



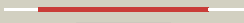
























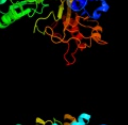



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3bg5C_	 Alignment		100.0	44	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate2 carboxylase
2	c3g8cB_	 Alignment		100.0	100	PDB header: ligase Chain: B: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
3	c2gpwC_	 Alignment		100.0	99	PDB header: ligase Chain: C: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of the biotin carboxylase subunit, f363a2 mutant, of acetyl-coa carboxylase from escherichia coli.
4	c1ulzA_	 Alignment		100.0	52	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
5	c3ouza_	 Alignment		100.0	50	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
6	c1w96B_	 Alignment		100.0	33	PDB header: ligase Chain: B: PDB Molecule: acetyl-coenzyme a carboxylase; PDBTitle: crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a
7	c3u9sE_	 Alignment		100.0	49	PDB header: ligase Chain: E: PDB Molecule: methylcrotonyl-coa carboxylase, alpha-subunit; PDBTitle: crystal structure of p. aeruginosa 3-methylcrotonyl-coa carboxylase2 (mcc) 750 kd holoenzyme, coa complex
8	c2vpqA_	 Alignment		100.0	53	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
9	c3n6rK_	 Alignment		100.0	46	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
10	c2hjaA_	 Alignment		100.0	33	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
11	c2dzdB_	 Alignment		100.0	45	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase

12	c2qf7A_	Alignment		100.0	45	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
13	c3gidB_	Alignment		100.0	33	PDB header: ligase Chain: B: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: the biotin carboxylase (bc) domain of human acetyl-coa2 carboxylase 2 (acc2) in complex with soraphen a
14	c1m6vE_	Alignment		100.0	23	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
15	c1kjjA_	Alignment		100.0	18	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycinamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
16	c2yyaB_	Alignment		100.0	19	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
17	c2xd4A_	Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
18	c3lp8A_	Alignment		100.0	14	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
19	c2ip4A_	Alignment		100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
20	c2ys6A_	Alignment		100.0	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
21	c2qk4A_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenosine-3; PDBTitle: human glycinamide ribonucleotide synthetase
22	c3uvzB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
23	c2dwcB_	Alignment	not modelled	100.0	16	PDB header: transferase Chain: B: PDB Molecule: 433aa long hypothetical phosphoribosylglycinamide formyl PDBTitle: crystal structure of probable phosphoribosylglycinamide formyl2 transferase from pyrococcus horikoshii ot3 complexed with adp
24	c1gsoA_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
25	c1vkzA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of phosphoribosylamine--glycine ligase (tm1250) from2 thermotoga maritima at 2.30 a resolution
26	c3q2oB_	Alignment	not modelled	100.0	19	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
27	c3k5iB_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminimidazole carboxylase;

27	c3k3bB_	Alignment	not modelled	100.0	17	PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimidazole ribonucleotide
28	c3orqA_	Alignment	not modelled	100.0	18	PDB header: ligase,biosynthetic protein Chain: A: PDB Molecule: n5-carboxyaminoimidazole ribonucleotide synthetase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthetase from2 staphylococcus aureus complexed with adp
29	c3etjB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure e. coli purk in complex with mg, adp, and2 pi
30	c2z04A_	Alignment	not modelled	100.0	17	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
31	d1a9xa5	Alignment	not modelled	100.0	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
32	d1w96a3	Alignment	not modelled	100.0	39	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
33	c2pn1A_	Alignment	not modelled	100.0	16	PDB header: ligase Chain: A: PDB Molecule: carbamoylphosphate synthase large subunit; PDBTitle: crystal structure of carbamoylphosphate synthase large subunit (split2 gene in mj) (zp_00538348.1) from exigubacterium sp. 255-15 at 2.00 a3 resolution
34	c1ehiB_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmdl2) of vancomycin-resistant2 leuconostoc mesenteroides
35	c3i12A_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: the crystal structure of the d-alanyl-alanine synthetase a from2 salmonella enterica subsp. enterica serovar typhimurium str. lt2
36	c2i80B_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: allosteric inhibition of staphylococcus aureus d-alanine:d-alanine2 ligase revealed by crystallographic studies
37	c3lwbA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of apo d-alanine:d-alanine ligase (ddl) from2 mycobacterium tuberculosis
38	c2dlnA_	Alignment	not modelled	100.0	23	PDB header: ligase(peptidoglycan synthesis) Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: vancomycin resistance: structure of d-alanine:d-alanine2 ligase at 2.3 angstroms resolution
39	c2zdgA_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine:d-alanine ligase with atp2 and d-alanine:d-alanine from thermus thermophilus hb8
40	c1e4eB_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lacate ligase
41	c3e5nA_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: d-alanine-d-alanine ligase a; PDBTitle: crystal structure of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
42	c2r85B_	Alignment	not modelled	100.0	18	PDB header: unknown function Chain: B: PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from pyrococcus furiosus complexed with amp
43	c3r23B_	Alignment	not modelled	100.0	12	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
44	d2j9ga3	Alignment	not modelled	100.0	100	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
45	c3k3pA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of the apo form of d-alanine:d-alanine ligase (ddl)2 from streptococcus mutans
46	d1a9xa6	Alignment	not modelled	100.0	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
47	c3se7A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
48	c2pvpB_	Alignment	not modelled	100.0	14	PDB header: ligase Chain: B: PDB Molecule: d-alanine-d-alanine ligase; PDBTitle: crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
49	c3tqtB_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
50	d1ulza3	Alignment	not modelled	100.0	53	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
51	d1kjqaz	Alignment	not modelled	100.0	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like

