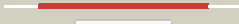



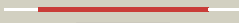



















# Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3423c_alr_3840374_3841600
Date	Fri Aug 9 18:20:09 BST 2019
Unique Job ID	99f3fcfe04319bf6

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c4bf5A_</a>	 Alignment		100.0	28	<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
2	<a href="#">c4fs9B_</a>	 Alignment		100.0	31	<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
3	<a href="#">c4y2wA_</a>	 Alignment		100.0	30	<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
4	<a href="#">c1vftA_</a>	 Alignment		100.0	47	<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
5	<a href="#">c4beqA_</a>	 Alignment		100.0	24	<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
6	<a href="#">c3mubB_</a>	 Alignment		100.0	33	<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
7	<a href="#">c5zl6A_</a>	 Alignment		100.0	28	<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 nbrc2 102480
8	<a href="#">c1niuA_</a>	 Alignment		100.0	36	<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
9	<a href="#">c3oo2A_</a>	 Alignment		100.0	33	<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
10	<a href="#">c3e6eC_</a>	 Alignment		100.0	36	<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
11	<a href="#">c4ec1A_</a>	 Alignment		100.0	30	<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

12	<a href="#">c4lusD_</a>	Alignment		100.0	33	<b>PDB header:</b> isomerase <b>Chain:</b> D: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> alanine racemase [clostridium difficile 630]
13	<a href="#">c1xfcB_</a>	Alignment		100.0	100	<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
14	<a href="#">c4dzaA_</a>	Alignment		100.0	22	<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
15	<a href="#">c3kw3B_</a>	Alignment		100.0	28	<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
16	<a href="#">c3hurA_</a>	Alignment		100.0	29	<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
17	<a href="#">c5irpA_</a>	Alignment		100.0	35	<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
18	<a href="#">c6a2fB_</a>	Alignment		100.0	31	<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
19	<a href="#">c2rigC_</a>	Alignment		100.0	35	<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
20	<a href="#">c2odoC_</a>	Alignment		100.0	34	<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
21	<a href="#">c5yycC_</a>	Alignment	not modelled	100.0	33	<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)
22	<a href="#">c3oo2B_</a>	Alignment	not modelled	100.0	32	<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
23	<a href="#">c2vd9A_</a>	Alignment	not modelled	100.0	36	<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
24	<a href="#">c2dy3B_</a>	Alignment	not modelled	100.0	43	<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
25	<a href="#">c3co8B_</a>	Alignment	not modelled	100.0	27	<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
26	<a href="#">c4tloB_</a>	Alignment	not modelled	100.0	29	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> alanine racemase; <b>PDBTitle:</b> alanine racemase from acinetobacter baumannii
27	<a href="#">c4bhyB_</a>	Alignment	not modelled	100.0	36	<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
28	<a href="#">d1vfa2</a>	Alignment	not modelled	100.0	47	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
						<b>PDB header:</b> unknown function

