

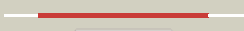

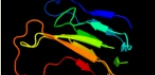






#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3h09B_	 Alignment		99.2	17	PDB header: hydrolase Chain: B: PDB Molecule: immunoglobulin a1 protease; PDBTitle: the structure of haemophilus influenzae iga1 protease
2	d1daba_	 Alignment		98.9	11	Fold: Single-stranded right-handed beta-helix Superfamily: Pectin lyase-like Family: Virulence factor P.69 pertactin
3	c3ml3A_	 Alignment		98.6	16	PDB header: protein transport Chain: A: PDB Molecule: outer membrane protein icsa autotransporter; PDBTitle: crystal structure of the icsa autochaperone region
4	c3syjA_	 Alignment		98.2	9	PDB header: cell adhesion Chain: A: PDB Molecule: adhesion and penetration protein autotransporter; PDBTitle: crystal structure of the haemophilus influenzae hap adhesin
5	c3ak5B_	 Alignment		89.9	14	PDB header: hydrolase Chain: B: PDB Molecule: hemoglobin-binding protease hbp; PDBTitle: hemoglobin protease (hbp) passenger missing domain-2
6	c2zj6A_	 Alignment		57.8	12	PDB header: hydrolase Chain: A: PDB Molecule: lipase; PDBTitle: crystal structure of d337a mutant of pseudomonas sp. mis38 lipase
7	c2qubG_	 Alignment		28.5	9	PDB header: hydrolase Chain: G: PDB Molecule: extracellular lipase; PDBTitle: crystal structure of extracellular lipase lipa from serratia2 marcescens
8	d1kapp1	 Alignment		18.5	20	Fold: Single-stranded right-handed beta-helix Superfamily: beta-Roll Family: Serralysin-like metalloprotease, C-terminal domain

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[c2agmA](#)

Alignment



16.2

15

PDB header:isomerase
Chain: A: **PDB Molecule:**poly(beta-d-mannuronate) c5 epimerase 4;
PDBTitle: solution structure of the r-module from alge4