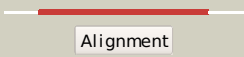
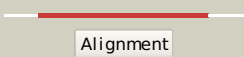
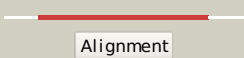
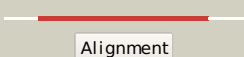
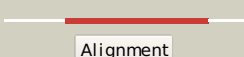
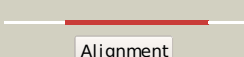
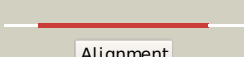
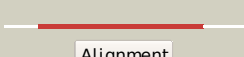
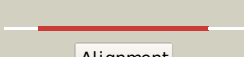
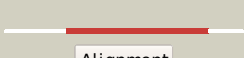
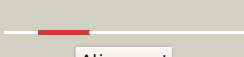


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1fpyE_	 Alignment		100.0	24	PDB header: ligase Chain: E: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from salmonella2 typhimurium with inhibitor phosphinothricin
2	c3ng0A_	 Alignment		100.0	22	PDB header: ligase Chain: A: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of glutamine synthetase from synechocystis sp. pcc2 6803
3	c1htoB_	 Alignment		100.0	24	PDB header: ligase Chain: B: PDB Molecule: glutamine synthetase; PDBTitle: crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
4	c2j9iL_	 Alignment		100.0	22	PDB header: ligase Chain: L: PDB Molecule: glutamate-ammonia ligase domain-containing PDBTitle: lengsin is a survivor of an ancient family of class i2 glutamine synthetases in eukaryotes that has undergone3 evolutionary re-engineering for a tissue-specific role4 in the vertebrate eye lens.
5	d1f52a2	 Alignment		100.0	24	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
6	d2bvca2	 Alignment		100.0	24	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
7	c2qc8J_	 Alignment		100.0	20	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
8	c2d3aJ_	 Alignment		100.0	16	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
9	c3fkyD_	 Alignment		100.0	20	PDB header: ligase Chain: D: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the glutamine synthetase gln1deltan182 from the yeast saccharomyces cerevisiae
10	c3o6xC_	 Alignment		100.0	22	PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
11	d1f52a1	 Alignment		99.9	19	Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain

12	d2bvca1	Alignment		99.9	23	Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
13	c1tt4B_	Alignment		99.0	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative cytoplasmic protein; PDBTitle: structure of np459575, a predicted glutathione synthase from2 salmonella typhimurium
14	d1tt4a_	Alignment		99.0	19	Fold: Glutamine synthetase/guano kinase Superfamily: Glutamine synthetase/guano kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
15	d1r8ga_	Alignment		98.9	18	Fold: Glutamine synthetase/guano kinase Superfamily: Glutamine synthetase/guano kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
16	c2gwcE_	Alignment		97.9	16	PDB header: ligase Chain: E: PDB Molecule: glutamate cysteine ligase; PDBTitle: crystal structure of plant glutamate cysteine ligase in complex with a2 transition state analogue
17	d1u8sa2	Alignment		32.8	9	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
18	c2jy5A_	Alignment		24.7	24	PDB header: signaling protein Chain: A: PDB Molecule: ubiquilin-1; PDBTitle: nmr structure of ubiquilin 1 uba domain
19	d1owxa_	Alignment		20.2	9	Fold: Ferredoxin-like Superfamily: RNA-binding domain, RBD Family: Canonical RBD
20	d1nxia_	Alignment		18.5	17	Fold: Ferredoxin-like Superfamily: Hypothetical protein VC0424 Family: Hypothetical protein VC0424
21	c3ln7A_	Alignment	not modelled	14.5	18	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurilla multocida
22	d1neka3	Alignment	not modelled	13.6	16	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
23	c3ns5B_	Alignment	not modelled	13.1	6	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: crystal structure of the rna recognition motif of yeast eif3b residues2 76-161
24	c2vxeA_	Alignment	not modelled	10.4	17	PDB header: transcription Chain: A: PDB Molecule: cg10686-pa; PDBTitle: solution structure of the lsm domain of drosophila2 melanogaster tral (trailer hitch)
25	c2k7rA_	Alignment	not modelled	10.4	14	PDB header: replication Chain: A: PDB Molecule: primosomal protein dna1; PDBTitle: n-terminal domain of the bacillus subtilis helicase-loading2 protein dna1
26	c3htnA_	Alignment	not modelled	9.9	12	PDB header: metal binding protein Chain: A: PDB Molecule: putative dna binding protein; PDBTitle: crystal structure of a putative dna binding protein (bt_1116) from2 bacteroides thetaiotaomicron vpi-5482 at 1.50 a resolution
27	d2z1ea1	Alignment	not modelled	9.5	17	Fold: Bacillus chorismate mutase-like Superfamily: PurM N-terminal domain-like Family: PurM N-terminal domain-like

