Email	l.a.kelley@imperial.ac.uk
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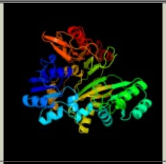
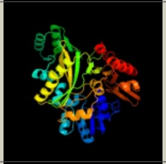
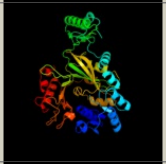
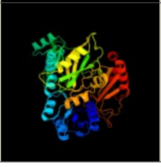
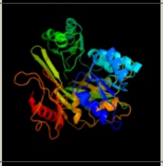
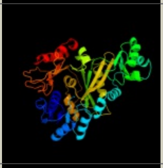
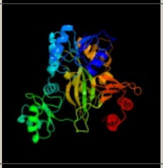
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2xd4A_	Alignment		100.0	54	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** nucleotide-bound structures of bacillus subtilis glycinamide2 ribonucleotide synthetase
2	c2yyaB_	Alignment		100.0	53	**PDB header:**ligase **Chain:** B: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of gar synthetase from aquifex aeolicus
3	c3lp8A_	Alignment		100.0	41	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine-glycine ligase; **PDBTitle:** crystal structure of phosphoribosylamine-glycine ligase from2 ehrlichia chaffeensis
4	c1gsoA_	Alignment		100.0	100	**PDB header:**ligase **Chain:** A: **PDB Molecule:**protein (glycinamide ribonucleotide synthetase); **PDBTitle:** glycinamide ribonucleotide synthetase (gar-syn) from e.2 coli.
5	c2ys6A_	Alignment		100.0	56	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide synthetase; **PDBTitle:** crystal structure of gar synthetase from geobacillus kaustophilus
6	c2qk4A_	Alignment		100.0	50	**PDB header:**ligase **Chain:** A: **PDB Molecule:**trifunctional purine biosynthetic protein adenosine-3; **PDBTitle:** human glycinamide ribonucleotide synthetase
7	c2ip4A_	Alignment		100.0	50	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylamine--glycine ligase; **PDBTitle:** crystal structure of glycinamide ribonucleotide synthetase from2 thermus thermophilus hb8
8	c1vkzA_	Alignment		100.0	35	**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
9	c3ouzA_	Alignment		100.0	15	**PDB header:**ligase **Chain:** A: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase-adp complex from campylobacter2 jejuni
10	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
11	c3g8cB_	Alignment		100.0	14	**PDB header:**ligase **Chain:** B: **PDB Molecule:**biotin carboxylase; **PDBTitle:** crystal structure of biotin carboxylase in complex with2 biotin, bicarbonate, adp and mg ion

12	c2vpqA_	Alignment		100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase; **PDBTitle:** crystal structure of biotin carboxylase from s. aureus2 complexed with amppnp
13	c1kjjA_	Alignment		100.0	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosylglycinamide formyltransferase 2; **PDBTitle:** crystal structure of glycniamide ribonucleotide2 transformylase in complex with mg-atp-gamma-s
14	c2dzdB_	Alignment		100.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
15	c3bg5C_	Alignment		100.0	15	**PDB header:**ligase **Chain:** C: **PDB Molecule:**pyruvate carboxylase; **PDBTitle:** crystal structure of staphylococcus aureus pyruvate2 carboxylase
16	c1m6vE_	Alignment		100.0	20	**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
17	c2hjwA_	Alignment		100.0	13	**PDB header:**ligase **Chain:** A: **PDB Molecule:**acetyl-coa carboxylase 2; **PDBTitle:** crystal structure of the bc domain of acc2
18	c2gpwC_	Alignment		100.0	15	**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.
