



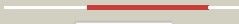









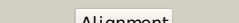

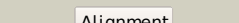



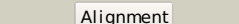







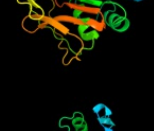




Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1keeH_	 Alignment		100.0	100	PDB header: ligase Chain: H: PDB Molecule: carbamoyl-phosphate synthetase small chain; PDBTitle: inactivation of the amidotransferase activity of carbamoyl phosphate2 synthetase by the antibiotic acivicin
2	d1a9xb1	 Alignment		100.0	100	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Carbamoyl phosphate synthetase, small subunit N-terminal domain Family: Carbamoyl phosphate synthetase, small subunit N-terminal domain
3	d1a9xb2	 Alignment		100.0	99	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
4	c2ywcC_	 Alignment		100.0	28	PDB header: ligase Chain: C: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
5	c1gpmD_	 Alignment		100.0	21	PDB header: transferase (glutamine amidotransferase) Chain: D: PDB Molecule: gmp synthetase; PDBTitle: escherichia coli gmp synthetase complexed with amp and pyrophosphate
6	c2vxob_	 Alignment		100.0	23	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: human gmp synthetase in complex with xmp
7	c3tqiB_	 Alignment		100.0	28	PDB header: ligase Chain: B: PDB Molecule: gmp synthase [glutamine-hydrolyzing]; PDBTitle: structure of the gmp synthase (guaa) from coxiella burnetii
8	d2a9va1	 Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
9	d1gpm2	 Alignment		100.0	21	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
10	d1wl8a1	 Alignment		100.0	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
11	d1qdlb_	 Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)

12	c3r74B_	Alignment		100.0	15	PDB header: lyase, biosynthetic protein Chain: B: PDB Molecule: anthranilate/para-aminobenzoate synthases component i; PDBTitle: crystal structure of 2-amino-2-desoxyisochorismate synthase (ad)2 synthase phze from burkholderia lata 383
13	dli7qb_	Alignment		100.0	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
14	c2vpiA_	Alignment		100.0	24	PDB header: ligase Chain: A: PDB Molecule: gmp synthase; PDBTitle: human gmp synthetase - glutaminase domain
15	c3uowB_	Alignment		100.0	25	PDB header: ligase Chain: B: PDB Molecule: gmp synthetase; PDBTitle: crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
16	clvcnA_	Alignment		100.0	21	PDB header: ligase Chain: A: PDB Molecule: ctp synthetase; PDBTitle: crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
17	dli1qb_	Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
18	cljvnB_	Alignment		100.0	20	PDB header: transferase Chain: B: PDB Molecule: bifunctional histidine biosynthesis protein hishf; PDBTitle: crystal structure of imidazole glycerol phosphate synthase: a tunnel2 through a (beta/alpha)8 barrel joins two active sites
19	dls1ma1	Alignment		100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
20	dlvcoa1	Alignment		100.0	26	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
21	c2ad5B_	Alignment	not modelled	100.0	23	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: mechanisms of feedback regulation and drug resistance of ctp2 synthetases: structure of the e. coli ctps/ctp complex at 2.8-3 angstrom resolution.
22	d2nv0a1	Alignment	not modelled	100.0	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
23	d1k9vf_	Alignment	not modelled	100.0	24	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
24	c3nvaB_	Alignment	not modelled	100.0	22	PDB header: ligase Chain: B: PDB Molecule: ctp synthase; PDBTitle: dimeric form of ctp synthase from sulfolobus solfataricus
25	c2v4uA_	Alignment	not modelled	100.0	21	PDB header: ligase Chain: A: PDB Molecule: ctp synthase 2; PDBTitle: human ctp synthetase 2 - glutaminase domain in complex with2 5-oxo-l-norleucine
26	d1ka9h_	Alignment	not modelled	100.0	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
27	c2w7tA_	Alignment	not modelled	100.0	24	PDB header: ligase Chain: A: PDB Molecule: putative cytidine triphosphate synthase; PDBTitle: trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
28	c3d54D_	Alignment	not modelled	100.0	20	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamidine synthase 1; PDBTitle: structure of purlqs from thermotoga maritima
						PDB header: structural genomics, unknown function

