


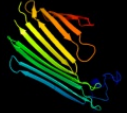

















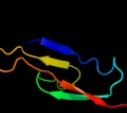




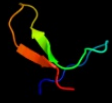
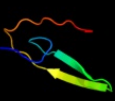

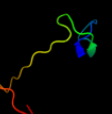



#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3rfzB_</a>	 Alignment		100.0	56	<b>PDB header:</b> cell adhesion/transport/chaperone <b>Chain:</b> B: <b>PDB Molecule:</b> outer membrane usher protein, type 1 fimbrial synthesis; <b>PDBTitle:</b> crystal structure of the fimd usher bound to its cognate fimc:fimh2 substrate
2	<a href="#">c3ohnA_</a>	 Alignment		99.9	55	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane usher protein fimd; <b>PDBTitle:</b> crystal structure of the fimd translocation domain
3	<a href="#">c2xetB_</a>	 Alignment		99.9	40	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> f1 capsule-anchoring protein; <b>PDBTitle:</b> conserved hydrophobic clusters on the surface of the caf1a usher2 c-terminal domain are important for f1 antigen assembly
4	<a href="#">c2vqiA_</a>	 Alignment		99.8	16	<b>PDB header:</b> transport <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane usher protein papc; <b>PDBTitle:</b> structure of the p pilus usher (papc) translocation pore
5	<a href="#">c3l48B_</a>	 Alignment		99.8	29	<b>PDB header:</b> transport protein <b>Chain:</b> B: <b>PDB Molecule:</b> outer membrane usher protein papc; <b>PDBTitle:</b> crystal structure of the c-terminal domain of the papc usher
6	<a href="#">c2x5pA_</a>	 Alignment		37.0	18	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> fibronectin binding protein; <b>PDBTitle:</b> crystal structure of the streptococcus pyogenes fibronectin binding2 protein fbab-b
7	<a href="#">d1aoza2</a>	 Alignment		32.0	9	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
8	<a href="#">d1uwya1</a>	 Alignment		30.9	12	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Carboxypeptidase regulatory domain-like <b>Family:</b> Carboxypeptidase regulatory domain
9	<a href="#">c2nsmA_</a>	 Alignment		27.3	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxypeptidase n catalytic chain; <b>PDBTitle:</b> crystal structure of the human carboxypeptidase n (kinase i)2 catalytic domain
10	<a href="#">c3nadB_</a>	 Alignment		24.4	19	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ferulate decarboxylase; <b>PDBTitle:</b> crystal structure of phenolic acid decarboxylase from bacillus pumilus2 ui-670
11	<a href="#">c2kywA_</a>	 Alignment		21.9	25	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> adhesion exoprotein; <b>PDBTitle:</b> solution nmr structure of a domain of adhesion exoprotein from2 pediococcus pentosaceus, northeast structural genomics consortium3 target ptr410

