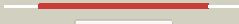



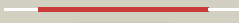






















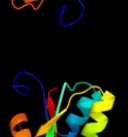
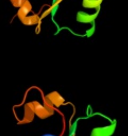



Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0A0G6
Date	Tue Jul 17 17:05:06 BST 2012
Unique Job ID	af71a9c07d345414

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2aifa1	 Alignment		99.8	26	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
2	dlw41a1	 Alignment		99.8	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
3	c3o85A_	 Alignment		99.8	24	PDB header: ribosomal protein Chain: A: PDB Molecule: ribosomal protein l7ae; PDBTitle: giardia lamblia 15.5kd rna binding protein
4	d1t0kb_	 Alignment		99.8	19	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
5	d2bo1a1	 Alignment		99.8	19	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
6	c3cpqB_	 Alignment		99.8	18	PDB header: ribosomal protein Chain: B: PDB Molecule: 50s ribosomal protein l30e; PDBTitle: crystal structure of l30e a ribosomal protein from2 methanocaldococcus jannaschii dsm2661 (mj1044)
7	c2lbaA_	 Alignment		99.8	22	PDB header: rna binding protein Chain: A: PDB Molecule: h/aca ribonucleoprotein complex subunit 2; PDBTitle: solution structure of the s. cerevisiae h/aca rnp protein nhp2p-s82w2 mutant
8	c4a1dG_	 Alignment		99.8	17	PDB header: ribosome Chain: G: PDB Molecule: rpl30; PDBTitle: t.thermophila 60s ribosomal subunit in complex with initiation2 factor 6. this file contains 26s rrna and proteins of3 molecule 4.
9	d1xbia1	 Alignment		99.8	34	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
10	c2zkr6_	 Alignment		99.8	18	PDB header: ribosomal protein/rna Chain: 6: PDB Molecule: 60s ribosomal protein l30e; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
11	d2ozba1	 Alignment		99.8	23	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins

12	d2czwa1	Alignment		99.8	34	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
13	d1rlga_	Alignment		99.8	31	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
14	d2fc3a1	Alignment		99.8	31	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
15	c3v7eB_	Alignment		99.8	35	PDB header: ribosomal protein/rna Chain: B: PDB Molecule: ribosome-associated protein l7ae-like; PDBTitle: crystal structure of ybxf bound to the sam-i riboswitch aptamer
16	d1vqof1	Alignment		99.8	21	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
17	d1jj2f_	Alignment		99.8	21	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
18	c2xznU	Alignment		99.8	21	PDB header: ribosome Chain: U: PDB Molecule: ribosomal protein l7ae containing protein; PDBTitle: crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 2
19	c3v7qB_	Alignment		99.8	19	PDB header: rna binding protein Chain: B: PDB Molecule: probable ribosomal protein ylxq; PDBTitle: crystal structure of b. subtilis ylxq at 1.55 a resolution
20	d2alea1	Alignment		99.8	23	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: L30e/L7ae ribosomal proteins
21	c3on1A_	Alignment	not modelled	99.8	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: bh2414 protein; PDBTitle: the structure of a protein with unknown function from bacillus2 halodurans c
22	c3u5cM_	Alignment	not modelled	99.8	24	PDB header: ribosome Chain: M: PDB Molecule: 40s ribosomal protein s12; PDBTitle: the structure of the eukaryotic ribosome at 3.0 a resolution. this2 entry contains proteins of the 40s subunit, ribosome a
23	c2zkrf_	Alignment	not modelled	99.7	21	PDB header: ribosomal protein/rna Chain: F: PDB Molecule: rna expansion segment es7 part iii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
24	c3iz5H_	Alignment	not modelled	99.7	20	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein l7a (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
25	c4a1eF_	Alignment	not modelled	99.7	29	PDB header: ribosome Chain: F: PDB Molecule: rpl7a; PDBTitle: t thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
26	c3izcH_	Alignment	not modelled	99.7	20	PDB header: ribosome Chain: H: PDB Molecule: 60s ribosomal protein rpl8 (l7ae); PDBTitle: localization of the large subunit ribosomal proteins into a 6.1 a2 cryo-em map of saccharomyces cerevisiae translating 80s ribosome
27	c1s1iG_	Alignment	not modelled	99.6	20	PDB header: ribosome Chain: G: PDB Molecule: 60s ribosomal protein l8-a; PDBTitle: structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and

						protein3 components into a 11.7 a cryo-em map. this file, 1s1i,4 contains 60s subunit. the 40s ribosomal subunit is in file5 1s1h.
28	c3cg6A_	Alignment	not modelled	99.4	18	PDB header: cell cycle Chain: A: PDB Molecule: growth arrest and dna-damage-inducible 45 gamma; PDBTitle: crystal structure of gadd45 gamma
29	c2kg4A_	Alignment	not modelled	98.8	17	PDB header: cell cycle Chain: A: PDB Molecule: growth arrest and dna-damage-inducible protein gadd45 PDBTitle: three-dimensional structure of human gadd45alpha in solution by nmr
30	d1gz0f2	Alignment	not modelled	96.7	8	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
31	c2ktvA_	Alignment	not modelled	96.6	19	PDB header: translation Chain: A: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: human erf1 c-domain, "open" conformer
32	d2vgna3	Alignment	not modelled	96.5	17	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
33	d2qi2a3	Alignment	not modelled	96.4	18	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
34	d1gz0a2	Alignment	not modelled	96.3	13	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
35	c3ir9A_	Alignment	not modelled	96.0	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: c-terminal domain of peptide chain release factor from2 methanosarcina mazel.
36	d1x52a1	Alignment	not modelled	95.8	20	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
37	d1dt9a2	Alignment	not modelled	95.7	22	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: ERF1/Dom34 C-terminal domain-like
38	c2qi2A_	Alignment	not modelled	95.4	18	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein pelota related protein; PDBTitle: crystal structure of the thermoplasma acidophilum pelota2 protein
39	c2vgmA_	Alignment	not modelled	95.2	15	PDB header: cell cycle Chain: A: PDB Molecule: dom34; PDBTitle: structure of yeast dom34 : a protein related to translation2 termination factor erf1 and involved in no-go decay.
40	c3obyB_	Alignment	not modelled	95.1	19	PDB header: hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeoglobus fulgidus pelota reveals inter-2 domain structural plasticity
41	c3e20C_	Alignment	not modelled	95.0	15	PDB header: translation Chain: C: PDB Molecule: eukaryotic peptide chain release factor subunit 1; PDBTitle: crystal structure of s.pombe erf1/erf3 complex
42	c3mcaB_	Alignment	not modelled	94.6	21	PDB header: translation regulation/hydrolase Chain: B: PDB Molecule: protein dom34; PDBTitle: structure of the dom34-hbs1 complex and implications for its role in2 no-go decay
43	c3agiD_	Alignment	not modelled	94.2	11	PDB header: translation/hydrolase Chain: D: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
44	c3agiB_	Alignment	not modelled	94.2	11	PDB header: translation/hydrolase Chain: B: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of archaeal pelota and gtp-bound ef1 alpha complex
45	c1dt9A_	Alignment	not modelled	94.2	20	PDB header: translation Chain: A: PDB Molecule: protein (eukaryotic peptide chain release factor PDBTitle: the crystal structure of human eukaryotic release factor2 erf1-mechanism of stop codon recognition and peptidyl-trna3 hydrolysis
46	c3obwA_	Alignment	not modelled	94.1	16	PDB header: hydrolase Chain: A: PDB Molecule: protein pelota homolog; PDBTitle: crystal structure of two archaeal pelotas reveal inter-domain2 structural plasticity
47	c3j15A_	Alignment	not modelled	94.1	19	PDB header: translation/transport protein Chain: A: PDB Molecule: protein pelota; PDBTitle: model of ribosome-bound archaeal pelota and abce1
48	c3agkA_	Alignment	not modelled	94.0	15	PDB header: translation Chain: A: PDB Molecule: peptide chain release factor subunit 1; PDBTitle: crystal structure of archaeal translation termination factor, arf1
49	d1wo8a1	Alignment	not modelled	85.3	9	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
50	d1piia2	Alignment	not modelled	82.3	9	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
51	c3nklA_	Alignment	not modelled	78.8	11	PDB header: oxidoreductase/lyase Chain: A: PDB Molecule: udp-d-quinovosamine 4-dehydrogenase; PDBTitle: crystal structure of udp-d-quinovosamine 4-dehydrogenase from vibrio2 fischeri
52	d1vmda_	Alignment	not modelled	77.4	16	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA

53	d2ohwa1	Alignment	not modelled	75.2	16	Fold: Bacillus chorismate mutase-like Superfamily: Yuel-like Family: Yuel-like
54	d1a53a	Alignment	not modelled	74.7	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
55	d1i4na	Alignment	not modelled	73.1	14	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
56	c3gyqB	Alignment	not modelled	70.8	9	PDB header: transferase Chain: B: PDB Molecule: rrna (adenosine-2'-o-)-methyltransferase; PDBTitle: structure of the thiostrepton-resistance methyltransferase2 s-adenosyl-l-methionine complex
57	c2yvqA	Alignment	not modelled	64.9	12	PDB header: ligase Chain: A: PDB Molecule: carbamoyl-phosphate synthase; PDBTitle: crystal structure of mgs domain of carbamoyl-phosphate2 synthetase from homo sapiens
58	d1yova1	Alignment	not modelled	62.1	13	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
59	d1ko7a1	Alignment	not modelled	61.4	16	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phosphatase HprK N-terminal domain
60	c1y8qA	Alignment	not modelled	58.8	6	PDB header: ligase Chain: A: PDB Molecule: ubiquitin-like 1 activating enzyme e1a; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
61	c3h9gA	Alignment	not modelled	58.6	16	PDB header: transferase/antibiotic Chain: A: PDB Molecule: mccb protein; PDBTitle: crystal structure of e. coli mccb + mcca-n7isoasn
62	d1j5ta	Alignment	not modelled	58.1	15	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: Tryptophan biosynthesis enzymes
63	c1u0lB	Alignment	not modelled	56.7	14	PDB header: hydrolase Chain: B: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of yjeq from thermotoga maritima
64	d1a9xa2	Alignment	not modelled	51.5	12	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
65	c2yv5A	Alignment	not modelled	51.1	14	PDB header: hydrolase Chain: A: PDB Molecule: yjeq protein; PDBTitle: crystal structure of yjeq from aquifex aeolicus
66	d1u0la2	Alignment	not modelled	48.9	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
67	d1knxa1	Alignment	not modelled	46.3	14	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phosphatase HprK N-terminal domain
68	c3iygD	Alignment	not modelled	40.4	17	PDB header: chaperone Chain: D: PDB Molecule: t-complex protein 1 subunit delta; PDBTitle: ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
69	c2px0D	Alignment	not modelled	40.3	9	PDB header: biosynthetic protein Chain: D: PDB Molecule: flagellar biosynthesis protein flhf; PDBTitle: crystal structure of flhf complexed with gmppnp/mg(2+)
70	d1b74a1	Alignment	not modelled	39.6	20	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
71	d1x49a1	Alignment	not modelled	39.1	11	Fold: dsRBD-like Superfamily: dsRNA-binding domain-like Family: Double-stranded RNA-binding domain (dsRBD)
72	d1uyra1	Alignment	not modelled	38.8	18	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
73	c2c3zA	Alignment	not modelled	38.8	15	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of a truncated variant of indole-3-2 glycerol phosphate synthase from sulfolobus solfataricus
74	c3kc2A	Alignment	not modelled	37.8	14	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein ykr070w; PDBTitle: crystal structure of mitochondrial had-like phosphatase from2 saccharomyces cerevisiae
75	c3cmmA	Alignment	not modelled	37.7	13	PDB header: ligase/protein binding Chain: A: PDB Molecule: ubiquitin-activating enzyme e1 1; PDBTitle: crystal structure of the uba1-ubiquitin complex
76	c1yj5B	Alignment	not modelled	36.6	16	PDB header: transferase Chain: B: PDB Molecule: 5' polynucleotide kinase-3' phosphatase catalytic domain; PDBTitle: molecular architecture of mammalian polynucleotide kinase, a dna2 repair enzyme
77	c1t9hA	Alignment	not modelled	33.6	23	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: the crystal structure of yloq, a circularly permuted gtpase.
78	c3qjaA	Alignment	not modelled	32.7	13	PDB header: lyase Chain: A: PDB Molecule: indole-3-glycerol phosphate synthase; PDBTitle: crystal structure of the mycobacterium tuberculosis indole-3-glycerol2 phosphate synthase (trpc) in apo form PDB header: chaperone

