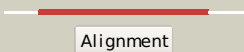

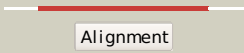







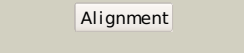

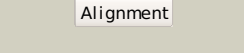

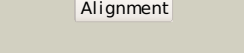



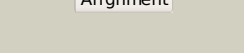

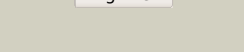












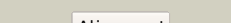
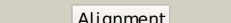


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1gshA_	 Alignment		100.0	19	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5
2	c1kjjA_	 Alignment		100.0	16	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase 2; PDBTitle: crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
3	c1uc8B_	 Alignment		100.0	28	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
4	c1m6vE_	 Alignment		100.0	19	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
5	c3lwbA_	 Alignment		100.0	19	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
6	c3bg5C_	 Alignment		100.0	16	PDB header: ligase Chain: C: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of staphylococcus aureus pyruvate2 carboxylase
7	c3i12A_	 Alignment		100.0	17	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
8	c2dzdB_	 Alignment		100.0	16	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
9	c2dlnA_	 Alignment		100.0	20	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
10	c3se7A_	 Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: vana; PDBTitle: ancient vana
11	c2i80B_	 Alignment		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

12	c2pvpB_	Alignment		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
13	c3g8cB_	Alignment		100.0	17	PDB header: ligase Chain: B: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion
14	c1e4eB_	Alignment		100.0	17	PDB header: ligase Chain: B: PDB Molecule: vancomycin/teicoplanin a-type resistance protein vana; PDBTitle: d-alanyl-d-lactate ligase
15	c3e5nA_	Alignment		100.0	17	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
16	c1ulzA_	Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase n-terminal domain; PDBTitle: crystal structure of the biotin carboxylase subunit of pyruvate2 carboxylase
17	c3tgtB_	Alignment		100.0	19	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: structure of the d-alanine-d-alanine ligase from coxiella burnetii
18	c3ouzA_	Alignment		100.0	16	PDB header: ligase Chain: A: PDB Molecule: biotin carboxylase; PDBTitle: crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
19	c1ehiB_	Alignment		100.0	16	PDB header: ligase Chain: B: PDB Molecule: d-alanine:d-lactate ligase; PDBTitle: d-alanine:d-lactate ligase (lmdl2) of vancomycin-resistant2 leuconostoc mesenteroides
20	c3etjB_	Alignment		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
21	c2zdqA_	Alignment	not modelled	100.0	17	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
22	c2vpqA_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase; PDBTitle: crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
23	c2xd4A_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
24	c3q2oB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole carboxylase, atpase subunit; PDBTitle: crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
25	c2yyaB_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: B: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of gar synthetase from aquifex aeolicus
26	c3lp8A_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine-glycine ligase; PDBTitle: crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
27	c1w96B_	Alignment	not modelled	100.0	17	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
						PDB header: lyase Chain: B: PDB Molecule: phosphoribosylaminoimidazole

28	c3uvzB_	Alignment	not modelled	100.0	15	carboxylase, atpase subunit; PDBTitle: crystal structure of phosphoribosylaminoimidazole carboxylase, atpase2 subunit from burkholderia ambifaria
29	c3ln6A_	Alignment	not modelled	100.0	25	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
30	c2hjaA_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: crystal structure of the bc domain of acc2
31	c3r23B_	Alignment	not modelled	100.0	15	PDB header: ligase Chain: B: PDB Molecule: d-alanine--d-alanine ligase; PDBTitle: crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
32	c1vkzA_	Alignment	not modelled	100.0	14	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
33	c3gidB_	Alignment	not modelled	100.0	17	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
34	c3ln7A_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurilla multocida
35	c3orgA_	Alignment	not modelled	100.0	15	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
36	c2dwcB_	Alignment	not modelled	100.0	19	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
37	c2ip4A_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylamine--glycine ligase; PDBTitle: crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
38	c2gpwC_	Alignment	not modelled	100.0	16	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.
39	c2p0aA_	Alignment	not modelled	100.0	14	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin-3; PDBTitle: the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
40	c3u9sE_	Alignment	not modelled	100.0	19	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
41	c2ys6A_	Alignment	not modelled	100.0	18	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylglycinamide synthetase; PDBTitle: crystal structure of gar synthetase from geobacillus kaustophilus
42	c3k5iB_	Alignment	not modelled	100.0	15	PDB header: lyase Chain: B: PDB Molecule: phosphoribosyl-aminoimidazole carboxylase; PDBTitle: crystal structure of n5-carboxyaminoimidazole synthase from2 aspergillus clavatus in complex with adp and 5-3 aminoimidazole ribonucleotide
43	c3k3pA_	Alignment	not modelled	100.0	13	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
44	c2qb5B_	Alignment	not modelled	100.0	18	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+
45	c1pk8D_	Alignment	not modelled	100.0	13	PDB header: membrane protein Chain: D: PDB Molecule: rat synapsin i; PDBTitle: crystal structure of rat synapsin i c domain complexed to2 ca.atp
46	c3n6rK_	Alignment	not modelled	100.0	17	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
47	c1i7nA_	Alignment	not modelled	100.0	16	PDB header: neuropeptide Chain: A: PDB Molecule: synapsin ii; PDBTitle: crystal structure analysis of the c domain of synapsin ii2 from rat brain
48	c2qk4A_	Alignment	not modelled	100.0	12	PDB header: ligase Chain: A: PDB Molecule: trifunctional purine biosynthetic protein adenosine-3; PDBTitle: human glycinamide ribonucleotide synthetase
49	c2pn1A_	Alignment	not modelled	99.9	17	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 exiguobacterium sp. 255-15 at 2.00 a3 resolution
50	c1gsoA_	Alignment	not modelled	99.9	17	PDB header: ligase Chain: A: PDB Molecule: protein (glycinamide ribonucleotide synthetase); PDBTitle: glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.