52	c3df7A_	Alignment	not modelled	100.0	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative atp-grasp superfamily protein; PDBTitle: crystal structure of a putative atp-grasp superfamily2 protein from archaeoglobus fulgidus
53	d1vkza3	Alignment	not modelled	100.0	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
54	d3etja3	Alignment	not modelled	100.0	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
55	d2j9ga1	Alignment	not modelled	99.9	100	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
56	c1uc8B_	Alignment	not modelled	99.9	20	PDB header: biosynthetic protein Chain: B: PDB Molecule: lysine biosynthesis enzyme; PDBTitle: crystal structure of a lysine biosynthesis enzyme, lysx,2 from thermus thermophilus hb8
57	d1ulza1	Alignment	not modelled	99.9	46	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
58	d1ehia2	Alignment	not modelled	99.9	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
59	d2r85a2	Alignment	not modelled	99.9	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
60	d2r7ka2	Alignment	not modelled	99.9	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
61	d2j9ga2	Alignment	not modelled	99.9	100	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
62	d1ulza2	Alignment	not modelled	99.9	56	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
63	d1w96a1	Alignment	not modelled	99.9	30	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
64	d1e4ea2	Alignment	not modelled	99.9	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
65	d1iowa2	Alignment	not modelled	99.9	22	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
66	d1gsoa3	Alignment	not modelled	99.9	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
67	d1w96a2	Alignment	not modelled	99.9	29	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
68	d1uc8a2	Alignment	not modelled	99.9	21	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain
69	c1i7nA_	Alignment	not modelled	99.8	13	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain
70	c1pk8D_	Alignment	not modelled	99.8	12	PDB header: membrane protein Chain: D: PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp
71	c2p0aA_	Alignment	not modelled	99.8	14	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
72	d1w96c1	Alignment	not modelled	99.8	32	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
73	c3ln6A_	Alignment	not modelled	99.8	18	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
74	c1gshA_	Alignment	not modelled	99.8	11	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
75	d1a9xa4	Alignment	not modelled	99.7	20	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
76	c3ln7A_	Alignment	not modelled	99.7	18	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
77	c1z2pX_	Alignment	not modelled	99.7	11	PDB header: transferase Chain: X: PDB Molecule: inositol 1,3,4-trisphosphate 5/6-kinase; PDBTitle: inositol 1,3,4-trisphosphate 5/6-kinase in complex with mg2+/amp-2 pcp/ins(1,3,4)p3
78	d1pk8a2	Alignment	not modelled	99.7	12	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like

