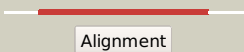

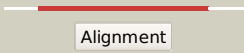



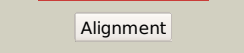



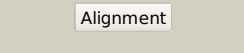

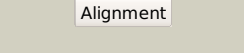



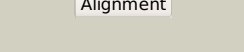

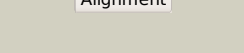
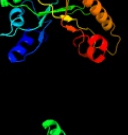
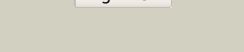
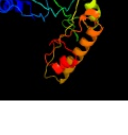


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1413_(-)_1589392_1589907
Date	Wed Jul 31 22:05:52 BST 2019
Unique Job ID	7c657924e03a3bfe

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3llxA_	 Alignment		100.0	25	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
2	c3gwqB_	 Alignment		100.0	20	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
3	c4kbxA_	 Alignment		100.0	18	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
4	c1w8gA_	 Alignment		99.9	19	PDB header: plp-binding protein Chain: A: PDB Molecule: hypothetical upf0001 protein yggs; PDBTitle: crystal structure of e. coli k-12 yggs
5	c3wqgB_	 Alignment		99.9	33	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
6	c4v15B_	 Alignment		99.9	28	PDB header: lyase Chain: B: PDB Molecule: d-threonine aldolase; PDBTitle: crystal structure of d-threonine aldolase from alcaligenes2 xylooxidans
7	c3cpgA_	 Alignment		99.9	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an unknown protein from bifidobacterium2 adolescentis
8	c3anuA_	 Alignment		99.9	25	PDB header: lyase Chain: A: PDB Molecule: d-serine dehydratase; PDBTitle: crystal structure of d-serine dehydratase from chicken kidney
9	c5nm8A_	 Alignment		99.9	11	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
10	d1vfsa2	 Alignment		99.9	18	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
11	c3r79B_	 Alignment		99.9	13	PDB header: structure genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of an uncharacterized protein from agrobacterium2 tumefaciens

12	c4y2wA_	Alignment		99.9	15	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 1; PDBTitle: crystal structure of a thermostable alanine racemase from2 thermoanaerobacter tengcongensis mb4
13	c1xfcB_	Alignment		99.9	13	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
14	c4ec1A_	Alignment		99.9	17	PDB header: isomerase Chain: A: PDB Molecule: serine racemase; PDBTitle: crystal structure of the cytoplasmic domain of vancomycin resistance2 serine racemase vantg
15	c5irpA_	Alignment		99.9	19	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 2; PDBTitle: crystal structure of the alanine racemase bsu17640 from bacillus2 subtilis
16	c5yycC_	Alignment		99.9	13	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from bacillus pseudofirmus (of4)
17	d1ct5a_	Alignment		99.9	14	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: "Hypothetical" protein ybl036c
18	c1vftA_	Alignment		99.9	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
19	c4bf5A_	Alignment		99.9	14	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: structure of broad spectrum racemase from aeromonas hydrophila
20	c2dy3B_	Alignment		99.9	23	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from corynebacterium glutamicum
21	c4fs9B_	Alignment	not modelled	99.9	17	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
22	d1bd0a2	Alignment	not modelled	99.9	15	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
23	c5zl6A_	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: A: PDB Molecule: histidine racemase; PDBTitle: histidine racemase from leuconostoc mesenteroides subsp. sake nbrc2 102480
24	c3kw3B_	Alignment	not modelled	99.9	12	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from bartonella henselae with2 covalently bound pyridoxal phosphate
25	c3e6eC_	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from e.faecalis2 complex with cycloserine
26	c4lusD_	Alignment	not modelled	99.9	17	PDB header: isomerase Chain: D: PDB Molecule: alanine racemase; PDBTitle: alanine racemase [clostridium difficile 630]
27	c3oo2A_	Alignment	not modelled	99.9	19	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
28	c4beqA_	Alignment	not modelled	99.8	16	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase 2; PDBTitle: structure of vibrio cholerae broad spectrum racemase double2 mutant r173a, n174a PDB header: isomerase

