










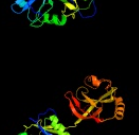


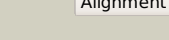

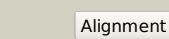
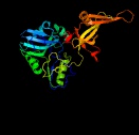















Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0938 (-)_1046140_1048419
Date	Fri Jul 26 01:50:53 BST 2019
Unique Job ID	727069981df62b44

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2iruA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: putative dna ligase-like protein rv0938/mt0965; PDBTitle: crystal structure of the polymerase domain from mycobacterium2 tuberculosis ligase d
2	c5op0B_	 Alignment		100.0	26	PDB header: transferase Chain: B: PDB Molecule: dna polymerase ligd, polymerase domain; PDBTitle: structure of prim-polc from mycobacterium smegmatis
3	c5dmuA_	 Alignment		100.0	32	PDB header: transferase Chain: A: PDB Molecule: nhej polymerase; PDBTitle: structure of the nhej polymerase from methanocella paludicola
4	c2faoB_	 Alignment		100.0	27	PDB header: hydrolase/transferase Chain: B: PDB Molecule: probable atp-dependent dna ligase; PDBTitle: crystal structure of pseudomonas aeruginosa ligd polymerase2 domain
5	c1x9nA_	 Alignment		100.0	28	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
6	c1vs0A_	 Alignment		100.0	98	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
7	c2hivA_	 Alignment		100.0	27	PDB header: ligase Chain: A: PDB Molecule: thermostable dna ligase; PDBTitle: atp-dependent dna ligase from s. solfataricus
8	c2cfmA_	 Alignment		100.0	31	PDB header: ligase Chain: A: PDB Molecule: thermostable dna ligase; PDBTitle: atp-dependent dna ligase from pyrococcus furiosus
9	c3gdeA_	 Alignment		100.0	31	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: the closed conformation of atp-dependent dna ligase from archaeoglobus2 fulgidus
10	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)
11	c3l2pA_	 Alignment		100.0	24	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

12	c5dmpA_	Alignment		100.0	45	PDB header: hydrolase Chain: A; PDB Molecule: uncharacterized protein; PDBTitle: structure of the archaeal nhej phosphoesterase from methanocella2 paludicola.
13	c3n9dA_	Alignment		100.0	44	PDB header: ligase Chain: A; PDB Molecule: probable atp-dependent dna ligase; PDBTitle: monoclinic structure of p. aeruginosa ligd phosphoesterase domain
14	c6rasI_	Alignment		100.0	24	PDB header: dna binding protein Chain: I; PDB Molecule: atp-dependent dna ligase; PDBTitle: pmar-lig_pre.
15	c6dt1E_	Alignment		100.0	20	PDB header: ligase/dna Chain: E; PDB Molecule: dna ligase; PDBTitle: crystal structure of the ligase from bacteriophage t4 complexed with2 dna intermediate
16	c3p43A_	Alignment		100.0	56	PDB header: hydrolase Chain: A; PDB Molecule: putative uncharacterized protein; PDBTitle: structure and activities of archaeal members of the ligd 3'2 phosphoesterase dna repair enzyme superfamily
17	c1a0iA_	Alignment		100.0	21	PDB header: ligase Chain: A; PDB Molecule: dna ligase; PDBTitle: atp-dependent dna ligase from bacteriophage t7 complex with2 atp
18	c3p4hA_	Alignment		100.0	50	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent dna ligase, n-terminal domain protein; PDBTitle: structures of archaeal members of the ligd 3'-phosphoesterase dna2 repair enzyme superfamily
19	c6imnB_	Alignment		100.0	21	PDB header: ligase/dna Chain: B; PDB Molecule: dna ligase; PDBTitle: the crystal structure of asfvlig:ct2 complex
20	c4d05A_	Alignment		100.0	21	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
21	c6gdrA_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A; PDB Molecule: dna ligase; PDBTitle: dna binding with a minimal scaffold: structure-function analysis of2 lig e dna ligases
22	c1p8lA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A; PDB Molecule: pbcv-1 dna ligase; PDBTitle: new crystal structure of chlorella virus dna ligase-adenylate
23	c2vugB_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: B; PDB Molecule: pab1020; PDBTitle: the structure of an archaeal homodimeric rna ligase
24	d1x9na3	Alignment	not modelled	100.0	28	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
25	d1fvia2	Alignment	not modelled	100.0	19	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
26	d1a0ia2	Alignment	not modelled	100.0	22	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: ATP-dependent DNA ligase catalytic domain
27	c3kyhC_	Alignment	not modelled	100.0	17	PDB header: protein binding Chain: C; PDB Molecule: mrna-capping enzyme subunit alpha; PDBTitle: saccharomyces cerevisiae cet1-ceg1 capping apparatus
28	d1x9na2	Alignment	not modelled	100.0	26	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
29	c1n16A_	Alignment	not modelled	100.0	21	PDB header: transferase Chain: A; PDB Molecule: mrna capping enzyme alpha subunit;

