Phyre^2

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Description	RVBD3062_(ligB)_3425581_3427104
Date	Thu Aug 8 16:20:23 BST 2019
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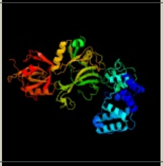
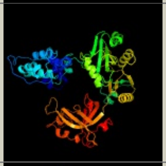
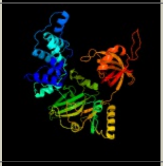
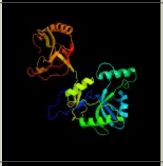
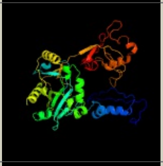
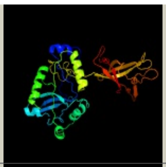
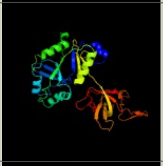
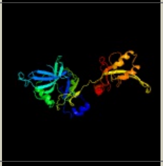
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1x9nA_	Alignment		100.0	30	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase i; **PDBTitle:** crystal structure of human dna ligase i bound to 5'-adenylated, nicked2 dna
2	c2cfmA_	Alignment		100.0	36	**PDB header:**ligase **Chain:** A: **PDB Molecule:**thermostable dna ligase; **PDBTitle:** atp-dependent dna ligase from pyrococcus furiosus
3	c2hivA_	Alignment		100.0	32	**PDB header:**ligase **Chain:** A: **PDB Molecule:**thermostable dna ligase; **PDBTitle:** atp-dependent dna ligase from s. solfataricus
4	c3gdeA_	Alignment		100.0	37	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** the closed conformation of atp-dependent dna ligase from archaeoglobus2 fulgidus
5	c3w1bA_	Alignment		100.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase 4; **PDBTitle:** crystal structure of human dna ligase iv-artemis complex (mercury2 derivative)
6	c3l2pA_	Alignment		100.0	26	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase 3; **PDBTitle:** human dna ligase iii recognizes dna ends by dynamic switching between2 two dna bound states
7	c6dt1E_	Alignment		100.0	16	**PDB header:**ligase/dna **Chain:** E: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of the ligase from bacteriophage t4 complexed with2 dna intermediate
8	c6rasI_	Alignment		100.0	22	**PDB header:**dna binding protein **Chain:** I: **PDB Molecule:**atp-dependent dna ligase; **PDBTitle:** pmar-lig_pre.
9	c1vs0A_	Alignment		100.0	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative dna ligase-like protein rv0938/mt0965; **PDBTitle:** crystal structure of the ligase domain from m. tuberculosis ligd at2 2.4a
10	c6imnB_	Alignment		100.0	16	**PDB header:**ligase/dna **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** the crystal structure of asfvlig:ct2 complex
11	c1a0iA_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** atp-dependent dna ligase from bacteriophage t7 complex with2 atp

12	c4d05A_	Alignment		100.0	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**atp-dependent dna ligase; **PDBTitle:** structure and activity of a minimal-type atp-dependent dna ligase from2 a psychrotolerant bacterium
13	c2vugB_	Alignment		100.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pab1020; **PDBTitle:** the structure of an archaeal homodimeric rna ligase
14	c1p8lA_	Alignment		100.0	19	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pbcv-1 dna ligase; **PDBTitle:** new crystal structure of chlorella virus dna ligase-adenylate
15	c6gdrA_	Alignment		100.0	25	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** dna binding with a minimal scaffold: structure-function analysis of2 lig e dna ligases
16	d1x9na3	Alignment		100.0	28	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**ATP-dependent DNA ligase catalytic domain
17	d1a0ia2	Alignment		100.0	22	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**ATP-dependent DNA ligase catalytic domain
18	c3kyhC_	Alignment		100.0	21	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**mrna-capping enzyme subunit alpha; **PDBTitle:** saccharomyces cerevisiae cet1-ceg1 capping apparatus
19	d1fvia2	Alignment		100.0	23	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**ATP-dependent DNA ligase catalytic domain
20	d1x9na2	Alignment		100.0	33	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
21	c1p16A_	Alignment	not modelled	100.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mrna capping enzyme alpha subunit; **PDBTitle:** structure of an mrna capping enzyme bound to the2 phosphorylated carboxyl-terminal domain of rna polymerase3 ii
22	d1x9na1	Alignment	not modelled	100.0	32	**Fold:**ATP-dependent DNA ligase DNA-binding domain **Superfamily:**ATP-dependent DNA ligase DNA-binding domain **Family:**ATP-dependent DNA ligase DNA-binding domain