28	c3dcgF	Alignment	not modelled	9.5	50	PDB header: ligase/viral protein Chain: F: PDB Molecule: virion infectivity factor; PDBTitle: crystal structure of the hiv vif bc-box in complex with human elonginb2 and elonginc
29	c2zuuA	Alignment	not modelled	9.2	20	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
30	c3bdkB	Alignment	not modelled	9.0	14	PDB header: lyase Chain: B: PDB Molecule: d-mannonate dehydratase; PDBTitle: crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
31	d2bs2a3	Alignment	not modelled	8.9	25	Fold: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Superfamily: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain Family: Succinate dehydrogenase/fumarate reductase flavoprotein, catalytic domain
32	c3ns6B	Alignment	not modelled	8.9	6	PDB header: translation Chain: B: PDB Molecule: eukaryotic translation initiation factor 3 subunit b; PDBTitle: crystal structure of hte rna recognition motif of yeast eif3b residues2 76-170
33	c1jqoA	Alignment	not modelled	8.8	17	PDB header: lyase Chain: A: PDB Molecule: phosphoenolpyruvate carboxylase; PDBTitle: crystal structure of c4-form phosphoenolpyruvate carboxylase from2 maize
34	d1jqoa	Alignment	not modelled	8.8	17	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase
35	c1nvpD	Alignment	not modelled	7.4	15	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia gamma chain; PDBTitle: human tfiia/tbp/dna complex
36	d2vxfa1	Alignment	not modelled	7.1	21	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: LSM14 N-terminal domain-like
37	d1z10a2	Alignment	not modelled	6.8	18	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
38	d2rgfa	Alignment	not modelled	6.7	20	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
39	d1prtc1	Alignment	not modelled	6.7	27	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
40	c3re3B	Alignment	not modelled	6.1	15	PDB header: lyase Chain: B: PDB Molecule: 2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; PDBTitle: crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
41	c3it5B	Alignment	not modelled	6.0	33	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
42	d1prtb1	Alignment	not modelled	5.8	20	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
43	c1nh2D	Alignment	not modelled	5.8	22	PDB header: transcription/dna Chain: D: PDB Molecule: transcription initiation factor iia small chain; PDBTitle: crystal structure of a yeast tfiia/tbp/dna complex
44	d2o3la1	Alignment	not modelled	5.7	16	Fold: Left-handed superhelix Superfamily: BH3980-like Family: BH3980-like
45	d1ihma	Alignment	not modelled	5.6	19	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Positive stranded ssRNA viruses Family: Caliciviridae-like VP
46	d1xv2a	Alignment	not modelled	5.6	28	Fold: AF0104/ALDC/Ptd012-like Superfamily: AF0104/ALDC/Ptd012-like Family: Alpha-acetolactate decarboxylase-like
47	d1eeja2	Alignment	not modelled	5.5	10	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
48	c2qw5B	Alignment	not modelled	5.5	13	PDB header: isomerase Chain: B: PDB Molecule: xylose isomerase-like tim barrel; PDBTitle: crystal structure of a putative sugar phosphate isomerase/epimerase2 (ava4194) from anabaena variabilis atcc 29413 at 1.78 a resolution
49	d2v0ea1	Alignment	not modelled	5.4	13	Fold: GYF/BRK domain-like Superfamily: BRK domain-like Family: BRK domain-like
50	d1t3ba2	Alignment	not modelled	5.1	14	Fold: Cystatin-like Superfamily: DsbC/DsbG N-terminal domain-like Family: DsbC/DsbG N-terminal domain-like
51	c1u8sB	Alignment	not modelled	5.1	7	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
52	d1jqna	Alignment	not modelled	5.1	21	Fold: TIM beta/alpha-barrel Superfamily: Phosphoenolpyruvate/pyruvate domain Family: Phosphoenolpyruvate carboxylase