

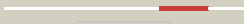


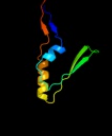
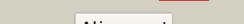

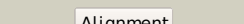

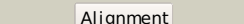

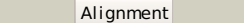

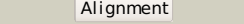

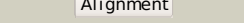

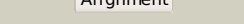

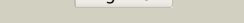









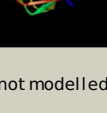


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2y9kG_</a>	 Alignment		98.2	14	<b>PDB header:</b> protein transport <b>Chain:</b> G: <b>PDB Molecule:</b> protein invg; <b>PDBTitle:</b> three-dimensional model of salmonella's needle complex at2 subnanometer resolution
2	<a href="#">c3gr5A_</a>	 Alignment		97.9	9	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> escsc; <b>PDBTitle:</b> periplasmic domain of the outer membrane secretin escsc from2 enteropathogenic e.coli (epec)
3	<a href="#">c2y3mA_</a>	 Alignment		96.2	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein transport protein hofq; <b>PDBTitle:</b> structure of the extra-membranous domain of the secretin2 hofq from actinobacillus actinomycetemcomitans
4	<a href="#">c2a02A_</a>	 Alignment		96.1	14	<b>PDB header:</b> membrane protein, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> ferric-pseudobactin 358 receptor; <b>PDBTitle:</b> solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter pupa from3 pseudomonas putida.
5	<a href="#">c3ezjA_</a>	 Alignment		96.1	10	<b>PDB header:</b> protein transport <b>Chain:</b> A: <b>PDB Molecule:</b> general secretion pathway protein gspd; <b>PDBTitle:</b> crystal structure of the n-terminal domain of the secretin gspd from2 etec determined with the assistance of a nanobody
6	<a href="#">c3hugl_</a>	 Alignment		95.7	12	<b>PDB header:</b> transcription/membrane protein <b>Chain:</b> J: <b>PDB Molecule:</b> probable conserved membrane protein; <b>PDBTitle:</b> crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
7	<a href="#">c3ossD_</a>	 Alignment		95.4	17	<b>PDB header:</b> protein transport <b>Chain:</b> D: <b>PDB Molecule:</b> type 2 secretion system, secretin gspd; <b>PDBTitle:</b> the crystal structure of enterotoxigenic escherichia coli gspc-gspd2 complex from the type ii secretion system
8	<a href="#">c2d1uA_</a>	 Alignment		94.9	10	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> iron(iii) dicitrate transport protein fecA; <b>PDBTitle:</b> solution structure of the periplasmic signaling domain of2 fecA from escherichia coli
9	<a href="#">c1zzvA_</a>	 Alignment		94.8	10	<b>PDB header:</b> membrane protein, metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> iron(iii) dicitrate transport protein fecA; <b>PDBTitle:</b> solution nmr structure of the periplasmic signaling domain2 of the outer membrane iron transporter fecA from3 escherichia coli.
10	<a href="#">c3eo6B_</a>	 Alignment		86.1	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> protein of unknown function (duf1255); <b>PDBTitle:</b> crystal structure of protein of unknown function (duf1255)2 (afe_2634) from acidithiobacillus ferrooxidans ncib8455 at3 0.97 a resolution
11	<a href="#">c3cddD_</a>	 Alignment		85.2	14	<b>PDB header:</b> structural protein <b>Chain:</b> D: <b>PDB Molecule:</b> prophage muso2, 43 kda tail protein; <b>PDBTitle:</b> crystal structure of prophage muso2, 43 kda tail protein from2 shewanella oneidensis

12	<a href="#">c3hqxA</a>	Alignment		85.1	18	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> upf0345 protein aciad0356; <b>PDBTitle:</b> crystal structure of protein of unknown function (duf1255, pf06865)2 from acinetobacter sp. adp1
13	<a href="#">d3cdda2</a>	Alignment		79.1	15	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
14	<a href="#">c2z2sD</a>	Alignment		78.7	8	<b>PDB header:</b> transcription <b>Chain:</b> D: <b>PDB Molecule:</b> anti-sigma factor chrr, transcriptional activator chrr; <b>PDBTitle:</b> crystal structure of rhodobacter sphaeroides sigE in complex with the2 anti-sigma chrr
15	<a href="#">d1uika1</a>	Alignment		74.2	11	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
16	<a href="#">d1uija1</a>	Alignment		71.0	8	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
17	<a href="#">c2eaaB</a>	Alignment		65.8	11	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> 7s globulin-3; <b>PDBTitle:</b> crystal structure of adzuki bean 7s globulin-3
18	<a href="#">c3s7eB</a>	Alignment		64.5	12	<b>PDB header:</b> allergen <b>Chain:</b> B: <b>PDB Molecule:</b> allergen ara h 1, clone p41b; <b>PDBTitle:</b> crystal structure of ara h 1
19	<a href="#">d2bnma2</a>	Alignment		62.8	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1459-like
20	<a href="#">c2pfwB</a>	Alignment		61.2	7	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel domain protein; <b>PDBTitle:</b> crystal structure of a rmlc-like cupin (sfri_3105) from shewanella2 frigidimarina ncimb 400 at 1.90 a resolution
21	<a href="#">c2cauA</a>	Alignment	not modelled	56.9	10	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> protein (canavalin); <b>PDBTitle:</b> canavalin from jack bean
22	<a href="#">d1yhfa1</a>	Alignment	not modelled	56.1	19	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
23	<a href="#">d1dgwa</a>	Alignment	not modelled	56.0	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
24	<a href="#">c2iaha</a>	Alignment	not modelled	54.7	14	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> ferripyoverdine receptor; <b>PDBTitle:</b> crystal structure of the ferripyoverdine receptor of the outer2 membrane of pseudomonas aeruginosa bound to ferripyoverdine.
25	<a href="#">d1fxza2</a>	Alignment	not modelled	51.7	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
26	<a href="#">c2bnoA</a>	Alignment	not modelled	50.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> epoxidase; <b>PDBTitle:</b> the structure of hydroxypropylphosphonic acid epoxidase2 from s. wedmorensis.
27	<a href="#">c1uija</a>	Alignment	not modelled	46.9	8	<b>PDB header:</b> sugar binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> beta subunit of beta conglycinin; <b>PDBTitle:</b> crystal structure of soybean beta-conglycinin beta2 homotrimer (i122m/k124w)
28	<a href="#">d2oyza1</a>	Alignment	not modelled	45.1	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> VPA0057-like

29	<a href="#">d1tkea1</a>	Alignment	not modelled	45.1	24	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
30	<a href="#">c2vz1A</a>	Alignment	not modelled	42.2	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> galactose oxidase; <b>PDBTitle:</b> prenat-galactose oxidase
31	<a href="#">c3es4B</a>	Alignment	not modelled	40.3	12	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein duf861 with a rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of protein of unknown function (duf861) with a rmlc-2 like cupin fold (17741406) from agrobacterium tumefaciens str. c583 (dupont) at 1.64 a resolution
32	<a href="#">c1wwtA</a>	Alignment	not modelled	38.4	15	<b>PDB header:</b> ligase <b>Chain:</b> A: <b>PDB Molecule:</b> threonyl-trna synthetase, cytoplasmic; <b>PDBTitle:</b> solution structure of the tgs domain from human threonyl-2 trna synthetase
33	<a href="#">d1dw0a</a>	Alignment	not modelled	38.0	19	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
34	<a href="#">d1yfua1</a>	Alignment	not modelled	36.7	8	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> 3-hydroxyanthranilic acid dioxygenase-like
35	<a href="#">d1y9qa2</a>	Alignment	not modelled	36.3	19	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Probable transcriptional regulator VC1968, C-terminal domain
36	<a href="#">d2j73a1</a>	Alignment	not modelled	36.2	11	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> PUD-like
37	<a href="#">c2ozjB</a>	Alignment	not modelled	34.8	12	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> cupin 2, conserved barrel; <b>PDBTitle:</b> crystal structure of a cupin superfamily protein (dsy2733) from2 desulfitobacterium hafniense dcb-2 at 1.60 a resolution
38	<a href="#">c3myxA</a>	Alignment	not modelled	32.8	8	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein pspto_0244; <b>PDBTitle:</b> crystal structure of a pspto_0244 (protein with unknown function which2 belongs to pfam duf861 family) from pseudomonas syringae pv. tomato3 str. dc3000 at 1.30 a resolution
39	<a href="#">c3kscD</a>	Alignment	not modelled	30.7	13	<b>PDB header:</b> plant protein <b>Chain:</b> D: <b>PDB Molecule:</b> lega class; <b>PDBTitle:</b> crystal structure of pea prolegumin, an 11s seed globulin2 from pisum sativum l.
40	<a href="#">d1j58a</a>	Alignment	not modelled	30.4	13	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
41	<a href="#">d2phla1</a>	Alignment	not modelled	30.3	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
42	<a href="#">d1j1la</a>	Alignment	not modelled	30.2	15	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Pirin-like
43	<a href="#">c3d37A</a>	Alignment	not modelled	30.0	7	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> tail protein, 43 kda; <b>PDBTitle:</b> the crystal structure of the tail protein from neisseria meningitidis2 mc58
44	<a href="#">c3bcwB</a>	Alignment	not modelled	29.6	9	<b>PDB header:</b> unknown function <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> crystal structure of a duf861 family protein with a rmlc-like cupin2 fold (bb1179) from bordetella bronchiseptica rb50 at 1.60 a3 resolution
45	<a href="#">d1gu2a</a>	Alignment	not modelled	28.7	14	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> monodomain cytochrome c
46	<a href="#">d1v8qa</a>	Alignment	not modelled	26.2	20	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Ribosomal L27 protein-like <b>Family:</b> Ribosomal L27 protein
47	<a href="#">d1o5ua</a>	Alignment	not modelled	25.9	21	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Hypothetical protein TM1112
48	<a href="#">d1od5a2</a>	Alignment	not modelled	25.8	7	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
49	<a href="#">c1wruA</a>	Alignment	not modelled	25.6	13	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> 43 kda tail protein; <b>PDBTitle:</b> structure of central hub elucidated by x-ray analysis of gene product2 44; baseplate component of bacteriophage mu
50	<a href="#">d2pyta1</a>	Alignment	not modelled	25.2	17	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> EutQ-like
51	<a href="#">d1wxma1</a>	Alignment	not modelled	25.1	26	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> Ubiquitin-like <b>Family:</b> Ras-binding domain, RBD
52	<a href="#">c3o5cA</a>	Alignment	not modelled	22.8	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c551 peroxidase; <b>PDBTitle:</b> cytochrome c peroxidase bccp of shewanella oneidensis
53	<a href="#">d1nyra2</a>	Alignment	not modelled	22.6	18	<b>Fold:</b> beta-Grasp (ubiquitin-like) <b>Superfamily:</b> TGS-like <b>Family:</b> TGS domain
54	<a href="#">d1wrua2</a>	Alignment	not modelled	21.8	13	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like

55	<a href="#">c1fxzC_</a>	Alignment	not modelled	21.7	10	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycinin g1; <b>PDBTitle:</b> crystal structure of soybean proglycinin a1ab1b homotrimer
56	<a href="#">c3kgIB_</a>	Alignment	not modelled	21.7	15	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> cruciferin; <b>PDBTitle:</b> crystal structure of procruciferin, 11s globulin from2 brassica napus
57	<a href="#">d1od5a1</a>	Alignment	not modelled	21.6	14	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
58	<a href="#">c2oziA_</a>	Alignment	not modelled	21.3	9	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein rpa4178; <b>PDBTitle:</b> structural genomics, the crystal structure of a putative2 protein rpa4178 from rhodopseudomonas palustris cga009
59	<a href="#">c2gu9B_</a>	Alignment	not modelled	21.3	6	<b>PDB header:</b> immune system <b>Chain:</b> B: <b>PDB Molecule:</b> tetracenomycin polyketide synthesis protein; <b>PDBTitle:</b> crystal structure of xc5357 from xanthomonas campestris: a2 putative tetracenomycin polyketide synthesis protein3 adopting a novel cupin subfamily structure
60	<a href="#">d1vj2a_</a>	Alignment	not modelled	21.2	12	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1459-like
61	<a href="#">c3ehkC_</a>	Alignment	not modelled	21.2	8	<b>PDB header:</b> plant protein <b>Chain:</b> C: <b>PDB Molecule:</b> prunin; <b>PDBTitle:</b> crystal structure of pru du amandin, an allergenic protein2 from prunus dulcis
62	<a href="#">d2oa4a1</a>	Alignment	not modelled	20.5	31	<b>Fold:</b> DNA/RNA-binding 3-helical bundle <b>Superfamily:</b> TrpR-like <b>Family:</b> SPO1678-like
63	<a href="#">c3hq7A_</a>	Alignment	not modelled	19.8	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> cytochrome c551 peroxidase; <b>PDBTitle:</b> ccpa from g. sulfurreducens, g94k/k97q/r100i variant
64	<a href="#">c2c1uB_</a>	Alignment	not modelled	19.7	15	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> di-haem cytochrome c peroxidase; <b>PDBTitle:</b> crystal structure of the di-haem cytochrome c peroxidase2 from paracoccus pantotrophus - oxidised form
65	<a href="#">c3qacA_</a>	Alignment	not modelled	19.7	10	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> 11s globulin seed storage protein; <b>PDBTitle:</b> structure of amaranth 11s proglobulin seed storage protein from2 amaranthus hypochondriacus l.
66	<a href="#">c3c3vA_</a>	Alignment	not modelled	19.5	10	<b>PDB header:</b> allergen <b>Chain:</b> A: <b>PDB Molecule:</b> arachin arah3 isoform; <b>PDBTitle:</b> crystal structure of peanut major allergen ara h 3
67	<a href="#">c3rnsA_</a>	Alignment	not modelled	19.0	14	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> cupin 2 conserved barrel domain protein; <b>PDBTitle:</b> cupin 2 conserved barrel domain protein from leptotrichia buccalis
68	<a href="#">d2f4pa1</a>	Alignment	not modelled	18.8	11	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> TM1287-like
69	<a href="#">c2e9qA_</a>	Alignment	not modelled	18.7	8	<b>PDB header:</b> plant protein <b>Chain:</b> A: <b>PDB Molecule:</b> 11s globulin subunit beta; <b>PDBTitle:</b> recombinant pro-11s globulin of pumpkin
70	<a href="#">c2vecA_</a>	Alignment	not modelled	18.7	10	<b>PDB header:</b> cytosolic protein <b>Chain:</b> A: <b>PDB Molecule:</b> pirin-like protein yahk; <b>PDBTitle:</b> the crystal structure of the protein yahk from escherichia2 coli
71	<a href="#">c2d5fB_</a>	Alignment	not modelled	18.6	14	<b>PDB header:</b> plant protein <b>Chain:</b> B: <b>PDB Molecule:</b> glycinin a3b4 subunit; <b>PDBTitle:</b> crystal structure of recombinant soybean proglycinin a3b4 subunit, its2 comparison with mature glycinin a3b4 subunit, responsible for hexamer3 assembly
72	<a href="#">d1eb7a2</a>	Alignment	not modelled	18.0	13	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
73	<a href="#">c3pdkB_</a>	Alignment	not modelled	17.9	20	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> phosphoglucosamine mutase; <b>PDBTitle:</b> crystal structure of phosphoglucosamine mutase from b. anthracis
74	<a href="#">d1mpga2</a>	Alignment	not modelled	16.9	10	<b>Fold:</b> TBP-like <b>Superfamily:</b> TATA-box binding protein-like <b>Family:</b> DNA repair glycosylase, N-terminal domain
75	<a href="#">c2i45C_</a>	Alignment	not modelled	16.4	15	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of protein nmb1881 from neisseria meningitidis
76	<a href="#">d2p5zx2</a>	Alignment	not modelled	16.3	7	<b>Fold:</b> Phage tail proteins <b>Superfamily:</b> Phage tail proteins <b>Family:</b> Baseplate protein-like
77	<a href="#">c1nmlA_</a>	Alignment	not modelled	15.9	8	<b>PDB header:</b> oxidoreductase <b>Chain:</b> A: <b>PDB Molecule:</b> di-haem cytochrome c peroxidase; <b>PDBTitle:</b> di-haemic cytochrome c peroxidase from pseudomonas nautica 617, form2 in (ph 4.0)
78	<a href="#">d1fxza1</a>	Alignment	not modelled	15.9	10	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Germin/Seed storage 7S protein
79	<a href="#">c2jrtA_</a>	Alignment	not modelled	15.4	25	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> nmr solution structure of the protein coded by gene2 rhos4_12090 of rhodobacter sphaeroides. northeast3 structural genomics target rhr5
80	<a href="#">c1v9qA_</a>	Alignment	not modelled	15.1	17	<b>PDB header:</b> transcription regulator <b>Chain:</b> A: <b>PDB Molecule:</b> transcriptional regulator, hth_3 family;

