


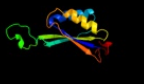
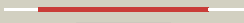












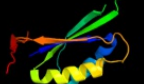





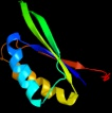
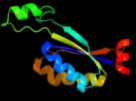


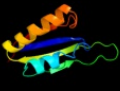
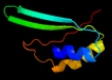



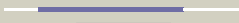
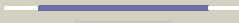
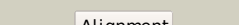
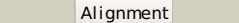
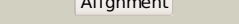
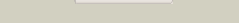

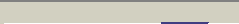


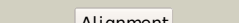
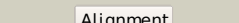
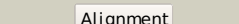
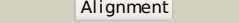
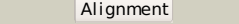
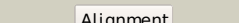
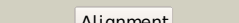

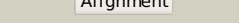


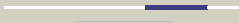



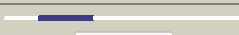


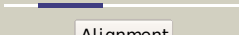
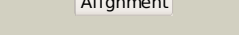
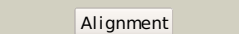

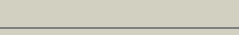

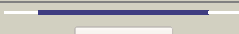


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2ns1b1	 Alignment		100.0	99	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
2	c3mhyC	 Alignment		100.0	68	PDB header: signaling protein Chain: C: PDB Molecule: pii-like protein pz; PDBTitle: a new pii protein structure
3	d1qy7a	 Alignment		100.0	56	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
4	d2piia	 Alignment		100.0	68	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
5	d1vfja	 Alignment		100.0	40	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
6	c2rd5D	 Alignment		100.0	45	PDB header: protein binding Chain: D: PDB Molecule: pii protein; PDBTitle: structural basis for the regulation of n-acetylglutamate kinase by pii2 in arabidopsis thaliana
7	c3ncpD	 Alignment		100.0	46	PDB header: signaling protein Chain: D: PDB Molecule: nitrogen regulatory protein p-ii (glnb-2); PDBTitle: glnk2 from archaeoglobus fulgidus
8	d1hwua	 Alignment		100.0	63	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
9	d1ul3a	 Alignment		100.0	55	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
10	c2j9dG	 Alignment		100.0	53	PDB header: membrane transport Chain: G: PDB Molecule: hypothetical nitrogen regulatory pii-like PDBTitle: structure of glnk1 with bound effectors indicates2 regulatory mechanism for ammonia uptake
11	c3bzqA	 Alignment		100.0	49	PDB header: signaling protein/transcription Chain: A: PDB Molecule: nitrogen regulatory protein p-ii; PDBTitle: high resolution crystal structure of nitrogen regulatory protein2 (rv2919c) of mycobacterium tuberculosis