					Family: Synapsin C-terminal domain
79	dli7na2	Alignment	not modelled	99.7	12 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
80	c2qb5B	Alignment	not modelled	99.6	12 PDB header: transferase Chain: B: PDB Molecule: inositol-tetrakisphosphate 1-kinase; PDBTitle: crystal structure of human inositol 1,3,4-trisphosphate 5/6-kinase2 (itpk1) in complex with adp and mn2+
81	c2cqyA	Alignment	not modelled	99.5	40 PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: solution structure of b domain from human propionyl-coa2 carboxylase alpha subunit
82	c3t9aA	Alignment	not modelled	99.5	11 PDB header: transferase Chain: A: PDB Molecule: inositol pyrophosphate kinase; PDBTitle: crystal structure of the catalytic domain of human diphosphoinositol2 pentakisphosphate kinase 2 (ppip5k2) in complex with amppnp at ph 7.0
83	dlgsaa2	Alignment	not modelled	99.5	14 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
84	c2r7mA	Alignment	not modelled	99.4	17 PDB header: ligase Chain: A: PDB Molecule: 5-formaminoimidazole-4-carboxamide-1-(beta)-d- PDBTitle: crystal structure of faicar synthetase (purp) from m.2 jannaschii complexed with amp
85	d1kjqaz	Alignment	not modelled	99.2	20 Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
86	d1a9xa3	Alignment	not modelled	99.2	26 Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
87	c1wr2A	Alignment	not modelled	99.1	19 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1789; PDBTitle: crystal structure of ph1788 from pyrococcus horikoshii ot3
88	c2pbzC	Alignment	not modelled	99.0	18 PDB header: ligase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis
89	c2nu9E	Alignment	not modelled	98.9	18 PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
90	c1eucB	Alignment	not modelled	98.7	20 PDB header: ligase Chain: B: PDB Molecule: succinyl-coa synthetase, beta chain; PDBTitle: crystal structure of dephosphorylated pig heart, gtp-2 specific succinyl-coa synthetase
91	d1eucb2	Alignment	not modelled	98.5	20 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain
92	d2pbza2	Alignment	not modelled	98.5	14 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
93	d2nu7b2	Alignment	not modelled	98.5	17 Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain
94	dlgsoa2	Alignment	not modelled	98.3	13 Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
95	c3tinA	Alignment	not modelled	97.5	19 PDB header: ligase Chain: A: PDB Molecule: ttl protein; PDBTitle: tubulin tyrosine ligase
96	dlgsoa1	Alignment	not modelled	97.3	10 Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
97	c3mwdA	Alignment	not modelled	97.3	8 PDB header: transferase Chain: A: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
98	dliowa1	Alignment	not modelled	97.2	27 Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
99	d2jfga1	Alignment	not modelled	97.2	17 Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
100	c3sc6F	Alignment	not modelled	97.1	16 PDB header: oxidoreductase Chain: F: PDB Molecule: ddtp-4-dehydrorhamnose reductase; PDBTitle: 2.65 angstrom resolution crystal structure of ddtp-4-dehydrorhamnose2 reductase (rfbd) from bacillus anthracis str. ames in complex with3 nadp
101	c2q1wC	Alignment	not modelled	97.1	14 PDB header: sugar binding protein Chain: C: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme wbmh in2 complex with nad+
102	c2we7A	Alignment	not modelled	96.8	15 PDB header: oxidoreductase Chain: A: PDB Molecule: xanthine dehydrogenase; PDBTitle: crystal structure of mycobacterium tuberculosis rv0376c2 homologue from mycobacterium smegmatis
103	d1vkza1	Alignment	not modelled	96.7	11 Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: BC C-terminal domain-like
					Fold: NAD(P)-binding Rossmann-fold domains

104	dlbxa_	Alignment	not modelled	96.7	14	Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
105	c2f00A_	Alignment	not modelled	96.6	11	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
106	dle5qa1	Alignment	not modelled	96.6	13	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
107	c3eywA_	Alignment	not modelled	96.6	17	PDB header: transport protein Chain: A: PDB Molecule: c-terminal domain of glutathione-regulated potassium-efflux PDBTitle: crystal structure of the c-terminal domain of e. coli kefc in complex2 with keff
108	dl1ssa_	Alignment	not modelled	96.6	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
109	dlpjqa1	Alignment	not modelled	96.6	10	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Siroheme synthase N-terminal domain-like
110	cle5lA_	Alignment	not modelled	96.6	13	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine reductase; PDBTitle: apo saccharopine reductase from magnaporthe grisea
111	c2g1uA_	Alignment	not modelled	96.6	14	PDB header: transport protein Chain: A: PDB Molecule: hypothetical protein tm1088a; PDBTitle: crystal structure of a putative transport protein (tm1088a) from2 thermotoga maritima at 1.50 a resolution
112	c3l4bG_	Alignment	not modelled	96.6	16	PDB header: transport protein Chain: G: PDB Molecule: trka k+ channel protien tm1088b; PDBTitle: crystal structure of an octomeric two-subunit trka k+ channel ring2 gating assembly, tm1088a:tm1088b, from thermotoga maritima
113	c1z45A_	Alignment	not modelled	96.4	8	PDB header: isomerase Chain: A: PDB Molecule: gal10 bifunctional protein; PDBTitle: crystal structure of the gal10 fusion protein galactose2 mutarotase/udp-galactose 4-epimerase from saccharomyces3 cerevisiae complexed with nad, udp-glucose, and galactose
114	dlp3da1	Alignment	not modelled	96.3	14	Fold: MurCD N-terminal domain Superfamily: MurCD N-terminal domain Family: MurCD N-terminal domain
115	c2yy7B_	Alignment	not modelled	96.3	19	PDB header: oxidoreductase Chain: B: PDB Molecule: l-threonine dehydrogenase; PDBTitle: crystal structure of thermolabile l-threonine dehydrogenase from2 flavobacterium frigidimaridis kuc-1
116	c3ay3C_	Alignment	not modelled	96.2	13	PDB header: oxidoreductase Chain: C: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of glucuronic acid dehydrogeanse from2 chromohalobacter salexigens
117	d2c5aa1	Alignment	not modelled	96.2	22	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
118	c3ic5A_	Alignment	not modelled	96.2	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative saccharopine dehydrogenase; PDBTitle: n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
119	dlhdoa_	Alignment	not modelled	96.1	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
120	c3gpiA_	Alignment	not modelled	96.1	31	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: structure of putative nad-dependent epimerase/dehydratase2 from methylobacillus flagellatus