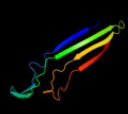
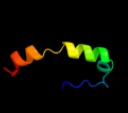
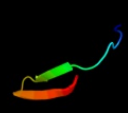
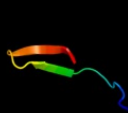
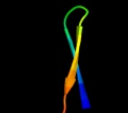
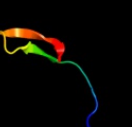
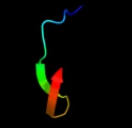
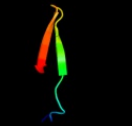


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1t16a_	 Alignment		47.6	22	Fold: Transmembrane beta-barrels Superfamily: Porins Family: Outer membrane protein transport protein
2	d1ew4a_	 Alignment		44.5	29	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
3	c3dwoX_	 Alignment		42.3	24	PDB header: membrane protein Chain: X: PDB Molecule: probable outer membrane protein; PDBTitle: crystal structure of a pseudomonas aeruginosa fadI homologue
4	c3pamB_	 Alignment		35.1	14	PDB header: transport protein Chain: B: PDB Molecule: transmembrane protein; PDBTitle: crystal structure of a domain of transmembrane protein of abc-type2 oligopeptide transport system from bartonella henselae str. houston-1
5	d1ekga_	 Alignment		28.4	32	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
6	d2ga5a1	 Alignment		25.9	25	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
7	c3lo4B_	 Alignment		25.7	53	PDB header: antimicrobial protein Chain: B: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (r24a mutant)
8	c3lo4A_	 Alignment		25.7	53	PDB header: antimicrobial protein Chain: A: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (r24a mutant)
9	d2fq1a1	 Alignment		23.7	25	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Frataxin-like
10	d1lib1a1	 Alignment		20.8	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
11	c2js3B_	 Alignment		17.9	35	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein q6n9a4_rhopa. northeast structural genomics2 consortium target rpt8

12	c3fzyA	Alignment		16.9	23	PDB header: toxin Chain: A: PDB Molecule: rtx toxin rtxa; PDBTitle: crystal structure of pre-cleavage form of cysteine protease domain2 from vibrio cholerae rtxa toxin
13	d1cta1	Alignment		14.6	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
14	c3brzA	Alignment		13.8	16	PDB header: transport protein Chain: A: PDB Molecule: todx; PDBTitle: crystal structure of the pseudomonas putida toluene2 transporter todx
15	d1u5sb1	Alignment		13.3	25	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
16	d1g90a	Alignment		11.5	24	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
17	c3gnyB	Alignment		10.8	47	PDB header: antimicrobial protein Chain: B: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (hnp1)
18	c3lvxB	Alignment		10.8	47	PDB header: antimicrobial protein Chain: B: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (i6a mutant)
19	c3lvxA	Alignment		10.8	47	PDB header: antimicrobial protein Chain: A: PDB Molecule: neutrophil defensin 1; PDBTitle: crystal structure of human alpha-defensin 1 (i6a mutant)
20	d1dfna	Alignment		10.6	47	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
21	d1j8ra	Alignment	not modelled	10.3	27	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: PapG adhesin receptor-binding domain
22	d1k0ha	Alignment	not modelled	9.9	44	Fold: Phage tail proteins Superfamily: Phage tail proteins Family: gpFII-like
23	d1pbya5	Alignment	not modelled	9.4	25	Fold: Streptavidin-like Superfamily: Quinohemoprotein amine dehydrogenase A chain, domain 3 Family: Quinohemoprotein amine dehydrogenase A chain, domain 3
24	c3eebB	Alignment	not modelled	9.3	18	PDB header: toxin Chain: B: PDB Molecule: rtx toxin rtxa; PDBTitle: structure of the v. cholerae rtx cysteine protease domain
25	c2pm4A	Alignment	not modelled	8.8	40	PDB header: antimicrobial protein Chain: A: PDB Molecule: neutrophil defensin 1 (hnp-1) (hp-1) (hp1) (defensin, alpha PDBTitle: human alpha-defensin 1 (multiple arg->lys mutant)
26	d2bbkl	Alignment	not modelled	8.7	22	Fold: Methylamine dehydrogenase, L chain Superfamily: Methylamine dehydrogenase, L chain Family: Methylamine dehydrogenase, L chain
27	d1qjpa	Alignment	not modelled	8.7	26	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
28	d1mdal	Alignment	not modelled	8.7	18	Fold: Methylamine dehydrogenase, L chain Superfamily: Methylamine dehydrogenase, L chain Family: Methylamine dehydrogenase, L chain
29	c2c75L	Alignment	not modelled	8.6	22	PDB header: oxidoreductase Chain: L: PDB Molecule: methylamine dehydrogenase light chain;

