






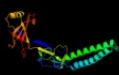
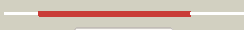


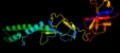

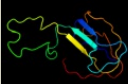



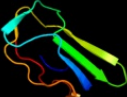

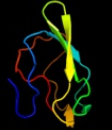

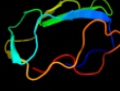


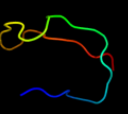
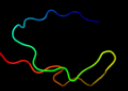

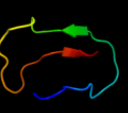
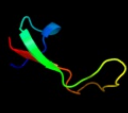


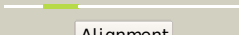
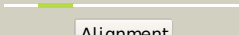
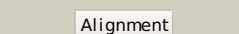


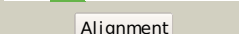



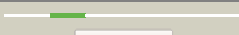
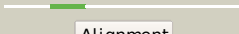
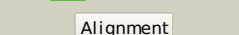
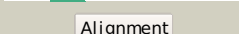
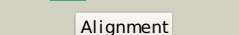
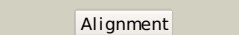



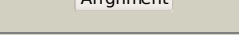
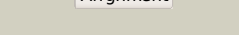
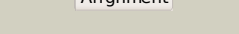





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h9iB_	 Alignment		100.0	20	PDB header: transport protein Chain: B: PDB Molecule: cation efflux system protein cusb; PDBTitle: crystal structure of the membrane fusion protein cusb from escherichia2 coli
2	c2f1mA_	 Alignment		99.9	76	PDB header: transport protein Chain: A: PDB Molecule: acriflavine resistance protein a; PDBTitle: conformational flexibility in the multidrug efflux system protein acra
3	c3fppB_	 Alignment		99.9	24	PDB header: membrane protein Chain: B: PDB Molecule: macrolide-specific efflux protein maca; PDBTitle: crystal structure of e.coli maca
4	c1t5eB_	 Alignment		99.8	59	PDB header: transport protein Chain: B: PDB Molecule: multidrug resistance protein mexa; PDBTitle: the structure of mexa
5	d1vf7a_	 Alignment		99.8	59	Fold: HlyD-like secretion proteins Superfamily: HlyD-like secretion proteins Family: HlyD-like secretion proteins
6	c3lnnB_	 Alignment		99.8	19	PDB header: metal transport Chain: B: PDB Molecule: membrane fusion protein (mfp) heavy metal cation efflux PDBTitle: crystal structure of zneb from cupriavidus metallidurans
7	c2k33A_	 Alignment		98.8	24	PDB header: membrane protein, transport protein Chain: A: PDB Molecule: acra; PDBTitle: solution structure of an n-glycosylated protein using in2 vitro glycosylation
8	c2b8gA_	 Alignment		97.3	27	PDB header: biosynthetic protein Chain: A: PDB Molecule: biotin/lipoyl attachment protein; PDBTitle: solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
9	c2ejgD_	 Alignment		97.1	33	PDB header: ligase Chain: D: PDB Molecule: 149aa long hypothetical methylmalonyl-coa decarboxylase PDBTitle: crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
10	d1dcza_	 Alignment		97.1	33	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
11	d1o78a_	 Alignment		97.0	27	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains

12	c2ejmA	Alignment		96.7	26	PDB header: ligase Chain: A: PDB Molecule: methylcrotonoyl-coa carboxylase subunit alpha; PDBTitle: solution structure of ruh-072, an apo-biotinyl domain form2 human acetyl coenzyme a carboxylase
13	c2dn8A	Alignment		96.2	23	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
14	c2kccA	Alignment		96.1	22	PDB header: ligase Chain: A: PDB Molecule: acetyl-coa carboxylase 2; PDBTitle: solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
15	c2l5tA	Alignment		96.1	29	PDB header: transferase Chain: A: PDB Molecule: lipamide acyltransferase; PDBTitle: solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
16	c3n6rK	Alignment		96.1	15	PDB header: ligase Chain: K: PDB Molecule: propionyl-coa carboxylase, alpha subunit; PDBTitle: crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
17	d1bdoa	Alignment		95.9	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
18	d1iyua	Alignment		95.9	21	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
19	d1ghja	Alignment		95.6	24	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
20	d1qlaf	Alignment		95.4	19	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
21	d1k8ma	Alignment	not modelled	95.3	11	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
22	d1qjoa	Alignment	not modelled	95.3	20	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
23	d2f3ga	Alignment	not modelled	95.2	19	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
24	d1laba	Alignment	not modelled	95.2	31	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
25	d2gprr	Alignment	not modelled	95.1	23	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
26	d1gprr	Alignment	not modelled	94.9	29	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Glucose permease-like
27	d1gjxa	Alignment	not modelled	94.9	17	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
28	d1y8ob1	Alignment	not modelled	94.5	22	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
29	c2qf7A	Alignment	not modelled	94.5	13	PDB header: ligase Chain: A: PDB Molecule: pyruvate carboxylase protein; PDBTitle: crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli

30	d2pnrc1	Alignment	not modelled	93.9	22	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
31	d1pmra	Alignment	not modelled	93.7	24	Fold: Barrel-sandwich hybrid Superfamily: Single hybrid motif Family: Biotinyl/lipoyl-carrier proteins and domains
32	d2tpa3	Alignment	not modelled	93.4	19	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
33	c2q8iB	Alignment	not modelled	93.3	25	PDB header: transferase Chain: B: PDB Molecule: dihydropyridine-residue acetyltransferase component of PDBTitle: pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
34	d1uoua3	Alignment	not modelled	93.3	17	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
35	d1brwa3	Alignment	not modelled	93.2	28	Fold: alpha/beta-Hammerhead Superfamily: Pyrimidine nucleoside phosphorylase C-terminal domain Family: Pyrimidine nucleoside phosphorylase C-terminal domain
36	c2dncA	Alignment	not modelled	92.8	19	PDB header: transferase Chain: A: PDB Molecule: pyruvate dehydrogenase protein x component; PDBTitle: solution structure of rsg1 ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
37	c2jkuA	Alignment	not modelled	92.1	26	PDB header: ligase Chain: A: PDB Molecule: propionyl-coa carboxylase alpha chain, PDBTitle: crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
38	c2dneA	Alignment	not modelled	91.9	13	PDB header: transferase Chain: A: PDB Molecule: dihydropyridine-residue acetyltransferase PDBTitle: solution structure of rsg1 ruh-058, a lipoyl domain of2 human 2-oxoacid dehydrogenase
39	c1otpA	Alignment	not modelled	90.8	19	PDB header: phosphorylase Chain: A: PDB Molecule: thymidine phosphorylase; PDBTitle: structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
40	c3h5qA	Alignment	not modelled	88.6	37	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside phosphorylase; PDBTitle: crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
41	c2j0fC	Alignment	not modelled	88.2	17	PDB header: transferase Chain: C: PDB Molecule: thymidine phosphorylase; PDBTitle: structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
42	c2dsjA	Alignment	not modelled	87.6	20	PDB header: transferase Chain: A: PDB Molecule: pyrimidine-nucleoside (thymidine) phosphorylase; PDBTitle: crystal structure of project id tt0128 from thermus thermophilus hb8
43	c1brwB	Alignment	not modelled	85.7	29	PDB header: transferase Chain: B: PDB Molecule: protein (pyrimidine nucleoside phosphorylase); PDBTitle: the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
44	c2hsiB	Alignment	not modelled	82.9	17	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative peptidase m23; PDBTitle: crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
45	c2gu1A	Alignment	not modelled	82.1	17	PDB header: hydrolase Chain: A: PDB Molecule: zinc peptidase; PDBTitle: crystal structure of a zinc containing peptidase from2 vibrio cholerae
46	d1ci3m2	Alignment	not modelled	82.0	28	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
47	c3fmcC	Alignment	not modelled	79.7	10	PDB header: hydrolase Chain: C: PDB Molecule: putative succinylglutamate desuccinylase / aspartoacylase; PDBTitle: crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
48	d1qwyA	Alignment	not modelled	77.4	17	Fold: Barrel-sandwich hybrid Superfamily: Duplicated hybrid motif Family: Peptidoglycan hydrolase LytM
49	c2qj8B	Alignment	not modelled	75.2	13	PDB header: hydrolase Chain: B: PDB Molecule: mlr6093 protein; PDBTitle: crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
50	c2aukA	Alignment	not modelled	75.0	25	PDB header: transferase Chain: A: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of e. coli rna polymerase beta' g/g' insert
51	d1e2wa2	Alignment	not modelled	73.7	44	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
52	c2jxmB	Alignment	not modelled	68.5	32	PDB header: electron transport Chain: B: PDB Molecule: cytochrome f; PDBTitle: ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
53	c2b44A	Alignment	not modelled	64.3	17	PDB header: hydrolase Chain: A: PDB Molecule: glycyl-glycine endopeptidase lytm; PDBTitle: truncated s. aureus lytm, p 32 2 1 crystal form

54	c3nyyA	 Alignment	not modelled	63.4	25	PDB header: hydrolase Chain: A: PDB Molecule: putative glycyl-glycine endopeptidase lytm; PDBTitle: crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
55	c3d4rE	 Alignment	not modelled	63.0	12	PDB header: unknown function Chain: E: PDB Molecule: domain of unknown function from the pfam-b_34464 family; PDBTitle: crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
56	c2aujD	 Alignment	not modelled	60.9	33	PDB header: transferase Chain: D: PDB Molecule: dna-directed rna polymerase beta' chain; PDBTitle: structure of thermus aquaticus rna polymerase beta'-subunit2 insert
57	d1qpoa2	 Alignment	not modelled	60.8	22	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
58	c3na6A	 Alignment	not modelled	59.7	16	PDB header: hydrolase Chain: A: PDB Molecule: succinylglutamate desuccinylase/aspartoacylase; PDBTitle: crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
59	c2xhaB	 Alignment	not modelled	59.1	22	PDB header: transcription Chain: B: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
60	c3it5B	 Alignment	not modelled	57.6	19	PDB header: hydrolase Chain: B: PDB Molecule: protease lasa; PDBTitle: crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
61	c3cdxB	 Alignment	not modelled	57.5	21	PDB header: hydrolase Chain: B: PDB Molecule: succinylglutamatedesuccinylase/aspartoacylase; PDBTitle: crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
62	d1o4ua2	 Alignment	not modelled	56.3	16	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
63	c1e2vB	 Alignment	not modelled	52.2	44	PDB header: electron transport proteins Chain: B: PDB Molecule: cytochrome f; PDBTitle: n153q mutant of cytochrome f from chlamydomonas reinhardtii
64	d1qapa2	 Alignment	not modelled	51.9	16	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
65	c1ctmA	 Alignment	not modelled	51.8	25	PDB header: electron transport(cytochrome) Chain: A: PDB Molecule: cytochrome f; PDBTitle: crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
66	c1tu2B	 Alignment	not modelled	49.5	38	PDB header: electron transport Chain: B: PDB Molecule: apocytochrome f; PDBTitle: the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
67	d1tu2b2	 Alignment	not modelled	49.4	38	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
68	c2xhcA	 Alignment	not modelled	48.7	22	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
69	c3csqC	 Alignment	not modelled	47.3	20	PDB header: hydrolase Chain: C: PDB Molecule: morphogenesis protein 1; PDBTitle: crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
70	c1q90A	 Alignment	not modelled	41.9	14	PDB header: photosynthesis Chain: A: PDB Molecule: apocytochrome f; PDBTitle: structure of the cytochrome b6f (plastohydroquinone : plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
71	c2e75C	 Alignment	not modelled	41.1	13	PDB header: photosynthesis Chain: C: PDB Molecule: apocytochrome f; PDBTitle: crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
72	d1hyoa2	 Alignment	not modelled	40.5	33	Fold: FAH Superfamily: FAH Family: FAH
73	c3r6oA	 Alignment	not modelled	38.1	41	PDB header: isomerase Chain: A: PDB Molecule: 2-hydroxyhepta-2,4-diene-1, 7-dioateisomerase; PDBTitle: crystal structure of a probable 2-hydroxyhepta-2,4-diene-1, 7-2 dioateisomerase from mycobacterium abscessus
74	c1wlfA	 Alignment	not modelled	36.3	32	PDB header: protein transport Chain: A: PDB Molecule: peroxisome biogenesis factor 1; PDBTitle: structure of the n-terminal domain of pex1 aaa-atpase:2 characterization of a putative adaptor-binding domain
75	c3a8jF	 Alignment	not modelled	36.0	17	PDB header: transferase/transport protein Chain: F: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of et-ehred complex
76	c2zpmA	 Alignment	not modelled	34.8	40	PDB header: hydrolase Chain: A: PDB Molecule: regulator of sigma e protease; PDBTitle: crystal structure analysis of pdz domain b
		 Alignment				PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide

77	c3gnaA	Alignment	not modelled	34.3	10	pyrophosphorylase; PDBTitle: crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
78	d1hcza2	Alignment	not modelled	34.2	25	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
79	c1o4uA	Alignment	not modelled	34.0	15	PDB header: transferase Chain: A: PDB Molecule: type ii quinolic acid phosphoribosyltransferase; PDBTitle: crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
80	c2j5uB	Alignment	not modelled	29.6	38	PDB header: cell shape regulation Chain: B: PDB Molecule: mrec protein; PDBTitle: mrec lysteria monocytogenes
81	c2qf4A	Alignment	not modelled	28.3	22	PDB header: structural protein Chain: A: PDB Molecule: cell shape determining protein mrec; PDBTitle: high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
82	c2jbmA	Alignment	not modelled	28.1	9	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: qprtase structure from human
83	c1qapA	Alignment	not modelled	28.0	9	PDB header: glycosyltransferase Chain: A: PDB Molecule: quinolinic acid phosphoribosyltransferase; PDBTitle: quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
84	c1hyoB	Alignment	not modelled	27.5	34	PDB header: hydrolase Chain: B: PDB Molecule: fumarylacetoacetate hydrolase; PDBTitle: crystal structure of fumarylacetoacetate hydrolase2 complexed with 4-(hydroxymethylphosphino)l-3-oxo-butanoic3 acid
85	c3paiA	Alignment	not modelled	26.4	9	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase, carboxylating; PDBTitle: 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
86	c1i7oC	Alignment	not modelled	25.8	26	PDB header: isomerase, lyase Chain: C: PDB Molecule: 4-hydroxyphenylacetate degradation bifunctional PDBTitle: crystal structure of hpce
87	c2dfuB	Alignment	not modelled	23.7	30	PDB header: isomerase Chain: B: PDB Molecule: probable 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase; PDBTitle: crystal structure of the 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase2 from thermus thermophilus hb8
88	c2b7pA	Alignment	not modelled	23.0	6	PDB header: transferase Chain: A: PDB Molecule: probable nicotinate-nucleotide pyrophosphorylase; PDBTitle: crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
89	c3pikA	Alignment	not modelled	22.5	12	PDB header: transport protein Chain: A: PDB Molecule: cation efflux system protein cusc; PDBTitle: outer membrane protein cusc
90	d1vf5c2	Alignment	not modelled	21.1	38	Fold: Barrel-sandwich hybrid Superfamily: Rudiment single hybrid motif Family: Cytochrome f, small domain
91	c3tqvA	Alignment	not modelled	20.8	8	PDB header: transferase Chain: A: PDB Molecule: nicotinate-nucleotide pyrophosphorylase; PDBTitle: structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
92	d2qamc2	Alignment	not modelled	20.8	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
93	d1wplA	Alignment	not modelled	20.2	12	Fold: Outer membrane efflux proteins (OEP) Superfamily: Outer membrane efflux proteins (OEP) Family: Outer membrane efflux proteins (OEP)
94	d1rl2a2	Alignment	not modelled	20.1	23	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Cold shock DNA-binding domain-like
95	c1wzoC	Alignment	not modelled	19.9	25	PDB header: isomerase Chain: C: PDB Molecule: hpce; PDBTitle: crystal structure of the hpce from thermus thermophilus hb8
96	d1vioa2	Alignment	not modelled	19.9	11	Fold: Alpha-L RNA-binding motif Superfamily: Alpha-L RNA-binding motif Family: Pseudouridine synthase RsuA N-terminal domain
97	d1nkqa	Alignment	not modelled	19.8	29	Fold: FAH Superfamily: FAH Family: FAH
98	d1sawa	Alignment	not modelled	19.4	21	Fold: FAH Superfamily: FAH Family: FAH
99	c3mxuA	Alignment	not modelled	19.4	22	PDB header: oxidoreductase Chain: A: PDB Molecule: glycine cleavage system h protein; PDBTitle: crystal structure of glycine cleavage system protein h from bartonella2 henselae