29	<a href="#">c4kbxA</a>	Alignment	not modelled	100.0	17	<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
30	<a href="#">d1bd0a2</a>	Alignment	not modelled	100.0	38	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
31	<a href="#">d1rcqa2</a>	Alignment	not modelled	100.0	35	<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="#">d1vfsa1</a>	Alignment	not modelled	100.0	47	<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
33	<a href="#">c3anuA</a>	Alignment	not modelled	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
34	<a href="#">d1bd0a1</a>	Alignment	not modelled	100.0	34	<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
35	<a href="#">d1rcqa1</a>	Alignment	not modelled	100.0	32	<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
36	<a href="#">c3wqgB</a>	Alignment	not modelled	100.0	20	<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
37	<a href="#">c1njjC</a>	Alignment	not modelled	100.0	16	<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
38	<a href="#">c2p3eA</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 aq1208 from aquifex aeolicus
39	<a href="#">c2j66A</a>	Alignment	not modelled	100.0	16	<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
40	<a href="#">c3llxA</a>	Alignment	not modelled	100.0	15	<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
41	<a href="#">c3gwqB</a>	Alignment	not modelled	100.0	15	<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
42	<a href="#">c2qghA</a>	Alignment	not modelled	100.0	15	<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
43	<a href="#">c4v15B</a>	Alignment	not modelled	100.0	22	<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 xylosoxidans
44	<a href="#">c3vabA</a>	Alignment	not modelled	100.0	18	<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
45	<a href="#">c5x7nA</a>	Alignment	not modelled	100.0	18	<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
46	<a href="#">c1tufA</a>	Alignment	not modelled	100.0	17	<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
47	<a href="#">c5bwaA</a>	Alignment	not modelled	100.0	14	<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
48	<a href="#">c3n2bD</a>	Alignment	not modelled	100.0	18	<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.
49	<a href="#">c5nm8A</a>	Alignment	not modelled	100.0	23	<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
50	<a href="#">c6n2fB</a>	Alignment	not modelled	100.0	15	<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)
51	<a href="#">c3r79B</a>	Alignment	not modelled	100.0	22	<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
52	<a href="#">c2nvaH</a>	Alignment	not modelled	100.0	12	<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 paramécie bursaria chlorella virus2 arginine decarboxylase bound to agmatine
53	<a href="#">c4xg1C</a>	Alignment	not modelled	100.0	15	<b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> psychromonas ingrahamii diaminopimelate decarboxylase with lp
54	<a href="#">c1w8gA</a>	Alignment	not modelled	100.0	17	<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

55	<a href="#">c5gjmB</a>	Alignment	not modelled	100.0	17	<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
56	<a href="#">d1ct5a</a>	Alignment	not modelled	100.0	14	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> "Hypothetical" protein ybl036c
57	<a href="#">c3cpgA</a>	Alignment	not modelled	100.0	20	<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
58	<a href="#">c2o0tB</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> lyase <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
59	<a href="#">c2pljA</a>	Alignment	not modelled	100.0	18	<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
60	<a href="#">c2yxxA</a>	Alignment	not modelled	100.0	15	<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)
61	<a href="#">c1knwA</a>	Alignment	not modelled	100.0	17	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> diaminopimelate decarboxylase; <b>PDBTitle:</b> crystal structure of diaminopimelate decarboxylase
62	<a href="#">c2on3A</a>	Alignment	not modelled	100.0	17	<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
63	<a href="#">c3btnA</a>	Alignment	not modelled	100.0	16	<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
64	<a href="#">d1f3ta2</a>	Alignment	not modelled	100.0	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="#">d7odca2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
66	<a href="#">c1d7kB</a>	Alignment	not modelled	99.9	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
67	<a href="#">d1hkva2</a>	Alignment	not modelled	99.9	21	<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="#">c3n29A</a>	Alignment	not modelled	99.9	12	<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
69	<a href="#">d1twia2</a>	Alignment	not modelled	99.9	17	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> PLP-binding barrel <b>Family:</b> Alanine racemase-like, N-terminal domain
70	<a href="#">d1d7ka2</a>	Alignment	not modelled	99.9	13	<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="#">c4aibC</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 of ornithine decarboxylase from entamoeba2 histolytica.
72	<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 mellioli
73	<a href="#">c3nzqB</a>	Alignment	not modelled	99.8	14	<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
74	<a href="#">d1knwa2</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
75	<a href="#">c3nzpA</a>	Alignment	not modelled	99.7	9	<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
76	<a href="#">c3n2oA</a>	Alignment	not modelled	99.7	15	<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
77	<a href="#">d1knwa1</a>	Alignment	not modelled	83.3	22	<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> Eukaryotic ODC-like
78	<a href="#">d1mxsa</a>	Alignment	not modelled	80.8	15	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
79	<a href="#">d1twia1</a>	Alignment	not modelled	80.7	20	<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> Eukaryotic ODC-like
						<b>PDB header:</b> structural genomics, unknown function

