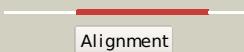

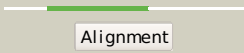
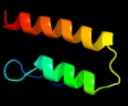


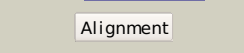



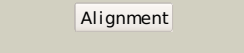
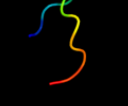
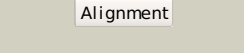
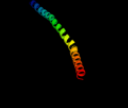
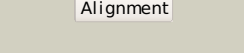



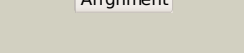

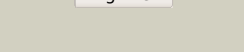
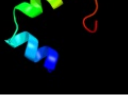


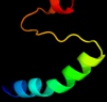

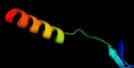


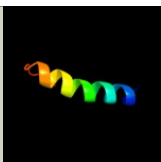


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c2kz6A_</a>	 Alignment		97.6	16	<b>PDB header:</b> structural genomics, unknown function <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein; <b>PDBTitle:</b> solution structure of protein cv0426 from chromobacterium violaceum, 2 northeast structural genomics consortium (nesg) target cvt2
2	<a href="#">c2kt9A_</a>	 Alignment		53.5	24	<b>PDB header:</b> ribosomal protein <b>Chain:</b> A: <b>PDB Molecule:</b> probable 30s ribosomal protein psrp-3; <b>PDBTitle:</b> solution nmr structure of probable 30s ribosomal protein2 psrp-3 (ycf65-like protein) from synechocystis sp. (strain3 pcc 6803), northeast structural genomics consortium target4 target sgr46
3	<a href="#">c3o0rC_</a>	 Alignment		37.3	23	<b>PDB header:</b> immune system/oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> nitric oxide reductase subunit c; <b>PDBTitle:</b> crystal structure of nitric oxide reductase from pseudomonas2 aeruginosa in complex with antibody fragment
4	<a href="#">d2oa5a1</a>	 Alignment		13.0	19	<b>Fold:</b> BLRF2-like <b>Superfamily:</b> BLRF2-like <b>Family:</b> BLRF2-like
5	<a href="#">d1ew4a_</a>	 Alignment		11.9	20	<b>Fold:</b> N domain of copper amine oxidase-like <b>Superfamily:</b> Frataxin/Nqo15-like <b>Family:</b> Frataxin-like
6	<a href="#">c2z8nB_</a>	 Alignment		10.9	36	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> 27.5 kda virulence protein; <b>PDBTitle:</b> structural basis for the catalytic mechanism of phosphothreonine lyase
7	<a href="#">c3ok8A_</a>	 Alignment		9.0	4	<b>PDB header:</b> protein binding <b>Chain:</b> A: <b>PDB Molecule:</b> brain-specific angiogenesis inhibitor 1-associated protein <b>PDBTitle:</b> i-bar of pinkbar
8	<a href="#">c1b35D_</a>	 Alignment		7.9	21	<b>PDB header:</b> virus <b>Chain:</b> D: <b>PDB Molecule:</b> protein (cricket paralysis virus, vp4); <b>PDBTitle:</b> cricket paralysis virus (crpv)
9	<a href="#">d2f2ac1</a>	 Alignment		7.6	24	<b>Fold:</b> Non-globular all-alpha subunits of globular proteins <b>Superfamily:</b> Glu-tRNA <sup>Gln</sup> amidotransferase C subunit <b>Family:</b> Glu-tRNA <sup>Gln</sup> amidotransferase C subunit
10	<a href="#">c2vzbA_</a>	 Alignment		7.6	10	<b>PDB header:</b> metal transport <b>Chain:</b> A: <b>PDB Molecule:</b> putative bacterioferritin-related protein; <b>PDBTitle:</b> a dodecameric thioferritin in the bacterial domain, characterization2 of the bacterioferritin-related protein from bacteroides fragilis
11	<a href="#">d2diia1</a>	 Alignment		7.2	7	<b>Fold:</b> BSD domain-like <b>Superfamily:</b> BSD domain-like <b>Family:</b> BSD domain

12	<a href="#">c1nwdC_</a>	Alignment		7.2	0	<b>PDB header:</b> binding protein/hydrolase <b>Chain:</b> C: <b>PDB Molecule:</b> glutamate decarboxylase; <b>PDBTitle:</b> solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
13	<a href="#">c1nwdB_</a>	Alignment		7.2	0	<b>PDB header:</b> binding protein/hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> glutamate decarboxylase; <b>PDBTitle:</b> solution structure of ca2+/calmodulin bound to the c-2 terminal domain of petunia glutamate decarboxylase
14	<a href="#">d2axpa1</a>	Alignment		7.1	28	<b>Fold:</b> P-loop containing nucleoside triphosphate hydrolases <b>Superfamily:</b> P-loop containing nucleoside triphosphate hydrolases <b>Family:</b> Nucleotide and nucleoside kinases
15	<a href="#">c2diiA_</a>	Alignment		6.8	7	<b>PDB header:</b> transcription <b>Chain:</b> A: <b>PDB Molecule:</b> tftiih basal transcription factor complex p62 <b>PDBTitle:</b> solution structure of the bsd domain of human tftiih basal2 transcription factor complex p62 subunit
16	<a href="#">d2paja1</a>	Alignment		6.8	12	<b>Fold:</b> Composite domain of metallo-dependent hydrolases <b>Superfamily:</b> Composite domain of metallo-dependent hydrolases <b>Family:</b> SAH/MTA deaminase-like
17	<a href="#">c3lvyB_</a>	Alignment		5.9	4	<b>PDB header:</b> lyase <b>Chain:</b> B: <b>PDB Molecule:</b> carboxymuconolactone decarboxylase family; <b>PDBTitle:</b> crystal structure of carboxymuconolactone decarboxylase2 family protein smu.961 from streptococcus mutans
18	<a href="#">c2d5kC_</a>	Alignment		5.5	10	<b>PDB header:</b> metal binding protein <b>Chain:</b> C: <b>PDB Molecule:</b> dps family protein; <b>PDBTitle:</b> crystal structure of dps from staphylococcus aureus

19 [d1bgva2](#)

Alignment



5.3

13

**Fold:**Aminoacid dehydrogenase-like, N-terminal domain  
**Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain  
**Family:**Aminoacid dehydrogenases