







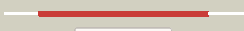
























Phyre2

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Description	RVBD2148c (-) _2406848_2407624
Date	Mon Aug 5 13:25:27 BST 2019
Unique Job ID	3174f782590566ae

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3cpgA_	 Alignment		100.0	34	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an unknown protein from bifidobacterium2 adolescentis
2	c1w8gA_	 Alignment		100.0	33	PDB header: plp-binding protein Chain: A: PDB Molecule: hypothetical upf0001 protein yggs; PDBTitle: crystal structure of e. coli k-12 yggs
3	c3r79B_	 Alignment		100.0	31	PDB header: structure genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from agrobacterium2 tumefaciens
4	d1ct5a_	 Alignment		100.0	28	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: "Hypothetical" protein ybl036c
5	c5nm8A_	 Alignment		100.0	35	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
6	c4y2wA_	 Alignment		100.0	15	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 1; PDBTitle: crystal structure of a thermostable alanine racemase from2 thermoanaerobacter tengcongensis mb4
7	c4bf5A_	 Alignment		100.0	15	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: structure of broad spectrum racemase from aeromonas hydrophila
8	c3oo2A_	 Alignment		100.0	14	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
9	d1bd0a2	 Alignment		100.0	15	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
10	c4fs9B_	 Alignment		100.0	20	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
11	d1vfsa2	 Alignment		100.0	17	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain

12	c2dy3B_	Alignment		100.0	15	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from corynebacterium glutamicum
13	c5zl6A_	Alignment		100.0	17	PDB header: isomerase Chain: A: PDB Molecule: histidine racemase; PDBTitle: histidine racemase from leuconostoc mesenteroides subsp. sake nbr2 102480
14	c3e6eC_	Alignment		100.0	16	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
15	c4ec1A_	Alignment		100.0	14	PDB header: isomerase Chain: A: PDB Molecule: serine racemase; PDBTitle: crystal structure of the cytoplasmic domain of vancomycin resistance2 serine racemase vantg
16	c4beqA_	Alignment		100.0	18	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 2; PDBTitle: structure of vibrio cholerae broad spectrum racemase double2 mutant r173a, n174a
17	c3mubB_	Alignment		100.0	15	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: the crystal structure of alanine racemase from streptococcus2 pneumoniae
18	c5irpA_	Alignment		100.0	13	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 2; PDBTitle: crystal structure of the alanine racemase bsu17640 from bacillus2 subtilis
19	c1xfcB_	Alignment		100.0	25	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
20	c5yycC_	Alignment		100.0	17	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from bacillus pseudofirmus (of4)
21	c3oo2B_	Alignment	not modelled	100.0	13	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
22	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
23	c3co8B_	Alignment	not modelled	100.0	17	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
24	c1vftA_	Alignment	not modelled	100.0	16	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
25	c3hurA_	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
26	c4lusD_	Alignment	not modelled	100.0	13	PDB header: isomerase Chain: D: PDB Molecule: alanine racemase; PDBTitle: alanine racemase [clostridium difficile 630]
27	c4dzaA_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: A: PDB Molecule: lysine racemase; PDBTitle: crystal structure of a lysine racemase within internal aldimine2 linkage
28	d1rcqa2	Alignment	not modelled	100.0	17	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
						PDB header: isomerase

29	c3kw3B_	Alignment	not modelled	100.0	13	Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
30	c2vd9A_	Alignment	not modelled	100.0	15	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
31	c6a2fB_	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase, biosynthetic; PDBTitle: crystal structure of biosynthetic alanine racemase from pseudomonas2 aeruginosa
32	c4kx9A_	Alignment	not modelled	100.0	22	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
33	c4tloB_	Alignment	not modelled	100.0	12	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: alanine racemase from acinetobacter baumannii
34	c2odoC_	Alignment	not modelled	100.0	18	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of pseudomonas fluorescens alanine racemase
35	c2rjgC_	Alignment	not modelled	100.0	15	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of biosynthetic alaine racemase from escherichia2 coli
36	c3wqgB_	Alignment	not modelled	100.0	19	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	c3anuA_	Alignment	not modelled	100.0	14	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of d-serine dehydratase from chicken kidney
38	c4v15B_	Alignment	not modelled	100.0	21	PDB header: lyase Chain: B: PDB Molecule: d-threonine aldolase; PDBTitle: crystal structure of d-threonine aldolase from alcaligenes2 xylosoxidans
39	c3llxA_	Alignment	not modelled	100.0	14	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
40	c3gwgB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: d-serine deaminase; PDBTitle: crystal structure of a putative d-serine deaminase (bx_e_a4060) from2 burkholderia xenovorans lb400 at 2.00 a resolution
41	c4bhyB_	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: structure of alanine racemase from aeromonas hydrophila
42	c2j66A_	Alignment	not modelled	99.9	12	PDB header: lyase Chain: A: PDB Molecule: btrk; PDBTitle: structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
43	c2qghA_	Alignment	not modelled	99.9	12	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
44	c2p3eA_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of aq1208 from aquifex aeolicus
45	c3n2bD_	Alignment	not modelled	99.9	18	PDB header: lyase Chain: D: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
46	c4xg1C_	Alignment	not modelled	99.9	16	PDB header: lyase Chain: C: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: psychromonas ingrahamii diaminopimelate decarboxylase with lp
47	c1njjC_	Alignment	not modelled	99.8	8	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
48	c3vabA_	Alignment	not modelled	99.8	17	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase 1; PDBTitle: crystal structure of diaminopimelate decarboxylase from brucella2 melitensis bound to plp
49	c5x7nA_	Alignment	not modelled	99.8	22	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of meso-diaminopimelate decarboxylase (dapdc) from2 corynebacterium glutamicum
50	c6n2fB_	Alignment	not modelled	99.8	18	PDB header: lyase Chain: B: PDB Molecule: diaminopimelate decarboxylase 2, chloroplastic; PDBTitle: meso-diaminopimelate decarboxylase from arabidopsis thaliana (isoform2 2)
51	c1tufA_	Alignment	not modelled	99.8	16	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
52	c5gjmB_	Alignment	not modelled	99.8	17	PDB header: lyase Chain: B: PDB Molecule: lysine/ornithine decarboxylase; PDBTitle: crystal structure of lysine decarboxylase from selenomonas ruminantium2 in c2 space group
53	d1twia2	Alignment	not modelled	99.8	17	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
						PDB header: lyase/lyase inhibitor

54	c5bwaA_	Alignment	not modelled	99.8	14	Chain: A: PDB Molecule: ornithine decarboxylase; PDBTitle: crystal structure of odc-plp-az1 ternary complex
55	d1hkva2	Alignment	not modelled	99.8	22	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
56	c2nvaH_	Alignment	not modelled	99.7	7	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
57	d7odca2	Alignment	not modelled	99.7	14	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
58	c2pljA_	Alignment	not modelled	99.7	15	PDB header: lyase Chain: A: PDB Molecule: lysine/ornithine decarboxylase; PDBTitle: crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
59	d1f3ta2	Alignment	not modelled	99.7	10	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
60	c2o0tB_	Alignment	not modelled	99.6	22	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
61	c1knwA_	Alignment	not modelled	99.6	18	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase
62	c2yxxA_	Alignment	not modelled	99.6	15	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure analysis of diaminopimelate decarboxylate (lysa)
63	d1d7ka2	Alignment	not modelled	99.5	13	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
64	c3btnA_	Alignment	not modelled	99.3	13	PDB header: biosynthetic protein Chain: A: PDB Molecule: antizyme inhibitor 1; PDBTitle: crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
65	c2on3A_	Alignment	not modelled	99.3	12	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
66	c3nzqB_	Alignment	not modelled	99.2	17	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
67	c3n29A_	Alignment	not modelled	99.2	12	PDB header: lyase Chain: A: PDB Molecule: carboxynorspermidine decarboxylase; PDBTitle: crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
68	d1knwa2	Alignment	not modelled	99.1	18	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
69	c1d7kB_	Alignment	not modelled	99.1	13	PDB header: lyase Chain: B: PDB Molecule: human ornithine decarboxylase; PDBTitle: crystal structure of human ornithine decarboxylase at 2.1 angstroms2 resolution
70	c3n2oA_	Alignment	not modelled	99.1	14	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
71	c4aibC_	Alignment	not modelled	99.0	15	PDB header: lyase Chain: C: PDB Molecule: ornithine decarboxylase; PDBTitle: crystal structure of ornithine decarboxylase from entamoeba2 histolytica.
72	c3nzpA_	Alignment	not modelled	98.9	13	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
73	c3mt1B_	Alignment	not modelled	98.5	14	PDB header: lyase Chain: B: PDB Molecule: putative carboxynorspermidine decarboxylase protein; PDBTitle: crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
74	c4nu7C_	Alignment	not modelled	94.0	15	PDB header: isomerase Chain: C: PDB Molecule: ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom crystal structure of ribulose-phosphate 3-epimerase from2 toxoplasma gondii.
75	c1izcA_	Alignment	not modelled	92.6	11	PDB header: lyase Chain: A: PDB Molecule: macrophomate synthase intermolecular diels-alderase; PDBTitle: crystal structure analysis of macrophomate synthase
76	d1izca_	Alignment	not modelled	92.6	11	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
77	d1tqxa_	Alignment	not modelled	92.4	11	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
78	c3qz6A_	Alignment	not modelled	89.9	13	PDB header: lyase Chain: A: PDB Molecule: hpcH/hpai aldolase; PDBTitle: the crystal structure of hpcH/hpai aldolase from desulfitobacterium2 hafniense dcb-2
79	d1h1ya_	Alignment	not modelled	89.6	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel

						Family: D-ribulose-5-phosphate 3-epimerase
80	d1dxea_	Alignment	not modelled	88.5	16	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Hpch/Hpal aldolase
81	c2vwtA_	Alignment	not modelled	85.9	23	PDB header: lyase Chain: A; PDB Molecule: yfau, 2-keto-3-deoxy sugar aldolase; PDBTitle: crystal structure of yfau, a metal ion dependent class ii aldolase from escherichia coli k12 - mg-pyruvate product3 complex
82	c3ct7E_	Alignment	not modelled	85.5	9	PDB header: isomerase Chain: E; PDB Molecule: d-allulose-6-phosphate 3-epimerase; PDBTitle: crystal structure of d-allulose 6-phosphate 3-epimerase2 from escherichia coli k-12
83	c3q94B_	Alignment	not modelled	85.4	18	PDB header: lyase Chain: B; PDB Molecule: fructose-bisphosphate aldolase, class ii; PDBTitle: the crystal structure of fructose 1,6-bisphosphate aldolase from2 bacillus anthracis str. 'ames ancestor'
84	d1tqja_	Alignment	not modelled	84.6	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
85	c4b5sB_	Alignment	not modelled	84.3	19	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
86	c2v5jB_	Alignment	not modelled	83.5	20	PDB header: lyase Chain: B; PDB Molecule: 2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase; PDBTitle: apo class ii aldolase hpch
87	c6oviA_	Alignment	not modelled	80.2	11	PDB header: lyase Chain: A; PDB Molecule: keto-deoxy-phosphogluconate aldolase; PDBTitle: crystal structure of kdpq aldolase from legionella pneumophila with2 pyruvate captured at low ph as a covalent carbinolamine intermediate
88	c4mf4F_	Alignment	not modelled	80.2	21	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
89	c6r62A_	Alignment	not modelled	73.5	17	PDB header: lyase Chain: A; PDB Molecule: hpch/hpai aldolase; PDBTitle: crystal structure of a class ii pyruvate aldolase from sphingomonas2 wittichii rw1 in complex with hydroxypyruvate
90	d1o4ua1	Alignment	not modelled	73.4	17	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
91	d2flia1	Alignment	not modelled	70.8	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
92	d1qvfa_	Alignment	not modelled	69.4	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
93	d1rpxa_	Alignment	not modelled	66.2	12	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
94	c3inpA_	Alignment	not modelled	63.3	14	PDB header: isomerase Chain: A; PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
95	d1qpoa1	Alignment	not modelled	54.6	26	Fold: TIM beta/alpha-barrel Superfamily: Nicotinate/Quinolinate PRTase C-terminal domain-like Family: NadC C-terminal domain-like
96	c3cu2A_	Alignment	not modelled	51.3	14	PDB header: isomerase Chain: A; PDB Molecule: ribulose-5-phosphate 3-epimerase; PDBTitle: crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
97	c2y85D_	Alignment	not modelled	51.0	20	PDB header: isomerase Chain: D; PDB Molecule: phosphoribosyl isomerase a; PDBTitle: crystal structure of mycobacterium tuberculosis phosphoribosyl2 isomerase with bound rcdrp
98	c2vkzH_	Alignment	not modelled	50.8	10	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
99	c1yoeA_	Alignment	not modelled	50.3	11	PDB header: hydrolase Chain: A; PDB Molecule: hypothetical protein ybek; PDBTitle: crystal structure of a the e. coli pyrimidine nucleoside hydrolase2 ybek with bound ribose
100	d1y0ea_	Alignment	not modelled	48.9	8	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: NanE-like
101	c1yadD_	Alignment	not modelled	40.5	5	PDB header: transcription Chain: D; PDB Molecule: regulatory protein teni; PDBTitle: structure of teni from bacillus subtilis
102	c4tv6A_	Alignment	not modelled	39.9	16	PDB header: lyase Chain: A; PDB Molecule: 2-dehydro-3-deoxyglucarate aldolase; PDBTitle: crystal structure of citrate synthase variant sbng e151q
103	c2c3zA_	Alignment	not modelled	39.7	14	PDB header: lyase Chain: A; PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
104	c5mj7B_	Alignment	not modelled	39.7	13	PDB header: hydrolase Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: structure of the c. elegans nucleoside hydrolase
105	c3oc3B_	Alignment	not modelled	38.7	12	PDB header: isomerase Chain: B; PDB Molecule: d-ribulose-5-phosphate-3-epimerase;

