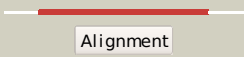

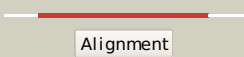

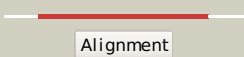

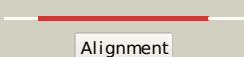

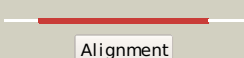

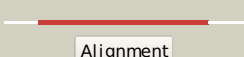

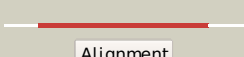

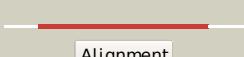

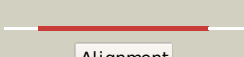

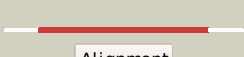











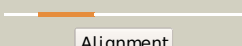

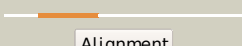

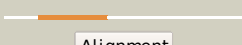

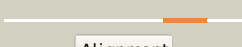









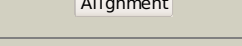
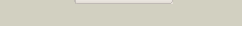
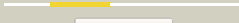



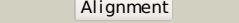



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ocda1	 Alignment		100.0	69	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
2	c2d6fA_	 Alignment		100.0	31	PDB header: ligase/rna Chain: A: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
3	c1zq1B_	 Alignment		100.0	30	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
4	d1zq1a2	 Alignment		100.0	30	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
5	c1wnfA_	 Alignment		100.0	36	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: crystal structure of ph0066 from pyrococcus horikoshii
6	d2d6fa2	 Alignment		100.0	30	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
7	d1nnsa_	 Alignment		100.0	25	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
8	d1wsaa_	 Alignment		100.0	24	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
9	c2wltA_	 Alignment		100.0	24	PDB header: hydrolase Chain: A: PDB Molecule: l-asparaginase; PDBTitle: the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution
10	d1agxa_	 Alignment		100.0	20	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
11	d1o7ja_	 Alignment		100.0	20	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase

12	d4pgaa_		Alignment		100.0	20	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
13	c3nxkE_		Alignment		100.0	23	PDB header: hydrolase Chain: E: PDB Molecule: cytoplasmic l-asparaginase; PDBTitle: crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
14	c1uz5A_		Alignment		91.0	22	PDB header: molybdopterin biosynthesis Chain: A: PDB Molecule: 402aa long hypothetical molybdopterin PDBTitle: the crystal structure of molybdopterin biosynthesis moea2 protein from pyrococcus horikosii
15	d1gtza_		Alignment		90.2	18	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
16	c2nqqA_		Alignment		86.8	17	PDB header: biosynthetic protein Chain: A: PDB Molecule: molybdopterin biosynthesis protein moea; PDBTitle: moea r137q
17	d1uz5a3		Alignment		86.3	21	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
18	d1gqoa_		Alignment		83.4	14	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
19	c2rjoA_		Alignment		81.2	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
20	c2q62A_		Alignment		79.0	12	PDB header: flavoprotein Chain: A: PDB Molecule: arsh; PDBTitle: crystal structure of arsh from sinorhizobium meliloti
21	d2ftsa3		Alignment	not modelled	76.6	11	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
22	d2nqra3		Alignment	not modelled	74.7	16	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
23	c2pr7A_		Alignment	not modelled	74.5	19	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
24	c3s81A_		Alignment	not modelled	73.6	15	PDB header: isomerase Chain: A: PDB Molecule: putative aspartate racemase; PDBTitle: crystal structure of putative aspartate racemase from salmonella2 typhimurium
25	d1wu2a3		Alignment	not modelled	72.8	20	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
26	c1powA_		Alignment	not modelled	72.2	13	PDB header: oxidoreductase(oxygen as acceptor) Chain: A: PDB Molecule: pyruvate oxidase; PDBTitle: the refined structures of a stabilized mutant and of wild-type2 pyruvate oxidase from lactobacillus plantarum
27	d1goxa_		Alignment	not modelled	71.3	21	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
28	c3d54D_		Alignment	not modelled	70.9	25	PDB header: ligase Chain: D: PDB Molecule: phosphoribosylformylglycinamide synthase 1; PDBTitle: stucture of purlqs from thermotoga maritima

