Email	l.a.kelley@imperial.ac.uk
Description	Q5H776
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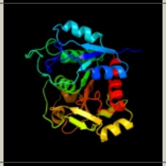
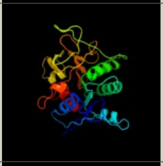
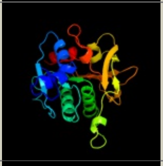
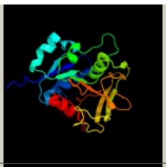
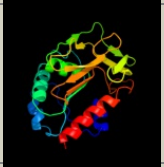
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3fijD_	Alignment		100.0	38	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**lin1909 protein; **PDBTitle:** crystal structure of a uncharacterized protein lin1909
2	c1l9xA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**gamma-glutamyl hydrolase; **PDBTitle:** structure of gamma-glutamyl hydrolase
3	d1l9xa_	Alignment		100.0	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
4	c2v4uA_	Alignment		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
5	d1s1ma1	Alignment		100.0	25	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
6	c2ad5B_	Alignment		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.
7	c3nvaB_	Alignment		100.0	24	**PDB header:**ligase **Chain:** B: **PDB Molecule:**ctp synthase; **PDBTitle:** dimeric form of ctp synthase from sulfolobus solfataricus
8	c1vcnA_	Alignment		100.0	26	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ctp synthetase; **PDBTitle:** crystal structure of t.th. hb8 ctp synthetase complex with sulfate2 anion
9	d1vcoa1	Alignment		100.0	24	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
10	c2w7tA_	Alignment		100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**putative cytidine triphosphate synthase; **PDBTitle:** trypanosoma brucei ctps - glutaminase domain with bound2 acivicin
11	d2a9va1	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)

12	c1gpmD_	Alignment		100.0	18	**PDB header:**transferase (glutamine amidotransferase) **Chain:** D: **PDB Molecule:**gmp synthetase; **PDBTitle:** escherichia coli gmp synthetase complexed with amp and pyrophosphate
13	d1gpma2	Alignment		100.0	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
14	c3d54D_	Alignment		100.0	18	**PDB header:**ligase **Chain:** D: **PDB Molecule:**phosphoribosylformylglycinamidine synthase 1; **PDBTitle:** stucture of purlqs from thermotoga maritima
15	c2ywcC_	Alignment		100.0	22	**PDB header:**ligase **Chain:** C: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** crystal structure of gmp synthetase from thermus thermophilus in2 complex with xmp
16	d1wl8a1	Alignment		100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
17	d1qdlb_	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
18	d1a9xb2	Alignment		100.0	27	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
19	c1keeH_	Alignment		100.0	27	**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
20	d1i7qb_	Alignment		100.0	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
21	c2vxoB_	Alignment	not modelled	100.0	20	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** human gmp synthetase in complex with xmp
22	d1q7ra_	Alignment	not modelled	100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
23	c3tqiB_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthase [glutamine-hydrolyzing]; **PDBTitle:** structure of the gmp synthase (guaa) from coxiella burnetii
24	d1i1qb_	Alignment	not modelled	100.0	23	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
25	c2vpiA_	Alignment	not modelled	100.0	21	**PDB header:**ligase **Chain:** A: **PDB Molecule:**gmp synthase; **PDBTitle:** human gmp synthetase - glutaminase domain
26	d2nv0a1	Alignment	not modelled	100.0	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
27	c3uowB_	Alignment	not modelled	100.0	19	**PDB header:**ligase **Chain:** B: **PDB Molecule:**gmp synthetase; **PDBTitle:** crystal structure of pf10_0123, a gmp synthetase from plasmodium2 falciparum
28	c2ywdA_	Alignment	not modelled	100.0	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of glutamine amidotransferase
29	d1jvna2	Alignment	not modelled	100.0	21	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like

						Family: Class I glutamine amidotransferases (GAT)
30	c2ywjA_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** crystal structure of uncharacterized conserved protein from2 methanocaldococcus jannaschii
31	d2abwa1	Alignment	not modelled	99.9	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
32	c2issF_	Alignment	not modelled	99.9	20	**PDB header:**lyase, transferase **Chain:** F: **PDB Molecule:**glutamine amidotransferase subunit pdxt; **PDBTitle:** structure of the plp synthase holoenzyme from thermotoga maritima
33	d1k9vf_	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
34	c1jvnB_	Alignment	not modelled	99.9	23	**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
35	d1ka9h_	Alignment	not modelled	99.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
36	c3l7nA_	Alignment	not modelled	99.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
37	c3r74B_	Alignment	not modelled	99.9	16	**PDB header:**lyase, biosynthetic protein **Chain:** B: **PDB Molecule:**anthranilate/para-aminobenzoate synthases component i; **PDBTitle:** crystal structure of 2-amino-2-desoxyisochorismate synthase (adic)2 synthase phze from burkholderia lata 383