29	c6a2fB_	Alignment	not modelled	99.8	17	Chain: B: PDB Molecule: alanine racemase, biosynthetic; PDBTitle: crystal structure of biosynthetic alanine racemase from pseudomonas2 aeruginosa
30	c3mubB_	Alignment	not modelled	99.8	17	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: the crystal structure of alanine racemase from streptococcus2 pneumoniae
31	c3hurA_	Alignment	not modelled	99.8	17	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
32	d1rcqa2	Alignment	not modelled	99.8	15	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
33	c4dzaA_	Alignment	not modelled	99.8	12	PDB header: isomerase Chain: A: PDB Molecule: lysine racemase; PDBTitle: crystal structure of a lysine racemase within internal aldimine2 linkage
34	c2odoC_	Alignment	not modelled	99.8	12	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of pseudomonas fluorescens alanine racemase
35	c3oo2B_	Alignment	not modelled	99.8	19	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
36	c3co8B_	Alignment	not modelled	99.8	18	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: crystal structure of alanine racemase from oenococcus oeni
37	c1niuA_	Alignment	not modelled	99.8	14	PDB header: isomerase Chain: A: PDB Molecule: alanine racemase; PDBTitle: alanine racemase with bound inhibitor derived from l-2 cycloserine
38	c2p3eA_	Alignment	not modelled	99.8	14	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of aq1208 from aquifex aeolicus
39	c2rjgC_	Alignment	not modelled	99.8	18	PDB header: isomerase Chain: C: PDB Molecule: alanine racemase; PDBTitle: crystal structure of biosynthetic alaine racemase from escherichia2 coli
40	c3vabA_	Alignment	not modelled	99.7	19	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase 1; PDBTitle: crystal structure of diaminopimelate decarboxylase from brucella2 melitensis bound to plp
41	c3n2bD_	Alignment	not modelled	99.7	15	PDB header: lyase Chain: D: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: 1.8 angstrom resolution crystal structure of diaminopimelate2 decarboxylase (lysa) from vibrio cholerae.
42	c4xg1C_	Alignment	not modelled	99.7	18	PDB header: lyase Chain: C: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: psychromonas ingrahamii diaminopimelate decarboxylase with lp
43	c4tloB_	Alignment	not modelled	99.7	11	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: alanine racemase from acinetobacter baumannii
44	c2qghA_	Alignment	not modelled	99.7	18	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from helicobacter2 pylori complexed with l-lysine
45	c1tufA_	Alignment	not modelled	99.7	17	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase from m.2 jannaschi
46	c6n2fB_	Alignment	not modelled	99.7	17	PDB header: lyase Chain: B: PDB Molecule: diaminopimelate decarboxylase 2, chloroplastic; PDBTitle: meso-diaminopimelate decarboxylase from arabidopsis thaliana (isoform2 2)
47	c2vd9A_	Alignment	not modelled	99.7	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
48	c1njc_	Alignment	not modelled	99.7	11	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
49	c2j66A_	Alignment	not modelled	99.7	17	PDB header: lyase Chain: A: PDB Molecule: btrk; PDBTitle: structural characterisation of btrk decarboxylase from2 butirosin biosynthesis
50	c5gjmB_	Alignment	not modelled	99.7	22	PDB header: lyase Chain: B: PDB Molecule: lysine/ornithine decarboxylase; PDBTitle: crystal structure of lysine decarboxylase from selenomonas ruminantium2 in c2 space group
51	c5bwaA_	Alignment	not modelled	99.6	14	PDB header: lyase/lyase inhibitor Chain: A: PDB Molecule: ornithine decarboxylase; PDBTitle: crystal structure of odc-plp-az1 ternary complex
52	c2nvaH_	Alignment	not modelled	99.6	11	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
53	d1hkva2	Alignment	not modelled	99.6	22	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
54	c1knwA_	Alignment	not modelled	99.6	18	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of diaminopimelate decarboxylase
						PDB header: lyase