29	d1tuba1		Alignment	not modelled	70.1	13	Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
30	c2fu3A		Alignment	not modelled	68.1	9	PDB header: biosynthetic protein/structural protein Chain: A: PDB Molecule: gephyrin; PDBTitle: crystal structure of gephyrin e-domain
31	c3ffsC		Alignment	not modelled	67.3	5	PDB header: oxidoreductase Chain: C: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: the crystal structure of cryptosporidium parvum inosine-5'-2 monophosphate dehydrogenase
32	c3o8nA		Alignment	not modelled	67.2	16	PDB header: transferase Chain: A: PDB Molecule: 6-phosphofructokinase, muscle type; PDBTitle: structure of phosphofructokinase from rabbit skeletal muscle
33	d2ioja1		Alignment	not modelled	66.7	32	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: DRTGG domain
34	d1h05a		Alignment	not modelled	66.2	24	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
35	d1tb3a1		Alignment	not modelled	65.6	14	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
36	c1wu2B		Alignment	not modelled	65.3	18	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
37	d1uqra		Alignment	not modelled	64.2	18	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinase dehydratase Family: Type II 3-dehydroquinase dehydratase
38	c3n8kG		Alignment	not modelled	63.0	24	PDB header: lyase Chain: G: PDB Molecule: 3-dehydroquinase dehydratase; PDBTitle: type ii dehydroquinase from mycobacterium tuberculosis complexed with2 citrazinic acid
39	c2cdh1		Alignment	not modelled	62.0	20	PDB header: transferase Chain: 1: PDB Molecule: enoyl reductase; PDBTitle: architecture of the thermomyces lanuginosus fungal fatty2 acid synthase at 5 angstrom resolution.
40	c2z6jB		Alignment	not modelled	61.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: trans-2-enoyl-acp reductase ii; PDBTitle: crystal structure of s. pneumoniae enoyl-acyl carrier2 protein reductase (fabk) in complex with an inhibitor
41	d1dxya2		Alignment	not modelled	61.5	18	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
42	d1slma1		Alignment	not modelled	60.8	13	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
43	c2hmcA		Alignment	not modelled	60.0	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: the crystal structure of dihydrodipicolinate synthase dapa from2 agrobacterium tumefaciens
44	d1q7ra		Alignment	not modelled	57.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
45	c1jcnA		Alignment	not modelled	56.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: inosine monophosphate dehydrogenase i; PDBTitle: binary complex of human type-i inosine monophosphate dehydrogenase2 with 6-cl-imp
46	c3o1hB		Alignment	not modelled	55.6	11	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
47	d1fuia2		Alignment	not modelled	55.6	9	Fold: Fucl/AraA N-terminal and middle domains Superfamily: Fucl/AraA N-terminal and middle domains Family: L-fucose isomerase, N-terminal and second domains
48	d1ka9h		Alignment	not modelled	55.0	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
49	c2zskA		Alignment	not modelled	54.8	15	PDB header: unknown function Chain: A: PDB Molecule: 226aa long hypothetical aspartate racemase; PDBTitle: crystal structure of ph1733, an aspartate racemase2 homologue, from pyrococcus horikoshii ot3
50	c3brsA		Alignment	not modelled	54.2	13	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein/laci transcriptional regulator; PDBTitle: crystal structure of sugar transporter from clostridium2 phytofermentans
51	c2dgdD		Alignment	not modelled	53.6	12	PDB header: lyase Chain: D: PDB Molecule: 223aa long hypothetical arylmalonate decarboxylase; PDBTitle: crystal structure of st0656, a function unknown protein from2 sulfolobus tokodaii
52	c3mc3A		Alignment	not modelled	53.0	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dsre/dsrf-like family protein; PDBTitle: crystal structure of dsre/dsrf-like family protein (np_342589.1) from2 sulfolobus solfataricus at 1.49 a resolution
53	c2e77B		Alignment	not modelled	52.4	9	PDB header: oxidoreductase Chain: B: PDB Molecule: lactate oxidase; PDBTitle: crystal structure of l-lactate oxidase with pyruvate