29	c1p1vA	Alignment	not modelled	100.0	21	PDBTitle: structure of an mrna capping enzyme bound to the2 phosphorylated carboxyl-terminal domain of rna polymerase3 ii PDB header: capping enzyme
30	c1cknA	Alignment	not modelled	99.9	18	Chain: A; PDB Molecule: mrna capping enzyme; PDBTitle: structure of guanylylated mrna capping enzyme complexed2 with gtp
31	c3s24F	Alignment	not modelled	99.9	21	PDB header: hydrolase, transferase Chain: F; PDB Molecule: mrna-capping enzyme; PDBTitle: crystal structure of human mrna guanylyltransferase
32	d1ckma2	Alignment	not modelled	99.9	16	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: mRNA capping enzyme
33	c4pz8A	Alignment	not modelled	99.9	22	PDB header: transferase/transcription Chain: A; PDB Molecule: mrna-capping enzyme subunit alpha; PDBTitle: pce1 guanylyltransferase bound to spt5 ctd
34	d1p16a2	Alignment	not modelled	99.9	20	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: mRNA capping enzyme
35	c3vnnA	Alignment	not modelled	99.9	17	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
36	c3qwvA	Alignment	not modelled	99.9	19	PDB header: ligase Chain: A; PDB Molecule: dna ligase; PDBTitle: putative atp-dependent dna ligase from aquifex aeolicus.
37	c5covA	Alignment	not modelled	99.7	16	PDB header: ligase Chain: A; PDB Molecule: naegleria gruberi rna ligase; PDBTitle: structure and mechanism of a eukaryal nick-sealing rna ligase k170m+mn
38	d1a0ia1	Alignment	not modelled	99.0	22	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
39	d1fvia1	Alignment	not modelled	98.9	21	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: DNA ligase/mRNA capping enzyme postcatalytic domain
40	c5d1pB	Alignment	not modelled	98.8	22	PDB header: ligase Chain: B; PDB Molecule: atp-dependent rna ligase; PDBTitle: archaeal atp-dependent rna ligase - form 2
41	d1b04a	Alignment	not modelled	98.6	18	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
42	c3pn1A	Alignment	not modelled	98.6	18	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
43	c3jsIA	Alignment	not modelled	98.6	16	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
44	c3bacA	Alignment	not modelled	98.5	18	PDB header: ligase Chain: A; PDB Molecule: dna ligase; PDBTitle: structural basis for the inhibition of bacterial nad+2 dependent dna ligase
45	c2owoA	Alignment	not modelled	98.5	18	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
46	c4glwA	Alignment	not modelled	98.5	18	PDB header: ligase/ligase inhibitor Chain: A; PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
47	c4glxA	Alignment	not modelled	98.5	20	PDB header: ligase/ligase inhibitor/dna Chain: A; PDB Molecule: dna ligase; PDBTitle: dna ligase a in complex with inhibitor
48	d1s68a	Alignment	not modelled	98.5	17	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: RNA ligase
49	d1ta8a	Alignment	not modelled	98.4	16	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
50	c3gjxE	Alignment	not modelled	98.3	19	PDB header: protein transport Chain: E; PDB Molecule: snurportin-1; PDBTitle: crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
51	c3sgIA	Alignment	not modelled	98.3	21	PDB header: ligase Chain: A; PDB Molecule: dna ligase; PDBTitle: crystal structure of dna ligase a brct domain deleted mutant of2 mycobacterium tuberculosis
52	d1v9pa3	Alignment	not modelled	98.3	18	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
53	c1dgsB	Alignment	not modelled	98.2	17	PDB header: ligase Chain: B; PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase from t.2 filiformis
54	c3gb8B	Alignment	not modelled	98.2	17	PDB header: transport protein Chain: B; PDB Molecule: snurportin-1; PDBTitle: crystal structure of crm1/snurportin-1 complex
55	d1dgsa3	Alignment	not modelled	98.1	16	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: Adenylation domain of NAD+-dependent DNA ligase
						PDB header: ligase