80	<a href="#">c3c2qA</a>	Alignment	not modelled	78.7	21	<b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized conserved protein; <b>PDBTitle:</b> crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
81	<a href="#">c4e38A</a>	Alignment	not modelled	78.5	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-hydroxyglutarate-aldolase/keto-deoxy-phosphogluconate <b>PDBTitle:</b> crystal structure of probable keto-hydroxyglutarate-aldolase from2 vibionales bacterium swat-3 (target efi-502156)
82	<a href="#">c2jfoB</a>	Alignment	not modelled	75.5	15	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
83	<a href="#">c6oviA</a>	Alignment	not modelled	73.5	18	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> keto-deoxy-phosphogluconate aldolase; <b>PDBTitle:</b> crystal structure of kdpg aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
84	<a href="#">c3qz6A</a>	Alignment	not modelled	73.0	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hpch/hpai aldolase; <b>PDBTitle:</b> the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
85	<a href="#">c3b8fF</a>	Alignment	not modelled	71.7	13	<b>PDB header:</b> lyase <b>Chain:</b> F: <b>PDB Molecule:</b> pa4872 oxaloacetate decarboxylase; <b>PDBTitle:</b> crystal structure of oxaloacetate decarboxylase from pseudomonas2 aeruginosa (pa4872) in complex with oxalate and mg2+
86	<a href="#">c2vvtA</a>	Alignment	not modelled	65.2	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> yfau, 2-keto-3-deoxy sugar aldolase; <b>PDBTitle:</b> crystal structure of yfau, a metal ion dependent class ii2 aldolase from escherichia coli k12 - mg-pyruvate product3 complex
87	<a href="#">d1a3xa2</a>	Alignment	not modelled	64.3	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Pyruvate kinase
88	<a href="#">c4x2rA</a>	Alignment	not modelled	63.9	17	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) <b>PDBTitle:</b> crystal structure of pria from actinomyces urogenitalis
89	<a href="#">d2toda1</a>	Alignment	not modelled	56.7	21	<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> Eukaryotic ODC-like
90	<a href="#">c3u80A</a>	Alignment	not modelled	53.2	21	<b>PDB header:</b> unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquininate dehydratase, type ii; <b>PDBTitle:</b> 1.60 angstrom resolution crystal structure of a 3-dehydroquininate2 dehydratase-like protein from bifidobacterium longum
91	<a href="#">c2x7vA</a>	Alignment	not modelled	53.0	14	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> probable endonuclease 4; <b>PDBTitle:</b> crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
92	<a href="#">c2gzmb</a>	Alignment	not modelled	52.9	12	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> crystal structure of the glutamate racemase from bacillus anthracis
93	<a href="#">c2ohoA</a>	Alignment	not modelled	50.4	12	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> glutamate racemase; <b>PDBTitle:</b> structural basis for glutamate racemase inhibitor
94	<a href="#">d1hkva1</a>	Alignment	not modelled	50.0	28	<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> Eukaryotic ODC-like
95	<a href="#">d1njib1</a>	Alignment	not modelled	49.2	17	<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> Eukaryotic ODC-like
96	<a href="#">c1uheA</a>	Alignment	not modelled	48.6	21	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> aspartate 1-decarboxylase alpha chain; <b>PDBTitle:</b> crystal structure of aspartate decarboxylase, isoasparagine complex
97	<a href="#">c2bibA</a>	Alignment	not modelled	45.7	5	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> teichoic acid phosphorylcholine esterase/ choline binding <b>PDBTitle:</b> crystal structure of the complete modular teichoic acid2 phosphorylcholine esterase pce (cbpe) from streptococcus pneumoniae
98	<a href="#">d1dxea</a>	Alignment	not modelled	44.1	12	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> HpcH/Hpal aldolase
99	<a href="#">d1y0ya1</a>	Alignment	not modelled	43.4	30	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Aminoamidase/glucanase lid domain <b>Family:</b> Aminoamidase/glucanase lid domain
100	<a href="#">d1vqoe2</a>	Alignment	not modelled	42.2	21	<b>Fold:</b> Ribosomal protein L6 <b>Superfamily:</b> Ribosomal protein L6 <b>Family:</b> Ribosomal protein L6
101	<a href="#">c4b5sB</a>	Alignment	not modelled	41.7	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; <b>PDBTitle:</b> crystal structures of divalent metal dependent pyruvate aldolase,2 hpai, in complex with pyruvate
102	<a href="#">d2grea1</a>	Alignment	not modelled	37.0	21	<b>Fold:</b> Domain of alpha and beta subunits of F1 ATP synthase-like <b>Superfamily:</b> Aminoamidase/glucanase lid domain <b>Family:</b> Aminoamidase/glucanase lid domain
103	<a href="#">c2v5jB</a>	Alignment	not modelled	36.8	20	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; <b>PDBTitle:</b> apo class ii aldolase hpch
104	<a href="#">c3plxB</a>	Alignment	not modelled	35.9	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> aspartate 1-decarboxylase; <b>PDBTitle:</b> the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168