105	c9qc3B_	Alignment	not modelled	38.7	12	PDBTitle: crystal structure of a d-ribulose-5-phosphate-3-epimerase (np_954699)2 from homo sapiens at 2.20 a resolution
106	d1kica_	Alignment	not modelled	34.5	9	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
107	c2w5fB_	Alignment	not modelled	33.8	13	PDB header: hydrolase Chain: B: PDB Molecule: endo-1,4-beta-xylanase y; PDBTitle: high resolution crystallographic structure of the clostridium2 thermocellum n-terminal endo-1,4-beta-d-xylanase 10b (xyn10b) cbm22-3 1- gh10 modules complexed with xylohexaose
108	d1rvga_	Alignment	not modelled	31.1	9	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class II FBP aldolase
109	c3ve9B_	Alignment	not modelled	30.0	23	PDB header: lyase Chain: B: PDB Molecule: orotidine-5'-phosphate decarboxylase; PDBTitle: crystal structure of orotidine 5'-monophosphate decarboxylase from2 metallosphaera sedula
110	c3ewbX_	Alignment	not modelled	27.8	10	PDB header: transferase Chain: X: PDB Molecule: 2-isopropylmalate synthase; PDBTitle: crystal structure of n-terminal domain of putative 2-isopropylmalate2 synthase from listeria monocytogenes
111	c1qpoA_	Alignment	not modelled	23.8	27	PDB header: transferase Chain: A: PDB Molecule: quinolinate acid phosphoribosyl transferase; PDBTitle: quinolinate phosphoribosyl transferase (qaprtase) apoenzyme from2 mycobacterium tuberculosis
112	c2b7pA_	Alignment	not modelled	22.2	14	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori with phthalic acid
113	c5u4nA_	Alignment	not modelled	22.2	17	PDB header: lyase Chain: A: PDB Molecule: fructose-1; PDBTitle: crystal structure of a fructose-bisphosphate aldolase from neisseria2 gonorrhoeae
114	d1pkla2	Alignment	not modelled	22.1	20	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Pyruvate kinase