29	c3fijD_	Alignment	not modelled	100.0	20	Chain: D: PDB Molecule: lin1909 protein; PDBTitle: crystal structure of a uncharacterized protein lin1909
30	d1jvna2	Alignment	not modelled	100.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
31	d1q7ra_	Alignment	not modelled	100.0	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
32	c2issF_	Alignment	not modelled	99.9	18	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
33	c1l9xA_	Alignment	not modelled	99.9	20	PDB header: hydrolase Chain: A: PDB Molecule: gamma-glutamyl hydrolase; PDBTitle: structure of gamma-glutamyl hydrolase
34	d1l9xa_	Alignment	not modelled	99.9	20	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
35	c3l83A_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: A: PDB Molecule: glutamine amido transferase; PDBTitle: crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
36	c2ywjA_	Alignment	not modelled	99.9	16	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
37	c3l7nA_	Alignment	not modelled	99.9	25	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
38	d1o1ya_	Alignment	not modelled	99.9	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
39	c2ywdA_	Alignment	not modelled	99.9	17	PDB header: transferase Chain: A: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: crystal structure of glutamine amidotransferase
40	d2abwa1	Alignment	not modelled	99.9	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
41	d1t3ta2	Alignment	not modelled	99.9	15	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
42	d2ghra1	Alignment	not modelled	99.8	12	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: HTS-like
43	c2h2wA_	Alignment	not modelled	99.7	14	PDB header: transferase Chain: A: PDB Molecule: homoserine o-succinyltransferase; PDBTitle: crystal structure of homoserine o-succinyltransferase (ec 2.3.1.46)2 (homoserine o-transsuccinylase) (hts) (tm0881) from thermotoga3 maritima at 2.52 a resolution
44	c1t3tA_	Alignment	not modelled	98.5	16	PDB header: ligase Chain: A: PDB Molecule: phosphoribosylformylglycinamide synthase; PDBTitle: structure of formylglycinamide synthetase
45	c1sy7B_	Alignment	not modelled	98.1	15	PDB header: oxidoreductase Chain: B: PDB Molecule: catalase 1; PDBTitle: crystal structure of the catalase-1 from neurospora crassa, native2 structure at 1.75a resolution.
46	c3uk7B_	Alignment	not modelled	98.0	27	PDB header: transferase Chain: B: PDB Molecule: class i glutamine amidotransferase-like domain-containing PDBTitle: crystal structure of arabidopsis thaliana dj-1d
47	d1vhqa_	Alignment	not modelled	97.9	11	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: DJ-1/Pfpl
48	c3l3bA_	Alignment	not modelled	97.8	12	PDB header: biosynthetic protein Chain: A: PDB Molecule: es1 family protein; PDBTitle: crystal structure of isoprenoid biosynthesis protein with2 amidotransferase-like domain from ehrlichia chaffeensis at 1.90a3 resolution
49	d1sy7a1	Alignment	not modelled	97.8	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
50	c3fseB_	Alignment	not modelled	97.6	14	PDB header: hydrolase Chain: B: PDB Molecule: two-domain protein containing dj-1/thij/pfpi-like and PDBTitle: crystal structure of a two-domain protein containing dj-1/thij/pfpi-2 like and ferritin-like domains (ava_4496) from anabaena variabilis3 atcc 29413 at 1.90 a resolution
51	c3cneD_	Alignment	not modelled	97.5	19	PDB header: hydrolase Chain: D: PDB Molecule: putative protease i; PDBTitle: crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
52	c3kkIA_	Alignment	not modelled	97.5	18	PDB header: hydrolase Chain: A: PDB Molecule: probable chaperone protein hsp33; PDBTitle: crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
53	d1p80a1	Alignment	not modelled	97.4	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Catalase, C-terminal domain
54	c3n7tA_	Alignment	not modelled	97.3	15	PDB header: protein binding Chain: A: PDB Molecule: macrophage binding protein; PDBTitle: crystal structure of a macrophage binding protein from coccidioides2 immitis

