




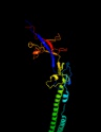





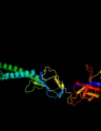

















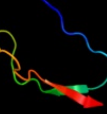

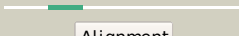
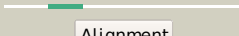
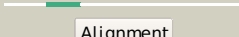


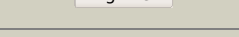

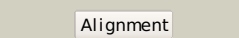
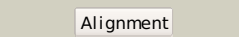

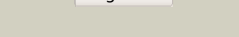
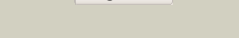



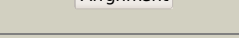
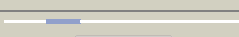
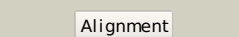
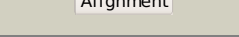




#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3h9iB_</a>	 Alignment		100.0	20	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> cation efflux system protein cusb; <b>PDBTitle:</b> crystal structure of the membrane fusion protein cusb from escherichia2 coli
2	<a href="#">c2f1mA_</a>	 Alignment		99.9	98	<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
3	<a href="#">c3fppB_</a>	 Alignment		99.9	18	<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
4	<a href="#">c1t5eB_</a>	 Alignment		99.9	60	<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
5	<a href="#">d1vf7a_</a>	 Alignment		99.9	58	<b>Fold:</b> HlyD-like secretion proteins <b>Superfamily:</b> HlyD-like secretion proteins <b>Family:</b> HlyD-like secretion proteins
6	<a href="#">c3l1nnB_</a>	 Alignment		99.9	20	<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
7	<a href="#">c2k33A_</a>	 Alignment		98.9	27	<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
8	<a href="#">c2b8gA_</a>	 Alignment		97.1	28	<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)
9	<a href="#">d1dcza_</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
10	<a href="#">c2ejgD_</a>	 Alignment		96.9	19	<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
11	<a href="#">c3n6rK_</a>	 Alignment		96.8	14	<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)

12	<a href="#">d1o78a_</a>	Alignment		96.7	23	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
13	<a href="#">c2l5tA_</a>	Alignment		96.7	32	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> lipoamide acyltransferase; <b>PDBTitle:</b> solution nmr structure of e2 lipoyl domain from thermoplasma2 acidophilum
14	<a href="#">c2dn8A_</a>	Alignment		96.7	23	<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
15	<a href="#">c2ejmA_</a>	Alignment		96.6	29	<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
16	<a href="#">c2kccA_</a>	Alignment		96.6	22	<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
17	<a href="#">d1iyua_</a>	Alignment		96.6	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
18	<a href="#">d1bdoa_</a>	Alignment		96.6	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
19	<a href="#">d1ghja_</a>	Alignment		96.4	24	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
20	<a href="#">d1k8ma_</a>	Alignment		96.2	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
21	<a href="#">d1qjoa_</a>	Alignment	not modelled	96.0	15	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
22	<a href="#">d1laba_</a>	Alignment	not modelled	95.5	26	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
23	<a href="#">d1gjxa_</a>	Alignment	not modelled	95.4	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
24	<a href="#">d1glaf_</a>	Alignment	not modelled	95.4	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
25	<a href="#">d1y8ob1</a>	Alignment	not modelled	95.4	23	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
26	<a href="#">d2f3ga_</a>	Alignment	not modelled	95.2	21	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
27	<a href="#">d2pnrc1</a>	Alignment	not modelled	95.1	23	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
28	<a href="#">c2qf7A_</a>	Alignment	not modelled	95.1	22	<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
29	<a href="#">d2gprra_</a>	Alignment	not modelled	95.1	17	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif

						<b>Family:</b> Glucose permease-like
30	<a href="#">d1pmra</a>	Alignment	not modelled	95.1	18	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
31	<a href="#">c2q8iB</a>	Alignment	not modelled	94.9	25	<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
32	<a href="#">d1uoua3</a>	Alignment	not modelled	94.9	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
33	<a href="#">d1gpra</a>	Alignment	not modelled	94.9	27	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Glucose permease-like
34	<a href="#">d1brwa3</a>	Alignment	not modelled	94.5	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
35	<a href="#">c2dncA</a>	Alignment	not modelled	94.3	25	<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
36	<a href="#">d2tpta3</a>	Alignment	not modelled	94.0	23	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Pyrimidine nucleoside phosphorylase C-terminal domain <b>Family:</b> Pyrimidine nucleoside phosphorylase C-terminal domain
37	<a href="#">c2dneA</a>	Alignment	not modelled	93.6	13	<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
38	<a href="#">c2jkuA</a>	Alignment	not modelled	93.4	20	<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
39	<a href="#">c1otpA</a>	Alignment	not modelled	93.1	23	<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
40	<a href="#">c3h5qA</a>	Alignment	not modelled	91.3	37	<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
41	<a href="#">c2j0fC</a>	Alignment	not modelled	91.3	26	<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
42	<a href="#">c2dsjA</a>	Alignment	not modelled	90.9	26	<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
43	<a href="#">c1brwB</a>	Alignment	not modelled	89.8	26	<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
44	<a href="#">c3fmcC</a>	Alignment	not modelled	88.4	12	<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
45	<a href="#">c2hsiB</a>	Alignment	not modelled	86.9	22	<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
46	<a href="#">c2qj8B</a>	Alignment	not modelled	86.9	13	<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
47	<a href="#">c2gu1A</a>	Alignment	not modelled	86.7	17	<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
48	<a href="#">c2aukA</a>	Alignment	not modelled	83.8	20	<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
49	<a href="#">d1qwya</a>	Alignment	not modelled	82.9	13	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Duplicated hybrid motif <b>Family:</b> Peptidoglycan hydrolase LytM
50	<a href="#">c3na6A</a>	Alignment	not modelled	79.4	9	<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
51	<a href="#">c3cdxB</a>	Alignment	not modelled	79.1	16	<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
						<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> transcription antitermination protein

52	<a href="#">c2xhaB_</a>	Alignment	not modelled	76.7	17	nusg; <b>PDBTitle:</b> crystal structure of domain 2 of thermotoga maritima n-utilization2 substance g (nusg)
53	<a href="#">d1qpoa2</a>	Alignment	not modelled	76.5	17	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
54	<a href="#">c2b44A_</a>	Alignment	not modelled	75.2	13	<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
55	<a href="#">c3d4rE_</a>	Alignment	not modelled	73.7	10	<b>PDB header:</b> unknown function <b>Chain:</b> E: <b>PDB Molecule:</b> domain of unknown function from the pfam-b_34464 family; <b>PDBTitle:</b> crystal structure of a duf2118 family protein (mmp0046) from2 methanococcus maripaludis at 2.20 a resolution
56	<a href="#">d1o4ua2</a>	Alignment	not modelled	70.9	26	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
57	<a href="#">d1ci3m2</a>	Alignment	not modelled	70.4	31	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
58	<a href="#">d1e2wa2</a>	Alignment	not modelled	69.7	31	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
59	<a href="#">c3it5B_</a>	Alignment	not modelled	69.3	14	<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
60	<a href="#">d1qapa2</a>	Alignment	not modelled	69.0	16	<b>Fold:</b> alpha/beta-Hammerhead <b>Superfamily:</b> Nicotinate/Quinolinate PRTase N-terminal domain-like <b>Family:</b> NadC N-terminal domain-like
61	<a href="#">c2aujD_</a>	Alignment	not modelled	66.1	28	<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
62	<a href="#">c2xhcA_</a>	Alignment	not modelled	63.0	22	<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)
63	<a href="#">c3nyyA_</a>	Alignment	not modelled	60.2	21	<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
64	<a href="#">c3csqC_</a>	Alignment	not modelled	55.1	20	<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
65	<a href="#">c1o4uA_</a>	Alignment	not modelled	53.4	23	<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
66	<a href="#">c3a8jF_</a>	Alignment	not modelled	50.5	22	<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
67	<a href="#">c2edgA_</a>	Alignment	not modelled	50.4	8	<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
68	<a href="#">c3iftA_</a>	Alignment	not modelled	50.1	16	<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.
69	<a href="#">c3gnnA_</a>	Alignment	not modelled	49.9	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
70	<a href="#">c2jbmA_</a>	Alignment	not modelled	49.8	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> qprtase structure from human
71	<a href="#">d1onla_</a>	Alignment	not modelled	49.2	16	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
72	<a href="#">c1ctmA_</a>	Alignment	not modelled	49.2	25	<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
73	<a href="#">c3pajA_</a>	Alignment	not modelled	48.9	7	<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
74	<a href="#">c1e2vB_</a>	Alignment	not modelled	48.7	31	<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
75	<a href="#">c2jxmB_</a>	Alignment	not modelled	48.3	31	<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

