Phyre2

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Description	RVBD1293_(lysA)_1448034_1449377
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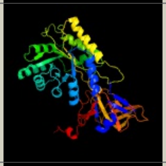
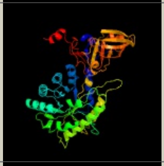
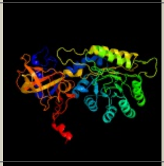
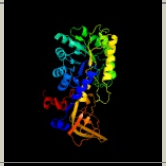
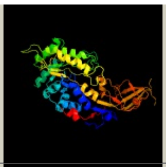
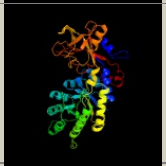
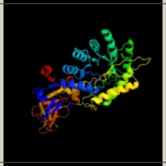
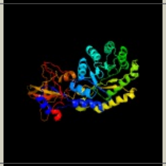
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2o0tB_	Alignment		100.0	98	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** the three dimensional structure of diaminopimelate decarboxylase from2 mycobacterium tuberculosis reveals a tetrameric enzyme organisation
2	c5x7nA_	Alignment		100.0	58	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal strcuture of meso-diaminopimelate decarboxylase (dapdc) from2 corynebacterium glutamicum
3	c1tufA_	Alignment		100.0	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
4	c6n2fB_	Alignment		100.0	27	**PDB header:**lyase **Chain:** B: **PDB Molecule:**diaminopimelate decarboxylase 2, chloroplastic; **PDBTitle:** meso-diaminopimelate decarboxylase from arabidopsis thaliana (isoform2 2)
5	c3vabA_	Alignment		100.0	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase 1; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from brucella2 melitensis bound to plp
6	c4xg1C_	Alignment		100.0	27	**PDB header:**lyase **Chain:** C: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** psychromonas ingrahamii diaminopimelate decarboxylase with llp
7	c3n2bD_	Alignment		100.0	31	**PDB header:**lyase **Chain:** D: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
8	c2p3eA_	Alignment		100.0	35	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of aq1208 from aquifex aeolicus
9	c1knwA_	Alignment		100.0	27	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase
10	c2qghA_	Alignment		100.0	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
11	c2j66A_	Alignment		100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**btrk; **PDBTitle:** structural characterisation of btrk decarboxylase from2 butirosin biosynthesis

12	c1d7kB_	Alignment		100.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**human ornithine decarboxylase; **PDBTitle:** crystal structure of human ornithine decarboxylase at 2.1 angstroms2 resolution
13	c2on3A_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** a structural insight into the inhibition of human and leishmania2 donovani ornithine decarboxylases by 3-aminooxy-1-aminopropane
14	c2yxxA_	Alignment		100.0	33	**PDB header:**lyase **Chain:** A: **PDB Molecule:**diaminopimelate decarboxylase; **PDBTitle:** crystal structure analysis of diaminopimelate decarboxylate (lysa)
15	c3nzpA_	Alignment		100.0	20	**PDB header:**lyase **Chain:** A: **PDB Molecule:**arginine decarboxylase; **PDBTitle:** crystal structure of the biosynthetic arginine decarboxylase spea from2 campylobacter jejuni, northeast structural genomics consortium target3 br53
16	c3nzqB_	Alignment		100.0	24	**PDB header:**lyase **Chain:** B: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** crystal structure of biosynthetic arginine decarboxylase adc (spea)2 from escherichia coli, northeast structural genomics consortium3 target er600
17	c3btnA_	Alignment		100.0	19	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**antizyme inhibitor 1; **PDBTitle:** crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
18	c3n2oA_	Alignment		100.0	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**biosynthetic arginine decarboxylase; **PDBTitle:** x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
19	c5gjmB_	Alignment		100.0	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**lysine/ornithine decarboxylase; **PDBTitle:** crystal strcuture of lysine decarboxylase from selenomonas ruminantium2 in c2 space group
20	c2pljA_	Alignment		100.0	25	**PDB header:**lyase **Chain:** A: **PDB Molecule:**lysine/ornithine decarboxylase; **PDBTitle:** crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
21	c3n29A_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carboxynorspermidine decarboxylase; **PDBTitle:** crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
22	c3mt1B_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative carboxynorspermidine decarboxylase protein; **PDBTitle:** crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
23	c2nvaH_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** H: **PDB Molecule:**arginine decarboxylase, a207r protein; **PDBTitle:** the x-ray crystal structure of the paramecium bursaria chlorella virus2 arginine decarboxylase bound to agmatine
24	c1njjC_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure determination of t. brucei ornithine decarboxylase2 bound to d-ornithine and to g418
25	c5bwaA_	Alignment	not modelled	100.0	20	**PDB header:**lyase/lyase inhibitor **Chain:** A: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure of odc-plp-az1 ternary complex
26	c4aibC_	Alignment	not modelled	100.0	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**ornithine decarboxylase; **PDBTitle:** crystal structure of ornithine decarboxylase from entamoeba2 histolytica.
