





















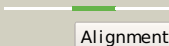

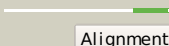

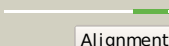




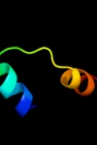
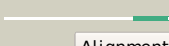

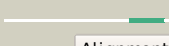

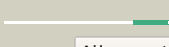


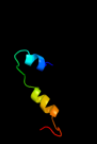
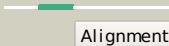

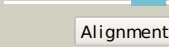
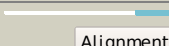

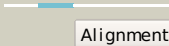
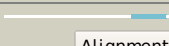




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2d32a1	 Alignment		100.0	99	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase
2	c3nztA	 Alignment		100.0	35	PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase; PDBTitle: 2.0 angstrom crystal structure of glutamate--cysteine ligase (gsha)2 from francisella tularensis in complex with amp
3	c3ln6A	 Alignment		100.0	32	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 streptococcus agalactiae
4	c3ln7A	 Alignment		100.0	27	PDB header: ligase Chain: A: PDB Molecule: glutathione biosynthesis bifunctional protein gshab; PDBTitle: crystal structure of a bifunctional glutathione synthetase from2 pasteurilla multocida
5	d1r8ga	 Alignment		100.0	19	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
6	d1tt4a	 Alignment		100.0	19	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamate-cysteine ligase family 2 (GCS2)
7	c1tt4B	 Alignment		100.0	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
8	c2gwcE	 Alignment		99.8	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
9	c3lvwA	 Alignment		81.1	15	PDB header: ligase Chain: A: PDB Molecule: glutamate--cysteine ligase; PDBTitle: glutathione-inhibited scgcl
10	d2bvca2	 Alignment		62.1	15	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Glutamine synthetase catalytic domain
11	c3lgaA	 Alignment		58.3	10	PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase cecr1; PDBTitle: crystal structure of human adenosine deaminase growth factor, 2 adenosine deaminase type 2 (ada2) complexed with transition state3 analogue, coformycin

12	dlf52a2	 Alignment		57.7	18	Fold: Glutamine synthetase/guano kinase Superfamily: Glutamine synthetase/guano kinase Family: Glutamine synthetase catalytic domain
13	dljv1a_	 Alignment		53.0	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
14	c2yqsA_	 Alignment		50.2	28	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of uridine-diphospho-n-acetylglucosamine2 pyrophosphorylase from candida albicans, in the product-binding form
15	clhtoB_	 Alignment		49.5	15	PDB header: ligase Chain: B: PDB Molecule: glutamine synthetase; PDBTitle: crystallographic structure of a relaxed glutamine synthetase from2 mycobacterium tuberculosis
16	d2ixoa1	 Alignment		49.3	21	Fold: PTPA-like Superfamily: PTPA-like Family: PTPA-like
17	c3oc9A_	 Alignment		47.1	20	PDB header: transferase Chain: A: PDB Molecule: udp-n-acetylglucosamine pyrophosphorylase; PDBTitle: crystal structure of putative udp-n-acetylglucosamine2 pyrophosphorylase from entamoeba histolytica
18	dlgsua2	 Alignment		43.5	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
19	dlvm8a_	 Alignment		43.3	24	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
20	c2g62A_	 Alignment		42.0	24	PDB header: hydrolase activator Chain: A: PDB Molecule: protein phosphatase 2a, regulatory subunit b' (pr 53); PDBTitle: crystal structure of human ptpa
21	d2d6fc3	 Alignment	not modelled	41.0	15	Fold: Glutamine synthetase/guano kinase Superfamily: Glutamine synthetase/guano kinase Family: GatB/GatE catalytic domain-like
22	dl1tja_	 Alignment	not modelled	39.6	30	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
23	c3lq7B_	 Alignment	not modelled	39.3	33	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: crystal structure of glutathione s-transferase from2 agrobacterium tumefaciens str. c58
24	dlrpxa_	 Alignment	not modelled	35.9	26	Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phosphate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
25	dlzqlc3	 Alignment	not modelled	34.5	19	Fold: Glutamine synthetase/guano kinase Superfamily: Glutamine synthetase/guano kinase Family: GatB/GatE catalytic domain-like
26	d2f2ab2	 Alignment	not modelled	34.1	15	Fold: Glutamine synthetase/guano kinase Superfamily: Glutamine synthetase/guano kinase Family: GatB/GatE catalytic domain-like
27	c1tu8A_	 Alignment	not modelled	32.2	30	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase 2; PDBTitle: structure of onchocerca volvulus pi-class glutathione s-2 transferase with its kompetitive inhibitor s-hexyl-gsh
28	dl1tu7a2	 Alignment	not modelled	30.1	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
29	c3llkA_	 Alignment	not modelled	28.8	14	PDB header: oxidoreductase Chain: A: PDB Molecule: sulfhydryl oxidase 1;

