
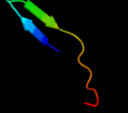
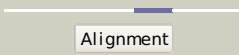
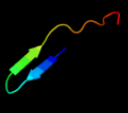
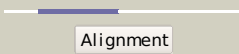
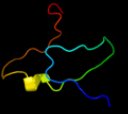
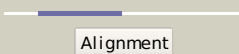
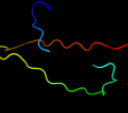
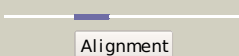
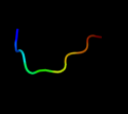
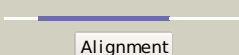



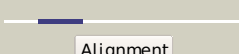
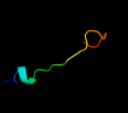
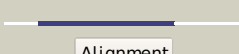

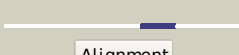

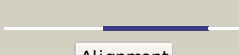
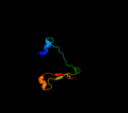
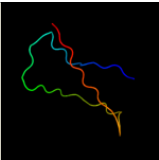


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3jwdA_	 Alignment		18.5	63	PDB header: viral protein Chain: A: PDB Molecule: hiv-1 gp120 envelope glycoprotein; PDBTitle: structure of hiv-1 gp120 with gp41-interactive region: layered2 architecture and basis of conformational mobility
2	c3ngbl_	 Alignment		15.5	58	PDB header: viral protein/immune system Chain: I: PDB Molecule: envelope glycoprotein gp160; PDBTitle: crystal structure of broadly and potently neutralizing antibody vrc012 in complex with hiv-1 gp120
3	d1oe1a2	 Alignment		14.9	18	Fold: Cupredoxin-like Superfamily: Cupredoxins Family: Multidomain cupredoxins
4	c4a02A_	 Alignment		11.6	19	PDB header: chitin binding protein Chain: A: PDB Molecule: chitin binding protein; PDBTitle: x-ray crystallographic structure of efcbm33a
5	c2bf1A_	 Alignment		10.9	30	PDB header: virus protein Chain: A: PDB Molecule: exterior membrane glycoprotein gp120; PDBTitle: structure of an unliganded and fully-glycosylated siv gp1202 envelope glycoprotein
6	d1tvca1	 Alignment		10.3	20	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
7	d2b4cq1	 Alignment		8.1	41	Fold: gp120 core Superfamily: gp120 core Family: gp120 core
8	c2fgvA_	 Alignment		6.7	55	PDB header: lyase Chain: A: PDB Molecule: carboxysome shell polypeptide; PDBTitle: beta carbonic anhydrase from the carboxysomal shell of2 halothiobacillus neapolitanus (csosca)
9	d1gvha2	 Alignment		6.3	14	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
10	c1fqjC_	 Alignment		6.3	54	PDB header: signaling protein Chain: C: PDB Molecule: retinal rod rhodopsin-sensitive cgmp 3',5'- PDBTitle: crystal structure of the heterotrimeric complex of the rgs2 domain of rgs9, the gamma subunit of phosphodiesterase and3 the gt/i1 chimera alpha subunit [(rgs9)-(pdegamma)-4 (gt/i1alpha)-(gdp)-(alf4-)-(mg2+)]
11	d1w07a3	 Alignment		5.4	23	Fold: Acyl-CoA dehydrogenase NM domain-like Superfamily: Acyl-CoA dehydrogenase NM domain-like Family: acyl-CoA oxidase N-terminal domains

12 [d2bema_](#)

Alignment



5.0

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Fold:Immunoglobulin-like beta-sandwich
Superfamily:E set domains
Family:E-set domains of sugar-utilizing enzymes