19	c3gidB_	Alignment		100.0	13	**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
20	c1w96B_	Alignment		100.0	16	**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
21	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)
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	c3u9sE_	Alignment	not modelled	100.0	17	**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
24	c3k5iB_	Alignment	not modelled	100.0	17	**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 aminoimadazole ribonucleotide
25	c3orqA_	Alignment	not modelled	100.0	14	**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
26	c2dwcB_	Alignment	not modelled	100.0	18	**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

27	c3q2oB_	Alignment	not modelled	100.0	14	**PDB header:**lyase **Chain:** B: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase, atpase subunit; **PDBTitle:** crystal structure of purk: n5-carboxyaminoimidazole ribonucleotide2 synthetase
28	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
29	c2z04A_	Alignment	not modelled	100.0	21	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphoribosylaminoimidazole carboxylase atpase **PDBTitle:** crystal structure of phosphoribosylaminoimidazole2 carboxylase atpase subunit from aquifex aeolicus
30	c3i12A_	Alignment	not modelled	100.0	15	**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
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	c2pn1A_	Alignment	not modelled	100.0	19	**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
33	d1vkza3	Alignment	not modelled	100.0	33	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
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 (lmddl2) of vancomycin-resistant2 leuconostoc mesenteroides
35	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
36	c2i80B_	Alignment	not modelled	100.0	12	**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	c1e4eB_	Alignment	not modelled	100.0	15	**PDB header:**ligase **Chain:** B: **PDB Molecule:**vancomycin/teicoplanin a-type resistance protein vana; **PDBTitle:** d-alanyl-d-lacate ligase
38	c2dlnA_	Alignment	not modelled	100.0	16	**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	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 thermophius hb8
40	c3tqtB_	Alignment	not modelled	100.0	13	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** structure of the d-alanine-d-alanine ligase from coxiella burnetii
41	d1gsoa3	Alignment	not modelled	100.0	96	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
42	c3se7A_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**vana; **PDBTitle:** ancient vana
43	c3e5nA_	Alignment	not modelled	100.0	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**d-alanine-d-alanine ligase a; **PDBTitle:** crystal strucutre of d-alanine-d-alanine ligase from2 xanthomonas oryzae pv. oryzae kacc10331
44	d1a9xa6	Alignment	not modelled	100.0	21	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
45	c2qf7A_	Alignment	not modelled	100.0	18	**PDB header:**ligase **Chain:** A: **PDB Molecule:**pyruvate carboxylase protein; **PDBTitle:** crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
46	c2pvpB_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine-d-alanine ligase; **PDBTitle:** crystal structure of d-alanine-d-alanine ligase from helicobacter2 pylori
47	c3df7A_	Alignment	not modelled	100.0	15	**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
48	c2r85B_	Alignment	not modelled	100.0	13	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**purp protein pf1517; **PDBTitle:** crystal structure of purp from pyrococcus furiosus complexed with amp
49	c3r23B_	Alignment	not modelled	100.0	17	**PDB header:**ligase **Chain:** B: **PDB Molecule:**d-alanine--d-alanine ligase; **PDBTitle:** crystal structure of d-alanine--d-alanine ligase from bacillus2 anthracis
50	d1w96a3	Alignment	not modelled	100.0	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
51	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
52	d1ulza3	Alignment	not modelled	100.0	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
53	d2j9ga3	Alignment	not modelled	100.0	19	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
54	c1uc8B_	Alignment	not modelled	100.0	19	**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
55	d1kjqa3	Alignment	not modelled	100.0	14	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
56	d3etja3	Alignment	not modelled	99.9	16	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**BC ATP-binding domain-like
57	d2r7ka2	Alignment	not modelled	99.9	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
58	d2r85a2	Alignment	not modelled	99.9	14	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
59	d1e4ea2	Alignment	not modelled	99.9	19	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
60	d1ehia2	Alignment	not modelled	99.9	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
61	d1iowa2	Alignment	not modelled	99.9	17	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
62	d1uc8a2	Alignment	not modelled	99.9	24	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Lysine biosynthesis enzyme LysX ATP-binding domain
63	c3ln6A_	Alignment	not modelled	99.9	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
64	c1pk8D_	Alignment	not modelled	99.9	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
65	c1i7nA_	Alignment	not modelled	99.9	11	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin ii; **PDBTitle:** crystal structure analysis of the c domain of synapsin ii2 from rat brain
66	c3ln7A_	Alignment	not modelled	99.9	27	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutathione biosynthesis bifunctional protein gshab; **PDBTitle:** crystal structure of a bifunctional glutathione synthetase from2 pasteurella multocida
67	c2p0aA_	Alignment	not modelled	99.9	17	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin-3; **PDBTitle:** the crystal structure of human synapsin iii (syn3) in complex with2 amppnp
68	c1z2pX_	Alignment	not modelled	99.8	10	**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
69	d1gsoa2	Alignment	not modelled	99.8	100	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
70	c1gshA_	Alignment	not modelled	99.8	13	**PDB header:**glutathione biosynthesis ligase **Chain:** A: **PDB Molecule:**glutathione biosynthetic ligase; **PDBTitle:** structure of escherichia coli glutathione synthetase at ph 7.5
71	d1i7na2	Alignment	not modelled	99.8	15	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
72	d1pk8a2	Alignment	not modelled	99.8	12	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
73	c2qb5B_	Alignment	not modelled	99.8	16	**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+
74	d1gsaa2	Alignment	not modelled	99.7	14	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**ATP-binding domain of peptide synthetases
75	d1gsoa1	Alignment	not modelled	99.7	98	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
76	c3t9aA_	Alignment	not modelled	99.7	15	**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
77	c2cqyA_	Alignment	not modelled	99.6	27	**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

78	d1vkza1	Alignment	not modelled	99.5	42	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
79	d1vkza2	Alignment	not modelled	99.5	36	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
80	c2r7mA_	Alignment	not modelled	99.4	13	**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
81	c1wr2A_	Alignment	not modelled	99.4	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein ph1789; **PDBTitle:** crystal structure of ph1788 from pyrococcus horikoshii ot3
82	d1a9xa4	Alignment	not modelled	99.3	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
83	d1kjqa2	Alignment	not modelled	99.2	23	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
84	c2nu9E_	Alignment	not modelled	99.1	24	**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	d1eucb2	Alignment	not modelled	99.0	22	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
86	c1eucB_	Alignment	not modelled	99.0	24	**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	99.0	25	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Succinyl-CoA synthetase, beta-chain, N-terminal domain
88	d1a9xa3	Alignment	not modelled	99.0	15	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
89	c2pbzC_	Alignment	not modelled	98.5	14	**PDB header:**ligase **Chain:** C: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of an imp biosynthesis protein purp from2 thermococcus kodakaraensis
90	d2pbza2	Alignment	not modelled	98.5	14	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**PurP ATP-binding domain-like
91	c3tinA_	Alignment	not modelled	98.3	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ttl protein; **PDBTitle:** tubulin tyrosine ligase
92	c3mwdA_	Alignment	not modelled	98.3	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**atp-citrate synthase; **PDBTitle:** truncated human atp-citrate lyase with citrate bound
93	d1ulza2	Alignment	not modelled	98.1	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
94	d2j9ga2	Alignment	not modelled	98.1	16	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
95	c3ic5A_	Alignment	not modelled	97.7	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative saccharopine dehydrogenase; **PDBTitle:** n-terminal domain of putative saccharopine dehydrogenase from ruegeria2 pomeroyi.