12	<a href="#">d1nkgal</a>	Alignment		21.5	10	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Starch-binding domain-like <b>Family:</b> Rhamnogalacturonase B, RhgB, middle domain
13	<a href="#">d2je6i3</a>	Alignment		18.8	33	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
14	<a href="#">c2ww8A_</a>	Alignment		18.8	12	<b>PDB header:</b> cell adhesion <b>Chain:</b> A: <b>PDB Molecule:</b> cell wall surface anchor family protein; <b>PDBTitle:</b> structure of the pilus adhesin (rrga) from streptococcus2 pneumoniae
15	<a href="#">d2ey4c1</a>	Alignment		18.2	14	<b>Fold:</b> Reductase/isomerase/elongation factor common domain <b>Superfamily:</b> Translation proteins <b>Family:</b> Gar1-like SnoRNP
16	<a href="#">c2hvyB_</a>	Alignment		17.6	14	<b>PDB header:</b> isomerase/biosynthetic protein/rna <b>Chain:</b> B: <b>PDB Molecule:</b> small nucleolar rnp similar to gar1; <b>PDBTitle:</b> crystal structure of an h/aca box rnp from pyrococcus furiosus
17	<a href="#">d1ci3m2</a>	Alignment		17.5	27	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
18	<a href="#">d2ja9a2</a>	Alignment		15.5	21	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
19	<a href="#">c3ilaG_</a>	Alignment		15.4	21	<b>PDB header:</b> signaling protein <b>Chain:</b> G: <b>PDB Molecule:</b> ryanodine receptor 1; <b>PDBTitle:</b> crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
20	<a href="#">c1h8la_</a>	Alignment		13.3	9	<b>PDB header:</b> carboxypeptidase <b>Chain:</b> A: <b>PDB Molecule:</b> carboxypeptidase gp180 residues 503-882; <b>PDBTitle:</b> duck carboxypeptidase d domain ii in complex with gemsa
21	<a href="#">d1hfua2</a>	Alignment	not modelled	13.1	14	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
22	<a href="#">d1e2wa2</a>	Alignment	not modelled	12.5	28	<b>Fold:</b> Barrel-sandwich hybrid <b>Superfamily:</b> Rudiment single hybrid motif <b>Family:</b> Cytochrome f, small domain
23	<a href="#">d1h8la1</a>	Alignment	not modelled	12.0	8	<b>Fold:</b> Prealbumin-like <b>Superfamily:</b> Carboxypeptidase regulatory domain-like <b>Family:</b> Carboxypeptidase regulatory domain
24	<a href="#">c1yukB_</a>	Alignment	not modelled	11.4	29	<b>PDB header:</b> cell adhesion <b>Chain:</b> B: <b>PDB Molecule:</b> integrin beta-2 b chain; <b>PDBTitle:</b> the crystal structure of the psi/hybrid domain/ i-egf12 segment from the human integrin beta2 at 1.8 resolution
25	<a href="#">d2gc9a1</a>	Alignment	not modelled	11.0	14	<b>Fold:</b> Lipocalins <b>Superfamily:</b> Lipocalins <b>Family:</b> Phenolic acid decarboxylase (PAD)
26	<a href="#">d1gyca2</a>	Alignment	not modelled	10.4	9	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
27	<a href="#">d1lnza1</a>	Alignment	not modelled	9.9	30	<b>Fold:</b> Obg-fold <b>Superfamily:</b> Obg GTP-binding protein N-terminal domain <b>Family:</b> Obg GTP-binding protein N-terminal domain
28	<a href="#">d1zvca1</a>	Alignment	not modelled	8.5	18	<b>Fold:</b> AOC barrel-like <b>Superfamily:</b> Allene oxide cyclase-like <b>Family:</b> Allene oxide cyclase-like
29	<a href="#">c1wv8A_</a>	Alignment	not modelled	8.4	11	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> aminomethyltransferase;

