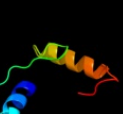
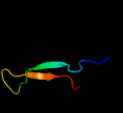
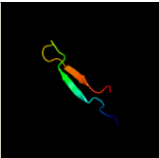
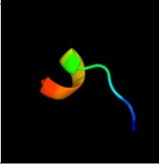


Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2b5dx1	 Alignment		32.8	56	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: AmyC C-terminal domain-like
2	c3bghB_	 Alignment		21.6	60	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative neuraminylactose-binding hemagglutinin homolog; PDBTitle: crystal structure of putative neuraminylactose-binding hemagglutinin2 homolog from helicobacter pylori
3	d1ufaa1	 Alignment		17.5	59	Fold: immunoglobulin/albumin-binding domain-like Superfamily: Families 57/38 glycoside transferase middle domain Family: AmyC C-terminal domain-like
4	c2i9iA_	 Alignment		16.6	47	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of helicobacter pylori protein hp0492
5	d2i9ia1	 Alignment		16.6	47	Fold: Anticodon-binding domain-like Superfamily: XCC0632-like Family: NLBH-like
6	d2cu1a1	 Alignment		14.9	37	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
7	d1jt6a2	 Alignment		12.8	30	Fold: Tetracyclin repressor-like, C-terminal domain Superfamily: Tetracyclin repressor-like, C-terminal domain Family: Tetracyclin repressor-like, C-terminal domain
8	d2dloa2	 Alignment		12.2	22	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
9	c2rbgB_	 Alignment		12.0	24	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative uncharacterized protein st0493; PDBTitle: crystal structure of hypothetical protein(st0493) from2 sulfolobus tokodaii
10	d2nptb1	 Alignment		11.1	27	Fold: beta-Grasp (ubiquitin-like) Superfamily: CAD & PB1 domains Family: PB1 domain
11	d1f2ja_	 Alignment		6.6	36	Fold: TIM beta/alpha-barrel Superfamily: Aldolase Family: Class I aldolase

12	c3kx6C_	Alignment		6.6	32	PDB header: lyase Chain: C: PDB Molecule: fructose-bisphosphate aldolase; PDBTitle: crystal structure of fructose-1,6-bisphosphate aldolase from babesia2 bovis at 2.1a resolution
13	c1xrxD_	Alignment		6.1	60	PDB header: replication inhibitor Chain: D: PDB Molecule: sega protein; PDBTitle: crystal structure of a dna-binding protein

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[dlxrxal](#)

Alignment



6.1

60

Fold:Ribbon-helix-helix
Superfamily:Ribbon-helix-helix
Family:SeqA N-terminal domain-like