29	c3c79L_	Alignment	not modelled	8.0	42	PDBTitle: paracoccus versutus methylamine dehydrogenase in complex2 with amicyanin
30	d1qj8a_	Alignment	not modelled	8.4	17	Fold: Transmembrane beta-barrels Superfamily: OMPA-like Family: Outer membrane protein
31	d1jmx5	Alignment	not modelled	8.3	18	Fold: Streptavidin-like Superfamily: Quinohemoprotein amine dehydrogenase A chain, domain 3 Family: Quinohemoprotein amine dehydrogenase A chain, domain 3
32	c3nb3C_	Alignment	not modelled	7.4	26	PDB header: virus Chain: C: PDB Molecule: outer membrane protein a; PDBTitle: the host outer membrane proteins ompa and ompc are packed at specific2 sites in the shigella phage sf6 virion as structural components
33	c3lvuB_	Alignment	not modelled	7.4	21	PDB header: transport protein Chain: B: PDB Molecule: abc transporter, periplasmic substrate-binding protein; PDBTitle: crystal structure of abc transporter, periplasmic substrate-binding2 protein spo2066 from silicibacter pomeroyi
34	d1bdsa_	Alignment	not modelled	6.7	50	Fold: Defensin-like Superfamily: Defensin-like Family: Defensin
35	c3qraA_	Alignment	not modelled	6.5	28	PDB header: cell invasion Chain: A: PDB Molecule: attachment invasion locus protein; PDBTitle: the crystal structure of ail, the attachment invasion locus protein of2 yersinia pestis
36	d1qdl_	Alignment	not modelled	6.3	26	Fold: ADC synthase Superfamily: ADC synthase Family: ADC synthase
37	c2vcpE_	Alignment	not modelled	6.0	44	PDB header: structural protein Chain: E: PDB Molecule: neural wiskott-aldrich syndrome protein; PDBTitle: crystal structure of n-wasp vc domain in complex with2 skeletal actin
38	c3h8aF_	Alignment	not modelled	5.8	63	PDB header: lyase/protein binding Chain: F: PDB Molecule: rnase e; PDBTitle: crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain
39	d3eipa_	Alignment	not modelled	5.8	44	Fold: FKBP-like Superfamily: Colicin E3 immunity protein Family: Colicin E3 immunity protein
40	d1imla1	Alignment	not modelled	5.7	27	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
41	c3h8aE_	Alignment	not modelled	5.7	56	PDB header: lyase/protein binding Chain: E: PDB Molecule: rnase e; PDBTitle: crystal structure of e. coli enolase bound to its cognate rnase e2 recognition domain
42	d1g8sa_	Alignment	not modelled	5.5	14	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Fibrillarlin homologue
43	d1pgja1	Alignment	not modelled	5.5	19	Fold: 6-phosphogluconate dehydrogenase C-terminal domain-like Superfamily: 6-phosphogluconate dehydrogenase C-terminal domain-like Family: Hydroxyisobutyrate and 6-phosphogluconate dehydrogenase domain