29	<a href="#">c1wslA_</a>	Alignment	not modelled	8.4	11	<b>PDBTitle:</b> crystal structure of human t-protein of glycine cleavage2 system
30	<a href="#">d1v8ha1</a>	Alignment	not modelled	8.2	13	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> E set domains <b>Family:</b> SoxZ-like
31	<a href="#">d1udxa1</a>	Alignment	not modelled	7.9	30	<b>Fold:</b> Obg-fold <b>Superfamily:</b> Obg GTP-binding protein N-terminal domain <b>Family:</b> Obg GTP-binding protein N-terminal domain
32	<a href="#">d1wkqa_</a>	Alignment	not modelled	7.6	20	<b>Fold:</b> Cytidine deaminase-like <b>Superfamily:</b> Cytidine deaminase-like <b>Family:</b> Deoxycytidylate deaminase-like
33	<a href="#">d1mlsa_</a>	Alignment	not modelled	7.5	11	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> MSP-like
34	<a href="#">d1v76a_</a>	Alignment	not modelled	7.5	15	<b>Fold:</b> Rof/RNase P subunit-like <b>Superfamily:</b> Rof/RNase P subunit-like <b>Family:</b> RNase P subunit p29-like
35	<a href="#">c2zaeC_</a>	Alignment	not modelled	7.3	15	<b>PDB header:</b> hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> ribonuclease p protein component 1; <b>PDBTitle:</b> crystal structure of protein ph1601p in complex with protein ph1771p2 of archaeal ribonuclease p from pyrococcus horikoshii ot3
36	<a href="#">d2nn6g3</a>	Alignment	not modelled	7.3	16	<b>Fold:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Superfamily:</b> Eukaryotic type KH-domain (KH-domain type I) <b>Family:</b> Eukaryotic type KH-domain (KH-domain type I)
37	<a href="#">d1fr5a_</a>	Alignment	not modelled	7.0	28	<b>Fold:</b> RNA bacteriophage capsid protein <b>Superfamily:</b> RNA bacteriophage capsid protein <b>Family:</b> RNA bacteriophage capsid protein
38	<a href="#">d1kyaa2</a>	Alignment	not modelled	6.9	9	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
39	<a href="#">d2hqya1</a>	Alignment	not modelled	6.5	31	<b>Fold:</b> Acyl-CoA N-acyltransferases (Nat) <b>Superfamily:</b> Acyl-CoA N-acyltransferases (Nat) <b>Family:</b> FemXAB nonribosomal peptidyltransferases
40	<a href="#">c1fw3A_</a>	Alignment	not modelled	6.0	31	<b>PDB header:</b> hydrolase, membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> outer membrane phospholipase a; <b>PDBTitle:</b> outer membrane phospholipase a from escherichia coli
41	<a href="#">c2eqnA_</a>	Alignment	not modelled	5.6	10	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> hypothetical protein loc92345; <b>PDBTitle:</b> solution structure of the naf1 domain of hypothetical2 protein bc008207 [homo sapiens]
42	<a href="#">c2jxmB_</a>	Alignment	not modelled	5.5	24	<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
43	<a href="#">c2gw4C_</a>	Alignment	not modelled	5.4	17	<b>PDB header:</b> luminescent protein <b>Chain:</b> C: <b>PDB Molecule:</b> kaede; <b>PDBTitle:</b> crystal structure of stony coral fluoresent protein kaede, red form
44	<a href="#">d2q9oa2</a>	Alignment	not modelled	5.3	9	<b>Fold:</b> Cupredoxin-like <b>Superfamily:</b> Cupredoxins <b>Family:</b> Multidomain cupredoxins
45	<a href="#">c2ja9A_</a>	Alignment	not modelled	5.3	13	<b>PDB header:</b> rna-binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> exosome complex exonuclease rrp40; <b>PDBTitle:</b> structure of the n-terminal deletion of yeast exosome2 component rrp40
46	<a href="#">d1rowa_</a>	Alignment	not modelled	5.3	9	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> PapD-like <b>Family:</b> MSP-like
47	<a href="#">c3mn8A_</a>	Alignment	not modelled	5.2	13	<b>PDB header:</b> hydrolase <b>Chain:</b> A: <b>PDB Molecule:</b> lp15968p; <b>PDBTitle:</b> structure of drosophila melanogaster carboxypeptidase d isoform 1b2 short
48	<a href="#">c3nx2B_</a>	Alignment	not modelled	5.2	12	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> ferulic acid decarboxylase; <b>PDBTitle:</b> enterobacter sp. px6-4 ferulic acid decarboxylase in complex with2 substrate analogues
49	<a href="#">d1gyva_</a>	Alignment	not modelled	5.2	18	<b>Fold:</b> Immunoglobulin-like beta-sandwich <b>Superfamily:</b> Clathrin adaptor appendage domain <b>Family:</b> gamma-adaptin C-terminal appendage domain-like
50	<a href="#">c2brqA_</a>	Alignment	not modelled	5.1	7	<b>PDB header:</b> structural protein <b>Chain:</b> A: <b>PDB Molecule:</b> filamin a; <b>PDBTitle:</b> crystal structure of the filamin a repeat 21 complexed with2 the integrin beta7 cytoplasmic tail peptide
51	<a href="#">c3iswB_</a>	Alignment	not modelled	5.1	7	<b>PDB header:</b> structural protein <b>Chain:</b> B: <b>PDB Molecule:</b> filamin-a; <b>PDBTitle:</b> crystal structure of filamin-a immunoglobulin-like repeat 21 bound to2 an n-terminal peptide of cfr