105	<a href="#">c2c3zA_</a>	Alignment	not modelled	35.8	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> indole-3-glycerol phosphate synthase; <b>PDBTitle:</b> crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
106	<a href="#">d1ppya_</a>	Alignment	not modelled	35.6	26	<b>Fold:</b> Double psi beta-barrel <b>Superfamily:</b> ADC-like <b>Family:</b> Pyruvoyl dependent aspartate decarboxylase, ADC
107	<a href="#">d1wbha1</a>	Alignment	not modelled	33.6	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
108	<a href="#">d1muma_</a>	Alignment	not modelled	33.5	19	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Phosphoenolpyruvate/pyruvate domain <b>Family:</b> Phosphoenolpyruvate mutase/Isocitrate lyase-like
109	<a href="#">d1vhca_</a>	Alignment	not modelled	33.5	13	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
110	<a href="#">c2kzhA_</a>	Alignment	not modelled	32.5	16	<b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan biosynthesis protein trpcf; <b>PDBTitle:</b> three-dimensional structure of a truncated phosphoribosylanthranilate2 isomerase (residues 255-384) from escherichia coli
111	<a href="#">c4axkB_</a>	Alignment	not modelled	31.2	17	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> 1-(5-phosphoribosyl)-5-((5'-phosphoribosylamino) <b>PDBTitle:</b> crystal structure of subhisa from the thermophile corynebacterium2 efficiens
112	<a href="#">d1wraa1</a>	Alignment	not modelled	30.8	5	<b>Fold:</b> Metallo-hydrolase/oxidoreductase <b>Superfamily:</b> Metallo-hydrolase/oxidoreductase <b>Family:</b> Pce catalytic domain-like
113	<a href="#">c5lp5F_</a>	Alignment	not modelled	30.3	18	<b>PDB header:</b> hydrolase/antibiotic <b>Chain:</b> F: <b>PDB Molecule:</b> rod shape-determining protein (mrec); <b>PDBTitle:</b> complex between penicillin-binding protein (pbp2) and mrec from2 helicobacter pylori
114	<a href="#">c2ftpA_</a>	Alignment	not modelled	29.6	25	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> hydroxymethylglutaryl-coa lyase; <b>PDBTitle:</b> crystal structure of hydroxymethylglutaryl-coa lyase from pseudomonas2 aeruginosa
115	<a href="#">c5k9xA_</a>	Alignment	not modelled	29.2	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> tryptophan synthase alpha chain; <b>PDBTitle:</b> crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
116	<a href="#">c2pfuA_</a>	Alignment	not modelled	29.1	19	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> biopolymer transport exbd protein; <b>PDBTitle:</b> nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
117	<a href="#">d1khia1</a>	Alignment	not modelled	26.0	22	<b>Fold:</b> SH3-like barrel <b>Superfamily:</b> Translation proteins SH3-like domain <b>Family:</b> eIF5a N-terminal domain-like
118	<a href="#">d2bmwa1</a>	Alignment	not modelled	25.5	21	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Riboflavin synthase domain-like <b>Family:</b> Ferredoxin reductase FAD-binding domain-like
119	<a href="#">c4rz0B_</a>	Alignment	not modelled	25.2	33	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pfl0690c; <b>PDBTitle:</b> crystal structure of plasmodium falciparum putative histone2 methyltransferase pfl0690c
120	<a href="#">c5wb4H_</a>	Alignment	not modelled	22.7	9	<b>PDB header:</b> transferase <b>Chain:</b> H: <b>PDB Molecule:</b> n-acetylglucosaminyldiphosphoundecaprenol n-acetyl-beta-d- <b>PDBTitle:</b> crystal structure of the tara wall teichoic acid glycosyltransferase