Phyre^2

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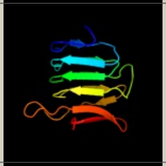
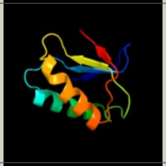
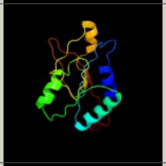
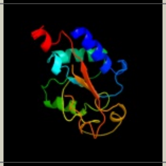
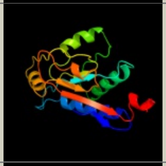
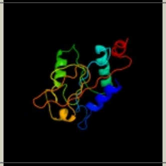
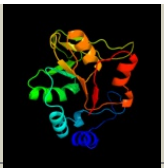
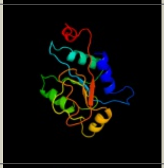
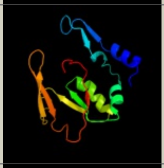
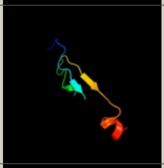
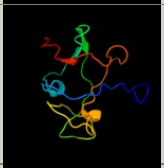
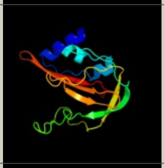
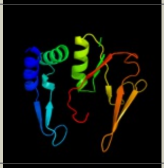
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1hf2A_	Alignment		100.0	23	**PDB header:**cell division protein **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the bacterial cell-division inhibitor2 minc from t. maritima
2	d1hf2a1	Alignment		100.0	27	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Cell-division inhibitor MinC, C-terminal domain **Family:**Cell-division inhibitor MinC, C-terminal domain
3	c3ghfA_	Alignment		99.8	83	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**septum site-determining protein minc; **PDBTitle:** crystal structure of the septum site-determining protein2 minc from salmonella typhimurium
4	d1hf2a2	Alignment		98.5	16	**Fold:**Cell-division inhibitor MinC, N-terminal domain **Superfamily:**Cell-division inhibitor MinC, N-terminal domain **Family:**Cell-division inhibitor MinC, N-terminal domain
5	c1tf2A_	Alignment		90.6	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of seca:adp in an open conformation from2 bacillus subtilis
6	c1nl3B_	Alignment		86.7	27	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**preprotein translocase seca 1 subunit; **PDBTitle:** crystal structure of the seca protein translocation atpase2 from mycobacterium tuberculosis in apo form
7	c3dl8B_	Alignment		84.1	22	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca
8	c3dinB_	Alignment		83.0	25	**PDB header:**membrane protein, protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** crystal structure of the protein-translocation complex formed by the2 secy channel and the seca atpase
9	c3juxA_	Alignment		82.2	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the translocation atpase seca from thermotoga2 maritima
10	c2fsgA_	Alignment		81.9	25	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** complex seca:atp from escherichia coli
11	d1nkta4	Alignment		79.0	29	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain

12	d1mzva_	Alignment		75.7	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
13	c2vdaA_	Alignment		74.2	26	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**translocase subunit seca; **PDBTitle:** solution structure of the seca-signal peptide complex
14	c2dy0A_	Alignment		65.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**adenine phosphoribosyltransferase; **PDBTitle:** crystal structure of project jw0458 from escherichia coli
15	c2pfuA_	Alignment		61.4	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**biopolymer transport exbd protein; **PDBTitle:** nmr strcuture determination of the periplasmic domain of exbd from2 e.coli
16	c2ipcB_	Alignment		53.1	29	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of the translocation atpase seca from thermus2 thermophilus reveals a parallel, head-to-head dimer
17	d1zunb1	Alignment		41.3	18	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
18	c3l7nA_	Alignment		40.1	8	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of smu.1228c
19	d1g2qa_	Alignment		37.6	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
20	d1o57a2	Alignment		37.1	13	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
21	d1n0ua1	Alignment	not modelled	36.8	33	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
22	c2jwlB_	Alignment	not modelled	33.3	6	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**protein tolr; **PDBTitle:** solution structure of periplasmic domain of tolr from h.2 influenzae with saxs data
23	c3k4iC_	Alignment	not modelled	31.0	20	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of uncharacterized protein pspto_3204 from2 pseudomonas syringae pv. tomato str. dc3000
24	d2bv3a1	Alignment	not modelled	27.3	21	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
25	d1jnya1	Alignment	not modelled	26.4	15	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
26	c2i5kB_	Alignment	not modelled	26.3	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**utp--glucose-1-phosphate uridylyltransferase; **PDBTitle:** crystal structure of ugp1p