56	c1v9pB_	Alignment	not modelled	98.1	18	Chain: B: PDB Molecule: dna ligase; PDBTitle: crystal structure of nad+-dependent dna ligase
57	c4e6nC_	Alignment	not modelled	98.1	23	PDB header: protein binding Chain: C: PDB Molecule: metallophosphoesterase; PDBTitle: crystal structure of bacterial pnpk-c/hen1-n heterodimer
58	c1zauA_	Alignment	not modelled	98.0	21	PDB header: ligase Chain: A: PDB Molecule: dna ligase; PDBTitle: adenylation domain of nad+ dependent dna ligase from m.tuberculosis
59	c2hvsA_	Alignment	not modelled	98.0	21	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
60	c3ty8A_	Alignment	not modelled	98.0	20	PDB header: transferase Chain: A: PDB Molecule: polynucleotide 2',3'-cyclic phosphate phosphodiesterase / PDBTitle: crystal structure of c. thermocellum pnpk ligase domain apo form
61	c1xk5A_	Alignment	not modelled	98.0	17	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
62	d1zt2a1	Alignment	not modelled	97.5	20	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
63	c4limA_	Alignment	not modelled	96.3	21	PDB header: transferase Chain: A: PDB Molecule: dna primase small subunit; PDBTitle: crystal structure of the catalytic subunit of yeast primase
64	d1v33a_	Alignment	not modelled	96.2	23	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
65	c4bpxC_	Alignment	not modelled	96.1	24	PDB header: transferase Chain: C: PDB Molecule: dna primase small subunit; PDBTitle: crystal structure of human primase in complex with the primase-2 binding motif of dna polymerase alpha
66	d1g71a_	Alignment	not modelled	95.9	25	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: PriA-like
67	d1xdna_	Alignment	not modelled	95.5	22	Fold: ATP-grasp Superfamily: DNA ligase/mRNA capping enzyme, catalytic domain Family: RNA ligase
68	c4xruE_	Alignment	not modelled	91.5	18	PDB header: protein binding Chain: E: PDB Molecule: rnl; PDBTitle: structure of pnpk1/rnl/hen1 complex
69	d1k1sa2	Alignment	not modelled	74.5	15	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
70	c5todD_	Alignment	not modelled	74.2	32	PDB header: lipid transport Chain: D: PDB Molecule: transmembrane protein 24; PDBTitle: transmembrane protein 24 smp domain
71	d1ro0a_	Alignment	not modelled	71.9	19	Fold: Prim-pol domain Superfamily: Prim-pol domain Family: Bifunctional DNA primase/polymerase N-terminal domain
72	d1im4a_	Alignment	not modelled	70.5	14	Fold: DNA/RNA polymerases Superfamily: DNA/RNA polymerases Family: Lesion bypass DNA polymerase (Y-family), catalytic domain
73	c5gl6A_	Alignment	not modelled	63.0	11	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosome maturation factor rimp; PDBTitle: msmeg rimp
74	c6a9wA_	Alignment	not modelled	61.6	24	PDB header: replication Chain: A: PDB Molecule: primase; PDBTitle: structure of the bifunctional dna primase-polymerase from phage nrs-1
75	c2bf9A_	Alignment	not modelled	58.7	15	PDB header: hormone Chain: A: PDB Molecule: pancreatic hormone; PDBTitle: anisotropic refinement of avian (turkey) pancreatic polypeptide at 0.2 99 angstroms resolution.
76	c1tz5A_	Alignment	not modelled	57.8	18	PDB header: hormone/growth factor Chain: A: PDB Molecule: chimera of pancreatic hormone and neuropeptide y; PDBTitle: [pnpy19-23]-hpp bound to dpc micelles
77	c3ebkA_	Alignment	not modelled	57.2	27	PDB header: allergen Chain: A: PDB Molecule: allergen bla g 4; PDBTitle: crystal structure of major allergens, bla g 4 from cockroaches
78	c2dezA_	Alignment	not modelled	53.2	18	PDB header: neuropeptide Chain: A: PDB Molecule: peptide yy; PDBTitle: structure of human pyy
79	c1ronA_	Alignment	not modelled	52.4	19	PDB header: neuropeptide Chain: A: PDB Molecule: neuropeptide y; PDBTitle: nmr solution structure of human neuropeptide y
80	d2oyra1	Alignment	not modelled	50.7	23	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: YhiQ-like
81	c2xj9B_	Alignment	not modelled	47.5	24	PDB header: replication Chain: B: PDB Molecule: mipz; PDBTitle: dimer structure of the bacterial cell division regulator mipz
82	c4d1lB_	Alignment	not modelled	41.2	23	PDB header: hydrolase Chain: B: PDB Molecule: beta-galactosidase, putative, bgl35a; PDBTitle: the structure of the gh35 beta-galactosidase bgl35a from2 cellvibrio japonicus