23	c1cknA_	Alignment	not modelled	100.0	21	**PDB header:**capping enzyme **Chain:** A: **PDB Molecule:**mrna capping enzyme; **PDBTitle:** structure of guanylylated mrna capping enzyme complexed2 with gtp
24	c3s24F_	Alignment	not modelled	100.0	18	**PDB header:**hydrolase, transferase **Chain:** F: **PDB Molecule:**mrna-capping enzyme; **PDBTitle:** crystal structure of human mrna guanylyltransferase
25	c4htoA_	Alignment	not modelled	100.0	20	**PDB header:**ligase, dna binding protein **Chain:** A: **PDB Molecule:**dna ligase 4; **PDBTitle:** crystal structure of the dbd domain of human dna ligase iv apo form
26	c4pz8A_	Alignment	not modelled	100.0	20	**PDB header:**transferase/transcription **Chain:** A: **PDB Molecule:**mrna-capping enzyme subunit alpha; **PDBTitle:** pce1 guanylyltransferase bound to spt5 ctd
27	d1ckma2	Alignment	not modelled	100.0	17	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**mRNA capping enzyme
28	d1p16a2	Alignment	not modelled	100.0	25	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**mRNA capping enzyme
						PDB header:ligase

29	c3qwuA_	Alignment	not modelled	100.0	18	**Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** putative atp-dependent dna ligase from aquifex aeolicus.
30	c3vnnA_	Alignment	not modelled	99.9	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase 4; **PDBTitle:** crystal structure of a sub-domain of the nucleotidyltransferase2 (adenylation) domain of human dna ligase iv
31	c5covA_	Alignment	not modelled	99.9	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**naegleria gruberi rna ligase; **PDBTitle:** structure and mechanism of a eukaryal nick-sealing rna ligase k170m+mn
32	c5d1pB_	Alignment	not modelled	99.3	25	**PDB header:**ligase **Chain:** B: **PDB Molecule:**atp-dependent rna ligase; **PDBTitle:** archaeal atp-dependent rna ligase - form 2
33	c4glxA_	Alignment	not modelled	99.2	25	**PDB header:**ligase/ligase inhibitor/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** dna ligase a in complex with inhibitor
34	c2owoA_	Alignment	not modelled	99.2	25	**PDB header:**ligase/dna **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
35	d1b04a_	Alignment	not modelled	99.1	23	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
36	c3bacA_	Alignment	not modelled	99.0	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** structural basis for the inhibition of bacterial nad+2 dependent dna ligase
37	d1fvia1	Alignment	not modelled	99.0	10	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
38	c3pn1A_	Alignment	not modelled	98.9	23	**PDB header:**ligase/ligase inhibitor **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
39	c3jslA_	Alignment	not modelled	98.9	20	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of the adenylation domain of nad+-2 dependent dna ligase from staphylococcus aureus
40	c4glwA_	Alignment	not modelled	98.9	22	**PDB header:**ligase/ligase inhibitor **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** dna ligase a in complex with inhibitor
41	c1dgsB_	Alignment	not modelled	98.8	22	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase from t.2 filiformis
42	c1v9pB_	Alignment	not modelled	98.8	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of nad+-dependent dna ligase
43	c3sgiA_	Alignment	not modelled	98.8	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** crystal structure of dna ligase a brct domain deleted mutant of2 mycobacterium tuberculosis
44	d1ta8a_	Alignment	not modelled	98.8	19	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
45	d1s68a_	Alignment	not modelled	98.7	18	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**RNA ligase
46	d1a0ia1	Alignment	not modelled	98.7	20	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
47	c1zauA_	Alignment	not modelled	98.7	22	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase; **PDBTitle:** adenylation domain of nad+ dependent dna ligase from m.tuberculosis
48	c3ty8A_	Alignment	not modelled	98.6	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polynucleotide 2',3'-cyclic phosphate phosphodiesterase / **PDBTitle:** crystal structure of c. thermocellum pnkp ligase domain apo form
49	d1v9pa3	Alignment	not modelled	98.6	21	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