79	c3aq1B_	Alignment	not modelled	32.2	10	Chain: B: PDB Molecule: thermosome subunit; PDBTitle: open state monomer of a group ii chaperonin from methanococcus2 burtonii
80	c4a2iV_	Alignment	not modelled	31.6	14	PDB header: ribosome/hydrolase Chain: V: PDB Molecule: putative ribosome biogenesis gtpase rsga; PDBTitle: cryo-electron microscopy structure of the 30s subunit in complex with2 the yjeq biogenesis factor
81	d2ioja1	Alignment	not modelled	30.9	23	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: DRTGG domain
82	d1ipaa2	Alignment	not modelled	29.8	18	Fold: Bacillus chorismate mutase-like Superfamily: L30e-like Family: RNA 2'-O ribose methyltransferase substrate binding domain
83	c1u8cB_	Alignment	not modelled	28.0	21	PDB header: cell adhesion Chain: B: PDB Molecule: integrin beta-3; PDBTitle: a novel adaptation of the integrin psi domain revealed from its2 crystal structure
84	c4e2i3_	Alignment	not modelled	27.6	21	PDB header: hydrolase/dna binding protein Chain: 3: PDB Molecule: dna polymerase alpha subunit b; PDBTitle: the complex structure of the sv40 helicase large t antigen and p682 subunit of dna polymerase alpha-primase
85	d2h6ca1	Alignment	not modelled	27.4	8	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
86	d1kyqa1	Alignment	not modelled	26.8	8	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
87	c3iygE_	Alignment	not modelled	26.8	8	PDB header: chaperone Chain: E: PDB Molecule: t-complex protein 1 subunit; PDBTitle: ca model of bovine tric/cct derived from a 4.0 angstrom2 cryo-em map
88	c2yhsA_	Alignment	not modelled	26.7	12	PDB header: cell cycle Chain: A: PDB Molecule: cell division protein ftsy; PDBTitle: structure of the e. coli srp receptor ftsy
89	d2oz6a1	Alignment	not modelled	26.5	22	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
90	c2rcnA_	Alignment	not modelled	26.3	17	PDB header: hydrolase Chain: A: PDB Molecule: probable gtpase engc; PDBTitle: crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
91	d1agxa_	Alignment	not modelled	26.1	19	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
92	c1knxF_	Alignment	not modelled	25.0	17	PDB header: transferase/hydrolase Chain: F: PDB Molecule: probable hpr(ser) kinase/phosphatase; PDBTitle: hpr kinase/phosphatase from mycoplasma pneumoniae
93	d1oi7a1	Alignment	not modelled	24.9	17	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
94	c2kebA_	Alignment	not modelled	24.8	21	PDB header: dna binding protein Chain: A: PDB Molecule: dna polymerase subunit alpha b; PDBTitle: nmr solution structure of the n-terminal domain of the dna polymerase2 alpha p68 subunit
95	c3ff6D_	Alignment	not modelled	24.1	21	PDB header: ligase Chain: D: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: human acc2 ct domain with cp-640186
96	d1i5za1	Alignment	not modelled	24.1	19	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
97	d1t9ha2	Alignment	not modelled	24.0	19	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
98	d1b93a_	Alignment	not modelled	23.9	21	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Methylglyoxal synthase, MgsA
99	d1pixa2	Alignment	not modelled	23.8	12	Fold: ClpP/crotonase Superfamily: ClpP/crotonase Family: Biotin dependent carboxylase carboxyltransferase domain
100	d1m1na_	Alignment	not modelled	23.7	7	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: Nitrogenase iron-molybdenum protein
101	c2jfoB_	Alignment	not modelled	23.7	23	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of enterococcus faecalis glutamate2 racemase in complex with d- and l-glutamate
102	c3kydB_	Alignment	not modelled	23.6	14	PDB header: ligase Chain: B: PDB Molecule: sumo-activating enzyme subunit 2; PDBTitle: human sumo e1~sumo1-amp tetrahedral intermediate mimic
103	c2khpA_	Alignment	not modelled	22.7	13	PDB header: electron transport Chain: A: PDB Molecule: glutaredoxin; PDBTitle: solution structure of glutaredoxin from brucella melitensis
104	c3gucB_	Alignment	not modelled	22.7	7	PDB header: transferase Chain: B: PDB Molecule: ubiquitin-like modifier-activating enzyme 5; PDBTitle: human ubiquitin-activating enzyme 5 in complex with amppnp
105	c3hfrA_	Alignment	not modelled	22.5	15	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase;