83	c3u7vA	Alignment	not modelled	37.0	26	PDB header: hydrolase Chain: A: PDB Molecule: beta-galactosidase; PDBTitle: the structure of a putative beta-galactosidase from caulobacter2 crescentus cb15.
84	c5yrzD	Alignment	not modelled	36.8	22	PDB header: antitoxin/hydrolase Chain: D: PDB Molecule: hica; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
85	c5kodA	Alignment	not modelled	36.7	23	PDB header: ligase Chain: A: PDB Molecule: indole-3-acetic acid-amido synthetase gh3.5; PDBTitle: crystal structure of gh3.5 acyl acid amido synthetase from arabidopsis2 thaliana
86	c5yrzB	Alignment	not modelled	36.6	22	PDB header: antitoxin/hydrolase Chain: B: PDB Molecule: hica; PDBTitle: toxin-antitoxin complex from streptococcus pneumoniae
87	c2qjpC	Alignment	not modelled	35.5	17	PDB header: hydrolase Chain: C: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: bifunctional dctp deaminase:dutpase from mycobacterium tuberculosis,2 apo form
88	c2qxxA	Alignment	not modelled	34.2	17	PDB header: hydrolase Chain: A: PDB Molecule: deoxycytidine triphosphate deaminase; PDBTitle: bifunctional dctp deaminase: dutpase from mycobacterium tuberculosis2 in complex with dttp
89	c1s21A	Alignment	not modelled	33.3	30	PDB header: chaperone Chain: A: PDB Molecule: orf2; PDBTitle: crystal structure of avrpphf orf2, a type iii effector from p.2 syringae
90	d1s21a	Alignment	not modelled	33.3	30	Fold: ADP-ribosylation Superfamily: ADP-ribosylation Family: AvrPphF ORF2, a type III effector
91	d1xv2a	Alignment	not modelled	32.6	56	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: Alpha-acetolactate decarboxylase-like
92	c3m1mA	Alignment	not modelled	31.0	19	PDB header: replication Chain: A: PDB Molecule: orf904; PDBTitle: crystal structure of the primase-polymerase from sulfobolus islandicus
93	c5j96C	Alignment	not modelled	29.4	45	PDB header: virus Chain: C: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of slow bee paralysis virus at 3.4a resolution
94	c4kxbA	Alignment	not modelled	28.4	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
95	c5yhkB	Alignment	not modelled	28.4	44	PDB header: metal binding protein Chain: B: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterobacter2 aerogenes
96	c3osrA	Alignment	not modelled	27.3	15	PDB header: fluorescent protein, transport protein Chain: A: PDB Molecule: maltose-binding periplasmic protein,green fluorescent PDBTitle: maltose-bound maltose sensor engineered by insertion of circularly2 permuted green fluorescent protein into e. coli maltose binding3 protein at position 311
97	c5xneA	Alignment	not modelled	26.9	56	PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: x-ray crystal structure of alpha-acetolactate decarboxylase from2 bacillus subtilis strain 168
98	c4euvA	Alignment	not modelled	26.9	16	PDB header: signaling protein Chain: A: PDB Molecule: peld; PDBTitle: crystal structure of peld 158-ct from pseudomonas aeruginosa pao1, in2 complex with c-di-gmp, form 1
99	c5yhoA	Alignment	not modelled	26.5	44	PDB header: metal binding protein Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: crystal structure of acetolactate decarboxylase from enterobacter2 cloacae
100	c4bt7A	Alignment	not modelled	26.4	44	PDB header: lyase Chain: A: PDB Molecule: alpha-acetolactate decarboxylase; PDBTitle: acetolactate decarboxylase with a bound phosphate ion
101	c4ep1A	Alignment	not modelled	25.6	13	PDB header: ligase Chain: A: PDB Molecule: jasmonic acid-amido synthetase jar1; PDBTitle: crystal structure of arabidopsis thaliana gh3.11 (jar1) in complex2 with ja-ile
102	c3k9gA	Alignment	not modelled	25.4	16	PDB header: biosynthetic protein Chain: A: PDB Molecule: pf-32 protein; PDBTitle: crystal structure of a plasmid partition protein from borrelia2 burgdorferi at 2.25a resolution, iodide soak
103	d2r7ka2	Alignment	not modelled	25.1	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
104	c3k6gA	Alignment	not modelled	24.0	27	PDB header: protein binding Chain: A: PDB Molecule: telomeric repeat-binding factor 2-interacting protein 1; PDBTitle: crystal structure of rap1 and trf2 complex
105	d1v95a	Alignment	not modelled	23.9	18	Fold: Anticodon-binding domain-like Superfamily: Class II aaRS ABD-related Family: Anticodon-binding domain of Class II aaRS
106	c4aaqA	Alignment	not modelled	23.8	33	PDB header: viral protein Chain: A: PDB Molecule: l2 protein iii (penton base); PDBTitle: dodecahedron formed of penton base protein from adenovirus ad3
107	c4ki0A	Alignment	not modelled	22.4	19	PDB header: calcium binding protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the effector protein xoo4466
108	c5c5hA	Alignment	not modelled	22.3	16	PDB header: ligase Chain: A: PDB Molecule: 2-succinylbenzoate--coa ligase;