38	c3l83A_	Alignment	not modelled	99.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
39	d1t3ta2	Alignment	not modelled	99.9	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
40	d1o1ya_	Alignment	not modelled	99.9	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
41	d2ghra1	Alignment	not modelled	99.7	18	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**HTS-like
42	c2h2wA_	Alignment	not modelled	99.7	20	**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
43	c1t3tA_	Alignment	not modelled	98.9	17	**PDB header:**ligase **Chain:** A: **PDB Molecule:**phosphoribosylformylglycinamidine synthase; **PDBTitle:** structure of formylglycinamide synthetase
44	c3l4eA_	Alignment	not modelled	98.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**uncharacterized peptidase lmo0363; **PDBTitle:** 1.5a crystal structure of a putative peptidase e protein from listeria2 monocytogenes egd-e
45	c1sy7B_	Alignment	not modelled	97.6	14	**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	97.0	21	**PDB header:**transferase **Chain:** B: **PDB Molecule:**class i glutamine amidotransferase-like domain-containing **PDBTitle:** crystal structure of arabidopsis thaliana dj-1d
47	d1sy7a1	Alignment	not modelled	96.9	17	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
48	d1p80a1	Alignment	not modelled	96.9	15	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Catalase, C-terminal domain
49	d1fyea_	Alignment	not modelled	96.8	14	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Aspartyl dipeptidase PepE
50	d1qvwa_	Alignment	not modelled	96.7	11	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
51	c3l3bA_	Alignment	not modelled	96.7	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
52	c3fseB_	Alignment	not modelled	96.7	19	**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
53	c3n7tA_	Alignment	not modelled	96.6	18	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**macrophage binding protein; **PDBTitle:** crystal structure of a macrophage binding protein from coccidioides2 immitis
						Fold: Flavodoxin-like

54	d1vhqa_	Alignment	not modelled	96.6	23	**Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
55	c3cneD_	Alignment	not modelled	96.4	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**putative protease i; **PDBTitle:** crystal structure of the putative protease i from bacteroides2 thetaiotaomicron
56	d1u9ca_	Alignment	not modelled	96.3	19	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
57	c1p81A_	Alignment	not modelled	96.3	16	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**catalase hpii; **PDBTitle:** crystal structure of the d181e variant of catalase hpii2 from e. coli
58	c3en0A_	Alignment	not modelled	96.2	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**cyanophycinase; **PDBTitle:** the structure of cyanophycinase
59	d1n57a_	Alignment	not modelled	95.1	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
60	c3kklA_	Alignment	not modelled	94.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable chaperone protein hsp33; **PDBTitle:** crystal structure of functionally unknown hsp33 from2 saccharomyces cerevisiae
61	d1xi8a3	Alignment	not modelled	94.8	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
62	d1oi4a1	Alignment	not modelled	94.2	31	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
63	c3f5dA_	Alignment	not modelled	93.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**protein ydea; **PDBTitle:** crystal structure of a protein of unknown function from2 bacillus subtilis
64	d1p5fa_	Alignment	not modelled	93.6	27	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
65	d1g2ia_	Alignment	not modelled	93.5	27	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
66	c3efeC_	Alignment	not modelled	93.2	27	**PDB header:**chaperone **Chain:** C: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** the crystal structure of the thij/pfpi family protein from bacillus2 anthracis
67	c2an1D_	Alignment	not modelled	91.9	23	**PDB header:**transferase **Chain:** D: **PDB Molecule:**putative kinase; **PDBTitle:** structural genomics, the crystal structure of a putative kinase from2 salmonella typhimurim lt2
68	d1wu2a3	Alignment	not modelled	91.0	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
69	d1uz5a3	Alignment	not modelled	90.6	24	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
70	c3pfnB_	Alignment	not modelled	90.6	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nad kinase; **PDBTitle:** crystal structure of human nad kinase
71	c3bhnA_	Alignment	not modelled	90.2	18	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thij/pfpi domain protein; **PDBTitle:** crystal structure of a dj-1/pfpi-like protein (shew_2856) from2 shewanella loihica pv-4 at 1.76 a resolution
72	c3ej6D_	Alignment	not modelled	90.2	13	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**catalase-3; **PDBTitle:** neurospora crassa catalase-3 crystal structure
73	d2fexa1	Alignment	not modelled	90.2	20	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
74	d2ftsa3	Alignment	not modelled	90.1	25	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
75	d2ab0a1	Alignment	not modelled	89.7	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**DJ-1/PfpI
76	c1uz5A_	Alignment	not modelled	89.4	23	**PDB header:**molybdopterin biosynthesis **Chain:** A: **PDB Molecule:**402aa long hypothetical molybdopterin **PDBTitle:** the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
77	c2nqqA_	Alignment	not modelled	89.2	16	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis protein moea; **PDBTitle:** moea r137q
78	c3nooB_	Alignment	not modelled	89.2	30	**PDB header:**lyase **Chain:** B: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of c101a isocyanide hydratase from pseudomonas2 fluorescens
79	c2fu3A_	Alignment	not modelled	88.6	30	**PDB header:**biosynthetic protein/structural protein **Chain:** A: **PDB Molecule:**gephyrin; **PDBTitle:** crystal structure of gephyrin e-domain
80	c3ot1B_	Alignment	not modelled	88.3	21	**PDB header:**structural genomics **Chain:** B: **PDB Molecule:**4-methyl-5(b-hydroxyethyl)-thiazole monophosphate **PDBTitle:** crystal structure of vc2308 protein
						PDB header:hydrolase

81	c2vrnA_	Alignment	not modelled	88.0	21	**Chain:** A: **PDB Molecule:**protease i; **PDBTitle:** the structure of the stress response protein dr1199 from2 deinococcus radiodurans: a member of the dj-1 superfamily
82	d1mkza_	Alignment	not modelled	86.7	15	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
83	d1y5ea1	Alignment	not modelled	86.6	11	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
84	c3mgkA_	Alignment	not modelled	86.5	22	**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
85	c3ewnA_	Alignment	not modelled	86.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**thij/pfpi family protein; **PDBTitle:** crystal structure of a thij/pfpi family protein from pseudomonas2 syringae
86	c2pjkA_	Alignment	not modelled	83.5	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**178aa long hypothetical molybdenum cofactor **PDBTitle:** structure of hypothetical molybdenum cofactor biosynthesis2 protein b from sulfolobus tokodaii
87	c3g85A_	Alignment	not modelled	82.5	9	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator (laci family); **PDBTitle:** crystal structure of laci family transcription regulator from2 clostridium acetobutylicum
88	c3afoB_	Alignment	not modelled	82.1	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nadh kinase pos5; **PDBTitle:** crystal structure of yeast nadh kinase complexed with nadh
89	c3graA_	Alignment	not modelled	81.3	20	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, arac family; **PDBTitle:** crystal structure of arac family transcriptional regulator from2 pseudomonas putida
90	c3dzvB_	Alignment	not modelled	81.2	17	**PDB header:**transferase **Chain:** B: **PDB Molecule:**4-methyl-5-(beta-hydroxyethyl)thiazole kinase; **PDBTitle:** crystal structure of 4-methyl-5-(beta-hydroxyethyl)thiazole2 kinase (np_816404.1) from enterococcus faecalis v583 at3 2.57 a resolution
91	c3d8tB_	Alignment	not modelled	80.2	15	**PDB header:**lyase **Chain:** B: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** thermus thermophilus uroporphyrinogen iii synthase
92	c2is8A_	Alignment	not modelled	79.1	18	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**molybdopterin biosynthesis enzyme, moab; **PDBTitle:** crystal structure of the molybdopterin biosynthesis enzyme moab2 (ttha0341) from thermus theromophilus hb8
93	d2f7wa1	Alignment	not modelled	77.4	17	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
94	c1wu2B_	Alignment	not modelled	76.0	19	**PDB header:**structural genomics,biosynthetic protein **Chain:** B: **PDB Molecule:**molybdopterin biosynthesis moea protein; **PDBTitle:** crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikoshii ot3
95	c2zkiH_	Alignment	not modelled	75.6	16	**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)
96	d1sc6a2	Alignment	not modelled	74.6	18	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
97	c1zuwA_	Alignment	not modelled	74.3	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutamate racemase 1; **PDBTitle:** crystal structure of b.subtilis glutamate racemase (race) with d-glu
98	d1wd7a_	Alignment	not modelled	73.2	22	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
99	c3er6D_	Alignment	not modelled	73.2	20	**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
100	c2zuuA_	Alignment	not modelled	72.5	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**lacto-n-biose phosphorylase; **PDBTitle:** crystal structure of galacto-n-biose/lacto-n-biose i phosphorylase in2 complex with glcnac
101	c2higA_	Alignment	not modelled	71.3	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**6-phospho-1-fructokinase; **PDBTitle:** crystal structure of phosphofructokinase apoenzyme from trypanosoma2 brucei.