					PDBTitle: sulfhydryl oxidase fragment of human qsox1
30	d2ixma1	Alignment	not modelled	28.6	24 Fold: PTPA-like Superfamily: PTPA-like Family: PTPA-like
31	d1f52a1	Alignment	not modelled	27.5	17 Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
32	c3h0mE_	Alignment	not modelled	27.2	26 PDB header: ligase Chain: E: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase PDBTitle: structure of trna-dependent amidotransferase gatcab from2 aquifex aeolicus
33	d2bvca1	Alignment	not modelled	27.0	22 Fold: beta-Grasp (ubiquitin-like) Superfamily: Glutamine synthetase, N-terminal domain Family: Glutamine synthetase, N-terminal domain
34	c2g5iB_	Alignment	not modelled	26.9	15 PDB header: ligase Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase PDBTitle: structure of trna-dependent amidotransferase gatcab2 complexed with adp-alf4
35	c3rysA_	Alignment	not modelled	26.8	19 PDB header: hydrolase Chain: A: PDB Molecule: adenosine deaminase 1; PDBTitle: the crystal structure of adenine deaminase (aaur1117) from2 arthrobacter aurescens
36	d2cvda2	Alignment	not modelled	26.5	29 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
37	d2ixna1	Alignment	not modelled	26.4	30 Fold: PTPA-like Superfamily: PTPA-like Family: PTPA-like
38	d1okta2	Alignment	not modelled	26.2	32 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
39	c2qm2B_	Alignment	not modelled	25.6	56 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative hopj type iii effector protein; PDBTitle: putative hopj type iii effector protein from vibrio parahaemolyticus
40	d2fnoa2	Alignment	not modelled	25.0	30 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
41	c3al0B_	Alignment	not modelled	23.9	26 PDB header: ligase/rna Chain: B: PDB Molecule: aspartyl/glutamyl-trna(asn/gln) amidotransferase subunit b; PDBTitle: crystal structure of the glutamine transamidosome from thermotoga2 maritima in the glutamylation state.
42	c2fnoB_	Alignment	not modelled	23.4	30 PDB header: transferase Chain: B: PDB Molecule: agr_pat_752p; PDBTitle: crystal structure of a glutathione s-transferase (atu5508) from2 agrobacterium tumefaciens str. c58 at 2.00 a resolution
43	c1zq1D_	Alignment	not modelled	23.3	19 PDB header: lyase Chain: D: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit e; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
44	c2jfkD_	Alignment	not modelled	23.2	14 PDB header: transferase Chain: D: PDB Molecule: fatty acid synthase; PDBTitle: structure of the mat domain of human fas with malonyl-coa
45	d1k3ya2	Alignment	not modelled	23.1	36 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
46	c2d6fC_	Alignment	not modelled	21.8	15 PDB header: ligase/rna Chain: C: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit e; PDBTitle: crystal structure of glu-trna(gln) amidotransferase in the2 complex with trna(gln)
47	d2amxa1	Alignment	not modelled	21.3	19 Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
48	d1ml6a2	Alignment	not modelled	21.0	32 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
49	d1oe8a2	Alignment	not modelled	20.8	36 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
50	c2d3aj_	Alignment	not modelled	20.3	44 PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the maize glutamine synthetase2 complexed with adp and methionine sulfoximine phosphate
51	d2a2ra2	Alignment	not modelled	20.2	29 Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
52	d1tqxa_	Alignment	not modelled	20.0	21 Fold: TIM beta/alpha-barrel Superfamily: Ribulose-phoshate binding barrel Family: D-ribulose-5-phosphate 3-epimerase
53	c3ogzA_	Alignment	not modelled	19.7	22 PDB header: transferase Chain: A: PDB Molecule: udp-sugar pyrophosphorylase; PDBTitle: protein structure of usp from l. major in apo-form
54	d2icya2	Alignment	not modelled	19.0	39 Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
					Fold: OsmC-like

