a>	 Alignment		100.0	20	<b>PDB header:</b> lyase <b>Chain:</b> B; <b>PDB Molecule:</b> d-threonine aldolase; <b>PDBTitle:</b> crystal structure of d-threonine aldolase from alcaligenes2 xylooxidans
5	<a href="#">c3anuA_</a>	 Alignment		100.0	19	<b>PDB header:</b> lyase <b>Chain:</b> A; <b>PDB Molecule:</b> d-serine dehydratase; <b>PDBTitle:</b> crystal structure of d-serine dehydratase from chicken kidney
6	<a href="#">c4kxkA_</a>	 Alignment		100.0	13	<b>PDB header:</b> unknown function <b>Chain:</b> A; <b>PDB Molecule:</b> uncharacterized protein yhfx; <b>PDBTitle:</b> crystal structure of the pyridoxal-5'-phosphate dependent protein yhfx2 from escherichia coli
7	<a href="#">c5lrpA_</a>	 Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine racemase 2; <b>PDBTitle:</b> crystal structure of the alanine racemase bsu17640 from bacillus2 subtilis
8	<a href="#">c4y2wA_</a>	 Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A; <b>PDB Molecule:</b> alanine racemase 1; <b>PDBTitle:</b> crystal structure of a thermostable alanine racemase from2 thermoanaerobacter tengcongensis mb4
9	<a href="#">c2dy3B_</a>	 Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from corynebacterium glutamicum
10	<a href="#">c5yycC_</a>	 Alignment		100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> C; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from bacillus pseudofirmus (of4)
11	<a href="#">c1xfcB_</a>	 Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B; <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the 1.9 a crystal structure of alanine racemase from mycobacterium2 tuberculosis contains a conserved entryway into the active site

12	<a href="#">c3oo2B_</a>	Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase 1; <b>PDBTitle:</b> 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
13	<a href="#">c4ec1A_</a>	Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> serine racemase; <b>PDBTitle:</b> crystal structure of the cytoplasmic domain of vancomycin resistance2 serine racemase vantg
14	<a href="#">c1vftA_</a>	Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
15	<a href="#">c5zl6A_</a>	Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> histidine racemase; <b>PDBTitle:</b> histidine racemase from leuconostoc mesenteroides subsp. sake nbr2 102480
16	<a href="#">c4lusD_</a>	Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> alanine racemase [clostridium difficile 630]
17	<a href="#">c3hurA_</a>	Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from oenococcus oeni
18	<a href="#">c3oo2A_</a>	Alignment		100.0	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase 1; <b>PDBTitle:</b> 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
19	<a href="#">c4bf5A_</a>	Alignment		100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> structure of broad spectrum racemase from aeromonas hydrophila
20	<a href="#">c3e6eC_</a>	Alignment		100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
21	<a href="#">c1niuA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> alanine racemase with bound inhibitor derived from l-2 cycloserine
22	<a href="#">c4dzaA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine racemase; <b>PDBTitle:</b> crystal structure of a lysine racemase within internal aldimine2 linkage
23	<a href="#">c4fs9B_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> broad specificity amino acid racemase; <b>PDBTitle:</b> complex structure of a broad specificity amino acid racemase (bar)2 within the reactive intermediate
24	<a href="#">c3n2bD_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
25	<a href="#">c4beqA_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase 2; <b>PDBTitle:</b> structure of vibrio cholerae broad spectrum racemase double2 mutant r173a, n174a
26	<a href="#">c3co8B_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from oenococcus oeni
27	<a href="#">c3kw3B_</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
28	<a href="#">c2j66A_</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> btrk; <b>PDBTitle:</b> structural characterisation of btrk decarboxylase from2 butirosin biosynthesis

29	<a href="#">c2p3eA</a>	Alignment	not modelled	100.0	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of aq1208 from aquifex aeolicus
30	<a href="#">c3mubB</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the crystal structure of alanine racemase from streptococcus2 pneumoniae
31	<a href="#">d1bd0a2</a>	Alignment	not modelled	100.0	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
32	<a href="#">c6a2fB</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase, biosynthetic; <b>PDBTitle:</b> crystal structure of biosynthetic alanine racemase from pseudomonas2 aeruginosa
33	<a href="#">c2odoC</a>	Alignment	not modelled	100.0	20	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of pseudomonas fluorescens alanine racemase
34	<a href="#">c2rjgC</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> crystal structure of biosynthetic alaine racemase from escherichia2 coli
35	<a href="#">c2qghA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