81	c2f00A_	Alignment	not modelled	91.0	20	Chain: A: PDB Molecule: udp-n-acetylmuramate--l-alanine ligase; PDBTitle: escherichia coli murc
82	c1j6uA_	Alignment	not modelled	90.9	12	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-alanine ligase murc; PDBTitle: crystal structure of udp-n-acetylmuramate-alanine ligase2 murc (tm0231) from thermotoga maritima at 2.3 a resolution
83	d1fmfa_	Alignment	not modelled	90.6	18	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
84	c3en0A_	Alignment	not modelled	89.8	18	PDB header: hydrolase Chain: A: PDB Molecule: cyanophycinase; PDBTitle: the structure of cyanophycinase
85	c3mgkA_	Alignment	not modelled	89.5	23	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: intracellular protease/amidase related enzyme PDBTitle: crystal structure of probable protease/amidase from2 clostridium acetobutylicum atcc 824
86	c2dc1A_	Alignment	not modelled	89.1	15	PDB header: oxidoreductase Chain: A: PDB Molecule: l-aspartate dehydrogenase; PDBTitle: crystal structure of l-aspartate dehydrogenase from2 hyperthermophilic archaeon archaeoglobus fulgidus
87	c3hn7A_	Alignment	not modelled	88.6	19	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate-l-alanine ligase; PDBTitle: crystal structure of a murein peptide ligase mpl (psyc_0032) from2 psychrobacter arcticus 273-4 at 1.65 a resolution
88	c2zkiH_	Alignment	not modelled	87.7	20	PDB header: transcription Chain: H: PDB Molecule: 199aa long hypothetical trp repressor binding PDBTitle: crystal structure of hypothetical trp repressor binding2 protein from sul folobus tokodaii (st0872)
89	c3r6mD_	Alignment	not modelled	87.7	22	PDB header: hydrolase Chain: D: PDB Molecule: yeaz, resuscitation promoting factor; PDBTitle: crystal structure of vibrio parahaemolyticus yeaz
90	d1t0ba_	Alignment	not modelled	87.2	9	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: ThuA-like
91	d1b74a1	Alignment	not modelled	87.1	26	Fold: ATC-like Superfamily: Aspartate/glutamate racemase Family: Aspartate/glutamate racemase
92	c2dlnA_	Alignment	not modelled	87.1	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
93	c3rhtB_	Alignment	not modelled	85.8	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: (gatase1)-like protein; PDBTitle: crystal structure of type 1 glutamine amidotransferase (gatase1)-like2 protein from planctomyces limnophilus
94	c1y80A_	Alignment	not modelled	85.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: predicted cobalamin binding protein; PDBTitle: structure of a corrinoid (factor iim)-binding protein from2 moorella thermoacetica
95	c2rjoA_	Alignment	not modelled	85.6	17	PDB header: signaling protein Chain: A: PDB Molecule: twin-arginine translocation pathway signal protein; PDBTitle: crystal structure of twin-arginine translocation pathway signal2 protein from burkholderia phytofirmans
96	c4a26B_	Alignment	not modelled	85.5	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative c-1-tetrahydrofolate synthase, cytoplasmic; PDBTitle: the crystal structure of leishmania major n5,n10-2 methylenetetrahydrofolate dehydrogenase/cyclohydrolase
97	c1xeaD_	Alignment	not modelled	85.2	24	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of a gfo/ldh/moca family oxidoreductase2 from vibrio cholerae
98	d1ccwa_	Alignment	not modelled	85.2	15	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
99	c2pv7B_	Alignment	not modelled	83.8	15	PDB header: isomerase, oxidoreductase Chain: B: PDB Molecule: t-protein [includes: chorismate mutase (ec 5.4.99.5) (cm) PDBTitle: crystal structure of chorismate mutase / prephenate dehydrogenase2 (tyra) (1574749) from haemophilus influenzae rd at 2.00 a resolution
100	c3gfgB_	Alignment	not modelled	83.4	9	PDB header: oxidoreductase Chain: B: PDB Molecule: uncharacterized oxidoreductase yvaa; PDBTitle: structure of putative oxidoreductase yvaa from bacillus subtilis in2 triclinic form
101	c1b74A_	Alignment	not modelled	83.4	24	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: glutamate racemase from aquifex pyrophilus
102	c3eagA_	Alignment	not modelled	82.8	16	PDB header: ligase Chain: A: PDB Molecule: udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-meso- PDBTitle: the crystal structure of udp-n-acetylmuramate:l-alanyl-gamma-d-2 glutamyl-meso-diaminopimelate ligase (mpl) from neisseria3 meningitidis
103	d1a9xa3	Alignment	not modelled	81.8	16	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
104	c3evnA_	Alignment	not modelled	80.7	13	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of putative oxidoreductase from streptococcus2 agalactiae 2603v/r
						Fold: Molybdenum cofactor biosynthesis proteins