102	c2d0iC_	Alignment	not modelled	70.3	13	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**dehydrogenase; **PDBTitle:** crystal structure ph0520 protein from pyrococcus horikoshii ot3
103	d1vpea_	Alignment	not modelled	68.4	17	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
104	d1jlja_	Alignment	not modelled	68.1	19	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
						PDB header:transferase

105	c3s40C_	Alignment	not modelled	66.7	17	**Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** the crystal structure of a diacylglycerol kinases from bacillus2 anthracis str. sterne
106	d1gdha2	Alignment	not modelled	65.5	8	**Fold:**Flavodoxin-like **Superfamily:**Formate/glycerate dehydrogenase catalytic domain-like **Family:**Formate/glycerate dehydrogenases, substrate-binding domain
107	d2nqra3	Alignment	not modelled	65.0	16	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MoeA central domain-like
108	d1uuya_	Alignment	not modelled	64.2	13	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
109	c2duwA_	Alignment	not modelled	63.4	16	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**putative coa-binding protein; **PDBTitle:** solution structure of putative coa-binding protein of2 klebsiella pneumoniae
110	d16pka_	Alignment	not modelled	62.8	13	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
111	d1phpa_	Alignment	not modelled	62.1	15	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase
112	d1u0ta_	Alignment	not modelled	61.9	10	**Fold:**NAD kinase/diacylglycerol kinase-like **Superfamily:**NAD kinase/diacylglycerol kinase-like **Family:**NAD kinase-like
113	d2g2ca1	Alignment	not modelled	60.1	8	**Fold:**Molybdenum cofactor biosynthesis proteins **Superfamily:**Molybdenum cofactor biosynthesis proteins **Family:**MogA-like
114	c3n7uD_	Alignment	not modelled	59.7	14	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**formate dehydrogenase; **PDBTitle:** nad-dependent formate dehydrogenase from higher-plant arabidopsis2 thaliana in complex with nad and azide
115	c3k9cA_	Alignment	not modelled	59.3	27	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**transcriptional regulator, laci family protein; **PDBTitle:** crystal structure of laci transcriptional regulator from rhodococcus2 species.
116	c1ybaC_	Alignment	not modelled	58.9	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase; **PDBTitle:** the active form of phosphoglycerate dehydrogenase
117	c1jr2A_	Alignment	not modelled	58.1	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**uroporphyrinogen-iii synthase; **PDBTitle:** structure of uroporphyrinogen iii synthase
118	d1jr2a_	Alignment	not modelled	58.1	16	**Fold:**HemD-like **Superfamily:**HemD-like **Family:**HemD-like
119	c3q3vA_	Alignment	not modelled	57.2	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoglycerate kinase; **PDBTitle:** crystal structure of phosphoglycerate kinase from campylobacter2 jejuni.
120	d1fw8a_	Alignment	not modelled	56.9	16	**Fold:**Phosphoglycerate kinase **Superfamily:**Phosphoglycerate kinase **Family:**Phosphoglycerate kinase