27	d1o1ya_	Alignment	not modelled	24.1	10	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**Class I glutamine amidotransferases (GAT)
28	c2zwaA_	Alignment	not modelled	23.9	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**leucine carboxyl methyltransferase 2; **PDBTitle:** crystal structure of trna wybutosine synthesizing enzyme2 tyw4
						PDB header:transferase

29	c3cr8C_	Alignment	not modelled	23.9	8	**Chain:** C: **PDB Molecule:**sulfate adenylyltranferase, adenylylsulfate **PDBTitle:** hexameric aps kinase from thiobacillus denitrificans
30	d1l1qa_	Alignment	not modelled	22.4	12	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
31	d1qb7a_	Alignment	not modelled	21.9	15	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
32	d2f69a1	Alignment	not modelled	21.4	29	**Fold:**open-sided beta-meander **Superfamily:**Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain **Family:**Histone H3 K4-specific methyltransferase SET7/9 N-terminal domain
33	d1f60a1	Alignment	not modelled	20.0	12	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
34	c2idcA_	Alignment	not modelled	19.9	17	**PDB header:**replication/chaperone **Chain:** A: **PDB Molecule:**anti-silencing protein 1 and histone h3 chimera; **PDBTitle:** structure of the histone h3-asf1 chaperone interaction
35	d1roca_	Alignment	not modelled	18.8	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ASF1-like **Family:**ASF1-like
36	d2icya1	Alignment	not modelled	17.9	24	**Fold:**Single-stranded left-handed beta-helix **Superfamily:**Trimeric LpxA-like enzymes **Family:**GlmU C-terminal domain-like
37	c2i32A_	Alignment	not modelled	17.8	22	**PDB header:**replication chaperone **Chain:** A: **PDB Molecule:**anti-silencing factor 1 paralog a; **PDBTitle:** structure of a human asf1a-hira complex and insights into2 specificity of histone chaperone complex assembly
38	d2i32a1	Alignment	not modelled	17.8	22	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ASF1-like **Family:**ASF1-like
39	d2c78a1	Alignment	not modelled	16.7	10	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
40	d1v30a_	Alignment	not modelled	16.6	56	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
41	c3es1A_	Alignment	not modelled	16.6	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**cupin 2, conserved barrel domain protein; **PDBTitle:** crystal structure of protein with a cupin-like fold and unknown2 function (yp_001165807.1) from novosphingobium aromaticivorans dsm3 12444 at 1.91 a resolution
42	d1mvfd_	Alignment	not modelled	16.6	22	**Fold:**Double-split beta-barrel **Superfamily:**AbrB/MazE/MraZ-like **Family:**Kis/PemI addiction antidote
43	d2exda1	Alignment	not modelled	16.6	18	**Fold:**OB-fold **Superfamily:**NfeD domain-like **Family:**NfeD domain-like
44	c3agqA_	Alignment	not modelled	16.5	9	**PDB header:**translation,transferase **Chain:** A: **PDB Molecule:**elongation factor ts, elongation factor tu 1, linker, q **PDBTitle:** structure of viral polymerase form ii
45	c3tr5C_	Alignment	not modelled	16.4	18	**PDB header:**translation **Chain:** C: **PDB Molecule:**peptide chain release factor 3; **PDBTitle:** structure of a peptide chain release factor 3 (prfc) from coxiella2 burnetii
46	d2cu9a1	Alignment	not modelled	16.1	17	**Fold:**Immunoglobulin-like beta-sandwich **Superfamily:**ASF1-like **Family:**ASF1-like
47	c2eqaA_	Alignment	not modelled	14.7	18	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**hypothetical protein st1526; **PDBTitle:** crystal structure of the hypothetical sua5 protein from2 sulfolobus tokodaii
48	c3k13A_	Alignment	not modelled	14.1	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**5-methyltetrahydrofolate-homocysteine methyltransferase; **PDBTitle:** structure of the pterin-binding domain metr of 5-2 methyltetrahydrofolate-homocysteine methyltransferase from3 bacteroides thetaiotaomicron
49	d1vkba_	Alignment	not modelled	14.0	44	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
50	c2h5eB_	Alignment	not modelled	13.7	16	**PDB header:**translation **Chain:** B: **PDB Molecule:**peptide chain release factor rf-3; **PDBTitle:** crystal structure of e.coli polypeptide release factor rf3
51	d1q1oa_	Alignment	not modelled	13.5	10	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
52	c2wmkB_	Alignment	not modelled	13.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fucolectin-related protein; **PDBTitle:** crystal structure of the catalytic module of a family 982 glycoside hydrolase from streptococcus pneumoniae sp3-bs713 (sp3gh98) in complex with the a-lewisy pentasaccharide4 blood group antigen.