12	c3o8wA_	Alignment		100.0	50	PDB header: signaling protein Chain: A: PDB Molecule: nitrogen regulatory protein p-ii (glnb-1); PDBTitle: archaeoglobus fulgidus glnk1
13	c3l7pA_	Alignment		99.9	48	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
14	d2cz4a1	Alignment		99.8	17	Fold: Ferredoxin-like Superfamily: GlnB-like Family: Prokaryotic signal transducing protein
15	c3ce8A_	Alignment		98.5	14	PDB header: unknown function Chain: A: PDB Molecule: putative pii-like nitrogen regulatory protein; PDBTitle: crystal structure of a duf3240 family protein (sbal_0098) from2 shewanella baltica os155 at 2.40 a resolution
16	c3m05A_	Alignment		98.2	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein pepe_1480; PDBTitle: the crystal structure of a functionally unknown protein2 pepe_1480 from pediococcus pentosaceus atcc 25745
17	d1o51a_	Alignment		96.6	21	Fold: Ferredoxin-like Superfamily: GlnB-like Family: DUF190/COG1993
18	c2dclB_	Alignment		95.3	26	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical upf0166 protein ph1503; PDBTitle: structure of ph1503 protein from pyrococcus horikoshii ot3
19	c2gx8B_	Alignment		92.6	25	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: nif3-related protein; PDBTitle: the crystal stucture of bacillus cereus protein related to nif3
20	d2gx8a1	Alignment		90.7	25	Fold: NIF3 (NGG1p interacting factor 3)-like Superfamily: NIF3 (NGG1p interacting factor 3)-like Family: NIF3 (NGG1p interacting factor 3)-like
21	c2nydB_	Alignment	not modelled	86.6	19	PDB header: unknown function Chain: B: PDB Molecule: upf0135 protein sa1388; PDBTitle: crystal structure of staphylococcus aureus hypothetical protein sa1388
22	d1nh8a2	Alignment	not modelled	84.3	9	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
23	c3hluA_	Alignment	not modelled	77.5	22	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein duf2179; PDBTitle: crystal structure of uncharacterized protein conserved in bacteria2 duf2179 from eubacterium ventriosum
24	c2vd3B_	Alignment	not modelled	75.3	12	PDB header: transferase Chain: B: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: the structure of histidine inhibited hisg from2 methanobacterium thermoautotrophicum
25	c1nh7A_	Alignment	not modelled	71.7	9	PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: atp phosphoribosyltransferase (atp-prtase) from mycobacterium2 tuberculosis
26	d1h3da2	Alignment	not modelled	60.3	13	Fold: Ferredoxin-like Superfamily: GlnB-like Family: ATP phosphoribosyltransferase (ATP-PRTase, HisG), regulatory C-terminal domain
27	c3dfeA_	Alignment	not modelled	59.8	25	PDB header: signaling protein Chain: A: PDB Molecule: putative pii-like signaling protein; PDBTitle: crystal structure of a putative pii-like signaling protein2 (yp_323533.1) from anabaena variabilis atcc 29413 at 2.35 a3 resolution
28	c3rrkA_	Alignment	not modelled	47.1	16	PDB header: proton transport Chain: A: PDB Molecule: v-type atpase 116 kda subunit; PDBTitle: crystal structure of the cytoplasmic n-terminal domain of

					subunit i, 2 homolog of subunit a, of v-atpase
29	c1q1kA_	Alignment	not modelled	44.0	13 PDB header: transferase Chain: A: PDB Molecule: atp phosphoribosyltransferase; PDBTitle: structure of atp-phosphoribosyltransferase from e. coli complexed with 2 pr-atp
30	c2f06B_	Alignment	not modelled	32.5	19 PDB header: structural genomics, unknown function Chain: B: PDB Molecule: conserved hypothetical protein; PDBTitle: crystal structure of protein bt0572 from bacteroides thetaiotaomicron
31	c2cz9A_	Alignment	not modelled	26.3	14 PDB header: transferase Chain: A: PDB Molecule: probable galactokinase; PDBTitle: crystal structure of galactokinase from pyrococcus horikoshi
32	d2hmfa2	Alignment	not modelled	24.9	20 Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
33	d1w1oa1	Alignment	not modelled	24.4	16 Fold: Ferredoxin-like Superfamily: FAD-linked oxidases, C-terminal domain Family: Cytokinin dehydrogenase 1
34	c2zvyB_	Alignment	not modelled	23.5	12 PDB header: membrane protein Chain: B: PDB Molecule: chemotaxis protein motb; PDBTitle: structure of the periplasmic domain of motb from salmonella2 (crystal form ii)
35	c2hk3A_	Alignment	not modelled	22.4	10 PDB header: lyase Chain: A: PDB Molecule: diphosphomevalonate decarboxylase; PDBTitle: crystal structure of mevalonate diphosphate decarboxylase2 from staphylococcus aureus (orthorhombic form)
36	d1zhva2	Alignment	not modelled	21.2	19 Fold: Ferredoxin-like Superfamily: ACT-like Family: Atu0741-like
37	d2j0wa3	Alignment	not modelled	19.3	4 Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
38	c2dtjA_	Alignment	not modelled	19.0	15 PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: crystal structure of regulatory subunit of aspartate kinase2 from corynebacterium glutamicum
39	c3mahA_	Alignment	not modelled	19.0	13 PDB header: transferase Chain: A: PDB Molecule: aspartokinase; PDBTitle: a putative c-terminal regulatory domain of aspartate kinase from2 porphyromonas gingivalis w83.
40	d2f06a2	Alignment	not modelled	17.4	28 Fold: Ferredoxin-like Superfamily: ACT-like Family: BT0572-like
41	d1wjwa_	Alignment	not modelled	17.2	30 Fold: TBP-like Superfamily: Phosphoglucumutase, C-terminal domain Family: Phosphoglucumutase, C-terminal domain
42	c2nuxB_	Alignment	not modelled	15.4	19 PDB header: lyase Chain: B: PDB Molecule: 2-keto-3-deoxygluconate/2-keto-3-deoxy-6-phospho gluconate PDBTitle: 2-keto-3-deoxygluconate aldolase from sulfolobus acidocaldarius, 2 native structure in p6522 at 2.5 a resolution
43	d1v6za2	Alignment	not modelled	15.3	23 Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
44	d2cdqa3	Alignment	not modelled	15.3	24 Fold: Ferredoxin-like Superfamily: ACT-like Family: Aspartokinase allosteric domain-like
45	d1x8da1	Alignment	not modelled	14.3	17 Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: YjiL-like
46	c3fluD_	Alignment	not modelled	13.4	19 PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from the pathogen2 neisseria meningitidis
47	c2qlxA_	Alignment	not modelled	13.3	11 PDB header: isomerase Chain: A: PDB Molecule: l-rhamnose mutarotase; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
48	c2qlwA_	Alignment	not modelled	13.3	11 PDB header: isomerase Chain: A: PDB Molecule: rhau; PDBTitle: crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
49	c1zr6A_	Alignment	not modelled	12.4	27 PDB header: oxidoreductase Chain: A: PDB Molecule: glucooligosaccharide oxidase; PDBTitle: the crystal structure of an acremonium strictum glucooligosaccharide2 oxidase reveals a novel flavinylation
50	c3dz1A_	Alignment	not modelled	12.4	14 PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 rhodospseudomonas palustris at 1.87a resolution
51	c3nuhB_	Alignment	not modelled	12.1	18 PDB header: isomerase Chain: B: PDB Molecule: dna gyrase subunit b; PDBTitle: a domain insertion in e. coli gyrb adopts a novel fold that plays a2 critical role in gyrase function
52	c3n2xB_	Alignment	not modelled	11.8	19 PDB header: lyase Chain: B: PDB Molecule: uncharacterized protein yage; PDBTitle: crystal structure of yage, a prophage protein belonging to the2 dihydrodipicolinic acid synthase family from e. coli k12 in complex3 with pyruvate
53	d1vi2a2	Alignment	not modelled	11.8	17 Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
54	d2a5la1	Alignment	not modelled	11.0	15 Fold: Flavodoxin-like Superfamily: Flavoproteins Family: WrbA-like

55	c3nnqA	 Alignment	not modelled	11.0	12	PDB header: viral protein Chain: A: PDB Molecule: n-terminal domain of moloney murine leukemia virus PDBTitle: crystal structure of the n-terminal domain of moloney murine leukemia2 virus integrase, northeast structural genomics consortium target or3
56	c2hfvA	 Alignment	not modelled	10.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein rpa1041; PDBTitle: solution nmr structure of protein rpa1041 from pseudomonas2 aeruginosa. northeast structural genomics consortium3 target pat90.
57	c2yxgD	 Alignment	not modelled	10.3	19	PDB header: lyase Chain: D: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase (dapa)
58	c2re1A	 Alignment	not modelled	10.2	18	PDB header: transferase Chain: A: PDB Molecule: aspartokinase, alpha and beta subunits; PDBTitle: crystal structure of aspartokinase alpha and beta subunits
59	d1v7ra	 Alignment	not modelled	10.0	32	Fold: Anticodon-binding domain-like Superfamily: ITPase-like Family: ITPase (Ham1)
60	c3lerA	 Alignment	not modelled	10.0	20	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from2 campylobacter jejuni subsp. jejuni nctc 11168
61	d1mwza	 Alignment	not modelled	9.4	19	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
62	c2y3rC	 Alignment	not modelled	9.3	21	PDB header: oxidoreductase Chain: C: PDB Molecule: tamI; PDBTitle: structure of the tirandamycin-bound fad-dependent2 tirandamycin oxidase tamI in p21 space group
63	d1p77a2	 Alignment	not modelled	9.3	21	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
64	d1fx0a2	 Alignment	not modelled	9.2	25	Fold: Domain of alpha and beta subunits of F1 ATP synthase-like Superfamily: N-terminal domain of alpha and beta subunits of F1 ATP synthase Family: N-terminal domain of alpha and beta subunits of F1 ATP synthase
65	d2i0ka2	 Alignment	not modelled	9.0	13	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain
66	d1p5dx4	 Alignment	not modelled	9.0	23	Fold: TBP-like Superfamily: Phosphoglucosyltransferase, C-terminal domain Family: Phosphoglucosyltransferase, C-terminal domain
67	d1nvta2	 Alignment	not modelled	9.0	33	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
68	c3pueA	 Alignment	not modelled	8.8	15	PDB header: lyase Chain: A: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of the complex of dhydrodipicolinate synthase from2 acinetobacter baumannii with lysine at 2.6a resolution
69	d1nxza2	 Alignment	not modelled	8.8	20	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YggJ C-terminal domain-like
70	c2zodB	 Alignment	not modelled	8.5	17	PDB header: transferase Chain: B: PDB Molecule: selenide, water dikinase; PDBTitle: crystal structure of selenophosphate synthetase from2 aquifex aeolicus
71	c2gs8A	 Alignment	not modelled	8.4	17	PDB header: lyase Chain: A: PDB Molecule: mevalonate pyrophosphate decarboxylase; PDBTitle: structure of mevalonate pyrophosphate decarboxylase from streptococcus2 pyogenes
72	c1wveB	 Alignment	not modelled	8.4	12	PDB header: oxidoreductase Chain: B: PDB Molecule: 4-cresol dehydrogenase [hydroxylating] PDBTitle: p-cresol methylhydroxylase: alteration of the structure of2 the flavoprotein subunit upon its binding to the3 cytochrome subunit
73	d1ny5a2	 Alignment	not modelled	8.3	24	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Extended AAA-ATPase domain
74	c1f0xA	 Alignment	not modelled	8.3	9	PDB header: oxidoreductase Chain: A: PDB Molecule: d-lactate dehydrogenase; PDBTitle: crystal structure of d-lactate dehydrogenase, a peripheral2 membrane respiratory enzyme.
75	c2ipiD	 Alignment	not modelled	8.3	11	PDB header: oxidoreductase Chain: D: PDB Molecule: aclacinomycin oxidoreductase (aknox); PDBTitle: crystal structure of aclacinomycin oxidoreductase
76	d1nyta2	 Alignment	not modelled	8.3	25	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
77	c3b4uB	 Alignment	not modelled	8.3	14	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from agrobacterium2 tumefaciens str. c58
78	c3lciA	 Alignment	not modelled	8.1	19	PDB header: lyase Chain: A: PDB Molecule: n-acetylneuraminate lyase; PDBTitle: the d-sialic acid aldolase mutant v251w
79	d1sqsa	 Alignment	not modelled	8.0	13	Fold: Flavodoxin-like Superfamily: Flavoproteins Family: Hypothetical protein SP1951

80	c2bvfA	 Alignment	not modelled	8.0	22	PDB header: oxidase Chain: A: PDB Molecule: 6-hydroxy-d-nicotine oxidase; PDBTitle: crystal structure of 6-hydroxy-d-nicotine oxidase from2 arthrobacter nicotinovorans. crystal form 3 (p1)
81	c2otnB	 Alignment	not modelled	8.0	29	PDB header: isomerase Chain: B: PDB Molecule: diaminopimelate epimerase; PDBTitle: crystal structure of the catalytically active form of diaminopimelate2 epimerase from bacillus anthracis
82	c1z85B	 Alignment	not modelled	7.9	14	PDB header: transferase Chain: B: PDB Molecule: hypothetical protein tm1380; PDBTitle: crystal structure of a predicted rna methyltransferase (tm1380) from2 thermotoga maritima msb8 at 2.12 a resolution
83	c3pm9A	 Alignment	not modelled	7.9	13	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: crystal structure of a putative dehydrogenase (rpa1076) from2 rhodopseudomonas palustris cga009 at 2.57 a resolution
84	c3cprB	 Alignment	not modelled	7.6	17	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthetase; PDBTitle: the crystal structure of corynebacterium glutamicum2 dihydrodipicolinate synthase to 2.2 a resolution
85	c3daqB	 Alignment	not modelled	7.6	12	PDB header: lyase Chain: B: PDB Molecule: dihydrodipicolinate synthase; PDBTitle: crystal structure of dihydrodipicolinate synthase from methicillin-2 resistant staphylococcus aureus
86	c3popD	 Alignment	not modelled	7.5	21	PDB header: oxidoreductase Chain: D: PDB Molecule: gilr oxidase; PDBTitle: the crystal structure of gilr, an oxidoreductase that catalyzes the2 terminal step of gilvocarcin biosynthesis
87	c2hfuB	 Alignment	not modelled	7.5	21	PDB header: transferase Chain: B: PDB Molecule: mevalonate kinase, putative; PDBTitle: crystal structure of l. major mevalonate kinase in complex2 with r-mevalonate
88	d1vhka2	 Alignment	not modelled	7.3	17	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: Yggj C-terminal domain-like
89	c2zhoB	 Alignment	not modelled	7.2	22	PDB header: transferase Chain: B: PDB Molecule: aspartokinase; PDBTitle: crystal structure of the regulatory subunit of aspartate2 kinase from thermus thermophilus (ligand free form)
90	c2cx8B	 Alignment	not modelled	7.2	23	PDB header: transferase Chain: B: PDB Molecule: methyl transferase; PDBTitle: crystal structure of methyltransferase with ligand(sah)
91	c2wdwB	 Alignment	not modelled	7.1	21	PDB header: oxidoreductase Chain: B: PDB Molecule: putative hexose oxidase; PDBTitle: the native crystal structure of the primary hexose oxidase (2 dbv29) in antibiotic a40926 biosynthesis
92	c1zhvA	 Alignment	not modelled	7.1	14	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.
93	c3oonA	 Alignment	not modelled	7.0	20	PDB header: membrane protein Chain: A: PDB Molecule: outer membrane protein (tpn50); PDBTitle: the structure of an outer membrane protein from borrelia burgdorferi2 b31
94	c3fwaA	 Alignment	not modelled	7.0	21	PDB header: flavoprotein Chain: A: PDB Molecule: reticuline oxidase; PDBTitle: structure of berberine bridge enzyme, c166a variant in complex with2 (s)-reticuline
95	d1luxy1	 Alignment	not modelled	6.9	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: Uridine diphospho-N-Acetylenolpyruvylglucosamine reductase (MurB), N-terminal domain
96	d1xxa1	 Alignment	not modelled	6.9	14	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase
97	c2apnA	 Alignment	not modelled	6.7	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: protein hi1723; PDBTitle: hi1723 solution structure
98	c1i19B	 Alignment	not modelled	6.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: cholesterol oxidase; PDBTitle: crystal structure of cholesterol oxidase from b.sterolicum
99	d1e8ga2	 Alignment	not modelled	6.5	18	Fold: FAD-binding/transporter-associated domain-like Superfamily: FAD-binding/transporter-associated domain-like Family: FAD-linked oxidases, N-terminal domain