50	c4e6nC_	Alignment	not modelled	98.5	20	**PDB header:**protein binding **Chain:** C: **PDB Molecule:**metallophosphoesterase; **PDBTitle:** crystal structure of bacterial pnkp-c/hen1-n heterodimer
51	d1dgsa3	Alignment	not modelled	98.5	20	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**Adenylation domain of NAD+-dependent DNA ligase
52	c3gjxE_	Alignment	not modelled	98.4	20	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
53	c2hvsA_	Alignment	not modelled	98.3	17	**PDB header:**ligase/dna/rna **Chain:** A: **PDB Molecule:**t4 rna ligase 2; **PDBTitle:** structure of t4 rna ligase 2 with nicked 5'-adenylated nucleic acid2 duplex containing a 2'-deoxyribonucleotide at the nick
54	c3gb8B_	Alignment	not modelled	98.3	21	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of crm1/snurportin-1 complex
55	c1xk5A_	Alignment	not modelled	98.2	20	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**snurportin-1; **PDBTitle:** crystal structure of the m3g-cap-binding domain of2 snurportin1 in complex with a m3gpppg-cap dinucleotide

56	c4xruE_	Alignment	not modelled	95.7	16	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**rnl; **PDBTitle:** structure of pnkp1/rnl/hen1 complex
57	d1p16a1	Alignment	not modelled	92.8	14	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
58	d1xdna_	Alignment	not modelled	91.4	27	**Fold:**ATP-grasp **Superfamily:**DNA ligase/mRNA capping enzyme, catalytic domain **Family:**RNA ligase
59	d1ckma1	Alignment	not modelled	77.6	18	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
60	c6n0tA_	Alignment	not modelled	67.8	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trna ligase; **PDBTitle:** trna ligase
61	d2oyra1	Alignment	not modelled	58.7	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhiQ-like
62	d2pkwa1	Alignment	not modelled	50.8	21	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**YhiQ-like
63	c4ckcD_	Alignment	not modelled	43.5	17	**PDB header:**transferase/hydrolase **Chain:** D: **PDB Molecule:**mrna-capping enzyme catalytic subunit; **PDBTitle:** vaccinia virus capping enzyme complexed with sah (monoclinic form)
64	c2r6zA_	Alignment	not modelled	31.6	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**upf0341 protein in rsp 3' region; **PDBTitle:** crystal structure of the sam-dependent methyltransferase ngo1261 from2 neisseria gonorrhoeae, northeast structural genomics consortium3 target ngr48
65	c2hmcA_	Alignment	not modelled	27.5	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
66	d1xv2a_	Alignment	not modelled	24.9	56	**Fold:**AF0104/ALDC/Ptd012-like **Superfamily:**AF0104/ALDC/Ptd012-like **Family:**Alpha-acetolactate decarboxylase-like
67	c6daqA_	Alignment	not modelled	23.6	17	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phdj; **PDBTitle:** phdj bound to substrate intermediate
68	c5ud6B_	Alignment	not modelled	22.1	12	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dhdps from cyanidioschyzon merolae with lysine2 bound
69	c6arhA_	Alignment	not modelled	22.0	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** crystal structure of human nal at a resolution of 1.6 angstrom
70	c5c54D_	Alignment	not modelled	21.7	22	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase/n-acetylneuraminate lyase; **PDBTitle:** crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
71	c5yhkB_	Alignment	not modelled	21.6	56	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**alpha-acetolactate decarboxylase; **PDBTitle:** crystal structure of acetolactate decarboxylase from enterbacter2 aerogenes
72	d1xxxa1	Alignment	not modelled	21.1	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
73	c5xneA_	Alignment	not modelled	19.9	44	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-acetolactate decarboxylase; **PDBTitle:** x-ray crystal structure of alpha-acetolactate decarboxylase from2 bacillus subtilis strain 168
74	c2oemA_	Alignment	not modelled	19.8	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**2,3-diketo-5-methylthiopentyl-1-phosphate enolase; **PDBTitle:** crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohexane 1-phosphate
75	c3daqB_	Alignment	not modelled	19.7	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
76	c5yhoA_	Alignment	not modelled	19.7	56	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**alpha-acetolactate decarboxylase; **PDBTitle:** crystal structure of acetolactate decarboxylase from enterobacter2 cloacae
77	c4i7vD_	Alignment	not modelled	19.6	10	**PDB header:**biosynthetic protein **Chain:** D: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** agrobacterium tumefaciens dhdps with pyruvate
78	c4bt7A_	Alignment	not modelled	19.6	44	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-acetolactate decarboxylase; **PDBTitle:** acetolactate decarboxylase with a bound phosphate ion
79	c2v9dB_	Alignment	not modelled	18.6	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**yage; **PDBTitle:** crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
80	c2ehhE_	Alignment	not modelled	18.3	13	**PDB header:**lyase **Chain:** E: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
81	c2rfgB_	Alignment	not modelled	17.9	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthase;

		Alignment	not modelled			**PDBTitle:** crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
82	c4nasD_	Alignment	not modelled	17.6	17	**PDB header:**lyase **Chain:** D: **PDB Molecule:**ribulose-bisphosphate carboxylase; **PDBTitle:** the crystal structure of a rubisco-like protein (mtnw) from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
83	d1xkya1	Alignment	not modelled	17.5	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
84	c6h4eB_	Alignment	not modelled	17.3	8	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative n-acetylneuraminate lyase; **PDBTitle:** proteus mirabilis n-acetylneuraminate lyase
85	c4uxdC_	Alignment	not modelled	16.9	12	**PDB header:**lyase **Chain:** C: **PDB Molecule:**2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- **PDBTitle:** 2-keto 3-deoxygluconate aldolase from picrophilus torridus
86	c6daoB_	Alignment	not modelled	16.9	10	**PDB header:**lyase **Chain:** B: **PDB Molecule:**trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; **PDBTitle:** nahe wt selenomethionine
87	c2ogfD_	Alignment	not modelled	16.2	13	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein mj0408; **PDBTitle:** crystal structure of protein mj0408 from methanococcus jannaschii,2 pfam duf372
88	c3fkkA_	Alignment	not modelled	16.2	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**l-2-keto-3-deoxyarabonate dehydratase; **PDBTitle:** structure of l-2-keto-3-deoxyarabonate dehydratase
89	d1e5ra_	Alignment	not modelled	16.0	12	**Fold:**Double-stranded beta-helix **Superfamily:**Clavaminate synthase-like **Family:**Type II Proline 3-hydroxylase (proline oxidase)
90	c3cprB_	Alignment	not modelled	15.7	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dihydrodipicolinate synthetase; **PDBTitle:** the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
91	d2a6na1	Alignment	not modelled	14.6	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
92	c5afdA_	Alignment	not modelled	14.5	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**n-acetylneuraminate lyase; **PDBTitle:** native structure of n-acetylneuramininate lyase (sialic acid aldolase)2 from aliivibrio salmonicida
93	c3g0sA_	Alignment	not modelled	14.2	8	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from salmonella typhimurium lt2
94	c4l8lA_	Alignment	not modelled	14.0	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**3-dehydroquinate dehydratase 1; **PDBTitle:** crystal structure of the type ii dehydroquinase from pseudomonas2 aeruginosa
95	c3nwrA_	Alignment	not modelled	12.3	28	**PDB header:**lyase **Chain:** A: **PDB Molecule:**a rubisco-like protein; **PDBTitle:** crystal structure of a rubisco-like protein from burkholderia fungorum
96	d1f74a_	Alignment	not modelled	12.2	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
97	c4xkyC_	Alignment	not modelled	12.1	10	**PDB header:**lyase **Chain:** C: **PDB Molecule:**dihydrodipicolinate synthase; **PDBTitle:** structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
98	c2r94B_	Alignment	not modelled	11.8	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-keto-3-deoxy-(6-phospho-)gluconate aldolase; **PDBTitle:** crystal structure of kd(p)ga from t.tenax
99	c5ktlA_	Alignment	not modelled	11.7	13	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-tetrahydrodipicolinate synthase; **PDBTitle:** dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.