						PDBTitle: r195k e. coli mene with bound osb-ams
109	c5f4zB_	Alignment	not modelled	21.9	24	PDB header: hydrolase Chain: B: PDB Molecule: epoxide hydrolase; PDBTitle: the crystal structure of an epoxide hydrolase from streptomyces2 carzinostaticus subsp. neocarzinostaticus
110	c4oudB_	Alignment	not modelled	21.7	20	PDB header: ligase Chain: B: PDB Molecule: tyrosyl-trna synthetase; PDBTitle: engineered tyrosyl-trna synthetase with the nonstandard amino acid l-2 4,4-biphenylalanine
111	d1jh3a_	Alignment	not modelled	21.7	29	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Tyrosyl-tRNA synthetase (TyrRS), C-terminal domain
112	c3nezA_	Alignment	not modelled	21.6	11	PDB header: fluorescent protein Chain: A: PDB Molecule: mrojoa; PDBTitle: mrojoa
113	d1e8ga1	Alignment	not modelled	21.4	10	Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Vanillyl-alcohol oxidase-like
114	d1pfsa_	Alignment	not modelled	21.2	34	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Phage ssDNA-binding proteins
115	c2c5uA_	Alignment	not modelled	21.0	19	PDB header: ligase Chain: A: PDB Molecule: rna ligase; PDBTitle: t4 rna ligase (rn1) crystal structure
116	c2d8bA_	Alignment	not modelled	20.8	12	PDB header: protein binding Chain: A: PDB Molecule: twinfilin-1; PDBTitle: solution structure of the second tandem cofilin-domain of2 mouse twinfilin
117	c2icrD_	Alignment	not modelled	20.6	16	PDB header: fluorescent protein Chain: D: PDB Molecule: red fluorescent protein zoanrfp; PDBTitle: red fluorescent protein zrfp574 from zoanthus sp.
118	c2a5hC_	Alignment	not modelled	20.6	19	PDB header: isomerase Chain: C: PDB Molecule: l-lysine 2,3-aminomutase; PDBTitle: 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
119	d2hqva1	Alignment	not modelled	20.5	14	Fold: Heme iron utilization protein-like Superfamily: Heme iron utilization protein-like Family: ChuX-like