27	d1hkva2	Alignment	not modelled	100.0	100	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
28	d1twia2	Alignment	not modelled	100.0	31	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain

29	d1knwa2	Alignment	not modelled	100.0	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
30	d1d7ka2	Alignment	not modelled	100.0	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
31	d1f3ta2	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
32	d7odca2	Alignment	not modelled	100.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
33	c4v15B_	Alignment	not modelled	100.0	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-threonine aldolase; **PDBTitle:** crystal structure of d-threonine aldolase from alcaligenes2 xylosoxidans
34	c5yycC_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from bacillus pseudofirmus (of4)
35	d1hkva1	Alignment	not modelled	100.0	90	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
36	c3wqgB_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-threo-3-hydroxyaspartate dehydratase; **PDBTitle:** d-threo-3-hydroxyaspartate dehydratase c353a mutant in the metal-free2 form
37	c4y2wA_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 1; **PDBTitle:** crystal structure of a thermostable alanine racemase from2 thermoanaerobacter tengcongensis mb4
38	c3anuA_	Alignment	not modelled	100.0	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**d-serine dehydratase; **PDBTitle:** crystal structure of d-serine dehydratase from chicken kidney
39	c1xfcB_	Alignment	not modelled	100.0	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** the 1.9 a crystal structure of alanine racemase from mycobacterium2 tuberculosis contains a conserved entryway into the active site
40	c5irpA_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 2; **PDBTitle:** crystal structure of the alanine racemase bsu17640 from bacillus2 subtilis
41	c4bf5A_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** structure of broad spectrum racemase from aeromonas hydrophila
42	c3oo2B_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
43	c4fs9B_	Alignment	not modelled	100.0	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**broad specificity amino acid racemase; **PDBTitle:** complex structure of a broad specificity amino acid racemase (bar)2 within the reactive intermediate
44	c3kw3B_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
45	c4beqA_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 2; **PDBTitle:** structure of vibrio cholerae broad spectrum racemase double2 mutant r173a, n174a
46	c4lusD_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**alanine racemase; **PDBTitle:** alanine racemase [clostridium difficile 630]
47	c4eclA_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**serine racemase; **PDBTitle:** crystal structure of the cytoplasmic domain of vancomycin resistance2 serine racemase vantg
48	c3oo2A_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase 1; **PDBTitle:** 2.37 angstrom resolution crystal structure of an alanine racemase2 (alr) from staphylococcus aureus subsp. aureus col
49	d1knwa1	Alignment	not modelled	100.0	34	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
50	c1vftA_	Alignment	not modelled	100.0	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of l-cycloserine-bound form of alanine2 racemase from d-cycloserine-producing streptomyces3 lavendulae
51	d1twia1	Alignment	not modelled	100.0	30	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
52	c3llxA_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**predicted amino acid aldolase or racemase; **PDBTitle:** crystal structure of an ala racemase-like protein (il1761) from2 idiomarina loihiensis at 1.50 a resolution
53	c4dzaA_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**lysine racemase; **PDBTitle:** crystal structure of a lysine racemase within internal aldimine2 linkage
54	c5zl6A_	Alignment	not modelled	100.0	13	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**histidine racemase; **PDBTitle:** histidine racemase from leuconostoc mesenteroides subsp. sake nbrc2 102480