53	c2xexA_	Alignment	not modelled	13.1	13	**PDB header:**translation **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** crystal structure of staphylococcus aureus elongation factor2 g
						Fold: Double-stranded beta-helix

54	d1dcsa_	Alignment	not modelled	13.0	16	**Superfamily:**Clavaminate synthase-like **Family:**Penicillin synthase-like
55	c3mezA_	Alignment	not modelled	12.7	15	**PDB header:**sugar binding protein **Chain:** A: **PDB Molecule:**mannose-specific lectin 3 chain 1; **PDBTitle:** x-ray structural analysis of a mannose specific lectin from dutch2 crocus (crocus vernus)
56	c2kl8A_	Alignment	not modelled	12.2	23	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
57	d1iqoa_	Alignment	not modelled	12.2	21	**Fold:**Hypothetical protein MTH1880 **Superfamily:**Hypothetical protein MTH1880 **Family:**Hypothetical protein MTH1880
58	d1pqsa_	Alignment	not modelled	11.8	8	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains **Family:**PB1 domain
59	c3l83A_	Alignment	not modelled	11.7	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**glutamine amido transferase; **PDBTitle:** crystal structure of glutamine amido transferase from methylobacillus2 flagellatus
60	c3jubA_	Alignment	not modelled	11.3	38	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aig2-like domain-containing protein 1; **PDBTitle:** human gamma-glutamylamine cyclotransferase
61	d1omwa2	Alignment	not modelled	11.1	15	**Fold:**PH domain-like barrel **Superfamily:**PH domain-like **Family:**Pleckstrin-homology domain (PH domain)
62	c2rdo7_	Alignment	not modelled	10.8	13	**PDB header:**ribosome **Chain:** 7: **PDB Molecule:**elongation factor g; **PDBTitle:** 50s subunit with ef-g(gdpnp) and rrf bound
63	c2k5hA_	Alignment	not modelled	10.5	19	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved protein; **PDBTitle:** solution nmr structure of protein encoded by mth693 from2 methanobacterium thermoautotrophicum: northeast structural3 genomics consortium target tt824a
64	d1vm6a3	Alignment	not modelled	10.2	21	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
65	c3uotB_	Alignment	not modelled	10.0	13	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of mdc1 fha domain in complex with a phosphorylated2 peptide from the mdc1 n-terminus
66	c3cb4D_	Alignment	not modelled	10.0	14	**PDB header:**translation **Chain:** D: **PDB Molecule:**gtp-binding protein lepa; **PDBTitle:** the crystal structure of lepa
67	d1xhsa_	Alignment	not modelled	10.0	56	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
68	c2g0qA_	Alignment	not modelled	9.8	44	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**at5g39720.1 protein; **PDBTitle:** solution structure of at5g39720.1 from arabidopsis thaliana
69	c2vu9A_	Alignment	not modelled	9.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**botulinum neurotoxin a heavy chain; **PDBTitle:** crystal structure of botulinum neurotoxin serotype a2 binding domain in complex with gt1b
70	c2bm0A_	Alignment	not modelled	9.5	15	**PDB header:**elongation factor **Chain:** A: **PDB Molecule:**elongation factor g; **PDBTitle:** ribosomal elongation factor g (ef-g) fusidic acid resistant2 mutant t84a
71	c1qysA_	Alignment	not modelled	9.4	21	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**top7; **PDBTitle:** crystal structure of top7: a computationally designed2 protein with a novel fold
72	d1od5a2	Alignment	not modelled	9.2	21	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein
73	d2cvoa2	Alignment	not modelled	9.1	16	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**GAPDH-like
74	c3k3sG_	Alignment	not modelled	8.9	17	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**altronate hydrolase; **PDBTitle:** crystal structure of altronate hydrolase (fragment 1-84) from shigella2 flexneri.
75	c2q4jB_	Alignment	not modelled	8.9	16	**PDB header:**transferase **Chain:** B: **PDB Molecule:**probable utp-glucose-1-phosphate uridylyltransferase 2; **PDBTitle:** ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
76	c2jqvA_	Alignment	not modelled	8.8	44	**PDB header:**structural genomics **Chain:** A: **PDB Molecule:**aig2 protein-like; **PDBTitle:** solution structure at3g28950.1 from arabidopsis thaliana
77	c3cgiD_	Alignment	not modelled	8.8	36	**PDB header:**unknown function **Chain:** D: **PDB Molecule:**propanediol utilization protein pduu; **PDBTitle:** crystal structure of the pduu shell protein from the pdu2 microcompartment
78	c3mmyE_	Alignment	not modelled	8.8	16	**PDB header:**nuclear protein **Chain:** E: **PDB Molecule:**mrna export factor; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
79	d1ip9a_	Alignment	not modelled	8.7	9	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**CAD & PB1 domains

						Family:PB1 domain
80	c2d5nB_	Alignment	not modelled	8.7	18	**PDB header:**hydrolase, oxidoreductase **Chain:** B: **PDB Molecule:**riboflavin biosynthesis protein ribd; **PDBTitle:** crystal structure of a bifunctional deaminase and reductase2 involved in riboflavin biosynthesis
81	c2qikA_	Alignment	not modelled	8.7	50	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0131 protein ykqa; **PDBTitle:** crystal structure of ykqa from bacillus subtilis. northeast2 structural genomics target sr631
82	d1ofda1	Alignment	not modelled	8.7	14	**Fold:**Single-stranded right-handed beta-helix **Superfamily:**Alpha subunit of glutamate synthase, C-terminal domain **Family:**Alpha subunit of glutamate synthase, C-terminal domain
83	c2jvfA_	Alignment	not modelled	8.7	18	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**de novo protein m7; **PDBTitle:** solution structure of m7, a computationally-designed2 artificial protein
84	c2glvA_	Alignment	not modelled	8.6	15	**PDB header:**lyase **Chain:** A: **PDB Molecule:**(3r)-hydroxymyristoyl-acyl carrier protein **PDBTitle:** crystal structure of (3r)-hydroxyacyl-acyl carrier protein2 dehydratase(fabz) mutant(y100a) from helicobacter pylori
85	c3r0eC_	Alignment	not modelled	8.5	36	**PDB header:**sugar binding protein **Chain:** C: **PDB Molecule:**lectin; **PDBTitle:** structure of remusatia vivipara lectin
86	c2qv3A_	Alignment	not modelled	8.2	57	**PDB header:**toxin **Chain:** A: **PDB Molecule:**vacuolating cytotoxin; **PDBTitle:** crystal structure of the helicobacter pylori vacuolating toxin p552 domain
87	d2dy1a1	Alignment	not modelled	7.7	16	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**Elongation factors
88	c3b8hA_	Alignment	not modelled	7.7	24	**PDB header:**biosynthetic protein/transferase **Chain:** A: **PDB Molecule:**elongation factor 2; **PDBTitle:** structure of the eef2-exoa(e546a)-nad+ complex
89	c3ia0c_	Alignment	not modelled	7.6	27	**PDB header:**structural protein **Chain:** C: **PDB Molecule:**ethanolamine utilization protein euts; **PDBTitle:** ethanolamine utilization microcompartment shell subunit,2 euts-g39v mutant
90	c2jw5A_	Alignment	not modelled	7.5	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna polymerase lambda; **PDBTitle:** polymerase lambda brct domain
91	d1y13a_	Alignment	not modelled	7.5	19	**Fold:**T-fold **Superfamily:**Tetrahydrobiopterin biosynthesis enzymes-like **Family:**6-pyruvoyl tetrahydropterin synthase
92	c3jx9B_	Alignment	not modelled	7.4	18	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**putative phosphoheptose isomerase; **PDBTitle:** crystal structure of putative phosphoheptose isomerase2 (yp_001815198.1) from exiguobacterium sp. 255-15 at 1.95 a resolution
93	c1g2cN_	Alignment	not modelled	7.4	22	**PDB header:**viral protein **Chain:** N: **PDB Molecule:**fusion protein (f); **PDBTitle:** human respiratory syncytial virus fusion protein core
94	d2gsaa_	Alignment	not modelled	7.4	3	**Fold:**PLP-dependent transferase-like **Superfamily:**PLP-dependent transferases **Family:**GABA-aminotransferase-like
95	c2w18A_	Alignment	not modelled	7.1	30	**PDB header:**nuclear protein **Chain:** A: **PDB Molecule:**partner and localizer of brca2; **PDBTitle:** crystal structure of the c-terminal wd40 domain of human2 palb2
96	d1diha1	Alignment	not modelled	7.1	20	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
97	d1d9ea_	Alignment	not modelled	7.0	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I DAHP synthetase
98	c3mkqA_	Alignment	not modelled	7.0	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**coatomer beta'-subunit; **PDBTitle:** crystal structure of yeast alpha/betaprime-cop subcomplex of the copi2 vesicular coat
99	d1fxza2	Alignment	not modelled	7.0	18	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Germin/Seed storage 7S protein