105	c3m1A_	Alignment	not modelled	22.9	13	PDBTitle: crystal structure of glutamate racemase from listeria monocytogenes
106	c1y8qD_	Alignment	not modelled	22.5	14	PDB header: ligase Chain: D: PDB Molecule: ubiquitin-like 2 activating enzyme e1b; PDBTitle: sumo e1 activating enzyme sae1-sae2-mg-atp complex
107	c3uhfB_	Alignment	not modelled	22.5	23	PDB header: isomerase Chain: B: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase from campylobacter jejuni2 subsp. jejuni
108	c2iy3A_	Alignment	not modelled	22.3	12	PDB header: rna-binding Chain: A: PDB Molecule: signal recognition particle protein ffh; PDBTitle: structure of the e. coli signal recognition particle2 bound to a translating ribosome
109	d2ji7a1	Alignment	not modelled	22.2	7	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
110	d2obba1	Alignment	not modelled	22.2	22	Fold: HAD-like Superfamily: HAD-like Family: BT0820-like
111	d1n0ua2	Alignment	not modelled	21.5	16	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: G proteins
112	d1dnpa2	Alignment	not modelled	21.5	18	Fold: Cryptochrome/photolyase, N-terminal domain Superfamily: Cryptochrome/photolyase, N-terminal domain Family: Cryptochrome/photolyase, N-terminal domain
113	c2ohoA_	Alignment	not modelled	21.4	18	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: structural basis for glutamate racemase inhibitor
114	d1ft9a1	Alignment	not modelled	21.3	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: CAP C-terminal domain-like
115	c1uytC_	Alignment	not modelled	21.2	18	PDB header: transferase Chain: C: PDB Molecule: acetyl-coa carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
116	c2x24B_	Alignment	not modelled	21.1	21	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase; PDBTitle: bovine acc2 ct domain in complex with inhibitor
117	c3emxB_	Alignment	not modelled	20.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from aeropyrum pernix
118	c1od4C_	Alignment	not modelled	20.5	18	PDB header: ligase Chain: C: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: acetyl-coa carboxylase carboxyltransferase domain
119	c1k6mA_	Alignment	not modelled	20.2	17	PDB header: transferase, hydrolase Chain: A: PDB Molecule: 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2- PDBTitle: crystal structure of human liver 6-phosphofructo-2-kinase/fructose-2,2 6-bisphosphatase
120	c3p9ee_	Alignment	not modelled	20.2	16	PDB header: chaperone Chain: E: PDB Molecule: PDBTitle: the crystal structure of yeast cct reveals intrinsic asymmetry of 2 eukaryotic cytosolic chaperonins