					complex
54	d1ccwa_	Alignment	not modelled	52.2	17 Fold: Flavodoxin-like Superfamily: Cobalamin (vitamin B12)-binding domain Family: Cobalamin (vitamin B12)-binding domain
55	d1xi8a3	Alignment	not modelled	52.0	18 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MoeA central domain-like
56	d1jlja_	Alignment	not modelled	51.6	18 Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
57	d1i1qb_	Alignment	not modelled	51.4	14 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
58	c3bo9B	Alignment	not modelled	51.3	18 PDB header: oxidoreductase Chain: B: PDB Molecule: putative nitroalkan dioxygenase; PDBTitle: crystal structure of putative nitroalkan dioxygenase (tm0800) from2 thermotoga maritima at 2.71 a resolution
59	c2rduA_	Alignment	not modelled	50.9	16 PDB header: oxidoreductase Chain: A: PDB Molecule: hydroxyacid oxidase 1; PDBTitle: crystal structure of human glycolate oxidase in complex with2 glyoxylate
60	c3lloA_	Alignment	not modelled	50.5	18 PDB header: motor protein Chain: A: PDB Molecule: prestin; PDBTitle: crystal structure of the stas domain of motor protein prestin (anion2 transporter slc26a5)
61	c1jscA_	Alignment	not modelled	50.4	22 PDB header: lyase Chain: A: PDB Molecule: acetoxyhydroxy-acid synthase; PDBTitle: crystal structure of the catalytic subunit of yeast2 acetoxyhydroxyacid synthase: a target for herbicidal3 inhibitors
62	d2nv0a1	Alignment	not modelled	50.1	25 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
63	c3lwzC_	Alignment	not modelled	50.0	14 PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: 1.65 angstrom resolution crystal structure of type ii 3-2 dehydroquinate dehydratase (aroq) from yersinia pestis
64	d2csua3	Alignment	not modelled	49.8	15 Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
65	c2qs0A_	Alignment	not modelled	49.7	25 PDB header: biosynthetic protein Chain: A: PDB Molecule: quinolinate synthetase a; PDBTitle: quinolinate synthase from pyrococcus furiosus
66	d1wl8a1	Alignment	not modelled	49.5	14 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
67	c2xecD_	Alignment	not modelled	49.4	16 PDB header: isomerase Chain: D: PDB Molecule: putative maleate isomerase; PDBTitle: nocardia farcinica maleate cis-trans isomerase bound to2 tris
68	d1vcoa1	Alignment	not modelled	49.4	20 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
69	d2c4va1	Alignment	not modelled	49.0	33 Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
70	c3khjE_	Alignment	not modelled	48.9	15 PDB header: oxidoreductase Chain: E: PDB Molecule: inosine-5-monophosphate dehydrogenase; PDBTitle: c. parvum inosine monophosphate dehydrogenase bound by inhibitor c64
71	d2csua1	Alignment	not modelled	48.8	12 Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: CoA-binding domain
72	c3nurA_	Alignment	not modelled	48.5	7 PDB header: hydrolase Chain: A: PDB Molecule: amidohydrolase; PDBTitle: crystal structure of a putative amidohydrolase from staphylococcus2 aureus
73	c2opiB_	Alignment	not modelled	48.5	9 PDB header: lyase Chain: B: PDB Molecule: l-fucose-1-phosphate aldolase; PDBTitle: crystal structure of l-fucose-1-phosphate aldolase from bacteroides2 thetaiotaomicron
74	d1t3ta2	Alignment	not modelled	48.0	18 Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
75	c2r94B_	Alignment	not modelled	48.0	17 PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxy-(6-phospho-)gluconate aldolase; PDBTitle: crystal structure of kd(p)ga from t.tenax
76	d2btoa1	Alignment	not modelled	47.9	15 Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
77	d2hbva1	Alignment	not modelled	47.1	8 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: PP1699/LP2961-like
78	c2iexA_	Alignment	not modelled	47.0	18 PDB header: lyase Chain: A: PDB Molecule: dihydroxynaphthoic acid synthetase; PDBTitle: crystal structure of dihydroxynaphthoic acid synthetase (gk2873) from2 geobacillus kaustophilus hta426
79	d1j4aa2	Alignment	not modelled	46.7	18 Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain

80	d1q8fa_	Alignment	not modelled	46.5	20	Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase
81	d1r61a_	Alignment	not modelled	45.4	10	Fold: The "swivelling" beta/beta/alpha domain Superfamily: Putative cyclase Family: Putative cyclase
82	d1gpma2	Alignment	not modelled	44.4	16	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: Class I glutamine amidotransferases (GAT)
83	c3ojcD_	Alignment	not modelled	43.8	9	PDB header: isomerase Chain: D: PDB Molecule: putative aspartate/glutamate racemase; PDBTitle: crystal structure of a putative asp/glu racemase from yersinia pestis
84	c2uygF_	Alignment	not modelled	43.2	19	PDB header: lyase Chain: F: PDB Molecule: 3-dehydroquinase dehydratase; PDBTitle: crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
85	d1uuya_	Alignment	not modelled	43.1	13	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
86	d1y5ea1	Alignment	not modelled	42.0	22	Fold: Molybdenum cofactor biosynthesis proteins Superfamily: Molybdenum cofactor biosynthesis proteins Family: MogA-like
87	c2obnA_	Alignment	not modelled	41.8	24	PDB header: unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf1611 family protein (ava_3511) from anabaena2 variabilis atcc 29413 at 2.30 a resolution
88	c2fzvC_	Alignment	not modelled	41.5	11	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: putative arsenical resistance protein; PDBTitle: crystal structure of an apo form of a flavin-binding protein from2 shigella flexneri
89	c2v1bC_	Alignment	not modelled	41.4	14	PDB header: lyase Chain: C: PDB Molecule: arylmalonate decarboxylase; PDBTitle: structure of unliganded arylmalonate decarboxylase
90	c1ozhD_	Alignment	not modelled	41.0	16	PDB header: lyase Chain: D: PDB Molecule: acetolactate synthase, catabolic; PDBTitle: the crystal structure of klebsiella pneumoniae acetolactate2 synthase with enzyme-bound cofactor and with an unusual3 intermediate.
91	c2issF_	Alignment	not modelled	40.9	27	PDB header: lyase, transferase Chain: F: PDB Molecule: glutamine amidotransferase subunit pdxt; PDBTitle: structure of the plp synthase holoenzyme from thermotoga maritima
92	d2dl1a2	Alignment	not modelled	40.8	25	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
93	c3l7nA_	Alignment	not modelled	39.6	18	PDB header: transferase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of smu.1228c
94	c2a7rD_	Alignment	not modelled	39.3	10	PDB header: oxidoreductase Chain: D: PDB Molecule: gmp reductase 2; PDBTitle: crystal structure of human guanosine monophosphate2 reductase 2 (gmpr2)
95	d1p4ca_	Alignment	not modelled	38.9	16	Fold: TIM beta/alpha-barrel Superfamily: FMN-linked oxidoreductases Family: FMN-linked oxidoreductases
96	d1wzua1	Alignment	not modelled	38.9	35	Fold: NadA-like Superfamily: NadA-like Family: NadA-like
97	d1q6za1	Alignment	not modelled	38.4	12	Fold: DHS-like NAD/FAD-binding domain Superfamily: DHS-like NAD/FAD-binding domain Family: Pyruvate oxidase and decarboxylase, middle domain
98	c3kipU_	Alignment	not modelled	38.1	24	PDB header: lyase Chain: U: PDB Molecule: 3-dehydroquinase, type ii; PDBTitle: crystal structure of type-ii 3-dehydroquinase from c. albicans
99	c3g1wB_	Alignment	not modelled	37.8	13	PDB header: transport protein Chain: B: PDB Molecule: sugar abc transporter; PDBTitle: crystal structure of sugar abc transporter (sugar-binding protein)2 from bacillus halodurans
100	c2a7nA_	Alignment	not modelled	37.5	16	PDB header: oxidoreductase Chain: A: PDB Molecule: l(+)-mandelate dehydrogenase; PDBTitle: crystal structure of the g81a mutant of the active chimera of (s)-2 mandelate dehydrogenase
101	d1jcna1	Alignment	not modelled	37.2	16	Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
102	c1brwB_	Alignment	not modelled	37.2	17	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
103	d1mx3a2	Alignment	not modelled	37.1	18	Fold: Flavodoxin-like Superfamily: Formate/glycerate dehydrogenase catalytic domain-like Family: Formate/glycerate dehydrogenases, substrate-binding domain
104	c2htmB_	Alignment	not modelled	37.0	16	PDB header: biosynthetic protein Chain: B: PDB Molecule: thiazole biosynthesis protein thig; PDBTitle: crystal structure of ttha0676 from thermus thermophilus hb8
105	d1k9vf_	Alignment	not modelled	36.9	23	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like