36	<a href="#">c4xg1C</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> psychromonas ingrahamii diaminopimelate decarboxylase with lp
37	<a href="#">c4tloB</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> alanine racemase from acinetobacter baumannii
38	<a href="#">d1vfa2</a>	Alignment	not modelled	100.0	23	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
39	<a href="#">c5gjmB</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> lysine/ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of lysine decarboxylase from selenomonas ruminantium2 in c2 space group
40	<a href="#">c5x7nA</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of meso-diaminopimelate decarboxylase (dapdc) from2 corynebacterium glutamicum
41	<a href="#">c1w8gA</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> plp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical upf0001 protein yggs; <b>PDBTitle:</b> crystal structure of e. coli k-12 yggs
42	<a href="#">c1tufA</a>	Alignment	not modelled	100.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
43	<a href="#">c3vabA</a>	Alignment	not modelled	100.0	12	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase 1; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase from brucella2 melitensis bound to plp
44	<a href="#">c6n2fB</a>	Alignment	not modelled	100.0	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate decarboxylase 2, chloroplastic; <b>PDBTitle:</b> meso-diaminopimelate decarboxylase from arabidopsis thaliana (isoform2 2)
45	<a href="#">c5bwaA</a>	Alignment	not modelled	99.9	12	<b>PDB header:</b> lyase/lyase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of odc-plp-az1 ternary complex
46	<a href="#">c3cpgA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an unknown protein from bifidobacterium2 adolescentis
47	<a href="#">c3r79B</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> structure genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of an uncharacterized protein from agrobacterium2 tumefaciens
48	<a href="#">c5nm8A</a>	Alignment	not modelled	99.9	14	<b>PDB header:</b> plp-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> pipy; <b>PDBTitle:</b> structure of pipy, the cog0325 family member of synechococcus2 elongatus pcc7942, with plp bound
49	<a href="#">d1ct5a</a>	Alignment	not modelled	99.9	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> "Hypothetical" protein yb1036c
50	<a href="#">c1njcC</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> crystal structure determination of t. brucei ornithine decarboxylase2 bound to d-ornithine and to g418
51	<a href="#">c2yxxA</a>	Alignment	not modelled	99.9	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure analysis of diaminopimelate decarboxylate (lysa)
52	<a href="#">c2pljA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> lysine/ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
53	<a href="#">d1rcqa2</a>	Alignment	not modelled	99.9	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
54	<a href="#">c1knwA</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase
						<b>PDB header:</b> lyase

55	<a href="#">c2o0tB_</a>	Alignment	not modelled	99.9	16	<b>Chain:</b> B: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
56	<a href="#">c2nvaH_</a>	Alignment	not modelled	99.9	15	<b>PDB header:</b> lyase <b>Chain:</b> H: <b>PDB Molecule:</b> arginine decarboxylase, a207r protein; <b>PDBTitle:</b> the x-ray crystal structure of the paramecium bursaria chlorella virus2 arginine decarboxylase bound to agmatine
57	<a href="#">c2vd9A_</a>	Alignment	not modelled	99.9	19	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> the crystal structure of alanine racemase from bacillus2 anthracis (ba0252) with bound l-ala-p
58	<a href="#">d1hkva2</a>	Alignment	not modelled	99.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
59	<a href="#">c2on3A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> a structural insight into the inhibition of human and leishmania2 donovani ornithine decarboxylases by 3-aminooxy-1-aminopropane
60	<a href="#">c3btnA_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> antizyme inhibitor 1; <b>PDBTitle:</b> crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
61	<a href="#">c3mt1B_</a>	Alignment	not modelled	99.8	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative carboxynorspermidine decarboxylase protein; <b>PDBTitle:</b> crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
62	<a href="#">c3n29A_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxynorspermidine decarboxylase; <b>PDBTitle:</b> crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
63	<a href="#">c1d7kB_</a>	Alignment	not modelled	99.8	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> human ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of human ornithine decarboxylase at 2.1 angstroms2 resolution
64	<a href="#">d1f3ta2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
65	<a href="#">c4aibC_</a>	Alignment	not modelled	99.8	14	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> ornithine decarboxylase; <b>PDBTitle:</b> crystal structure of ornithine decarboxylase from entamoeba2 histolytica.
