

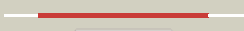





















#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2pc6C	 Alignment		100.0	29	PDB header: lyase Chain: C: PDB Molecule: probable acetolactate synthase isozyme iii (small subunit); PDBTitle: crystal structure of putative acetolactate synthase- small subunit2 from nitrosomonas europaea
2	c2fgcA	 Alignment		100.0	31	PDB header: transferase Chain: A: PDB Molecule: acetolactate synthase, small subunit; PDBTitle: crystal structure of acetolactate synthase- small subunit from2 thermotoga maritima
3	c2f1fA	 Alignment		100.0	30	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
4	d2fgca2	 Alignment		100.0	35	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
5	d2pc6a2	 Alignment		100.0	32	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
6	d2f1fa1	 Alignment		100.0	34	Fold: Ferredoxin-like Superfamily: ACT-like Family: IlvH-like
7	d2f06a2	 Alignment		99.5	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
8	d1sc6a3	 Alignment		99.4	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
9	d1vgya3	 Alignment		99.3	15	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phosphoglycerate dehydrogenase, regulatory (C-terminal) domain
10	c3ibwA	 Alignment		99.2	14	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
11	c1vgya	 Alignment		98.3	15	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis

12	c2f06B_	Alignment		98.2	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
13	d1u8sa2	Alignment		98.2	19	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
14	d1zpv1	Alignment		97.9	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: SP0238-like
15	d1u8sa1	Alignment		97.9	10	Fold: Ferredoxin-like Superfamily: ACT-like Family: Glycine cleavage system transcriptional repressor
16	c1y7pB_	Alignment		97.9	15	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein af1403; PDBTitle: 1.9 a crystal structure of a protein of unknown function2 af1403 from archaeoglobus fulgidus, probable metabolic3 regulator
17	c3n0vD_	Alignment		97.8	15	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
18	c2nyiB_	Alignment		97.8	9	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: unknown protein; PDBTitle: crystal structure of an unknown protein from galdieria2 sulphuraria
19	c3louB_	Alignment		97.7	15	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
20	d2qmwa2	Alignment		97.6	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
21	c1u8sB_	Alignment	not modelled	97.5	10	PDB header: transcription Chain: B: PDB Molecule: glycine cleavage system transcriptional PDBTitle: crystal structure of putative glycine cleavage system2 transcriptional repressor
22	c3obiC_	Alignment	not modelled	97.5	13	PDB header: hydrolase Chain: C: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of a formyltetrahydrofolate deformylase (np_949368)2 from rhodopseudomonas palustris cga009 at 1.95 a resolution
23	c3o1lB_	Alignment	not modelled	97.4	10	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
24	c3luyA_	Alignment	not modelled	97.4	17	PDB header: isomerase Chain: A: PDB Molecule: probable chorismate mutase; PDBTitle: putative chorismate mutase from bifidobacterium adolescentis
25	c3nrbd_	Alignment	not modelled	97.4	18	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
26	c2qmwA_	Alignment	not modelled	97.4	16	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
27	c3mwbA_	Alignment	not modelled	97.3	18	PDB header: lyase Chain: A: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of prephenate dehydratase in complex with l-phe2 from arthrobacter aurescens to 2.0a
						PDB header: oxidoreductase

28	c1ybaC_	Alignment	not modelled	97.3	17	Chain: C: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: the active form of phosphoglycerate dehydrogenase
29	c2qmxB_	Alignment	not modelled	97.3	16	PDB header: ligase Chain: B: PDB Molecule: prephenate dehydratase; PDBTitle: the crystal structure of l-phe inhibited prephenate dehydratase from2 chlorobium tepidum t1s
30	d1phza1	Alignment	not modelled	97.2	16	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
31	c3k5pA_	Alignment	not modelled	96.9	8	PDB header: oxidoreductase Chain: A: PDB Molecule: d-3-phosphoglycerate dehydrogenase; PDBTitle: crystal structure of amino acid-binding act: d-isomer specific 2-2 hydroxyacid dehydrogenase catalytic domain from brucella melitensis
32	c3mtjA_	Alignment	not modelled	96.9	21	PDB header: oxidoreductase Chain: A: PDB Molecule: homoserine dehydrogenase; PDBTitle: the crystal structure of a homoserine dehydrogenase from thiobacillus2 denitrificans to 2.15a
33	d2f06a1	Alignment	not modelled	96.8	11	Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
34	d2hmfa3	Alignment	not modelled	94.5	17	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
35	c2dtjA_	Alignment	not modelled	93.8	13	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
36	d2hmfa2	Alignment	not modelled	93.6	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
37	d2nzca1	Alignment	not modelled	93.2	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: TM1266-like
38	c3mahA_	Alignment	not modelled	92.8	14	PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
39	d2cdqa2	Alignment	not modelled	92.7	23	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
40	c2phmA_	Alignment	not modelled	91.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (phenylalanine-4-hydroxylase); PDBTitle: structure of phenylalanine hydroxylase dephosphorylated
41	c3p96A_	Alignment	not modelled	91.3	12	PDB header: hydrolase Chain: A: PDB Molecule: phosphoserine phosphatase serb; PDBTitle: crystal structure of phosphoserine phosphatase serb from mycobacterium2 avium, native form
42	c3mgjA_	Alignment	not modelled	91.2	11	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein mj1480; PDBTitle: crystal structure of the saccharop_dh_n domain of mj14802 protein from methanococcus jannaschii. northeast structural3 genomics consortium target mjr83a.
43	c1tdjA_	Alignment	not modelled	90.6	15	PDB header: allostery Chain: A: PDB Molecule: biosynthetic threonine deaminase; PDBTitle: threonine deaminase (biosynthetic) from e. coli
44	c2re1A_	Alignment	not modelled	90.3	16	PDB header: transferase Chain: A: PDB Molecule: aspartokinase, alpha and beta subunits; PDBTitle: crystal structure of aspartokinase alpha and beta subunits
45	d1rwua_	Alignment	not modelled	90.1	13	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: YbeD-like
46	c1rwuA_	Alignment	not modelled	90.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical upf0250 protein ybed; PDBTitle: solution structure of conserved protein ybed from e. coli
47	c2zhoB_	Alignment	not modelled	90.1	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)
48	d2cdqa3	Alignment	not modelled	88.6	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
49	c2rjzA_	Alignment	not modelled	87.5	19	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: pilo protein; PDBTitle: crystal structure of the type 4 fimbrial biogenesis protein pilo from2 pseudomonas aeruginosa
50	c3l76B_	Alignment	not modelled	87.4	16	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of aspartate kinase from synechocystis
51	c3ab4K_	Alignment	not modelled	87.1	15	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
52	d2j0wa2	Alignment	not modelled	84.0	25	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
53	c3c1nA_	Alignment	not modelled	81.0	12	PDB header: transferase Chain: A: PDB Molecule: probable aspartokinase; PDBTitle: crystal structure of allosteric inhibition threonine-sensitive2 aspartokinase from methanococcus jannaschii with l-threonine

54	c2az1B	Alignment	not modelled	74.4	20	PDB header: transferase Chain: B: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: structure of a halophilic nucleoside diphosphate kinase2 from halobacterium salinarum
55	c2dgbA	Alignment	not modelled	70.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein purs; PDBTitle: structure of thermus thermophilus purs in the p21 form
56	d2j0wa3	Alignment	not modelled	69.7	22	Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
57	c2cdqB	Alignment	not modelled	65.8	17	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of arabidopsis thaliana aspartate kinase2 complexed with lysine and s-adenosylmethionine
58	d1tdja2	Alignment	not modelled	50.1	14	Fold: Ferredoxin-like Superfamily: ACT-like Family: Allosteric threonine deaminase C-terminal domain
59	d1gtda	Alignment	not modelled	46.2	12	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
60	c2j0wA	Alignment	not modelled	45.7	20	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)
61	d2az3a1	Alignment	not modelled	38.5	19	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
62	c3cg4A	Alignment	not modelled	33.9	14	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: response regulator receiver domain protein (cheY-like); PDBTitle: crystal structure of response regulator receiver domain protein (cheY-2 like) from methanospirillum hungatei jf-1
63	d1p4xa2	Alignment	not modelled	32.7	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: MarR-like transcriptional regulators
64	c2jsxA	Alignment	not modelled	32.0	16	PDB header: chaperone Chain: A: PDB Molecule: protein napd; PDBTitle: solution structure of the e. coli tat proofreading2 chaperone protein napd
65	d1be4a	Alignment	not modelled	31.2	15	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
66	d1kona	Alignment	not modelled	31.1	15	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
67	c3r9lA	Alignment	not modelled	30.4	9	PDB header: transferase Chain: A: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of nucleoside diphosphate kinase from giardia2 lamblia featuring a disordered dinucleotide binding site
68	c3eodA	Alignment	not modelled	30.3	12	PDB header: signaling protein Chain: A: PDB Molecule: protein hnr; PDBTitle: crystal structure of n-terminal domain of e. coli rssb
69	d1qkka	Alignment	not modelled	28.1	8	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
70	d1dcfa	Alignment	not modelled	26.8	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: Receiver domain of the ethylene receptor
71	d2joqa1	Alignment	not modelled	25.7	12	Fold: Ferredoxin-like Superfamily: YbeD/HP0495-like Family: HP0495-like
72	d2a9pa1	Alignment	not modelled	25.0	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
73	c2zw2B	Alignment	not modelled	21.5	12	PDB header: ligase Chain: B: PDB Molecule: putative uncharacterized protein sts178; PDBTitle: crystal structure of formylglycinamide ribonucleotide amidotransferase2 iii from sulfobolus tokodaii (stpsurs)
74	c3crnA	Alignment	not modelled	21.0	15	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, cheY-like; PDBTitle: crystal structure of response regulator receiver domain protein (cheY-2 like) from methanospirillum hungatei jf-1
75	d1mb3a	Alignment	not modelled	19.2	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
76	c3hdgE	Alignment	not modelled	19.0	12	PDB header: structural genomics, unknown function Chain: E: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of the n-terminal domain of an2 uncharacterized protein (ws1339) from wolinetla3 succinogenes
77	d1t4aa	Alignment	not modelled	18.3	12	Fold: PurS-like Superfamily: PurS-like Family: PurS subunit of FGAM synthetase
78	c3cfyA	Alignment	not modelled	18.3	8	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative luxa repressor protein; PDBTitle: crystal structure of signal receiver domain of putative luxa2 repressor protein from vibrio parahaemolyticus
79	d2b3tb1	Alignment	not modelled	17.7	13	Fold: Release factor Superfamily: Release factor Family: Release factor
80	c3ot7A	Alignment	not modelled	17.7	10	PDB header: hydrolase Chain: A: PDB Molecule: sensor protein;