					Family: Class I glutamine amidotransferases (GAT)
106	dlvmea1	Alignment	not modelled	36.2	17 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Flavodoxin-related
107	dlqwga	Alignment	not modelled	36.2	25 Fold: TIM beta/alpha-barrel Superfamily: (2r)-phospho-3-sulfolactate synthase ComA Family: (2r)-phospho-3-sulfolactate synthase ComA
108	dleepa	Alignment	not modelled	36.1	9 Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
109	c2qneA	Alignment	not modelled	36.1	21 PDB header: transferase Chain: A: PDB Molecule: putative methyltransferase; PDBTitle: crystal structure of putative methyltransferase (zp_00558420.1) from2 desulfitobacterium hafniense y51 at 2.30 a resolution
110	dlisla2	Alignment	not modelled	36.0	22 Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
111	c1keeH	Alignment	not modelled	35.5	17 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
112	c3gdwA	Alignment	not modelled	35.5	22 PDB header: structural genomics, unknown function Chain: A: PDB Molecule: sigma-54 interaction domain protein; PDBTitle: crystal structure of sigma-54 interaction domain protein from2 enterococcus faecalis
113	dltubb1	Alignment	not modelled	35.2	17 Fold: Tubulin nucleotide-binding domain-like Superfamily: Tubulin nucleotide-binding domain-like Family: Tubulin, GTPase domain
114	c3bezC	Alignment	not modelled	35.2	28 PDB header: hydrolase Chain: C: PDB Molecule: protease 4; PDBTitle: crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
115	dljr1a1	Alignment	not modelled	34.9	18 Fold: TIM beta/alpha-barrel Superfamily: Inosine monophosphate dehydrogenase (IMPDH) Family: Inosine monophosphate dehydrogenase (IMPDH)
116	c2ax3A	Alignment	not modelled	34.6	19 PDB header: transferase Chain: A: PDB Molecule: hypothetical protein tm0922; PDBTitle: crystal structure of a putative carbohydrate kinase (tm0922) from2 thermotoga maritima msb8 at 2.25 a resolution
117	dlim5a	Alignment	not modelled	34.0	16 Fold: Isochorismatase-like hydrolases Superfamily: Isochorismatase-like hydrolases Family: Isochorismatase-like hydrolases
118	c3k2qA	Alignment	not modelled	33.6	17 PDB header: transferase Chain: A: PDB Molecule: pyrophosphate-dependent phosphofructokinase; PDBTitle: crystal structure of pyrophosphate-dependent2 phosphofructokinase from marinobacter aquaeolei, northeast3 structural genomics consortium target mqr88
119	c3ij6A	Alignment	not modelled	33.6	13 PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized metal-dependent hydrolase; PDBTitle: crystal structure of an uncharacterized metal-dependent2 hydrolase from lactobacillus acidophilus
120	dlezra	Alignment	not modelled	33.5	12 Fold: Nucleoside hydrolase Superfamily: Nucleoside hydrolase Family: Nucleoside hydrolase