55	d1qwia_	Alignment	not modelled	18.7	11	Superfamily: OsmC-like Family: Ohr/OsmC resistance proteins
56	d1o9aa1	Alignment	not modelled	18.5	35	Fold: Fnl-like domain Superfamily: Fnl-like domain Family: Fibronectin type I module
57	d1glqa2	Alignment	not modelled	18.2	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
58	c3js3C_	Alignment	not modelled	17.9	22	PDB header: lyase Chain: C: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystal structure of type i 3-dehydroquinate dehydratase (arod) from2 clostridium difficile with covalent reaction intermediate
59	c1nwdC_	Alignment	not modelled	17.2	56	PDB header: binding protein/hydrolase Chain: C: PDB Molecule: glutamate decarboxylase; PDBTitle: solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
60	c1nwdB_	Alignment	not modelled	17.2	56	PDB header: binding protein/hydrolase Chain: B: PDB Molecule: glutamate decarboxylase; PDBTitle: solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
61	d2c4ja2	Alignment	not modelled	17.0	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
62	c3o6xC_	Alignment	not modelled	16.9	13	PDB header: ligase Chain: C: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of the type iii glutamine synthetase from2 bacteroides fragilis
63	d1xfba1	Alignment	not modelled	16.6	34	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
64	c1m0uB_	Alignment	not modelled	16.6	25	PDB header: transferase Chain: B: PDB Molecule: gst2 gene product; PDBTitle: crystal structure of the drosophila glutathione s-2 transferase-2 in complex with glutathione
65	d1w5fa2	Alignment	not modelled	16.3	14	Fold: Bacillus chorismate mutase-like Superfamily: Tubulin C-terminal domain-like Family: Tubulin, C-terminal domain
66	d1xw6a2	Alignment	not modelled	15.9	21	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
67	c3inpA_	Alignment	not modelled	15.9	23	PDB header: isomerase Chain: A: PDB Molecule: d-ribulose-phosphate 3-epimerase; PDBTitle: 2.05 angstrom resolution crystal structure of d-ribulose-phosphate 3-2 epimerase from francisella tularensis.
68	c1c72A_	Alignment	not modelled	15.8	24	PDB header: transferase Chain: A: PDB Molecule: protein (glutathione s-transferase); PDBTitle: tyr115, gln165 and trp209 contribute to the 1,2-epoxy-3-(p-2 nitrophenoxy)propane conjugating activities of glutathione3 s-transferase cgstm1-1
69	d2gsta2	Alignment	not modelled	15.6	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
70	c3gwnA_	Alignment	not modelled	15.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: probable fad-linked sulfhydryl oxidase r596; PDBTitle: crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
71	c1oktA_	Alignment	not modelled	15.3	32	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: x-ray structure of glutathione s-transferase from the2 malarial parasite plasmodium falciparum
72	d1pd212	Alignment	not modelled	14.8	32	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
73	d1a4ma_	Alignment	not modelled	14.5	31	Fold: TIM beta/alpha-barrel Superfamily: Metallo-dependent hydrolases Family: Adenosine/AMP deaminase
74	d2f66c1	Alignment	not modelled	14.4	19	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS37 C-terminal domain-like
75	c1tw9C_	Alignment	not modelled	14.2	25	PDB header: transferase Chain: C: PDB Molecule: glutathione s-transferase 2; PDBTitle: glutathione transferase-2, apo form, from the nematode heligmosomoides2 polygyrus
76	c3qa8A_	Alignment	not modelled	13.9	19	PDB header: immune system, signaling protein Chain: A: PDB Molecule: mgc80376 protein; PDBTitle: crystal structure of inhibitor of kappa b kinase beta
77	d1fdja_	Alignment	not modelled	13.6	26	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
78	c2qc8J_	Alignment	not modelled	13.6	56	PDB header: ligase Chain: J: PDB Molecule: glutamine synthetase; PDBTitle: crystal structure of human glutamine synthetase in complex with adp2 and methionine sulfoximine phosphate
79	d2qapa1	Alignment	not modelled	13.5	35	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
80	d2fhea2	Alignment	not modelled	13.4	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
81	c2ganC_	Alignment	not modelled	13.4	35	PDB header: lyase Chain: C: PDB Molecule: fructose-1,6-bisphosphate aldolase;

