

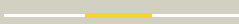










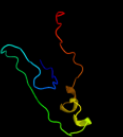








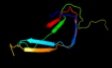




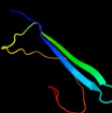





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2yjLC_	 Alignment		86.4	13	PDB header: lipid-binding protein Chain: C: PDB Molecule: exoenzyme s synthesis protein b; PDBTitle: structural characterization of a secretin pilot protein2 from the type iii secretion system (t3ss) of pseudomonas3 aeruginosa
2	d2b9va1	 Alignment		74.0	18	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
3	dlju3a1	 Alignment		64.7	25	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
4	c1lnsA_	 Alignment		56.9	9	PDB header: hydrolase Chain: A: PDB Molecule: x-prolyl dipeptidyl aminopetidase; PDBTitle: crystal structure analysis of the x-prolyl dipeptidyl2 aminopeptidase from lactococcus lactis
5	c2b9vB_	 Alignment		52.6	21	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: acetobacter turbidans alpha-amino acid ester hydrolase
6	c1mpxB_	 Alignment		51.9	25	PDB header: hydrolase Chain: B: PDB Molecule: alpha-amino acid ester hydrolase; PDBTitle: alpha-amino acid ester hydrolase labeled with selenomethionine
7	dle5ra_	 Alignment		44.1	12	Fold: Double-stranded beta-helix Superfamily: Clavaminat synthase-like Family: Type II Proline 3-hydroxylase (proline oxidase)
8	c3cm1C_	 Alignment		43.0	20	PDB header: cell cycle Chain: C: PDB Molecule: ssga-like sporulation-specific cell division protein; PDBTitle: crystal structure of ssga-like sporulation-specific cell division2 protein (yp_290167.1) from thermobifida fusca yx-er1 at 2.60 a3 resolution
9	c1l7qA_	 Alignment		40.6	23	PDB header: hydrolase Chain: A: PDB Molecule: cocaine esterase; PDBTitle: ser117ala mutant of bacterial cocaine esterase coce
10	dltg7a2	 Alignment		38.3	8	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: Beta-galactosidase LacA, domains 4 and 5
11	d2vnga1	 Alignment		37.7	14	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: NPCBM-like

12	d1lnsa2	Alignment		37.6	13	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
13	c3ib3A_	Alignment		23.3	12	PDB header: hydrolase Chain: A: PDB Molecule: coce/nond family hydrolase; PDBTitle: crystal structure of sacol2612 - coce/nond family hydrolase from2 staphylococcus aureus
14	d2vmha1	Alignment		21.1	12	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: NPCBM-like
15	d1wioa2	Alignment		19.8	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
16	c1ux6A_	Alignment		16.5	13	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-1; PDBTitle: structure of a thrombospondin c-terminal fragment reveals a2 novel calcium core in the type 3 repeats
17	d1mpxa1	Alignment		15.4	25	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: PepX C-terminal domain-like
18	c1wruA_	Alignment		14.7	19	PDB header: structural protein Chain: A: PDB Molecule: 43 kda tail protein; PDBTitle: structure of central hub elucidated by x-ray analysis of gene product2 44; baseplate component of bacteriophage mu
19	d2cc1a1	Alignment		13.6	23	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
20	d2icya1	Alignment		12.7	29	Fold: Single-stranded left-handed beta-helix Superfamily: Trimeric LpxA-like enzymes Family: GlmU C-terminal domain-like
21	c2qeaB_	Alignment	not modelled	12.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: putative general stress protein 26; PDBTitle: crystal structure of a putative general stress protein 26 (jann_0955)2 from jannaschia sp. ccs1 at 2.46 a resolution
22	c1yo8A_	Alignment	not modelled	12.4	6	PDB header: cell adhesion Chain: A: PDB Molecule: thrombospondin-2; PDBTitle: structure of the c-terminal domain of human thrombospondin-2
23	c2giaB_	Alignment	not modelled	11.2	33	PDB header: translation Chain: B: PDB Molecule: mitochondrial rna-binding protein 1; PDBTitle: crystal structures of trypanosoma brucei mrp1/mrp2
24	d2giab1	Alignment	not modelled	11.2	33	Fold: ssDNA-binding transcriptional regulator domain Superfamily: ssDNA-binding transcriptional regulator domain Family: Guide RNA binding protein gBP
25	d1rhoa_	Alignment	not modelled	11.1	13	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: RhoGDI-like
26	d1yq2a3	Alignment	not modelled	10.2	16	Fold: Galactose-binding domain-like Superfamily: Galactose-binding domain-like Family: beta-Galactosidase/glucuronidase, N-terminal domain
27	c2qv8B_	Alignment	not modelled	10.2	22	PDB header: transport protein Chain: B: PDB Molecule: general secretion pathway protein h; PDBTitle: structure of the minor pseudopilin epsH from the type 2 secretion2 system of vibrio cholerae
28	d2oz4a1	Alignment	not modelled	9.8	17	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: C2 set domains
						Fold: Cupredoxin-like