80	c3gt7A	Alignment	not modelled	17.7	19	PDBTitle: crystal structure of signal receiver domain of signal2 transduction histidine kinase from syntrophus3 aciditrophicus
81	d1mw7a	Alignment	not modelled	17.4	15	Fold: YebC-like Superfamily: YebC-like Family: YebC-like
82	c1zbtA	Alignment	not modelled	17.2	10	PDB header: translation Chain: A: PDB Molecule: peptide chain release factor 1; PDBTitle: crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution
83	d2b4aa1	Alignment	not modelled	17.0	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
84	c2rjnA	Alignment	not modelled	16.4	14	PDB header: hydrolase Chain: A: PDB Molecule: response regulator receiver:metal-dependent PDBTitle: crystal structure of an uncharacterized protein q2bku2 from2 neptuniibacter caesariensis
85	d1xjca	Alignment	not modelled	16.1	14	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
86	d1wxma1	Alignment	not modelled	15.0	11	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
87	d1zh2a1	Alignment	not modelled	14.9	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
88	c2qxyB	Alignment	not modelled	14.9	19	PDB header: transcription Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of a response regulator from thermotoga2 maritima
89	d1kgsa2	Alignment	not modelled	14.8	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
90	c2rdmB	Alignment	not modelled	14.5	12	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
91	d2ayxa1	Alignment	not modelled	14.1	14	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
92	c2gwrA	Alignment	not modelled	13.8	14	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator mtra; PDBTitle: crystal structure of the response regulator protein mtra from2 mycobacterium tuberculosis
93	c2qr3A	Alignment	not modelled	13.7	23	PDB header: transcription Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: crystal structure of the n-terminal signal receiver domain of two-2 component system response regulator from bacteroides fragilis
94	c3ktoA	Alignment	not modelled	13.5	7	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
95	d1w25a1	Alignment	not modelled	13.2	12	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
96	c3r0jA	Alignment	not modelled	13.1	14	PDB header: dna binding protein Chain: A: PDB Molecule: possible two component system response transcriptional PDBTitle: structure of phop from mycobacterium tuberculosis
97	c2ayxA	Alignment	not modelled	13.1	13	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2 700-949) containing linker region and phosphoreceiver3 domain
98	c3cu5B	Alignment	not modelled	13.0	13	PDB header: transcription regulator Chain: B: PDB Molecule: two component transcriptional regulator, arac family; PDBTitle: crystal structure of a two component transcriptional regulator arac2 from clostridium phytofermentans isdg
99	c3d5cX	Alignment	not modelled	13.0	16	PDB header: ribosome Chain: X: PDB Molecule: peptide chain release factor 1; PDBTitle: structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.