76	<a href="#">c2b7pA</a>	 Alignment	not modelled	46.1	10	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> probable nicotinate-nucleotide pyrophosphorylase; <b>PDBTitle:</b> crystal structure of quinolinic acid phosphoribosyltransferase from2 helicobacter pylori
77	<a href="#">c1qapA</a>	 Alignment	not modelled	44.7	9	<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
78	<a href="#">c3tqvA</a>	 Alignment	not modelled	43.7	6	<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.
79	<a href="#">c1tu2B</a>	 Alignment	not modelled	43.4	31	<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
80	<a href="#">c3mxuA</a>	 Alignment	not modelled	42.7	12	<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
81	<a href="#">d1hpca</a>	 Alignment	not modelled	40.2	12	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Single hybrid motif <b>Family:</b> Biotinyl/lipoyl-carrier proteins and domains
82	<a href="#">d1tu2b2</a>	 Alignment	not modelled	39.9	31	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
83	<a href="#">c2j5uB</a>	 Alignment	not modelled	38.4	43	<b>PDB header:</b> cell shape regulation <b>Chain:</b> B: <b>PDB Molecule:</b> mrec protein; <b>PDBTitle:</b> mrec lysteria monocytogenes
84	<a href="#">c3l0gD</a>	 Alignment	not modelled	38.2	9	<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
85	<a href="#">c1x1oC</a>	 Alignment	not modelled	35.8	9	<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
86	<a href="#">c2zpmA</a>	 Alignment	not modelled	29.3	57	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> regulator of sigma e protease; <b>PDBTitle:</b> crystal structure analysis of pdz domain b
87	<a href="#">c1qpoA</a>	 Alignment	not modelled	29.2	12	<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
88	<a href="#">c2qf4A</a>	 Alignment	not modelled	27.0	33	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> cell shape determining protein mrec; <b>PDBTitle:</b> high resolution structure of the major periplasmic domain from the2 cell shape-determining filament mrec (orthorhombic form)
89	<a href="#">d1hcza2</a>	 Alignment	not modelled	26.9	25	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
90	<a href="#">c3pikA</a>	 Alignment	not modelled	26.8	15	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> cation efflux system protein cusc; <b>PDBTitle:</b> outer membrane protein cusc
91	<a href="#">d1wplA</a>	 Alignment	not modelled	24.1	16	<b>Fold:</b> Outer membrane efflux proteins (OEP) <b>Superfamily:</b> Outer membrane efflux proteins (OEP) <b>Family:</b> Outer membrane efflux proteins (OEP)
92	<a href="#">c3tbiB</a>	 Alignment	not modelled	21.5	21	<b>PDB header:</b> transcription <b>Chain:</b> B: <b>PDB Molecule:</b> dna-directed rna polymerase subunit beta; <b>PDBTitle:</b> crystal structure of t4 gp33 bound to e. coli rnap beta-flap domain
93	<a href="#">c3p42D</a>	 Alignment	not modelled	21.4	11	<b>PDB header:</b> unknown function <b>Chain:</b> D: <b>PDB Molecule:</b> predicted protein; <b>PDBTitle:</b> structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon
94	<a href="#">c2e75C</a>	 Alignment	not modelled	21.1	17	<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
95	<a href="#">c2ka7A</a>	 Alignment	not modelled	20.4	16	<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
96	<a href="#">c1q90A</a>	 Alignment	not modelled	20.3	13	<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
97	<a href="#">d1vf5c2</a>	Alignment	not modelled	20.1	38	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
98	<a href="#">c2v4hA</a>	Alignment	not modelled	19.3	15	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> nf-kappa-b essential modulator; <b>PDBTitle:</b> nemo cc2-lz domain - 1d5 darpin complex
99	<a href="#">d1wp5a</a>	Alignment	not modelled	19.3	20	<b>Fold:</b> 6-bladed beta-propeller <b>Superfamily:</b> GyrA/ParC C-terminal domain-like <b>Family:</b> GyrA/ParC C-terminal domain-like