29	d1qhga_	Alignment	not modelled	9.1	9	Superfamily: Cupredoxins Family: Plastocyanin/azurin-like
30	d2vo8a1	Alignment	not modelled	8.6	8	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
31	c3hwaA_	Alignment	not modelled	8.5	7	PDB header: ligase Chain: A: PDB Molecule: e3 ubiquitin-protein ligase mycbp2; PDBTitle: crystal structure of the second phr domain of mouse myc-2 binding protein 2 (mycbp-2)
32	d2a6va1	Alignment	not modelled	8.1	20	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Lectin leg-like
33	c2ov7C_	Alignment	not modelled	8.1	16	PDB header: ribosomal protein Chain: C: PDB Molecule: 50s ribosomal protein l1; PDBTitle: the first domain of the ribosomal protein l1 from thermus2 thermophilus
34	d1cida1	Alignment	not modelled	8.1	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
35	c1cidaA_	Alignment	not modelled	7.7	32	PDB header: t-cell surface glycoprotein Chain: A: PDB Molecule: t cell surface glycoprotein cd4; PDBTitle: crystal structure of domains 3 & 4 of rat cd4 and their2 relationship to the nh2-terminal domains
36	c1c8uA_	Alignment	not modelled	7.3	14	PDB header: hydrolase Chain: A: PDB Molecule: acyl-coa thioesterase ii; PDBTitle: crystal structure of the e.coli thioesterase ii, a2 homologue of the human nef-binding enzyme
37	d1c1za5	Alignment	not modelled	7.1	17	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
38	d1mnga1	Alignment	not modelled	6.9	27	Fold: Long alpha-hairpin Superfamily: Fe,Mn superoxide dismutase (SOD), N-terminal domain Family: Fe,Mn superoxide dismutase (SOD), N-terminal domain
39	c3r7gB_	Alignment	not modelled	6.8	18	PDB header: protein binding Chain: B: PDB Molecule: formin-2; PDBTitle: crystal structure of spire kind domain in complex with the tail of2 fmn2
40	c3fbyC_	Alignment	not modelled	6.4	17	PDB header: cell adhesion Chain: C: PDB Molecule: cartilage oligomeric matrix protein; PDBTitle: the crystal structure of the signature domain of cartilage oligomeric2 matrix protein.
41	d1ux6a1	Alignment	not modelled	6.1	11	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Thrombospondin C-terminal domain
42	d1aoha_	Alignment	not modelled	5.8	31	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Carbohydrate-binding domain Family: Cellulose-binding domain family III
43	d2bs2c1	Alignment	not modelled	5.5	19	Fold: Heme-binding four-helical bundle Superfamily: Fumarate reductase respiratory complex transmembrane subunits Family: Fumarate reductase respiratory complex cytochrome b subunit, FrdC
44	c3bbjaA_	Alignment	not modelled	5.2	0	PDB header: hydrolase Chain: A: PDB Molecule: putative thioesterase ii; PDBTitle: crystal structure of a putative thioesterase ii (tfu_2367) from2 thermobifida fusca yx at 2.45 a resolution
45	d1quba5	Alignment	not modelled	5.2	17	Fold: Complement control module/SCR domain Superfamily: Complement control module/SCR domain Family: Complement control module/SCR domain
46	d2apsa_	Alignment	not modelled	5.1	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Cu,Zn superoxide dismutase-like Family: Cu,Zn superoxide dismutase-like