
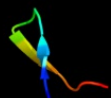















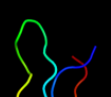



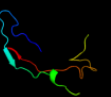


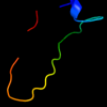



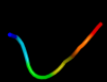
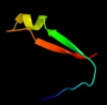
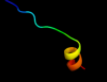


Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	A6X974
Date	Sun Jul 8 11:45:02 BST 2012
Unique Job ID	796354625ff4354a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kyjA_	 Alignment		32.1	54	PDB header: toxin Chain: A: PDB Molecule: litx; PDBTitle: structure of the scorpion toxin u1-liotoxin-lw1a
2	c3e3uA_	 Alignment		10.7	21	PDB header: hydrolase Chain: A: PDB Molecule: peptide deformylase; PDBTitle: crystal structure of mycobacterium tuberculosis peptide2 deformylase in complex with inhibitor
3	dlyfza1	 Alignment		10.2	30	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
4	clyfzA_	 Alignment		10.2	30	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: novel imp binding in feedback inhibition of hypoxanthine-guanine2 phosphoribosyltransferase from thermoanaerobacter tengcongensis
5	c3o7mD_	 Alignment		9.7	25	PDB header: transferase Chain: D: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
6	d2c4va1	 Alignment		8.8	35	Fold: Flavodoxin-like Superfamily: Type II 3-dehydroquinate dehydratase Family: Type II 3-dehydroquinate dehydratase
7	dlhgx_a	 Alignment		8.8	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
8	dlg9sa_	 Alignment		8.5	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
9	dlpzma_	 Alignment		8.3	27	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
10	dlel5a2	 Alignment		8.2	62	Fold: Streptavidin-like Superfamily: D-aminopeptidase, middle and C-terminal domains Family: D-aminopeptidase, middle and C-terminal domains
11	dlj8ra_	 Alignment		8.1	43	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: PapG adhesin receptor-binding domain

12	dltc1a_	Alignment		7.7	19	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
13	c3kb8A_	Alignment		7.3	26	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine phosphoribosyltransferase; PDBTitle: 2.09 angstrom resolution structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-1) from bacillus anthracis str. 'ames3 ancestor' in complex with gmp
14	d1stma_	Alignment		6.7	39	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Satellite viruses Family: Satellite viruses
15	c2ywtA_	Alignment		6.4	13	PDB header: transferase Chain: A: PDB Molecule: hypoxanthine-guanine phosphoribosyltransferase; PDBTitle: crystal structure of hypoxanthine-guanine2 phosphoribosyltransferase with gmp from thermus3 thermophilus hb8
16	d1p17b_	Alignment		6.3	27	Fold: PRTase-like Superfamily: PRTase-like Family: Phosphoribosyltransferases (PRTases)
17	c2uygF_	Alignment		5.5	33	PDB header: lyase Chain: F: PDB Molecule: 3-dehydroquinate dehydratase; PDBTitle: crystallographic structure of the typeii 3-dehydroquinase2 from thermus thermophilus
18	d1tf3a1	Alignment		5.4	67	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
19	c2x1kB_	Alignment		5.4	29	PDB header: hydrolase/rna Chain: B: PDB Molecule: csy4 endoribonuclease; PDBTitle: crystal structure of the csy4-crrna complex, orthorhombic form
20	d1gyta2	Alignment		5.1	31	Fold: Phosphorylase/hydrolase-like Superfamily: Zn-dependent exopeptidases Family: Leucine aminopeptidase, C-terminal domain
21	c1fmeA_	Alignment	not modelled	5.1	67	PDB header: de novo protein Chain: A: PDB Molecule: fsd-ey peptide; PDBTitle: solution structure of fsd-ey, a novel peptide assuming a2 beta-beta-alpha fold
22	c1fsdA_	Alignment	not modelled	5.0	67	PDB header: novel sequence Chain: A: PDB Molecule: full sequence design 1 of beta beta alpha motif; PDBTitle: full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures