

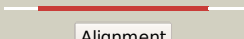

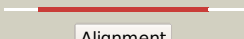




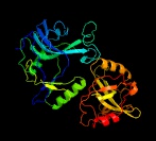
















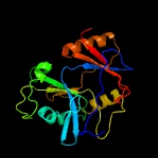



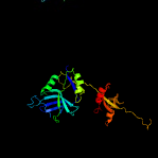


# Phyre2

Email mdejesus@rockefeller.edu  
 Description RVBD3731\_(ligC)\_4181936\_4183012  
 Date Fri Aug 9 18:20:43 BST 2019  
 Unique Job ID 086ba72bb9985ab7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c1x9nA_</a>	 Alignment		100.0	23	<b>PDB header:</b> ligase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase i; <b>PDBTitle:</b> crystal structure of human dna ligase i bound to 5'-adenylated, nicked2 dna
2	<a href="#">c2hivA_</a>	 Alignment		100.0	25	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable dna ligase; <b>PDBTitle:</b> atp-dependent dna ligase from s. solfataricus
3	<a href="#">c3gdeA_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> the closed conformation of atp-dependent dna ligase from archaeoglobus2 fulgidus
4	<a href="#">c2cfmA_</a>	 Alignment		100.0	24	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> thermostable dna ligase; <b>PDBTitle:</b> atp-dependent dna ligase from pyrococcus furiosus
5	<a href="#">c3w1bA_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase 4; <b>PDBTitle:</b> crystal structure of human dna ligase iv-artemis complex (mercury2 derivative)
6	<a href="#">c3l2pA_</a>	 Alignment		100.0	27	<b>PDB header:</b> ligase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase 3; <b>PDBTitle:</b> human dna ligase iii recognizes dna ends by dynamic switching between2 two dna bound states
7	<a href="#">c1vs0A_</a>	 Alignment		100.0	31	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dna ligase-like protein rv0938/mt0965; <b>PDBTitle:</b> crystal structure of the ligase domain from m. tuberculosis ligd at2 2.4a
8	<a href="#">c6dt1E_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase/dna <b>Chain:</b> E: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of the ligase from bacteriophage t4 complexed with2 dna intermediate
9	<a href="#">c6rasI_</a>	 Alignment		100.0	20	<b>PDB header:</b> dna binding protein <b>Chain:</b> I: <b>PDB Molecule:</b> atp-dependent dna ligase; <b>PDBTitle:</b> pmar-lig_pre.
10	<a href="#">c6imnB_</a>	 Alignment		100.0	20	<b>PDB header:</b> ligase/dna <b>Chain:</b> B: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> the crystal structure of asfvlig:ct2 complex
11	<a href="#">c1a0iA_</a>	 Alignment		100.0	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> atp-dependent dna ligase from bacteriophage t7 complex with2 atp

12	<a href="#">c4d05A_</a>	Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent dna ligase; <b>PDBTitle:</b> structure and activity of a minimal-type atp-dependent dna ligase from2 a psychrotolerant bacterium
13	<a href="#">c1p8lA_</a>	Alignment		100.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pbcv-1 dna ligase; <b>PDBTitle:</b> new crystal structure of chlorella virus dna ligase-adenylate
14	<a href="#">c6gdrA_</a>	Alignment		100.0	22	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> dna binding with a minimal scaffold: structure-function analysis of2 lig e dna ligases
15	<a href="#">c2vugB_</a>	Alignment		100.0	13	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> pab1020; <b>PDBTitle:</b> the structure of an archaeal homodimeric rna ligase
16	<a href="#">d1x9na3</a>	Alignment		100.0	22	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> ATP-dependent DNA ligase catalytic domain
17	<a href="#">d1a0ia2</a>	Alignment		100.0	19	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> ATP-dependent DNA ligase catalytic domain
18	<a href="#">d1fvia2</a>	Alignment		100.0	20	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> ATP-dependent DNA ligase catalytic domain
19	<a href="#">c3kyhC_</a>	Alignment		100.0	19	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> mrna-capping enzyme subunit alpha; <b>PDBTitle:</b> saccharomyces cerevisiae cet1-ceg1 capping apparatus
20	<a href="#">c1p16A_</a>	Alignment		100.0	22	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme alpha subunit; <b>PDBTitle:</b> structure of an mrna capping enzyme bound to the2 phosphorylated carboxyl-terminal domain of rna polymerase3 ii
21	<a href="#">c3s24F_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> hydrolase, transferase <b>Chain:</b> F: <b>PDB Molecule:</b> mrna-capping enzyme; <b>PDBTitle:</b> crystal structure of human mrna guanylyltransferase
22	<a href="#">c1cknA_</a>	Alignment	not modelled	100.0	18	<b>PDB header:</b> capping enzyme <b>Chain:</b> A: <b>PDB Molecule:</b> mrna capping enzyme; <b>PDBTitle:</b> structure of guanylylated mrna capping enzyme complexed2 with gtp
23	<a href="#">c4pz8A_</a>	Alignment	not modelled	100.0	21	<b>PDB header:</b> transferase/transcription <b>Chain:</b> A: <b>PDB Molecule:</b> mrna-capping enzyme subunit alpha; <b>PDBTitle:</b> pce1 guanylyltransferase bound to spt5 ctd
24	<a href="#">d1ckma2</a>	Alignment	not modelled	100.0	16	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> mRNA capping enzyme
25	<a href="#">d1x9na2</a>	Alignment	not modelled	100.0	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
26	<a href="#">c3qwUa_</a>	Alignment	not modelled	100.0	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> putative atp-dependent dna ligase from aquifex aeolicus.
27	<a href="#">d1p16a2</a>	Alignment	not modelled	100.0	21	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> mRNA capping enzyme
28	<a href="#">c3vnnA_</a>	Alignment	not modelled	100.0	19	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase 4; <b>PDBTitle:</b> crystal structure of a sub-domain of the nucleotidyltransferase2 (adenylation) domain of human dna ligase iv
29	<a href="#">c5cqvA_</a>	Alignment	not modelled	99.9	17	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> naegleria gruberi rna ligase;

29	<a href="#">c3c0vA</a>	Alignment	not modelled	99.5	17	<b>PDBTitle:</b> structure and mechanism of a eukaryal nick-sealing rna ligase k170m+mn
30	<a href="#">c5d1pB</a>	Alignment	not modelled	99.5	22	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> atp-dependent rna ligase; <b>PDBTitle:</b> archaeal atp-dependent rna ligase - form 2
31	<a href="#">c2owoA</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> ligase/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> last stop on the road to repair: structure of e.coli dna ligase bound2 to nicked dna-adenylate
32	<a href="#">c4glxA</a>	Alignment	not modelled	99.3	18	<b>PDB header:</b> ligase/ligase inhibitor/dna <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> dna ligase a in complex with inhibitor
33	<a href="#">c1dgsB</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of nad+-dependent dna ligase from t.2 filiformis
34	<a href="#">d1b04a</a>	Alignment	not modelled	99.0	13	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD+-dependent DNA ligase
35	<a href="#">c3pn1A</a>	Alignment	not modelled	99.0	15	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> novel bacterial nad+-dependent dna ligase inhibitors with broad2 spectrum potency and antibacterial efficacy in vivo
36	<a href="#">c3bacA</a>	Alignment	not modelled	99.0	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> structural basis for the inhibition of bacterial nad+2 dependent dna ligase
37	<a href="#">c3js1A</a>	Alignment	not modelled	98.9	16	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of the adenylation domain of nad+-2 dependent dna ligase from staphylococcus aureus
38	<a href="#">c3sg1A</a>	Alignment	not modelled	98.9	18	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of dna ligase a brct domain deleted mutant of2 mycobacterium tuberculosis
39	<a href="#">c4glwA</a>	Alignment	not modelled	98.9	11	<b>PDB header:</b> ligase/ligase inhibitor <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> dna ligase a in complex with inhibitor
40	<a href="#">c1v9pB</a>	Alignment	not modelled	98.9	14	<b>PDB header:</b> ligase <b>Chain:</b> B: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> crystal structure of nad+-dependent dna ligase
41	<a href="#">d1ta8a</a>	Alignment	not modelled	98.9	14	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD+-dependent DNA ligase
42	<a href="#">d1s68a</a>	Alignment	not modelled	98.9	17	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> RNA ligase
43	<a href="#">c3ty8A</a>	Alignment	not modelled	98.9	17	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> polynucleotide 2',3'-cyclic phosphate phosphodiesterase / <b>PDBTitle:</b> crystal structure of c. thermocellum pnkp ligase domain apo form
44	<a href="#">c3gjxE</a>	Alignment	not modelled	98.8	11	<b>PDB header:</b> protein transport <b>Chain:</b> E: <b>PDB Molecule:</b> snurportin-1; <b>PDBTitle:</b> crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
45	<a href="#">c4e6nC</a>	Alignment	not modelled	98.8	17	<b>PDB header:</b> protein binding <b>Chain:</b> C: <b>PDB Molecule:</b> metallophosphoesterase; <b>PDBTitle:</b> crystal structure of bacterial pnkp-c/hen1-n heterodimer
46	<a href="#">d1dgsa3</a>	Alignment	not modelled	98.7	16	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD+-dependent DNA ligase
47	<a href="#">c1zauA</a>	Alignment	not modelled	98.7	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> dna ligase; <b>PDBTitle:</b> adenylation domain of nad+ dependent dna ligase from m.tuberculosis
48	<a href="#">c3gb8B</a>	Alignment	not modelled	98.7	11	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> snurportin-1; <b>PDBTitle:</b> crystal structure of crm1/snurportin-1 complex
49	<a href="#">d1a0ia1</a>	Alignment	not modelled	98.6	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
50	<a href="#">d1v9pa3</a>	Alignment	not modelled	98.6	16	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> Adenylation domain of NAD+-dependent DNA ligase
51	<a href="#">c1xk5A</a>	Alignment	not modelled	98.6	11	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> snurportin-1; <b>PDBTitle:</b> crystal structure of the m3g-cap-binding domain of2 snurportin1 in complex with a m3gpppg-cap dinucleotide
52	<a href="#">c2hvsA</a>	Alignment	not modelled	98.5	15	<b>PDB header:</b> ligase/dna/rna <b>Chain:</b> A: <b>PDB Molecule:</b> t4 rna ligase 2; <b>PDBTitle:</b> structure of t4 rna ligase 2 with nicked 5'-adenylated nucleic acid2 duplex containing a 2'-deoxyribonucleotide at the nick
53	<a href="#">d1fvia1</a>	Alignment	not modelled	98.4	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
54	<a href="#">c4xruE</a>	Alignment	not modelled	97.8	20	<b>PDB header:</b> protein binding <b>Chain:</b> E: <b>PDB Molecule:</b> rnl; <b>PDBTitle:</b> structure of pnkp1/rnl/hen1 complex
55	<a href="#">d1xdna</a>	Alignment	not modelled	95.3	15	<b>Fold:</b> ATP-grasp <b>Superfamily:</b> DNA ligase/mRNA capping enzyme, catalytic domain <b>Family:</b> RNA ligase

56	<a href="#">c2r8wB</a>	Alignment	not modelled	71.4	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> agr_c_1641p; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase (atu0899) from2 agrobacterium tumefaciens str. c58
57	<a href="#">c5ud6B</a>	Alignment	not modelled	69.0	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dhds from cyanidioschyzon merolae with lysine2 bound
58	<a href="#">c6daoB</a>	Alignment	not modelled	66.2	11	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> trans-o-hydroxybenzylidenepyruvate hydratase-aldolase; <b>PDBTitle:</b> nahe wt selenomethionine
59	<a href="#">d1xxa1</a>	Alignment	not modelled	65.9	18	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
60	<a href="#">c2v9dB</a>	Alignment	not modelled	65.4	17	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to2 the dihydrodipicolinic acid synthase family from e. coli3 k12
61	<a href="#">d1xkya1</a>	Alignment	not modelled	65.1	11	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
62	<a href="#">c5afdA</a>	Alignment	not modelled	64.4	13	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> native structure of n-acetylneuramininate lyase (sialic acid aldolase)2 from aliivibrio salmonicida
63	<a href="#">d2a6na1</a>	Alignment	not modelled	64.2	9	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
64	<a href="#">c3noeA</a>	Alignment	not modelled	63.5	8	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from pseudomonas2 aeruginosa
65	<a href="#">c3bi8A</a>	Alignment	not modelled	62.4	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of dihydrodipicolinate synthase from clostridium2 botulinum
66	<a href="#">d1hl2a</a>	Alignment	not modelled	61.1	20	<b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
67	<a href="#">c6daqA</a>	Alignment	not modelled	61.0	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> phdj; <b>PDBTitle:</b> phdj bound to substrate intermediate
68	<a href="#">c6h4eB</a>	Alignment	not modelled	60.9	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative n-acetylneuraminate lyase; <b>PDBTitle:</b> proteus mirabilis n-acetylneuraminate lyase
69	<a href="#">c2rfgB</a>	Alignment	not modelled	60.8	13	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from hahella2 chejuensis at 1.5a resolution
70	<a href="#">c3g0sA</a>	Alignment	not modelled	60.7	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from salmonella typhimurium lt2
71	<a href="#">c3eb2A</a>	Alignment	not modelled	59.7	20	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodopseudomonas palustris at 2.0a resolution
72	<a href="#">c3fkkA</a>	Alignment	not modelled	58.8	11	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> l-2-keto-3-deoxyarabonate dehydratase; <b>PDBTitle:</b> structure of l-2-keto-3-deoxyarabonate dehydratase
73	<a href="#">c3daqB</a>	Alignment	not modelled	57.5	9	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
74	<a href="#">c2ehhE</a>	Alignment	not modelled	56.1	15	<b>PDB header:</b> lyase <b>Chain:</b> E: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 aquifex aeolicus
75	<a href="#">c4n4qD</a>	Alignment	not modelled	56.0	6	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> acylneuraminate lyase; <b>PDBTitle:</b> crystal structure of n-acetylneuramininate lyase from mycoplasma2 synoviae, crystal form ii
76	<a href="#">c3cprB</a>	Alignment	not modelled	55.4	21	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthetase; <b>PDBTitle:</b> the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
77	<a href="#">c4i7vD</a>	Alignment	not modelled	54.3	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> agrobacterium tumefaciens dhds with pyruvate
78	<a href="#">c3pueA</a>	Alignment	not modelled	54.2	6	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of the complex of dihydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
79	<a href="#">c5ktIA</a>	Alignment	not modelled	53.1	9	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from the industrial and evolutionarily2 important cyanobacteria anabaena variabilis.
80	<a href="#">c5c54D</a>	Alignment	not modelled	53.0	17	<b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase/n-acetylneuraminate lyase; <b>PDBTitle:</b> crystal structure of a novel n-acetylneuraminic acid lyase from2 corynebacterium glutamicum
81	<a href="#">c6arhA</a>	Alignment	not modelled	52.9	15	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminate lyase; <b>PDBTitle:</b> crystal structure of human nal at a resolution of 1.6

					angstrom
82	<a href="#">d1f74a_</a>	Alignment	not modelled	51.9	16 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
83	<a href="#">c2hmcA_</a>	Alignment	not modelled	51.8	15 <b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
84	<a href="#">c3na8A_</a>	Alignment	not modelled	51.2	13 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> putative dihydrodipicolinate synthetase; <b>PDBTitle:</b> crystal structure of a putative dihydrodipicolinate synthetase from2 pseudomonas aeruginosa
85	<a href="#">c3d0cB_</a>	Alignment	not modelled	51.2	11 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from oceanobacillus2 iheyensis at 1.9 a resolution
86	<a href="#">c4uxdC_</a>	Alignment	not modelled	50.5	11 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-dehydro-3-deoxy-d-gluconate/2-dehydro-3-deoxy- <b>PDBTitle:</b> 2-keto 3-deoxygluconate aldolase from picrophilus torridus
87	<a href="#">c6mqhA_</a>	Alignment	not modelled	50.5	13 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of 4-hydroxy-tetrahydrodipicolinate synthase (htpa2 synthase) from burkholderia mallei
88	<a href="#">c2vc6A_</a>	Alignment	not modelled	49.6	16 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of mosa from s. melloti with pyruvate bound
89	<a href="#">c3lciA_</a>	Alignment	not modelled	49.2	20 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> n-acetylneuraminatase lyase; <b>PDBTitle:</b> the d-sialic acid aldolase mutant v251w
90	<a href="#">c4icnB_</a>	Alignment	not modelled	49.0	14 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> dihydrodipicolinate synthase from shewanella benthica
91	<a href="#">c2yxqD_</a>	Alignment	not modelled	48.6	11 <b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase (dapa)
92	<a href="#">c3lerA_</a>	Alignment	not modelled	48.0	14 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from campylobacter2 jejuni subsp. jejuni nctc 11168
93	<a href="#">c5ui3C_</a>	Alignment	not modelled	46.5	11 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dhbps from chlamydomonas reinhardtii
94	<a href="#">c4xkyC_</a>	Alignment	not modelled	46.3	11 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> structure of dihydrodipicolinate synthase from the commensal bacterium2 bacteroides thetaiotaomicron at 2.1 a resolution
95	<a href="#">d1o5ka_</a>	Alignment	not modelled	46.1	13 <b>Fold:</b> TIM beta/alpha-barrel <b>Superfamily:</b> Aldolase <b>Family:</b> Class I aldolase
96	<a href="#">c3n2xB_</a>	Alignment	not modelled	45.5	16 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein yage; <b>PDBTitle:</b> crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
97	<a href="#">c3b4uB_</a>	Alignment	not modelled	45.5	19 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
98	<a href="#">c4nq1B_</a>	Alignment	not modelled	44.9	8 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 4-hydroxy-tetrahydrodipicolinate synthase; <b>PDBTitle:</b> legionella pneumophila dihydrodipicolinate synthase with first2 substrate pyruvate bound in the active site
99	<a href="#">c4l8IA_</a>	Alignment	not modelled	44.6	13 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 3-dehydroquinatase dehydratase 1; <b>PDBTitle:</b> crystal structure of the type ii dehydroquinase from pseudomonas2 aeruginosa
100	<a href="#">c4ah7C_</a>	Alignment	not modelled	44.4	17 <b>PDB header:</b> lyase <b>Chain:</b> C: <b>PDB Molecule:</b> n-acetylneuraminatase lyase; <b>PDBTitle:</b> structure of wild type staphylococcus aureus n-acetylneuraminic acid2 lyase in complex with pyruvate
101	<a href="#">c4dppB_</a>	Alignment	not modelled	44.2	9 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase 2, chloroplastic; <b>PDBTitle:</b> the structure of dihydrodipicolinate synthase 2 from arabidopsis2 thaliana
102	<a href="#">c2oemA_</a>	Alignment	not modelled	44.0	16 <b>PDB header:</b> isomerase <b>Chain:</b> A: <b>PDB Molecule:</b> 2,3-diketo-5-methylthiopentyl-1-phosphate enolase; <b>PDBTitle:</b> crystal structure of a rubisco-like protein from geobacillus2 kaustophilus liganded with mg2+ and 2,3-diketohehexane 1-phosphate
103	<a href="#">c4nasD_</a>	Alignment	not modelled	41.3	11 <b>PDB header:</b> lyase <b>Chain:</b> D: <b>PDB Molecule:</b> ribulose-bisphosphate carboxylase; <b>PDBTitle:</b> the crystal structure of a rubisco-like protein (mtnw) from2 alicyclobacillus acidocaldarius subsp. acidocaldarius dsm 446
104	<a href="#">c3si9B_</a>	Alignment	not modelled	40.4	13 <b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bartonella2 henselae
105	<a href="#">c3s5oA_</a>	Alignment	not modelled	35.9	9 <b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> 4-hydroxy-2-oxoglutarate aldolase, mitochondrial; <b>PDBTitle:</b> crystal structure of human 4-hydroxy-2-oxoglutarate aldolase bound to2 pyruvate <b>PDB header:</b> lyase

106	<a href="#">c3fluD</a>	Alignment	not modelled	35.7	14	<b>Chain:</b> D: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
107	<a href="#">c3qfeB</a>	Alignment	not modelled	35.6	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> putative dihydrodipicolinate synthase family protein; <b>PDBTitle:</b> crystal structures of a putative dihydrodipicolinate synthase family2 protein from coccidioides immitis
108	<a href="#">c3e96B</a>	Alignment	not modelled	34.5	16	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from bacillus2 clausii
109	<a href="#">c3nwrA</a>	Alignment	not modelled	32.9	22	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> a rubisco-like protein; <b>PDBTitle:</b> crystal structure of a rubisco-like protein from burkholderia fungorum
110	<a href="#">d1xv2a</a>	Alignment	not modelled	32.7	36	<b>Fold:</b> AF0104/ALDC/Ptd012-like <b>Superfamily:</b> AF0104/ALDC/Ptd012-like <b>Family:</b> Alpha-acetolactate decarboxylase-like
111	<a href="#">c2r94B</a>	Alignment	not modelled	30.8	15	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; <b>PDBTitle:</b> crystal structure of kd(p)ga from t.tenax
112	<a href="#">c5yhkB</a>	Alignment	not modelled	29.1	36	<b>PDB header:</b> metal binding protein <b>Chain:</b> B: <b>PDB Molecule:</b> alpha-acetolactate decarboxylase; <b>PDBTitle:</b> crystal structure of acetolactate decarboxylase from enterobacter2 aerogenes
113	<a href="#">c3dz1A</a>	Alignment	not modelled	28.4	14	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrodipicolinate synthase; <b>PDBTitle:</b> crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
114	<a href="#">c2nuxB</a>	Alignment	not modelled	28.3	10	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate <b>PDBTitle:</b> 2-keto-3-deoxygluconate aldolase from sulfobolus acidocaldarius,2 native structure in p6522 at 2.5 a resolution
115	<a href="#">c5xneA</a>	Alignment	not modelled	27.4	36	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-acetolactate decarboxylase; <b>PDBTitle:</b> x-ray crystal structure of alpha-acetolactate decarboxylase from2 bacillus subtilis strain 168
116	<a href="#">c4bt7A</a>	Alignment	not modelled	26.6	36	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-acetolactate decarboxylase; <b>PDBTitle:</b> acetolactate decarboxylase with a bound phosphate ion
117	<a href="#">c5yhoA</a>	Alignment	not modelled	26.6	36	<b>PDB header:</b> metal binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> alpha-acetolactate decarboxylase; <b>PDBTitle:</b> crystal structure of acetolactate decarboxylase from enterobacter2 cloacae
118	<a href="#">d1v6ba</a>	Alignment	not modelled	25.2	28	<b>Fold:</b> PDZ domain-like <b>Superfamily:</b> PDZ domain-like <b>Family:</b> PDZ domain
119	<a href="#">d1ckma1</a>	Alignment	not modelled	24.5	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> DNA ligase/mRNA capping enzyme postcatalytic domain
120	<a href="#">c2qygC</a>	Alignment	not modelled	21.6	20	<b>PDB header:</b> unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> ribulose bisphosphate carboxylase-like protein 2; <b>PDBTitle:</b> crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris