







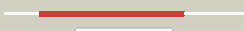










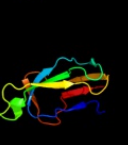


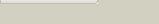

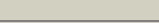
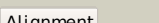
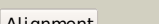
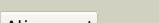

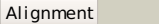


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d2f3ga_</a>	 Alignment		100.0	40	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
2	<a href="#">d1glaf_</a>	 Alignment		100.0	39	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
3	<a href="#">d2gpaa_</a>	 Alignment		100.0	31	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
4	<a href="#">d1gpaa_</a>	 Alignment		100.0	38	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
5	<a href="#">c3qngD_</a>	 Alignment		100.0	15	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> D: <b>PDB Molecule:</b> pts system, cellobiose-specific iic component; <b>PDBTitle:</b> crystal structure of the transporter chbc, the iic component from the 2 n,n'-diacetylchitobiose-specific phosphotransferase system
6	<a href="#">c3ipjB_</a>	 Alignment		99.9	27	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> pts system, iiaabc component; <b>PDBTitle:</b> the crystal structure of one domain of the pts system, iiaabc component2 from clostridium difficile
7	<a href="#">c1ibaA_</a>	 Alignment		99.9	34	<b>PDB header:</b> phosphotransferase <b>Chain:</b> A: <b>PDB Molecule:</b> glucose permease; <b>PDBTitle:</b> glucose permease (domain iib), nmr, 11 structures
8	<a href="#">d3bp8c1</a>	 Alignment		99.9	34	<b>Fold:</b> Homing endonuclease-like <b>Superfamily:</b> Glucose permease domain IIB <b>Family:</b> Glucose permease domain IIB
9	<a href="#">d1dcza_</a>	 Alignment		97.5	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
10	<a href="#">c3n6rK_</a>	 Alignment		97.2	18	<b>PDB header:</b> ligase <b>Chain:</b> K: <b>PDB Molecule:</b> propionyl-coa carboxylase, alpha subunit; <b>PDBTitle:</b> crystal structure of the holoenzyme of propionyl-coa carboxylase (pcc)
11	<a href="#">c2b44A_</a>	 Alignment		97.2	18	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> glycyl-glycine endopeptidase lytm; <b>PDBTitle:</b> truncated s. aureus lytm, p 32 2 1 crystal form

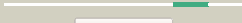
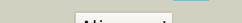
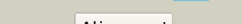







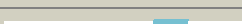

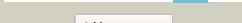
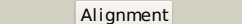


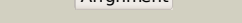
12	<a href="#">dlqwyA_</a>	Alignment		97.1	13	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Peptidoglycan hydrolase LytM
13	<a href="#">dlo78a_</a>	Alignment		97.0	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
14	<a href="#">dlbdoa_</a>	Alignment		97.0	27	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
15	<a href="#">c2gu1A_</a>	Alignment		96.8	11	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> zinc peptidase; <b>PDBTitle:</b> crystal structure of a zinc containing peptidase from2 vibrio cholerae
16	<a href="#">c2qf7A_</a>	Alignment		96.6	29	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate carboxylase protein; <b>PDBTitle:</b> crystal structure of a complete multifunctional pyruvate carboxylase2 from rhizobium etli
17	<a href="#">c2ejgD_</a>	Alignment		96.5	20	<b>PDB header:</b> ligase <b>Chain:</b> D: <b>PDB Molecule:</b> 149aa long hypothetical methylmalonyl-coa decarboxylase <b>PDBTitle:</b> crystal structure of the biotin protein ligase (mutation r48a) and2 biotin carboxyl carrier protein complex from pyrococcus horikoshii3 ot3
18	<a href="#">c2ejmA_</a>	Alignment		96.4	21	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> methylcrotonoyl-coa carboxylase subunit alpha; <b>PDBTitle:</b> solution structure of ruh-072, an apo-biotin domain form2 human acetyl coenzyme a carboxylase
19	<a href="#">d1vf7a_</a>	Alignment		96.1	34	<b>Fold:</b> HlyD-like secretion proteins <b>Superfamily:</b> HlyD-like secretion proteins <b>Family:</b> HlyD-like secretion proteins
20	<a href="#">c2dn8A_</a>	Alignment		96.0	20	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> solution structure of rsgi ruh-053, an apo-biotin carboxy2 carrier protein from human transcarboxylase
21	<a href="#">c2hsiB_</a>	Alignment	not modelled	96.0	21	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> putative peptidase m23; <b>PDBTitle:</b> crystal structure of putative peptidase m23 from2 pseudomonas aeruginosa, new york structural genomics3 consortium
22	<a href="#">c2b8gA_</a>	Alignment	not modelled	96.0	18	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> biotin/lipoyl attachment protein; <b>PDBTitle:</b> solution structure of bacillus subtilis blap biotinylated-2 form (energy minimized mean structure)
23	<a href="#">c3nyyA_</a>	Alignment	not modelled	95.8	20	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> putative glycyl-glycine endopeptidase lytm; <b>PDBTitle:</b> crystal structure of a putative glycyl-glycine endopeptidase lytm2 (rumgna_02482) from ruminococcus gnavus atcc 29149 at 1.60 a3 resolution
24	<a href="#">c2aukA_</a>	Alignment	not modelled	95.8	16	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> structure of e. coli rna polymerase beta' g/g' insert
25	<a href="#">d1ci3m2</a>	Alignment	not modelled	95.6	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
26	<a href="#">dliyuA_</a>	Alignment	not modelled	95.3	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
27	<a href="#">d1ghja_</a>	Alignment	not modelled	95.3	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
28	<a href="#">c1q90A_</a>	Alignment	not modelled	95.2	19	<b>PDB header:</b> photosynthesis <b>Chain:</b> A: <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> structure of the cytochrome b6f (plastohydroquinone :

						plastocyanin2 oxidoreductase) from chlamydomonas reinhardtii
29	<a href="#">c1e2vB_</a>	Alignment	not modelled	95.1	19	<b>PDB header:</b> electron transport proteins <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> n153q mutant of cytochrome f from chlamydomonas reinhardtii
30	<a href="#">c2jxmB_</a>	Alignment	not modelled	94.9	26	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> ensemble of twenty structures of the prochlorothrix2 hollandica plastocyanin- cytochrome f complex
31	<a href="#">d1k8ma_</a>	Alignment	not modelled	94.7	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
32	<a href="#">c2l5tA_</a>	Alignment	not modelled	94.6	19	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipamide acyltransferase; <b>PDBTitle:</b> solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
33	<a href="#">d1qjoa_</a>	Alignment	not modelled	94.6	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
34	<a href="#">d1laba_</a>	Alignment	not modelled	94.3	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
35	<a href="#">c3csqC_</a>	Alignment	not modelled	94.1	16	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> morphogenesis protein 1; <b>PDBTitle:</b> crystal and cryoem structural studies of a cell wall2 degrading enzyme in the bacteriophage phi29 tail
36	<a href="#">c2q8iB_</a>	Alignment	not modelled	94.0	23	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase component of <b>PDBTitle:</b> pyruvate dehydrogenase kinase isoform 3 in complex with antitumor drug2 radicicol
37	<a href="#">d1gjxa_</a>	Alignment	not modelled	94.0	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
38	<a href="#">c1tu2B_</a>	Alignment	not modelled	93.9	19	<b>PDB header:</b> electron transport <b>Chain:</b> B: <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> the complex of nostoc cytochrome f and plastocyanin determin with2 paramagnetic nmr. based on the structures of cytochrome f and3 plastocyanin, 10 structures
39	<a href="#">c2dncA_</a>	Alignment	not modelled	93.6	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component; <b>PDBTitle:</b> solution structure of rsgi ruh-054, a lipoyl domain from2 human 2-oxoacid dehydrogenase
40	<a href="#">d1y8ob1</a>	Alignment	not modelled	93.5	23	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
41	<a href="#">c3h9iB_</a>	Alignment	not modelled	92.8	38	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cation efflux system protein cusb; <b>PDBTitle:</b> crystal structure of the membrane fusion protein cusb from escherichia2 coli
42	<a href="#">c1t5eB_</a>	Alignment	not modelled	92.7	17	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> multidrug resistance protein mexa; <b>PDBTitle:</b> the structure of mexa
43	<a href="#">d1e2wa2</a>	Alignment	not modelled	92.6	22	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
44	<a href="#">c2kccA_</a>	Alignment	not modelled	92.5	14	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> acetyl-coa carboxylase 2; <b>PDBTitle:</b> solution structure of biotinoyl domain from human acetyl-2 coa carboxylase 2
45	<a href="#">d1uoua3</a>	Alignment	not modelled	92.2	19	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
46	<a href="#">c1ctmA_</a>	Alignment	not modelled	91.7	15	<b>PDB header:</b> electron transport(cytochrome) <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome f; <b>PDBTitle:</b> crystal structure of chloroplast cytochrome f reveals a2 novel cytochrome fold and unexpected heme ligation
47	<a href="#">c2f1mA_</a>	Alignment	not modelled	91.3	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acriflavine resistance protein a; <b>PDBTitle:</b> conformational flexibility in the multidrug efflux system protein acra
48	<a href="#">c3fppB_</a>	Alignment	not modelled	91.2	22	<b>PDB header:</b> membrane protein <b>Chain:</b> B: <b>PDB Molecule:</b> macrolide-specific efflux protein maca; <b>PDBTitle:</b> crystal structure of e.coli maca
49	<a href="#">c3l1nnB_</a>	Alignment	not modelled	91.0	31	<b>PDB header:</b> metal transport <b>Chain:</b> B: <b>PDB Molecule:</b> membrane fusion protein (mfp) heavy metal cation efflux <b>PDBTitle:</b> crystal structure of zneb from cupriavidus metallidurans
50	<a href="#">d1pmra_</a>	Alignment	not modelled	90.8	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
51	<a href="#">c2e75C_</a>	Alignment	not modelled	89.8	19	<b>PDB header:</b> photosynthesis <b>Chain:</b> C: <b>PDB Molecule:</b> apocytochrome f; <b>PDBTitle:</b> crystal structure of the cytochrome b6f complex with 2-nonyl-4-2 hydroxyquinoline n-oxide (nqno) from m.laminosus
52	<a href="#">c3fmcC_</a>	Alignment	not modelled	88.4	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> putative succinylglutamate desuccinylase / aspartoacylase; <b>PDBTitle:</b> crystal structure of a putative succinylglutamate desuccinylase /2 aspartoacylase family protein (sama_0604) from shewanella amazonensis3 sb2b at 1.80 a resolution
53	<a href="#">c2dneA_</a>	Alignment	not modelled	87.9	18	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> solution structure of rsgi ruh-058, a lipoyl domain of2

						human 2-oxoacid dehydrogenase
54	<a href="#">c2k33A_</a>	Alignment	not modelled	87.0	19	<b>PDB header:</b> membrane protein, transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> acra; <b>PDBTitle:</b> solution structure of an n-glycosylated protein using in2 vitro glycosylation
55	<a href="#">d1brwa3</a>	Alignment	not modelled	85.7	25	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
56	<a href="#">d2pnrc1</a>	Alignment	not modelled	84.3	28	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
57	<a href="#">d2tpa3</a>	Alignment	not modelled	83.3	21	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
58	<a href="#">c2aujD_</a>	Alignment	not modelled	82.6	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> dna-directed rna polymerase beta' chain; <b>PDBTitle:</b> structure of thermus aquaticus rna polymerase beta' - subunit2 insert
59	<a href="#">d1kl9a2</a>	Alignment	not modelled	82.2	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
60	<a href="#">d1q46a2</a>	Alignment	not modelled	79.2	12	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
61	<a href="#">c2qj8B_</a>	Alignment	not modelled	77.6	18	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> mlr6093 protein; <b>PDBTitle:</b> crystal structure of an aspartoacylase family protein (mlr6093) from2 mesorhizobium loti maff303099 at 2.00 a resolution
62	<a href="#">c3cdxB_</a>	Alignment	not modelled	77.2	17	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> succinylglutamatedesuccinylase/aspartoacylase; <b>PDBTitle:</b> crystal structure of2 succinylglutamatedesuccinylase/aspartoacylase from3 rhodobacter sphaeroides
63	<a href="#">c1brwB_</a>	Alignment	not modelled	76.2	25	<b>PDB header:</b> transferase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (pyrimidine nucleoside phosphorylase); <b>PDBTitle:</b> the crystal structure of pyrimidine nucleoside2 phosphorylase in a closed conformation
64	<a href="#">c3it5B_</a>	Alignment	not modelled	76.1	21	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protease lasa; <b>PDBTitle:</b> crystal structure of the lasa virulence factor from pseudomonas2 aeruginosa
65	<a href="#">c2dsjA_</a>	Alignment	not modelled	75.9	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine-nucleoside (thymidine) phosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0128 from thermus thermophilus hb8
66	<a href="#">c3h5qA_</a>	Alignment	not modelled	75.4	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyrimidine-nucleoside phosphorylase; <b>PDBTitle:</b> crystal structure of a putative pyrimidine-nucleoside phosphorylase2 from staphylococcus aureus
67	<a href="#">c1otpA_</a>	Alignment	not modelled	74.7	21	<b>PDB header:</b> phosphorylase <b>Chain:</b> A: <b>PDB Molecule:</b> thymidine phosphorylase; <b>PDBTitle:</b> structural and theoretical studies suggest domain movement produces an2 active conformation of thymidine phosphorylase
68	<a href="#">c2j0fC_</a>	Alignment	not modelled	74.2	21	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> thymidine phosphorylase; <b>PDBTitle:</b> structural basis for non-competitive product inhibition in2 human thymidine phosphorylase: implication for drug design
69	<a href="#">c3na6A_</a>	Alignment	not modelled	65.5	21	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> succinylglutamate desuccinylase/aspartoacylase; <b>PDBTitle:</b> crystal structure of a succinylglutamate desuccinylase (tm1040_2694)2 from silicibacter sp. tm1040 at 2.00 a resolution
70	<a href="#">c3a8jF_</a>	Alignment	not modelled	62.9	33	<b>PDB header:</b> transferase/transport protein <b>Chain:</b> F: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> crystal structure of et-ehred complex
71	<a href="#">d1o4ua2</a>	Alignment	not modelled	62.0	10	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
72	<a href="#">d1qpoa2</a>	Alignment	not modelled	61.5	25	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
73	<a href="#">c2jkuA_</a>	Alignment	not modelled	60.8	23	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> propionyl-coa carboxylase alpha chain, <b>PDBTitle:</b> crystal structure of the n-terminal region of the biotin2 acceptor domain of human propionyl-coa carboxylase
74	<a href="#">d2nn6h1</a>	Alignment	not modelled	57.9	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
75	<a href="#">d1at0a_</a>	Alignment	not modelled	56.4	12	<b>Fold:</b> Hedgehog/intein (Hint) domain <b>Superfamily:</b> Hedgehog/intein (Hint) domain <b>Family:</b> Hedgehog C-terminal (Hog) autoprocessing domain
76	<a href="#">d1qapa2</a>	Alignment	not modelled	55.7	20	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
77	<a href="#">c2xhaB_</a>	Alignment	not modelled	55.0	18	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)

78	<a href="#">c3i4oA</a>	 Alignment	not modelled	54.8	30	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor if-1; <b>PDBTitle:</b> crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
79	<a href="#">d2es2a1</a>	 Alignment	not modelled	53.1	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
80	<a href="#">c3a0jB</a>	 Alignment	not modelled	50.9	27	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> cold shock protein; <b>PDBTitle:</b> crystal structure of cold shock protein 1 from thermus2 thermophilus hb8
81	<a href="#">d1ah9a</a>	 Alignment	not modelled	50.2	25	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
82	<a href="#">c2ka7A</a>	 Alignment	not modelled	49.0	11	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> nmr solution structure of tm0212 at 40 c
83	<a href="#">c3gnnA</a>	 Alignment	not modelled	48.6	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide2 pyrophosphorylase from burkholderi pseudomallei
84	<a href="#">c2hc8A</a>	 Alignment	not modelled	48.4	20	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation-transporting atpase, p-type; <b>PDBTitle:</b> structure of the a. fulgidus copa a-domain
85	<a href="#">d1smxa</a>	 Alignment	not modelled	48.3	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
86	<a href="#">c1yz6A</a>	 Alignment	not modelled	48.2	17	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> probable translation initiation factor 2 alpha <b>PDBTitle:</b> crystal structure of intact alpha subunit of aif2 from2 pyrococcus abyssi
87	<a href="#">d2z0sa1</a>	 Alignment	not modelled	47.3	16	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
88	<a href="#">c3mxuA</a>	 Alignment	not modelled	46.7	21	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> crystal structure of glycine cleavage system protein h from bartonella2 henselae
89	<a href="#">d1oxxk1</a>	 Alignment	not modelled	46.0	18	<b>Fold:</b> OB-fold <b>Superfamily:</b> MOP-like <b>Family:</b> ABC-transporter additional domain
90	<a href="#">c3ic8D</a>	 Alignment	not modelled	45.4	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> uncharacterized gst-like proteinprotein; <b>PDBTitle:</b> the crystal structure of a gst-like protein from pseudomonas syringae2 to 2.4a
91	<a href="#">c3sy6A</a>	 Alignment	not modelled	45.4	25	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> fimbrial protein bf1861; <b>PDBTitle:</b> crystal structure of a fimbrial protein bf1861 [bacteroides fragilis2 nctc 9343] (bf1861) from bacteroides fragilis nctc 9343 at 1.90 a3 resolution
92	<a href="#">d1tu2b2</a>	 Alignment	not modelled	45.2	33	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
93	<a href="#">d1g6pa</a>	 Alignment	not modelled	44.2	17	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
94	<a href="#">c3tqvA</a>	 Alignment	not modelled	44.0	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> structure of the nicotinate-nucleotide pyrophosphorylase from2 francisella tularensis.
95	<a href="#">c3paiA</a>	 Alignment	not modelled	43.1	25	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase, carboxylating; <b>PDBTitle:</b> 2.00 angstrom resolution crystal structure of a quinolinate2 phosphoribosyltransferase from vibrio cholerae o1 biovar eltor str.3 n16961
96	<a href="#">c2xhcA</a>	 Alignment	not modelled	43.0	18	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> transcription antitermination protein nusg; <b>PDBTitle:</b> crystal structure of thermotoga maritima n-utilization substance g2 (nusg)
97	<a href="#">c3t2lA</a>	 Alignment	not modelled	41.5	17	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> putative cell adhesion protein; <b>PDBTitle:</b> crystal structure of a putative cell adhesion protein (bf1858) from2 bacteroides fragilis nctc 9343 at 2.33 a resolution
98	<a href="#">d1onla</a>	 Alignment	not modelled	41.5	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
99	<a href="#">d1hpca</a>	 Alignment	not modelled	41.3	14	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
100	<a href="#">c1vdzA</a>	 Alignment	not modelled	41.2	22	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> a-type atpase subunit a; <b>PDBTitle:</b> crystal structure of a-type atpase catalytic subunit a from2 pyrococcus horikoshii ot3
101	<a href="#">c3iftA</a>	 Alignment	not modelled	41.2	18	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> crystal structure of glycine cleavage system protein h from2 mycobacterium tuberculosis, using x-rays from the compact light3 source.
102	<a href="#">d2je6i2</a>	 Alignment	not modelled	40.8	19	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Ribosomal L27 protein-like