51	c2r85B	Alignment	not modelled	99.9	16	PDB header: unknown function Chain: B: PDB Molecule: purp protein pf1517; PDBTitle: crystal structure of purp from pyrococcus furiosus complexed with amp
52	c2z04A	Alignment	not modelled	99.9	14	PDB header: lyase Chain: A: PDB Molecule: phosphoribosylaminoimidazole carboxylase atpase PDBTitle: crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
53	d1uc8a2	Alignment	not modelled	99.9	29	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Lysine biosynthesis enzyme LysX ATP-binding domain
54	c3t9aA	Alignment	not modelled	99.9	18	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
55	c3df7A	Alignment	not modelled	99.9	19	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
56	c1z2pX	Alignment	not modelled	99.9	15	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
57	d1ehia2	Alignment	not modelled	99.9	18	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
58	d1e4ea2	Alignment	not modelled	99.9	19	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
59	d1w96a3	Alignment	not modelled	99.9	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
60	d1iowa2	Alignment	not modelled	99.9	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
61	d2j9ga3	Alignment	not modelled	99.9	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
62	d1kjqaz	Alignment	not modelled	99.9	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
63	d1a9xa5	Alignment	not modelled	99.9	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
64	d3etja3	Alignment	not modelled	99.9	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
65	d1pk8a2	Alignment	not modelled	99.9	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
66	d1vkza3	Alignment	not modelled	99.9	14	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
67	d1ulza3	Alignment	not modelled	99.9	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
68	d1gsaa2	Alignment	not modelled	99.9	23	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: ATP-binding domain of peptide synthetases
69	d1i7na2	Alignment	not modelled	99.9	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Synapsin C-terminal domain
70	d1a9xa6	Alignment	not modelled	99.8	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
71	d2r7ka2	Alignment	not modelled	99.8	13	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
72	d2r85a2	Alignment	not modelled	99.8	17	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
73	d1gsoa3	Alignment	not modelled	99.8	16	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: BC ATP-binding domain-like
74	c2qf7A	Alignment	not modelled	99.8	21	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
75	c2cqyA	Alignment	not modelled	99.0	15	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
76	c2r7mA	Alignment	not modelled	98.9	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
						Fold: PreATP-grasp domain