55	c3gwqB_	Alignment	not modelled	100.0	16	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-serine deaminase; **PDBTitle:** crystal structure of a putative d-serine deaminase (bxe_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
56	c6a2fB_	Alignment	not modelled	100.0	22	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase, biosynthetic; **PDBTitle:** crystal structure of biosynthetic alanine racemase from pseudomonas2 aeruginosa
57	c2dy3B_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from corynebacterium glutamicum
58	c1niuA_	Alignment	not modelled	100.0	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** alanine racemase with bound inhibitor derived from l-2 cycloserine
59	c4kbxA_	Alignment	not modelled	100.0	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein yhfx; **PDBTitle:** crystal structure of the pyridoxal-5'-phosphate dependent protein yhfx2 from escherichia coli
60	c3hurA_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from oenococcus oeni
61	c3e6eC_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
62	c3mubB_	Alignment	not modelled	100.0	14	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** the crystal structure of alanine racemase from streptococcus2 pneumoniae
63	c3co8B_	Alignment	not modelled	100.0	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of alanine racemase from oenococcus oeni
64	c4tloB_	Alignment	not modelled	100.0	16	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** alanine racemase from acinetobacter baumannii
65	c2odoC_	Alignment	not modelled	100.0	24	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of pseudomonas fluorescens alanine racemase
66	c2rjgC_	Alignment	not modelled	100.0	17	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**alanine racemase; **PDBTitle:** crystal structure of biosynthetic alaine racemase from escherichia2 coli
67	d7odca1	Alignment	not modelled	99.9	18	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
68	d1d7ka1	Alignment	not modelled	99.9	19	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
69	d1f3ta1	Alignment	not modelled	99.9	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
70	c2vd9A_	Alignment	not modelled	99.9	16	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**alanine racemase; **PDBTitle:** the crystal structure of alanine racemase from bacillus2 anthracis (ba0252) with bound l-ala-p
71	d2toda1	Alignment	not modelled	99.9	20	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
72	c5nm8A_	Alignment	not modelled	99.9	14	**PDB header:**plp-binding protein **Chain:** A: **PDB Molecule:**pipy; **PDBTitle:** structure of pipy, the cog0325 family member of synechococcus2 elongatus pcc7942, with plp bound
73	d1vfsa2	Alignment	not modelled	99.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
74	d1bd0a2	Alignment	not modelled	99.9	16	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
75	d1njjb1	Alignment	not modelled	99.8	21	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Eukaryotic ODC-like
76	c4bhyB_	Alignment	not modelled	99.8	19	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**alanine racemase; **PDBTitle:** structure of alanine racemase from aeromonas hydrophila
77	c1w8gA_	Alignment	not modelled	99.8	15	**PDB header:**plp-binding protein **Chain:** A: **PDB Molecule:**hypothetical upf0001 protein yggs; **PDBTitle:** crystal structure of e. coli k-12 yggs
78	d1rcqa2	Alignment	not modelled	99.8	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLP-binding barrel **Family:**Alanine racemase-like, N-terminal domain
79	c3r79B_	Alignment	not modelled	99.8	18	**PDB header:**structure genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an uncharactertized protein from agrobacterium2 tumefaciens
80	c3cpgA_	Alignment	not modelled	99.8	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of an unknown protein from bifidobacterium2 adolescentis
						Fold:TIM beta/alpha-barrel