66	<a href="#">d7odca2</a>	Alignment	not modelled	99.8	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
67	<a href="#">d1twia2</a>	Alignment	not modelled	99.7	16	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
68	<a href="#">c4bhyB_</a>	Alignment	not modelled	99.7	19	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> structure of alanine racemase from aeromonas hydrophila
69	<a href="#">c3nzqB_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
70	<a href="#">d1d7ka2</a>	Alignment	not modelled	99.7	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
71	<a href="#">c3n2oA_</a>	Alignment	not modelled	99.7	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> biosynthetic arginine decarboxylase; <b>PDBTitle:</b> x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
72	<a href="#">c3nzpA_</a>	Alignment	not modelled	99.6	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> arginine decarboxylase; <b>PDBTitle:</b> crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
73	<a href="#">d1knwa2</a>	Alignment	not modelled	99.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
74	<a href="#">d1rcqa1</a>	Alignment	not modelled	77.2	14	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Alanine racemase
75	<a href="#">d1bd0a1</a>	Alignment	not modelled	72.3	14	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Alanine racemase
76	<a href="#">c3iwpK_</a>	Alignment	not modelled	71.3	17	<b>PDB header:</b> metal binding protein <b>Chain:</b> K: <b>PDB Molecule:</b> copper homeostasis protein cutc homolog; <b>PDBTitle:</b> crystal structure of human copper homeostasis protein cutc
77	<a href="#">c2vvpA_</a>	Alignment	not modelled	65.6	19	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose dehydrogenase; <b>PDBTitle:</b> haloferax mediterranei glucose dehydrogenase in complex with nadph and2 zn.
78	<a href="#">d1vfa1</a>	Alignment	not modelled	56.1	12	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Alanine racemase C-terminal domain-like <b>Family:</b> Alanine racemase
79	<a href="#">c3cosD_</a>	Alignment	not modelled	52.4	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> alcohol dehydrogenase 4; <b>PDBTitle:</b> crystal structure of human class ii alcohol dehydrogenase (adh4) in2 complex with nad and zn
						<b>PDB header:</b> oxidoreductase

80	<a href="#">c4qi2B_</a>	Alignment	not modelled	47.8	26	<b>Chain:</b> B: <b>PDB Molecule:</b> crotonyl-coa carboxylase/reductase; <b>PDBTitle:</b> crotonyl-coa carboxylase/reductase
81	<a href="#">c3fp9E_</a>	Alignment	not modelled	46.2	9	<b>PDB header:</b> hydrolase <b>Chain:</b> E: <b>PDB Molecule:</b> proteasome-associated atpase; <b>PDBTitle:</b> crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
82	<a href="#">c3qf4B_</a>	Alignment	not modelled	45.6	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized abc transporter atp-binding protein <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
83	<a href="#">c1ma0B_</a>	Alignment	not modelled	45.5	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> glutathione-dependent formaldehyde dehydrogenase; <b>PDBTitle:</b> ternary complex of human glutathione-dependent formaldehyde2 dehydrogenase with nad+ and dodecanoic acid
84	<a href="#">c3b5xB_</a>	Alignment	not modelled	44.3	16	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> lipid a export atp-binding/permease protein msba; <b>PDBTitle:</b> crystal structure of msba from vibrio cholerae