80	<a href="#">c1y2qA</a>	Alignment	not modelled	13.1	17	<b>PDBTitle:</b> crystal structure of hth_3 family transcriptional regulator2 from vibrio cholerae <b>Fold:</b> Adenine nucleotide alpha hydrolase-like <b>Superfamily:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain <b>Family:</b> UDP-glucose/GDP-mannose dehydrogenase C-terminal domain
81	<a href="#">d1dlja3</a>	Alignment	not modelled	15.1	9	<b>PDB header:</b> biosynthetic protein <b>Chain:</b> C: <b>PDB Molecule:</b> uncharacterized protein with rmlc-like cupin fold; <b>PDBTitle:</b> crystal structure of a putative biosynthetic protein with rmlc-like2 cupin fold (reut_b4087) from ralstonia eutropha jmp134 at 1.90 a3 resolution
82	<a href="#">c3fjsC</a>	Alignment	not modelled	14.9	16	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
83	<a href="#">d1nmia2</a>	Alignment	not modelled	14.9	10	<b>PDB header:</b> lyase <b>Chain:</b> A: <b>PDB Molecule:</b> remf protein; <b>PDBTitle:</b> zink containing polyketide cyclase remf from streptomyces2 resistomycificus
84	<a href="#">c3ht2A</a>	Alignment	not modelled	14.8	11	<b>PDB header:</b> ribosome <b>Chain:</b> 0: <b>PDB Molecule:</b> 50s ribosomal protein l27; <b>PDBTitle:</b> t. thermophilus 70s ribosome in complex with mrna, trnas2 and ef-tu.gdp.kirromycin ternary complex, fitted to a 6.43 a cryo-em map. this file contains the 50s subunit.
85	<a href="#">c3fin0</a>	Alignment	not modelled	14.3	20	<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
86	<a href="#">c3i4oA</a>	Alignment	not modelled	13.9	9	<b>Fold:</b> Cytochrome c <b>Superfamily:</b> Cytochrome c <b>Family:</b> Di-heme cytochrome c peroxidase
87	<a href="#">d1iqca2</a>	Alignment	not modelled	13.5	10	<b>PDB header:</b> seed storage protein <b>Chain:</b> B: <b>PDB Molecule:</b> canavalin; <b>PDBTitle:</b> determination of three crystal structures of canavalin by molecular2 replacement
88	<a href="#">c1cauB</a>	Alignment	not modelled	13.3	8	<b>Fold:</b> Double-stranded beta-helix <b>Superfamily:</b> RmlC-like cupins <b>Family:</b> Type I phosphomannose isomerase
89	<a href="#">d1pmia</a>	Alignment	not modelled	13.3	6	<b>PDB header:</b> isomerase <b>Chain:</b> B: <b>PDB Molecule:</b> uncharacterized iolb-like protein; <b>PDBTitle:</b> crystal structure of an iolb-like protein (stm4420) from salmonella2 typhimurium lt2 at 1.90 a resolution
90	<a href="#">c2qjvB</a>	Alignment	not modelled	13.2	16	<b>Fold:</b> beta-clip <b>Superfamily:</b> dUTPase-like <b>Family:</b> dUTPase-like
91	<a href="#">d2bsya1</a>	Alignment	not modelled	12.8	8	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Ribosomal L27 protein-like <b>Family:</b> Ribosomal L27 protein
92	<a href="#">d2zjrt1</a>	Alignment	not modelled	12.7	18	<b>PDB header:</b> transcription <b>Chain:</b> C: <b>PDB Molecule:</b> sigma-e factor negative regulatory protein; <b>PDBTitle:</b> crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
93	<a href="#">c1or7C</a>	Alignment	not modelled	12.3	14	<b>Fold:</b> N-terminal, cytoplasmic domain of anti-sigmaE factor RseA <b>Superfamily:</b> N-terminal, cytoplasmic domain of anti-sigmaE factor RseA <b>Family:</b> N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
94	<a href="#">d1or7c</a>	Alignment	not modelled	12.3	14	<b>PDB header:</b> isomerase <b>Chain:</b> C: <b>PDB Molecule:</b> hypothetical protein; <b>PDBTitle:</b> crystal structure of a putative mannose-6-phosphate isomerase2 (reut_a1446) from ralstonia eutropha jmp134 at 2.10 a resolution
95	<a href="#">c2opkC</a>	Alignment	not modelled	12.2	17	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> cytochrome c551 peroxidase; <b>PDBTitle:</b> crystal structure of the di-haem cytochrome c peroxidase2 from pseudomonas aeruginosa - mixed valence form
96	<a href="#">c2vhdB</a>	Alignment	not modelled	11.9	13	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
97	<a href="#">d1ekxa1</a>	Alignment	not modelled	11.9	14	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
98	<a href="#">d1ml4a1</a>	Alignment	not modelled	11.1	19	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase
99	<a href="#">d1o1ha1</a>	Alignment	not modelled	10.9	19	<b>Fold:</b> ATC-like <b>Superfamily:</b> Aspartate/ornithine carbamoyltransferase <b>Family:</b> Aspartate/ornithine carbamoyltransferase