81	d1ct5a_	Alignment	not modelled	99.6	13	**Superfamily:**PLP-binding barrel **Family:**"Hypothetical" protein ybl036c
82	d1bd0a1	Alignment	not modelled	98.6	15	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
83	d1vfsa1	Alignment	not modelled	98.5	22	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
84	d1rcqa1	Alignment	not modelled	98.3	19	**Fold:**Domain of alpha and beta subunits of F1 ATP synthase-like **Superfamily:**Alanine racemase C-terminal domain-like **Family:**Alanine racemase
85	c1vc3B_	Alignment	not modelled	88.9	21	**PDB header:**lyase **Chain:** B: **PDB Molecule:**l-aspartate-alpha-decarboxylase heavy chain; **PDBTitle:** crystal structure of l-aspartate-alpha-decarboxylase
86	c3plxB_	Alignment	not modelled	87.2	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** the crystal structure of aspartate alpha-decarboxylase from2 campylobacter jejuni subsp. jejuni nctc 11168
87	c2uval_	Alignment	not modelled	82.2	16	**PDB header:**transferase **Chain:** I: **PDB Molecule:**fatty acid synthase beta subunits; **PDBTitle:** crystal structure of fatty acid synthase from thermomyces2 lanuginosus at 3.1 angstrom resolution. this file contains3 the beta subunits of the fatty acid synthase. the entire4 crystal structure consists of one heterododecameric fatty5 acid synthase and is described in remark 400
88	c2vkzH_	Alignment	not modelled	81.1	12	**PDB header:**transferase **Chain:** H: **PDB Molecule:**fatty acid synthase subunit beta; **PDBTitle:** structure of the cerulenin-inhibited fungal fatty acid synthase type i2 multienzyme complex
89	c4mf4F_	Alignment	not modelled	79.8	15	**PDB header:**lyase **Chain:** F: **PDB Molecule:**hpch/hpai aldolase/citrate lyase family protein; **PDBTitle:** crystal structure of a hpch/hpal aldolase/citrate lyase family protein2 from burkholderia cenocepacia j2315
90	c1pyuD_	Alignment	not modelled	74.8	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**aspartate 1-decarboxylase alfa chain; **PDBTitle:** processed aspartate decarboxylase mutant with ser25 mutated to cys
91	c1pt1B_	Alignment	not modelled	70.5	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** unprocessed pyruvoyl dependent aspartate decarboxylase with histidine2 11 mutated to alanine
92	c2c45F_	Alignment	not modelled	68.2	24	**PDB header:**lyase **Chain:** F: **PDB Molecule:**aspartate 1-decarboxylase; **PDBTitle:** native precursor of pyruvoyl dependent aspartate decarboxylase
93	c4gisB_	Alignment	not modelled	68.2	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**enolase; **PDBTitle:** crystal structure of an enolase family member from vibrio harveyi2 (efi-target 501692) with homology to mannonate dehydratase, with mg,3 glycerol and dicarboxylates bound (mixed loops, space group i4122)
94	c1uheA_	Alignment	not modelled	68.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aspartate 1-decarboxylase alpha chain; **PDBTitle:** crystal structure of aspartate decarboxylase, isoaspargine complex
95	c4b5sB_	Alignment	not modelled	66.0	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**4-hydroxy-2-oxo-heptane-1,7-dioate aldolase; **PDBTitle:** crystal structures of divalent metal dependent pyruvate aldolase,2 hpai, in complex with pyruvate
96	c3t8qA_	Alignment	not modelled	65.0	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme family **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing enzyme2 family protein from hoeflea phototrophica
97	d1ppya_	Alignment	not modelled	64.9	13	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Pyruvoyl dependent aspartate decarboxylase, ADC
98	d1olta_	Alignment	not modelled	64.5	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Radical SAM enzymes **Family:**Oxygen-independent coproporphyrinogen III oxidase HemN
99	d2gl5a1	Alignment	not modelled	63.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Enolase C-terminal domain-like **Family:**D-glucarate dehydratase-like