81	c2qapc	Alignment	not modelled	13.4	33	PDBTitle: fructose-1,6-bisphosphate aldolase from leishmania mexicana
82	d2gsqa2	Alignment	not modelled	13.0	29	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
83	d1a5ca	Alignment	not modelled	12.9	29	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
84	c3kk4B	Alignment	not modelled	12.7	21	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein bp1543; PDBTitle: uncharacterized protein bp1543 from bordetella pertussis tohama i
85	c2ws2B	Alignment	not modelled	12.7	25	PDB header: transferase Chain: B: PDB Molecule: glutathione s-transferase; PDBTitle: the 2 angstrom structure of a nu-class gst from haemonchus contortus
86	d3gtub2	Alignment	not modelled	12.6	25	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
87	c2qnlA	Alignment	not modelled	12.5	18	PDB header: signaling protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a putative dna damage-inducible protein2 (chu_0679) from cytophaga hutchinsonii atcc 33406 at 1.50 a3 resolution
88	d1zaia1	Alignment	not modelled	12.1	31	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
89	c3nrhA	Alignment	not modelled	11.7	18	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein bf1032; PDBTitle: crystal structure of protein bf1032 from bacteroides fragilis,2 northeast structural genomics consortium target bfr309
90	c1iyiA	Alignment	not modelled	11.5	29	PDB header: isomerase Chain: A: PDB Molecule: hematopoietic prostaglandin d synthase; PDBTitle: crystal structure of hematopoietic prostaglandin d synthase
91	c1yq1A	Alignment	not modelled	11.5	29	PDB header: transferase Chain: A: PDB Molecule: glutathione s-transferase; PDBTitle: structural genomics of caenorhabditis elegans: glutathione2 s-transferase
92	d1u5tb2	Alignment	not modelled	11.5	50	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: Vacuolar sorting protein domain
93	c3obeB	Alignment	not modelled	11.4	7	PDB header: isomerase Chain: B: PDB Molecule: sugar phosphate isomerase/epimerase; PDBTitle: crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
94	c2pc4B	Alignment	not modelled	11.3	29	PDB header: lyase Chain: B: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
95	d1a34a	Alignment	not modelled	11.2	33	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Satellite viruses Family: Satellite viruses
96	d2cazc1	Alignment	not modelled	11.0	19	Fold: Long alpha-hairpin Superfamily: Endosomal sorting complex assembly domain Family: VPS37 C-terminal domain-like
97	c2q4jB	Alignment	not modelled	11.0	39	PDB header: transferase Chain: B: PDB Molecule: probable utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
98	d1duga2	Alignment	not modelled	10.8	18	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione S-transferase (GST), N-terminal domain
99	c1gshA	Alignment	not modelled	10.7	35	PDB header: glutathione biosynthesis ligase Chain: A: PDB Molecule: glutathione biosynthetic ligase; PDBTitle: structure of escherichia coli glutathione synthetase at ph 7.5