						<b>Family:</b> ECR1 N-terminal domain-like
103	<a href="#">c1qapA</a>	 Alignment	not modelled	40.7	20	<b>PDB header:</b> glycosyltransferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinic acid phosphoribosyltransferase; <b>PDBTitle:</b> quinolinic acid phosphoribosyltransferase with bound2 quinolinic acid
104	<a href="#">c2eqsA</a>	 Alignment	not modelled	39.6	17	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> atp-dependent rna helicase dhx8; <b>PDBTitle:</b> solution structure of the s1 rna binding domain of human2 atp-dependent rna helicase dhx8
105	<a href="#">c2edgA</a>	 Alignment	not modelled	39.1	24	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> A: <b>PDB Molecule:</b> glycine cleavage system h protein; <b>PDBTitle:</b> solution structure of the gcv_h domain from mouse glycine
106	<a href="#">c1q46A</a>	 Alignment	not modelled	38.7	10	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> translation initiation factor 2 alpha subunit; <b>PDBTitle:</b> crystal structure of the eif2 alpha subunit from2 saccharomyces cerevisia
107	<a href="#">c1x1oC</a>	 Alignment	not modelled	38.0	25	<b>PDB header:</b> transferase <b>Chain:</b> C: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of project id tt0268 from thermus thermophilus hb8
108	<a href="#">c1q8kA</a>	 Alignment	not modelled	35.9	12	<b>PDB header:</b> translation <b>Chain:</b> A: <b>PDB Molecule:</b> eukaryotic translation initiation factor 2 <b>PDBTitle:</b> solution structure of alpha subunit of human eif2
109	<a href="#">c1o4uA</a>	 Alignment	not modelled	35.6	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> type ii quinolic acid phosphoribosyltransferase; <b>PDBTitle:</b> crystal structure of a nicotinate nucleotide pyrophosphorylase2 (tm1645) from thermotoga maritima at 2.50 a resolution
110	<a href="#">c3l0gD</a>	 Alignment	not modelled	34.7	25	<b>PDB header:</b> transferase <b>Chain:</b> D: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of nicotinate-nucleotide pyrophosphorylase from2 ehrlichia chaffeensis at 2.05a resolution
111	<a href="#">d1hcza2</a>	 Alignment	not modelled	34.6	19	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
112	<a href="#">c2kcmA</a>	 Alignment	not modelled	34.0	27	<b>PDB header:</b> nucleic acid binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> cold shock domain family protein; <b>PDBTitle:</b> solution nmr structure of the n-terminal ob-domain of so_1732 from2 shewanella oneidensis. northeast structural genomics consortium3 target sor210a.
113	<a href="#">d1d7qa</a>	 Alignment	not modelled	33.4	24	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
114	<a href="#">c2kncA</a>	 Alignment	not modelled	33.1	5	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> integrin alpha-iiB; <b>PDBTitle:</b> platelet integrin alfaIIB-beta3 transmembrane-cytoplasmic2 heterocomplex
115	<a href="#">c2jbmA</a>	 Alignment	not modelled	32.9	21	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> qprtase structure from human
116	<a href="#">d1y14b1</a>	 Alignment	not modelled	32.9	10	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
117	<a href="#">d1c9oa</a>	 Alignment	not modelled	32.3	20	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
118	<a href="#">c1qpoA</a>	 Alignment	not modelled	31.9	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> quinolinate acid phosphoribosyl transferase; <b>PDBTitle:</b> quinolinate phosphoribosyl transferase (qaprtase) apo-enzyme from2 mycobacterium tuberculosis
119	<a href="#">d2ba0a1</a>	 Alignment	not modelled	31.5	15	<b>Fold:</b> OB-fold <b>Superfamily:</b> Nucleic acid-binding proteins <b>Family:</b> Cold shock DNA-binding domain-like
120	<a href="#">d2uube1</a>	 Alignment	not modelled	31.0	15	<b>Fold:</b> Ribosomal protein S5 domain 2-like <b>Superfamily:</b> Ribosomal protein S5 domain 2-like <b>Family:</b> Translational machinery components