55	c5x7nA	Alignment	not modelled	99.6	20	Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure of meso-diaminopimelate decarboxylase (dapdc) from2 corynebacterium glutamicum
56	d1twia2	Alignment	not modelled	99.6	17	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
57	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
58	d1f3ta2	Alignment	not modelled	99.6	11	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
59	d1d7ka2	Alignment	not modelled	99.5	13	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
60	c2pljA	Alignment	not modelled	99.5	16	PDB header: lyase Chain: A: PDB Molecule: lysine/ornithine decarboxylase; PDBTitle: crystal structure of lysine/ornithine decarboxylase complexed with2 putrescine from vibrio vulnificus
61	c3btnA	Alignment	not modelled	99.4	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: antizyme inhibitor 1; PDBTitle: crystal structure of antizyme inhibitor, an ornithine2 decarboxylase homologous protein
62	d7odca2	Alignment	not modelled	99.4	12	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
63	c2on3A	Alignment	not modelled	99.4	14	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
64	c1d7kB	Alignment	not modelled	99.4	13	PDB header: lyase Chain: B: PDB Molecule: human ornithine decarboxylase; PDBTitle: crystal structure of human ornithine decarboxylase at 2.1 angstroms2 resolution
65	d1knwa2	Alignment	not modelled	99.4	18	Fold: TIM beta/alpha-barrel Superfamily: PLP-binding barrel Family: Alanine racemase-like, N-terminal domain
66	c3n2oA	Alignment	not modelled	99.3	13	PDB header: lyase Chain: A: PDB Molecule: biosynthetic arginine decarboxylase; PDBTitle: x-ray crystal structure of arginine decarboxylase complexed with2 arginine from vibrio vulnificus
67	c3nzqB	Alignment	not modelled	99.3	13	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
68	c3nzpA	Alignment	not modelled	99.1	10	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
69	c2yxxA	Alignment	not modelled	99.0	18	PDB header: lyase Chain: A: PDB Molecule: diaminopimelate decarboxylase; PDBTitle: crystal structure analysis of diaminopimelate decarboxylate (lysa)
70	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.
71	c3n29A	Alignment	not modelled	98.9	8	PDB header: lyase Chain: A: PDB Molecule: carboxynorspermidine decarboxylase; PDBTitle: crystal structure of carboxynorspermidine decarboxylase complexed with2 norspermidine from campylobacter jejuni
72	c4bhyB	Alignment	not modelled	98.7	11	PDB header: isomerase Chain: B: PDB Molecule: alanine racemase; PDBTitle: structure of alanine racemase from aeromonas hydrophila
73	c3mt1B	Alignment	not modelled	98.4	13	PDB header: lyase Chain: B: PDB Molecule: putative carboxynorspermidine decarboxylase protein; PDBTitle: crystal structure of putative carboxynorspermidine decarboxylase2 protein from sinorhizobium meliloti
74	c2x7vA	Alignment	not modelled	85.2	10	PDB header: hydrolase Chain: A: PDB Molecule: probable endonuclease 4; PDBTitle: crystal structure of thermotoga maritima endonuclease iv in2 the presence of zinc
75	c1yoeA	Alignment	not modelled	79.1	19	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
76	c4mwaA	Alignment	not modelled	76.1	16	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: 1.85 angstrom crystal structure of gcpe protein from bacillus2 anthracis
77	c3fz0C	Alignment	not modelled	72.8	15	PDB header: hydrolase Chain: C: PDB Molecule: nucleoside hydrolase, putative; PDBTitle: inosine-guanosine nucleoside hydrolase (ig-nh)
78	c5mj7B	Alignment	not modelled	71.3	15	PDB header: hydrolase Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: structure of the c. elegans nucleoside hydrolase
79	c4kpnE	Alignment	not modelled	70.0	23	PDB header: hydrolase Chain: E: PDB Molecule: nucleoside n-ribohydrolase 1; PDBTitle: plant nucleoside hydrolase - ppnrh1 enzyme

80	c4wr2A	Alignment	not modelled	68.9	22	PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine-specific ribonucleoside hydrolase riha; PDBTitle: crystal structure of a putative pyrimidine-specific ribonucleoside2 hydrolase (riha) protein from shewanella loihica pv-4 (shew_0697.3 target psi-029635) with divalent cation and peg 400 bound at the4 active site
81	d1ezra	Alignment	not modelled	68.5	18	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
82	c6ba0D	Alignment	not modelled	64.0	23	PDB header: hydrolase Chain: D: PDB Molecule: cytidine/uridine-specific hydrolase; PDBTitle: pyrimidine-specific ribonucleoside hydrolase from gardnerella2 vaginalis
83	d1qtwa	Alignment	not modelled	63.6	17	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: Endonuclease IV
84	d1q8fa	Alignment	not modelled	62.3	16	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
85	d2masa	Alignment	not modelled	62.1	18	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
86	c1k98A	Alignment	not modelled	60.9	30	PDB header: transferase Chain: A: PDB Molecule: methionine synthase; PDBTitle: adomet complex of meth c-terminal fragment
87	c3b9xA	Alignment	not modelled	60.0	17	PDB header: hydrolase Chain: A: PDB Molecule: pyrimidine-specific ribonucleoside hydrolase rihb; PDBTitle: crystal structure of the e. coli pyrimidine nucleoside hydrolase yeik2 in complex with inosine
88	c4kpoB	Alignment	not modelled	56.6	19	PDB header: hydrolase Chain: B: PDB Molecule: nucleoside n-ribohydrolase 3; PDBTitle: plant nucleoside hydrolase - zmrh3 enzyme
89	c6ba1C	Alignment	not modelled	54.6	20	PDB header: hydrolase Chain: C: PDB Molecule: inosine-uridine preferring nucleoside hydrolase; PDBTitle: purine-preferring ribonucleoside hydrolase from gardnerella vaginalis
90	c3t8jA	Alignment	not modelled	49.5	22	PDB header: hydrolase Chain: A: PDB Molecule: purine nucleosidase, (iunh-1); PDBTitle: structural analysis of thermostable s. solfataricus pyrimidine-2 specific nucleoside hydrolase
91	d1jvna1	Alignment	not modelled	40.7	20	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Histidine biosynthesis enzymes
92	d1ub3a	Alignment	not modelled	40.1	18	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
93	c2c40B	Alignment	not modelled	39.9	20	PDB header: hydrolase Chain: B: PDB Molecule: inosine-uridine preferring nucleoside hydrolase family PDBTitle: crystal structure of inosine-uridine preferring nucleoside2 hydrolase from bacillus anthracis at 2.2a resolution
94	c4as2D	Alignment	not modelled	34.9	21	PDB header: hydrolase Chain: D: PDB Molecule: phosphorylcholine phosphatase; PDBTitle: pseudomonas aeruginosa phosphorylcholine phosphatase. monoclinic form
95	c4x2rA	Alignment	not modelled	29.7	19	PDB header: isomerase Chain: A: PDB Molecule: 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino) PDBTitle: crystal structure of pria from actinomyces urogenitalis
96	d2hqsc1	Alignment	not modelled	29.5	18	Fold: Bacillus chorismate mutase-like Superfamily: OmpA-like Family: OmpA-like
97	d1o0ya	Alignment	not modelled	29.4	20	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
98	d1mzha	Alignment	not modelled	27.4	17	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
99	c4o1fB	Alignment	not modelled	27.2	6	PDB header: transferase Chain: B: PDB Molecule: dihydropteroate synthase dhps; PDBTitle: structure of a methyltransferase component in complex with thf2 involved in o-demethylation
100	c1fcbA	Alignment	not modelled	26.1	23	PDB header: oxidoreductase (ch-oh(d)-cytochrome(a)) Chain: A: PDB Molecule: flavocytochrome b2; PDBTitle: molecular structure of flavocytochrome b2 at 2.4 angstroms resolution
101	d1ad1a	Alignment	not modelled	25.9	16	Fold: TIM beta/alpha-barrel Superfamily: Dihydropteroate synthetase-like Family: Dihydropteroate synthetase
102	c5dbul	Alignment	not modelled	25.7	15	PDB header: lyase Chain: I: PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of 2-deoxyribose-5-phosphate aldolase (1-220) from2 streptococcus suis
103	d1tz9a	Alignment	not modelled	25.1	15	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: UxuA-like
104	c3qz6A	Alignment	not modelled	24.4	13	PDB header: lyase Chain: A: PDB Molecule: hpch/hpai aldolase; PDBTitle: the crystal structure of hpch/hpai aldolase from desulfitobacterium2 hafniense dcb-2 PDB header: lyase

105	c3oa3A_	Alignment	not modelled	22.9	18	Chain: A; PDB Molecule: aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from <i>Toxoplasma gondii</i>
106	c1jvnB_	Alignment	not modelled	22.6	21	PDB header: transferase Chain: B; PDB Molecule: bifunctional histidine biosynthesis protein hisH; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel through a (beta/alpha) ₈ barrel joins two active sites
107	c3ngjC_	Alignment	not modelled	22.4	21	PDB header: lyase Chain: C; PDB Molecule: deoxyribose-phosphate aldolase; PDBTitle: crystal structure of a putative deoxyribose-phosphate aldolase from <i>Entamoeba histolytica</i>
108	c3cssA_	Alignment	not modelled	21.6	27	PDB header: hydrolase Chain: A; PDB Molecule: 6-phosphogluconolactonase; PDBTitle: crystal structure of 6-phosphogluconolactonase from <i>Leishmania guyanensis</i>
109	c3t8iC_	Alignment	not modelled	20.9	19	PDB header: hydrolase Chain: C; PDB Molecule: purine nucleosidase, (iunh-2); PDBTitle: structural analysis of thermostable <i>S. solfataricus</i> purine-specific nucleoside hydrolase