96	d1w96a2	Alignment	not modelled	97.4	17	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**BC N-terminal domain-like
97	c2axqA_	Alignment	not modelled	97.2	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine dehydrogenase; **PDBTitle:** apo histidine-tagged saccharopine dehydrogenase (l-glu2 forming) from saccharomyces cerevisiae
98	c2z2vA_	Alignment	not modelled	97.1	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**hypothetical protein ph1688; **PDBTitle:** crystal structure of l-lysine dehydrogenase from2 hyperthermophilic archaeon pyrococcus horikoshii
99	c1e5lA_	Alignment	not modelled	97.1	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**saccharopine reductase; **PDBTitle:** apo saccharopine reductase from magnaporthe grisea
100	c3nklA_	Alignment	not modelled	97.1	12	**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
101	d1kewa_	Alignment	not modelled	97.0	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
102	c3ezyB_	Alignment	not modelled	96.9	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure of probable dehydrogenase tm_0414 from2 thermotoga maritima
103	c3e9mC_	Alignment	not modelled	96.8	9	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oxidoreductase, gfo/idh/moca family; **PDBTitle:** crystal structure of an oxidoreductase from enterococcus2 faecalis
104	c3bioB	Alignment	not modelled	96.8	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase, gfo/idh/moca family;

104	[illegible]	Alignment	not modelled	96.8	10	**PDBTitle:** crystal structure of oxidoreductase (gfo/idh/moca family member) from2 porphyromonas gingivalis w83
105	c3m2tA_	Alignment	not modelled	96.8	15	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**probable dehydrogenase; **PDBTitle:** the crystal structure of dehydrogenase from chromobacterium2 violaceum
106	c2pk3B_	Alignment	not modelled	96.8	21	**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
107	c3euwB_	Alignment	not modelled	96.7	21	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**myo-inositol dehydrogenase; **PDBTitle:** crystal structure of a myo-inositol dehydrogenase from corynebacterium2 glutamicum atcc 13032
108	d1vl0a_	Alignment	not modelled	96.7	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
109	c2p5uC_	Alignment	not modelled	96.7	13	**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
110	d1e5qa1	Alignment	not modelled	96.6	15	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
111	c3kuxA_	Alignment	not modelled	96.5	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative oxidoreductase; **PDBTitle:** structure of the ypo2259 putative oxidoreductase from yersinia pestis
112	d2dt5a2	Alignment	not modelled	96.5	18	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Transcriptional repressor Rex, C-terminal domain
113	d2jfga1	Alignment	not modelled	96.5	16	**Fold:**MurCD N-terminal domain **Superfamily:**MurCD N-terminal domain **Family:**MurCD N-terminal domain
114	d1n2sa_	Alignment	not modelled	96.5	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Tyrosine-dependent oxidoreductases
115	c2ggsB_	Alignment	not modelled	96.4	23	**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
116	d1w96c1	Alignment	not modelled	96.4	12	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
117	c2dc1A_	Alignment	not modelled	96.4	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**l-aspartate dehydrogenase; **PDBTitle:** crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
118	d1lssa_	Alignment	not modelled	96.4	14	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Potassium channel NAD-binding domain
119	d2j9ga1	Alignment	not modelled	96.4	10	**Fold:**Barrel-sandwich hybrid **Superfamily:**Rudiment single hybrid motif **Family:**BC C-terminal domain-like
120	c3q2kB_	Alignment	not modelled	96.4	12	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**oxidoreductase; **PDBTitle:** crystal structure of the wlba dehydrogenase from bordetella pertussis2 in complex with nadh and udp-glcnaca