77	d1gsaa1	Alignment	not modelled	98.7	18	Superfamily: PreATP-grasp domain Family: Prokaryotic glutathione synthetase, N-terminal domain
78	d1uc8a1	Alignment	not modelled	98.5	23	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: Lysine biosynthesis enzyme LysX, N-terminal domain
79	c2pbzC	Alignment	not modelled	98.4	12	PDB header: ligase Chain: C: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis
80	d1a9xa4	Alignment	not modelled	98.4	21	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
81	d1kja2	Alignment	not modelled	98.3	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
82	c3tinA	Alignment	not modelled	98.3	19	PDB header: ligase Chain: A: PDB Molecule: ttl protein; PDBTitle: tubulin tyrosine ligase
83	d1eucb2	Alignment	not modelled	98.0	15	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain
84	c2nu9E	Alignment	not modelled	98.0	23	PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
85	c1wr2A	Alignment	not modelled	97.8	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ph1789; PDBTitle: crystal structure of ph1788 from pyrococcus horikoshii ot3
86	c1eucB	Alignment	not modelled	97.7	18	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
87	d2nu7b2	Alignment	not modelled	97.6	23	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: Succinyl-CoA synthetase, beta-chain, N-terminal domain
88	d1a9xa3	Alignment	not modelled	97.6	25	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
89	d1iowa1	Alignment	not modelled	97.5	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
90	d2pbza2	Alignment	not modelled	97.4	12	Fold: ATP-grasp Superfamily: Glutathione synthetase ATP-binding domain-like Family: PurP ATP-binding domain-like
91	d1ulza2	Alignment	not modelled	96.8	16	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
92	c3mwdA	Alignment	not modelled	96.7	16	PDB header: transferase Chain: A: PDB Molecule: atp-citrate synthase; PDBTitle: truncated human atp-citrate lyase with citrate bound
93	d2j9ga2	Alignment	not modelled	96.6	13	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
94	c2ioaA	Alignment	not modelled	95.8	14	PDB header: ligase, hydrolase Chain: A: PDB Molecule: bifunctional glutathionylspermidine PDBTitle: e. coli bifunctional glutathionylspermidine2 synthetase/amidase incomplex with mg2+ and adp and3 phosphinate inhibitor
95	c3n6xA	Alignment	not modelled	95.4	18	PDB header: ligase Chain: A: PDB Molecule: putative glutathionylspermidine synthase; PDBTitle: crystal structure of a putative glutathionylspermidine synthase2 (mf1a_0391) from methylobacillus flagellatus kt at 2.35 a resolution
96	c3eywA	Alignment	not modelled	95.3	16	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
97	d1e4ea1	Alignment	not modelled	94.7	14	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: D-Alanine ligase N-terminal domain
98	c3m2pD	Alignment	not modelled	94.0	29	PDB header: isomerase Chain: D: PDB Molecule: udp-n-acetylglucosamine 4-epimerase; PDBTitle: the crystal structure of udp-n-acetylglucosamine 4-epimerase2 from bacillus cereus
99	c2pk3B	Alignment	not modelled	93.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: gdp-6-deoxy-d-lyxo-4-hexulose reductase; PDBTitle: crystal structure of a gdp-4-keto-6-deoxy-d-mannose reductase
100	c3icpA	Alignment	not modelled	93.7	23	PDB header: isomerase Chain: A: PDB Molecule: nad-dependent epimerase/dehydratase; PDBTitle: crystal structure of udp-galactose 4-epimerase
101	c2x4gA	Alignment	not modelled	93.7	19	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate-sugar epimerase; PDBTitle: crystal structure of pa4631, a nucleoside-diphosphate-sugar2 epimerase from pseudomonas aeruginosa
102	d1udca	Alignment	not modelled	93.6	29	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases

103	c2issF_	 Alignment	not modelled	93.6	24	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
104	d2a9va1	 Alignment	not modelled	93.5	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
105	d1w96a2	 Alignment	not modelled	93.4	14	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
106	d2blla1	 Alignment	not modelled	93.4	21	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
107	c2p5uC_	 Alignment	not modelled	93.2	26	PDB header: isomerase Chain: C: PDB Molecule: udp-glucose 4-epimerase; PDBTitle: crystal structure of thermus thermophilus hb8 udp-glucose 4-2 epimerase complex with nad
108	d2c5aa1	 Alignment	not modelled	93.1	15	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
109	c2pzlB_	 Alignment	not modelled	93.1	32	PDB header: sugar binding protein Chain: B: PDB Molecule: putative nucleotide sugar epimerase/dehydratase; PDBTitle: crystal structure of the bordetella bronchiseptica enzyme2 wbmj in complex with nad and udp
110	d2f1ka2	 Alignment	not modelled	93.0	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
111	d1lssa_	 Alignment	not modelled	92.5	24	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Potassium channel NAD-binding domain
112	c2jjmH_	 Alignment	not modelled	92.4	22	PDB header: transferase Chain: H: PDB Molecule: glycosyl transferase, group 1 family protein; PDBTitle: crystal structure of a family gt4 glycosyltransferase from2 bacillus anthracis orf ba1558.
113	d1vl0a_	 Alignment	not modelled	92.3	18	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Tyrosine-dependent oxidoreductases
114	c2p6pB_	 Alignment	not modelled	92.2	22	PDB header: transferase Chain: B: PDB Molecule: glycosyl transferase; PDBTitle: x-ray crystal structure of c-c bond-forming dtdp-d-olivose-transferase2 urdgt2
115	d2nv0a1	 Alignment	not modelled	91.9	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
116	d1mv8a2	 Alignment	not modelled	91.8	30	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: 6-phosphogluconate dehydrogenase-like, N-terminal domain
117	c2ggsB_	 Alignment	not modelled	91.8	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 273aa long hypothetical dtdp-4-dehydrorhamnose PDBTitle: crystal structure of hypothetical dtdp-4-dehydrorhamnose2 reductase from sulfolobus tokodaii
118	c3oh8A_	 Alignment	not modelled	91.8	16	PDB header: isomerase Chain: A: PDB Molecule: nucleoside-diphosphate sugar epimerase (sua family); PDBTitle: crystal structure of the nucleoside-diphosphate sugar epimerase from2 corynebacterium glutamicum. northeast structural genomics consortium3 target cgr91
119	c2q1wC_	 Alignment	not modelled	91.6	29	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+
120	c2f1kD_	 Alignment	not modelled	91.4	24	PDB header: oxidoreductase Chain: D: PDB Molecule: prephenate dehydrogenase; PDBTitle: crystal structure of synechocystis arogenate dehydrogenase