85	<a href="#">c3ukoA_</a>	Alignment	not modelled	42.9	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase class-3; <b>PDBTitle:</b> crystal structure of s-nitrosogluthatione reductase from arabidopsis2 thaliana, complex with nadh
86	<a href="#">c2dxcG_</a>	Alignment	not modelled	42.4	19	<b>PDB header:</b> hydrolase <b>Chain:</b> G: <b>PDB Molecule:</b> thiocyanate hydrolase subunit alpha; <b>PDBTitle:</b> recombinant thiocyanate hydrolase, fully-matured form
87	<a href="#">c4rqUA_</a>	Alignment	not modelled	40.8	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase crystal structure in complex with nad
88	<a href="#">c2ouiB_</a>	Alignment	not modelled	40.8	36	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> d275p mutant of alcohol dehydrogenase from protozoa entamoeba2 histolytica
89	<a href="#">d1p3ha_</a>	Alignment	not modelled	38.6	14	<b>Fold:</b> GroES-like <b>Superfamily:</b> GroES-like <b>Family:</b> GroES
90	<a href="#">c5mkkA_</a>	Alignment	not modelled	37.8	9	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrab, a2 homolog of the antigen translocation complex tap
91	<a href="#">c6dkhC_</a>	Alignment	not modelled	37.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> l-idonate 5-dehydrogenase (nad(p)(+)); <b>PDBTitle:</b> the crystal structure of l-idonate 5-dehydrogenase from escherichia2 coli str. k-12 substr. mg1655
92	<a href="#">c5ylnB_</a>	Alignment	not modelled	36.5	33	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase, zinc-containing; <b>PDBTitle:</b> zinc dependent alcohol dehydrogenase 2 from streptococcus pneumonia -2 apo form
93	<a href="#">c4cpdA_</a>	Alignment	not modelled	36.4	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase tadh from thermus sp. atn1
94	<a href="#">c5vm2A_</a>	Alignment	not modelled	35.2	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of eck1772, an oxidoreductase/dehydrogenase of2 unknown specificity involved in membrane biogenesis from escherichia3 coli
95	<a href="#">c2eihA_</a>	Alignment	not modelled	34.0	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of nad-dependent alcohol dehydrogenase
96	<a href="#">c1kolA_</a>	Alignment	not modelled	33.8	30	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dehydrogenase; <b>PDBTitle:</b> crystal structure of formaldehyde dehydrogenase
97	<a href="#">c1r37B_</a>	Alignment	not modelled	33.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nad-dependent alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase from sulfolobus solfataricus2 complexed with nad(h) and 2-ethoxyethanol
98	<a href="#">c5kiaA_</a>	Alignment	not modelled	33.7	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of l-threonine 3-dehydrogenase from burkholderia2 thailandensis
99	<a href="#">c5k1sD_</a>	Alignment	not modelled	33.2	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> D: <b>PDB Molecule:</b> oxidoreductase, zinc-binding dehydrogenase family; <b>PDBTitle:</b> crystal structure of aibc
100	<a href="#">c3qf4A_</a>	Alignment	not modelled	32.1	13	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> abc transporter, atp-binding protein; <b>PDBTitle:</b> crystal structure of a heterodimeric abc transporter in its inward-2 facing conformation
101	<a href="#">c3qz9D_</a>	Alignment	not modelled	31.6	32	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> co-type nitrile hydratase beta subunit; <b>PDBTitle:</b> crystal structure of co-type nitrile hydratase beta-y215f from2 pseudomonas putida.
102	<a href="#">c3hr8A_</a>	Alignment	not modelled	31.5	21	<b>PDB header:</b> recombination <b>Chain:</b> A: <b>PDB Molecule:</b> protein reca; <b>PDBTitle:</b> crystal structure of thermotoga maritima reca
103	<a href="#">c1kevB_</a>	Alignment	not modelled	30.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> nadp-dependent alcohol dehydrogenase; <b>PDBTitle:</b> structure of nadp-dependent alcohol dehydrogenase
104	<a href="#">c1h2bA_</a>	Alignment	not modelled	30.2	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> crystal structure of the alcohol dehydrogenase from the2 hyperthermophilic archaeon aeropyrum pernix at 1.65a resolution <b>PDB header:</b> hydrolase <b>Chain:</b> F: <b>PDB Molecule:</b> atp-binding cassette sub-family b member

105	<a href="#">c5ochF_</a>	Alignment	not modelled	30.1	3	8, mitochondrial; <b>PDBTitle:</b> the crystal structure of human abcb8 in an outward-facing state
106	<a href="#">c2dphA_</a>	Alignment	not modelled	29.8	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> formaldehyde dismutase; <b>PDBTitle:</b> crystal structure of formaldehyde dismutase
107	<a href="#">c1e3jA_</a>	Alignment	not modelled	29.6	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> nadp(h)-dependent ketose reductase; <b>PDBTitle:</b> ketose reductase (sorbitol dehydrogenase) from silverleaf2 whitefly
108	<a href="#">d1ugpb_</a>	Alignment	not modelled	29.6	32	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Nitrile hydratase beta chain
109	<a href="#">c2ejvA_</a>	Alignment	not modelled	29.4	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> l-threonine 3-dehydrogenase; <b>PDBTitle:</b> crystal structure of threonine 3-dehydrogenase complexed with nad+
110	<a href="#">c5ochH_</a>	Alignment	not modelled	29.3	3	<b>PDB header:</b> hydrolase <b>Chain:</b> H: <b>PDB Molecule:</b> atp-binding cassette sub-family b member 8, mitochondrial; <b>PDBTitle:</b> the crystal structure of human abcb8 in an outward-facing state
111	<a href="#">c5mkkB_</a>	Alignment	not modelled	29.1	10	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance abc transporter atp-binding and <b>PDBTitle:</b> crystal structure of the heterodimeric abc transporter tmrAB, a2 homolog of the antigen translocation complex tap
112	<a href="#">c1cdoB_</a>	Alignment	not modelled	28.8	20	<b>PDB header:</b> oxidoreductase (ch-oh(d)-nad(a)) <b>Chain:</b> B: <b>PDB Molecule:</b> alcohol dehydrogenase; <b>PDBTitle:</b> alcohol dehydrogenase (e.c.1.1.1.1) (ee isozyme) complexed with2 nicotinamide adenine dinucleotide (nad), and zinc
113	<a href="#">c4a2cB_</a>	Alignment	not modelled	28.6	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> galactitol-1-phosphate 5-dehydrogenase; <b>PDBTitle:</b> crystal structure of galactitol-1-phosphate dehydrogenase from2 escherichia coli
114	<a href="#">c1o89A_</a>	Alignment	not modelled	28.4	10	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> yhdh; <b>PDBTitle:</b> crystal structure of e. coli k-12 yhdh
115	<a href="#">c4ilkB_</a>	Alignment	not modelled	27.5	16	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> starvation sensing protein rspb; <b>PDBTitle:</b> crystal structure of short chain alcohol dehydrogenase (rspb) from e.2 coli cft073 (efi target efi-506413) complexed with cofactor nadh
116	<a href="#">c1yoeA_</a>	Alignment	not modelled	27.2	33	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein ybek; <b>PDBTitle:</b> crystal structure of a the e. coli pyrimidine nucleoside hydrolase2 ybek with bound ribose
117	<a href="#">d1v29b_</a>	Alignment	not modelled	26.9	16	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Electron transport accessory proteins <b>Family:</b> Nitrile hydratase beta chain
118	<a href="#">c5c76D_</a>	Alignment	not modelled	26.3	10	<b>PDB header:</b> transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> wlab protein; <b>PDBTitle:</b> atp-driven lipid-linked oligosaccharide flippase pglk in apo-inward2 facing state (2)
119	<a href="#">c1hf3A_</a>	Alignment	not modelled	25.9	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> alcohol dehydrogenase e chain; <b>PDBTitle:</b> atomic x-ray structure of liver alcohol dehydrogenase containing2 cadmium and a hydroxide adduct to nadh
120	<a href="#">c6daoB_</a>	Alignment	not modelled	24.9	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; <b>PDBTitle:</b> nahe wt selenomethionine