100	c2xioA_	Alignment	not modelled	63.6	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative deoxyribonuclease tatdn1; **PDBTitle:** structure of putative deoxyribonuclease tatdn1 isoform a
101	c2pjuD_	Alignment	not modelled	63.0	10	**PDB header:**transcription **Chain:** D: **PDB Molecule:**propionate catabolism operon regulatory protein; **PDBTitle:** crystal structure of propionate catabolism operon regulatory protein2 prpr
102	c3qz6A_	Alignment	not modelled	62.5	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**hpch/hpai aldolase; **PDBTitle:** the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2
103	d1jsca3	Alignment	not modelled	60.7	17	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
104	d1juba_	Alignment	not modelled	60.4	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**FMN-linked oxidoreductases **Family:**FMN-linked oxidoreductases
105	d1vhca_	Alignment	not modelled	59.6	10	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase

						Family: Class I aldolase
106	c3dfhC_	Alignment	not modelled	58.2	11	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**mandelate racemase; **PDBTitle:** crystal structure of putative mandelate racemase / muconate2 lactonizing enzyme from vibrionales bacterium swat-3
107	c3gy1B_	Alignment	not modelled	58.0	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of putative mandelate racemase/muconate lactonizing2 protein from clostridium beijerinckii ncimb 8052
108	c4ip4B_	Alignment	not modelled	57.8	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme-like **PDBTitle:** crystal structure of l-fuconate dehydratase from silicibacter sp.2 tm1040 liganded with mg
109	d1j6oa_	Alignment	not modelled	55.9	18	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
110	d1izca_	Alignment	not modelled	54.4	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Phosphoenolpyruvate/pyruvate domain **Family:**HpcH/HpaI aldolase
111	c1izcA_	Alignment	not modelled	54.4	14	**PDB header:**lyase **Chain:** A: **PDB Molecule:**macrophomate synthase intermolecular diels-alderase; **PDBTitle:** crystal structure analysis of macrophomate synthase
112	c3lq1A_	Alignment	not modelled	52.8	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1- **PDBTitle:** crystal structure of 2-succinyl-6-hydroxy-2,4-cyclohexadiene 1-2 carboxylic acid synthase/2-oxoglutarate decarboxylase from listeria3 monocytogenes str. 4b f2365
113	c2v5jB_	Alignment	not modelled	51.9	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; **PDBTitle:** apo class ii aldolase hpch
114	c2qjjC_	Alignment	not modelled	51.3	8	**PDB header:**lyase **Chain:** C: **PDB Molecule:**mandelate racemase/muconate lactonizing enzyme; **PDBTitle:** crystal structure of d-mannonate dehydratase from novosphingobium2 aromaticivorans
115	d1vd6a1	Alignment	not modelled	51.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**PLC-like phosphodiesterases **Family:**Glycerophosphoryl diester phosphodiesterase
116	c3jw7E_	Alignment	not modelled	50.9	15	**PDB header:**isomerase **Chain:** E: **PDB Molecule:**dipeptide epimerase; **PDBTitle:** crystal structure of dipeptide epimerase from enterococcus faecalis2 v583 complexed with mg and dipeptide l-ile-l-tyr
117	c4q9dA_	Alignment	not modelled	50.3	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**benzoylformate decarboxylase; **PDBTitle:** x-ray structure of a putative thiamin diphosphate-dependent enzyme2 isolated from mycobacterium smegmatis
118	c3nm3D_	Alignment	not modelled	49.5	11	**PDB header:**transferase **Chain:** D: **PDB Molecule:**thiamine biosynthetic bifunctional enzyme; **PDBTitle:** the crystal structure of candida glabrata thi6, a bifunctional enzyme2 involved in thiamin biosyhthesis of eukaryotes
119	d2ji7a3	Alignment	not modelled	49.0	19	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase PP module
120	c2hxtA_	Alignment	not modelled	48.8	19	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**l-fuconate dehydratase; **PDBTitle:** crystal structure of l-fuconate dehydratase from xanthomonas2 campestris liganded with mg++ and d-erythronohydroxamate