105	d1xi8a3	Alignment	not modelled	80.2	12	Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
106	c1vjta_	Alignment	not modelled	80.2	20	PDB header: hydrolase Chain: A: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of alpha-glucosidase (tm0752) from thermotoga2 maritima at 2.50 a resolution
107	c3er6D_	Alignment	not modelled	80.2	15	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: putative transcriptional regulator protein; PDBTitle: crystal structure of a putative transcriptional regulator2 protein from vibrio parahaemolyticus
108	d7reqa2	Alignment	not modelled	80.1	14	Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
109	c3sozC_	Alignment	not modelled	80.0	17	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: cytoplasmic protein stm1381; PDBTitle: cytoplasmic protein stm1381 from salmonella typhimurium lt2
110	c3db2C_	Alignment	not modelled	79.0	14	PDB header: oxidoreductase Chain: C: PDB Molecule: putative nadph-dependent oxidoreductase; PDBTitle: crystal structure of a putative nadph-dependent oxidoreductase2 (dhaf_2064) from desulfitobacterium hafniense dcb-2 at 1.70 a3 resolution
111	c3e18A_	Alignment	not modelled	78.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of nad-binding protein from listeria innocua
112	c2dzdB_	Alignment	not modelled	78.3	14	PDB header: ligase Chain: B: PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of the biotin carboxylase domain of2 pyruvate carboxylase
113	c2ho3D_	Alignment	not modelled	78.1	13	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, gfo/ldh/moca family; PDBTitle: crystal structure of oxidoreductase, gfo/ldh/moca family from2 streptococcus pneumoniae
114	d1mkza_	Alignment	not modelled	78.0	10	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
115	c3dhyC_	Alignment	not modelled	77.9	13	PDB header: hydrolase Chain: C: PDB Molecule: adenosylhomocysteinase; PDBTitle: crystal structures of mycobacterium tuberculosis s-adenosyl-l-2 homocysteine hydrolase in ternary complex with substrate and3 inhibitors
116	c2jfnA_	Alignment	not modelled	77.6	24	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of escherichia coli glutamate racemase2 in complex with l-glutamate and activator udp-murac-ala
117	d1tjya_	Alignment	not modelled	77.3	16	Fold: Periplasmic binding protein-like I Superfamily: Periplasmic binding protein-like I Family: L-arabinose binding protein-like
118	c2r47C_	Alignment	not modelled	76.7	26	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: uncharacterized protein mth_862; PDBTitle: crystal structure of mth_862 protein of unknown function from2 methanothermobacter thermautotrophicus
119	c3o1hB_	Alignment	not modelled	76.7	15	PDB header: signaling protein Chain: B: PDB Molecule: periplasmic protein tort; PDBTitle: crystal structure of the tors sensor domain - tort complex in the2 presence of tmao
120	c2dwuA_	Alignment	not modelled	75.9	20	PDB header: isomerase Chain: A: PDB Molecule: glutamate racemase; PDBTitle: crystal structure of glutamate racemase isoform race1 from bacillus2 anthracis