







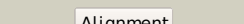

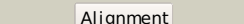

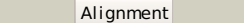

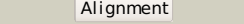
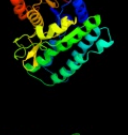
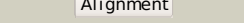

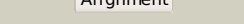

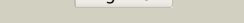


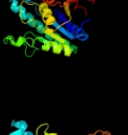






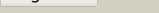


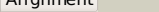
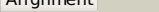
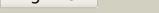
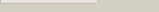
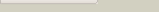

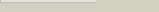
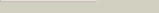
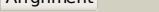
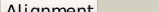
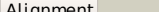

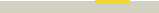



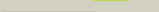
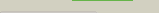


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2j0wA_	 Alignment		100.0	100	PDB header: transferase Chain: A: PDB Molecule: lysine-sensitive aspartokinase 3; PDBTitle: crystal structure of e. coli aspartokinase iii in complex2 with aspartate and adp (r-state)
2	c2cdqB_	 Alignment		100.0	34	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
3	c3c1nA_	 Alignment		100.0	30	PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine
4	c3l76B_	 Alignment		100.0	30	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
5	c3ab4K_	 Alignment		100.0	27	PDB header: transferase Chain: K: PDB Molecule: aspartokinase; PDBTitle: crystal structure of feedback inhibition resistant mutant of aspartate2 kinase from corynebacterium glutamicum in complex with lysine and3 threonine
6	d2cdqa1	 Alignment		100.0	33	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
7	d2j0wa1	 Alignment		100.0	100	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
8	d2hmfa1	 Alignment		100.0	35	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
9	d1ybda1	 Alignment		100.0	21	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
10	c2e9yA_	 Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: carbamate kinase; PDBTitle: crystal structure of project ape1968 from aeropyrum pernix k1
11	d2bnea1	 Alignment		100.0	25	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like

12	c3k4yB_	Alignment		100.0	17	PDB header: transferase Chain: B: PDB Molecule: isopentenyl phosphate kinase; PDBTitle: crystal structure of isopentenyl phosphate kinase from m. jannaschii2 in complex with ipp
13	c3l19A_	Alignment		100.0	20	PDB header: transferase Chain: A: PDB Molecule: isopentenyl phosphate kinase; PDBTitle: x-ray structures of isopentenyl phosphate kinase
14	c3ek5A_	Alignment		100.0	25	PDB header: transferase Chain: A: PDB Molecule: uridylate kinase; PDBTitle: unique gtp-binding pocket and allostery of ump kinase from a gram-2 negative phytopathogen bacterium
15	d2a1fa1	Alignment		100.0	24	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
16	d1z9da1	Alignment		100.0	24	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
17	d1gs5a_	Alignment		100.0	19	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
18	d1e19a_	Alignment		99.9	15	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: Carbamate kinase
19	c3nwyB_	Alignment		99.9	25	PDB header: transferase Chain: B: PDB Molecule: uridylate kinase; PDBTitle: structure and allosteric regulation of the uridine monophosphate2 kinase from mycobacterium tuberculosis
20	d2bufa1	Alignment		99.9	20	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
21	c2jjxC_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: C: PDB Molecule: uridylate kinase; PDBTitle: the crystal structure of ump kinase from bacillus anthracis2 (ba1797)
22	c3l86A_	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: acetylglutamate kinase; PDBTitle: the crystal structure of smu.665 from streptococcus mutans ua159
23	c2rd5A_	Alignment	not modelled	99.9	18	PDB header: protein binding Chain: A: PDB Molecule: acetylglutamate kinase-like protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
24	d2brxa1	Alignment	not modelled	99.9	26	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
25	d1b7ba_	Alignment	not modelled	99.9	16	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: Carbamate kinase
26	c3l15C_	Alignment	not modelled	99.9	18	PDB header: transferase Chain: C: PDB Molecule: gamma-glutamyl kinase related protein; PDBTitle: crystal structure of t. acidophilum isopentenyl phosphate kinase2 product complex
27	d2ij9a1	Alignment	not modelled	99.9	25	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
28	c2zhoB_	Alignment	not modelled	99.9	20	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
						PDB header: structural genomics, unknown function

29	c2egxA	Alignment	not modelled	99.9	22	Chain: A: PDB Molecule: putative acetylglutamate kinase; PDBTitle: crystal structure of the putative acetylglutamate kinase from thermus2 thermophilus
30	c2va1A	Alignment	not modelled	99.9	23	PDB header: transferase Chain: A: PDB Molecule: uridylyl kinase; PDBTitle: crystal structure of ump kinase from ureaplasma parvum
31	c2dtjA	Alignment	not modelled	99.9	19	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
32	c3mahA	Alignment	not modelled	99.9	29	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
33	d2btya1	Alignment	not modelled	99.9	18	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
34	c2re1A	Alignment	not modelled	99.9	18	PDB header: transferase Chain: A: PDB Molecule: aspartokinase, alpha and beta subunits; PDBTitle: crystal structure of aspartokinase alpha and beta subunits
35	d2akoa1	Alignment	not modelled	99.9	17	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: PyrH-like
36	c2j4kC	Alignment	not modelled	99.9	23	PDB header: transferase Chain: C: PDB Molecule: uridylyl kinase; PDBTitle: crystal structure of uridylyl kinase from sulfolobus2 solfataricus in complex with ump to 2.2 angstrom3 resolution
37	c2v5hB	Alignment	not modelled	99.9	17	PDB header: transcription Chain: B: PDB Molecule: acetylglutamate kinase; PDBTitle: controlling the storage of nitrogen as arginine: the2 complex of pii and acetylglutamate kinase from3 synechococcus elongatus pcc 7942
38	c2w21A	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: glutamate 5-kinase; PDBTitle: crystal structure of the aminoacid kinase domain of the2 glutamate 5 kinase of escherichia coli.
39	c3d40A	Alignment	not modelled	99.9	22	PDB header: transferase Chain: A: PDB Molecule: foma protein; PDBTitle: crystal structure of fosfomycin resistance kinase foma from2 streptomyces wedmorensis complexed with diphosphate
40	d2ap9a1	Alignment	not modelled	99.9	24	Fold: Carbamate kinase-like Superfamily: Carbamate kinase-like Family: N-acetyl-l-glutamate kinase
41	c2j5fF	Alignment	not modelled	99.9	21	PDB header: transferase Chain: F: PDB Molecule: glutamate 5-kinase; PDBTitle: glutamate 5-kinase from escherichia coli complexed with2 glutamate
42	c2ogxB	Alignment	not modelled	99.8	24	PDB header: metal binding protein Chain: B: PDB Molecule: molybdenum storage protein subunit beta; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
43	c3kzfC	Alignment	not modelled	99.8	19	PDB header: transferase Chain: C: PDB Molecule: carbamate kinase; PDBTitle: structure of giardia carbamate kinase
44	c2ogxA	Alignment	not modelled	99.8	24	PDB header: metal binding protein Chain: A: PDB Molecule: molybdenum storage protein subunit alpha; PDBTitle: the crystal structure of the molybdenum storage protein from2 azotobacter vinelandii loaded with polyoxotungstates (wsto)
45	c2f06B	Alignment	not modelled	99.6	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
46	c2r98A	Alignment	not modelled	99.6	18	PDB header: transferase Chain: A: PDB Molecule: putative acetylglutamate synthase; PDBTitle: crystal structure of n-acetylglutamate synthase (selenomet2 substituted) from neisseria gonorrhoeae
47	d2j0wa3	Alignment	not modelled	99.5	100	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
48	d2hmfa2	Alignment	not modelled	99.4	28	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
49	d2cdqa3	Alignment	not modelled	99.4	40	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
50	d2hmfa3	Alignment	not modelled	99.3	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
51	d2cdqa2	Alignment	not modelled	99.2	37	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
52	d2j0wa2	Alignment	not modelled	99.1	100	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
53	c2nyiB	Alignment	not modelled	96.5	11	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria2 sulphuraria
54	c1u8sB	Alignment	not modelled	95.9	14	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor

55	c1zhvA		Alignment	not modelled	93.4	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein atu0741; PDBTitle: x-ray crystal structure protein atu0741 from agobacterium tumefaciens.2 northeast structural genomics consortium target atr8.
56	d1zhva2		Alignment	not modelled	92.3	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
57	c2fgcA		Alignment	not modelled	91.5	19	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
58	c2pc6C		Alignment	not modelled	89.8	13	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
59	c2f1fA		Alignment	not modelled	88.5	14	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase isozyme iii small subunit; PDBTitle: crystal structure of the regulatory subunit of2 acetohydroxyacid synthase isozyme iii from e. coli
60	d2f06a1		Alignment	not modelled	88.5	10	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
61	d1zvpa2		Alignment	not modelled	87.5	21	Fold: Ferredoxin-like Superfamily: ACT-like Family: VC0802-like
62	c1zvpB		Alignment	not modelled	87.3	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein vc0802; PDBTitle: crystal structure of a protein of unknown function vc0802 from vibrio2 cholerae, possible transport protein
63	d2pc6a2		Alignment	not modelled	83.9	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
64	d2fgca2		Alignment	not modelled	83.7	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
65	d2f1fa1		Alignment	not modelled	82.7	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
66	d1ygva3		Alignment	not modelled	81.5	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
67	d2f06a2		Alignment	not modelled	78.3	29	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
68	d1sc6a3		Alignment	not modelled	77.3	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
69	d1u8sa2		Alignment	not modelled	76.3	10	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
70	c3nrbD		Alignment	not modelled	76.3	16	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (puru_2 pp_1943) from pseudomonas putida kt2440 at 2.05 a resolution
71	c2qmxB		Alignment	not modelled	75.9	13	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
72	d1zpva1		Alignment	not modelled	75.4	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
73	c3ibwA		Alignment	not modelled	74.1	17	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase; PDBTitle: crystal structure of the act domain from gtp2 pyrophosphokinase of chlorobium tepidum. northeast3 structural genomics consortium target ctr148a
74	d1phza1		Alignment	not modelled	70.8	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
75	d1u8sa1		Alignment	not modelled	70.3	13	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
76	c3mwbA		Alignment	not modelled	68.8	16	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aureus to 2.0a
77	c1ygva		Alignment	not modelled	64.9	8	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis
78	d2qmwa2		Alignment	not modelled	62.5	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
79	c2qmwa		Alignment	not modelled	58.7	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of the prephenate dehydratase (pdt) from2 staphylococcus aureus subsp. aureus mu50
							PDB header: isomerase Chain: A: PDB Molecule: probable prephenate dehydratase

80	c3luyA_	Alignment	not modelled	56.1	7	Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
81	c2vcbA_	Alignment	not modelled	44.9	16	PDB header: hydrolase Chain: A: PDB Molecule: alpha-n-acetylglucosaminidase; PDBTitle: family 89 glycoside hydrolase from clostridium perfringens2 in complex with pugnac
82	d1a9xa4	Alignment	not modelled	42.4	15	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
83	c2k4mA_	Alignment	not modelled	40.8	16	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: upf0146 protein mth_1000; PDBTitle: solution nmr structure of m. thermoautotrophicum protein2 mth_1000, northeast structural genomics consortium target3 tr8
84	c3n0vD_	Alignment	not modelled	40.5	12	PDB header: hydrolase Chain: D: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pp_0327)2 from pseudomonas putida kt2440 at 2.25 a resolution
85	c2nu9E_	Alignment	not modelled	39.6	31	PDB header: ligase Chain: E: PDB Molecule: succinyl-coa synthetase beta chain; PDBTitle: c123at mutant of e. coli succinyl-coa synthetase2 orthorhombic crystal form
86	d2g0ta1	Alignment	not modelled	38.4	13	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
87	c3cuxA_	Alignment	not modelled	35.1	21	PDB header: transferase Chain: A: PDB Molecule: malate synthase; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
88	c3o1lB_	Alignment	not modelled	35.0	14	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution
89	c3mtjA_	Alignment	not modelled	34.7	25	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
90	c2fvgA_	Alignment	not modelled	33.3	11	PDB header: hydrolase Chain: A: PDB Molecule: endoglucanase; PDBTitle: crystal structure of endoglucanase (tm1049) from thermotoga maritima2 at 2.01 a resolution
91	d1tzoa_	Alignment	not modelled	33.3	23	Fold: Anthrax protective antigen Superfamily: Anthrax protective antigen Family: Anthrax protective antigen
92	c3nbuC_	Alignment	not modelled	27.0	21	PDB header: isomerase Chain: C: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: crystal structure of pgi glucosephosphate isomerase
93	c3cuzA_	Alignment	not modelled	25.2	20	PDB header: transferase Chain: A: PDB Molecule: malate synthase a; PDBTitle: atomic resolution structures of escherichia coli and2 bacillis anthracis malate synthase a: comparison with3 isoform g and implications for structure based drug design
94	c2wu8A_	Alignment	not modelled	24.4	17	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: structural studies of phosphoglucose isomerase from2 mycobacterium tuberculosis h37rv
95	d2fvga1	Alignment	not modelled	24.2	23	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: Amino peptidase/glucanase lid domain Family: Amino peptidase/glucanase lid domain
96	c3ewiB_	Alignment	not modelled	24.1	21	PDB header: transferase Chain: B: PDB Molecule: n-acylneuraminate cytidyltransferase; PDBTitle: structural analysis of the c-terminal domain of murine cmp-2 sialic acid synthetase
97	c3isrB_	Alignment	not modelled	22.1	20	PDB header: hydrolase Chain: B: PDB Molecule: transglutaminase-like enzymes, putative cysteine protease; PDBTitle: the crystal structure of a putative cysteine protease from cytophaga2 hutchinsonii to 1.9a
98	d1gzda_	Alignment	not modelled	22.0	23	Fold: SIS domain Superfamily: SIS domain Family: Phosphoglucose isomerase, PGI
99	c3ljkA_	Alignment	not modelled	21.4	17	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: glucose-6-phosphate isomerase from francisella tularensis.
100	c2o2cB_	Alignment	not modelled	21.2	19	PDB header: isomerase Chain: B: PDB Molecule: glucose-6-phosphate isomerase, glycosomal; PDBTitle: crystal structure of phosphoglucose isomerase from t. brucei2 containing glucose-6-phosphate in the active site
101	c3l7pA_	Alignment	not modelled	20.8	6	PDB header: transcription Chain: A: PDB Molecule: putative nitrogen regulatory protein pii; PDBTitle: crystal structure of smu.1657c, putative nitrogen regulatory protein2 pii from streptococcus mutans
102	c3hjbA_	Alignment	not modelled	20.7	23	PDB header: isomerase Chain: A: PDB Molecule: glucose-6-phosphate isomerase; PDBTitle: 1.5 angstrom crystal structure of glucose-6-phosphate isomerase from2 vibrio cholerae.