

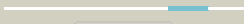




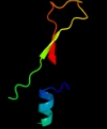



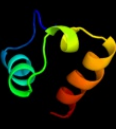

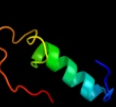



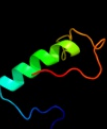










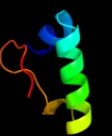

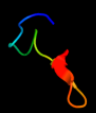


#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">d1kbhb_</a>	 Alignment		63.9	24	<b>Fold:</b> Nuclear receptor coactivator interlocking domain <b>Superfamily:</b> Nuclear receptor coactivator interlocking domain <b>Family:</b> Nuclear receptor coactivator interlocking domain
2	<a href="#">d1a9xa1</a>	 Alignment		37.1	24	<b>Fold:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Superfamily:</b> Carbamoyl phosphate synthetase, large subunit connection domain <b>Family:</b> Carbamoyl phosphate synthetase, large subunit connection domain
3	<a href="#">c3c7cB_</a>	 Alignment		25.5	10	<b>PDB header:</b> oxidoreductase <b>Chain:</b> B: <b>PDB Molecule:</b> octopine dehydrogenase; <b>PDBTitle:</b> a structural basis for substrate and stereo selectivity in2 octopine dehydrogenase (odh-nadh-l-arginine)
4	<a href="#">c1m6vE_</a>	 Alignment		24.3	23	<b>PDB header:</b> ligase <b>Chain:</b> E: <b>PDB Molecule:</b> carbamoyl phosphate synthetase large chain; <b>PDBTitle:</b> crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
5	<a href="#">c2xu8B_</a>	 Alignment		19.3	19	<b>PDB header:</b> structural genomics <b>Chain:</b> B: <b>PDB Molecule:</b> pa1645; <b>PDBTitle:</b> structure of pa1645
6	<a href="#">d1ej5a_</a>	 Alignment		19.2	18	<b>Fold:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain <b>Superfamily:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain <b>Family:</b> Wiscott-Aldrich syndrome protein, WASP, C-terminal domain
7	<a href="#">d1egaa2</a>	 Alignment		12.2	31	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
8	<a href="#">d1yvra1</a>	 Alignment		10.0	14	<b>Fold:</b> alpha-alpha superhelix <b>Superfamily:</b> TROVE domain-like <b>Family:</b> TROVE domain-like
9	<a href="#">c1egaB_</a>	 Alignment		9.1	29	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> protein (gtp-binding protein era); <b>PDBTitle:</b> crystal structure of a widely conserved gtpase era
10	<a href="#">d1rh6a_</a>	 Alignment		7.9	33	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Excisionase-like
11	<a href="#">d1p9qc1</a>	 Alignment		7.8	21	<b>Fold:</b> RuvA C-terminal domain-like <b>Superfamily:</b> Hypothetical protein AF0491, middle domain <b>Family:</b> Hypothetical protein AF0491, middle domain

12	<a href="#">d1pm6a_</a>	Alignment		7.1	33	<b>Fold:</b> Putative DNA-binding domain <b>Superfamily:</b> Putative DNA-binding domain <b>Family:</b> Excisionase-like
13	<a href="#">c1yvrA_</a>	Alignment		6.9	18	<b>PDB header:</b> rna binding protein <b>Chain:</b> A: <b>PDB Molecule:</b> 60-kda ss-a/ro ribonucleoprotein; <b>PDBTitle:</b> ro autoantigen
14	<a href="#">d1z0jb1</a>	Alignment		6.8	23	<b>Fold:</b> Long alpha-hairpin <b>Superfamily:</b> Rabenosyn-5 Rab-binding domain-like <b>Family:</b> Rabenosyn-5 Rab-binding domain-like
15	<a href="#">c1sseB_</a>	Alignment		6.7	24	<b>PDB header:</b> transcription activator <b>Chain:</b> B: <b>PDB Molecule:</b> ap-1 like transcription factor yap1; <b>PDBTitle:</b> solution structure of the oxidized form of the yap1 redox2 domain
16	<a href="#">c1gw4A_</a>	Alignment		6.7	38	<b>PDB header:</b> high density lipoproteins <b>Chain:</b> A: <b>PDB Molecule:</b> apoa-i; <b>PDBTitle:</b> the helix-hinge-helix structural motif in human2 apolipoprotein a-i determined by nmr spectroscopy, 13 structure
17	<a href="#">d1zoqc1</a>	Alignment		6.1	42	<b>Fold:</b> Nuclear receptor coactivator interlocking domain <b>Superfamily:</b> Nuclear receptor coactivator interlocking domain <b>Family:</b> Nuclear receptor coactivator interlocking domain
18	<a href="#">d1oj4a2</a>	Alignment		6.0	14	<b>Fold:</b> Ferredoxin-like <b>Superfamily:</b> GHMP Kinase, C-terminal domain <b>Family:</b> 4-(cytidine 5'-diphospho)-2C-methyl-D-erythritol kinase IspE
19	<a href="#">d1wf3a2</a>	Alignment		6.0	24	<b>Fold:</b> Alpha-lytic protease prodomain-like <b>Superfamily:</b> Prokaryotic type KH domain (KH-domain type II) <b>Family:</b> Prokaryotic type KH domain (KH-domain type II)
20	<a href="#">d1g47a1</a>	Alignment		5.9	22	<b>Fold:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Superfamily:</b> Glucocorticoid receptor-like (DNA-binding domain) <b>Family:</b> LIM domain
21	<a href="#">c2nrzB_</a>	Alignment	not modelled	5.7	20	<b>PDB header:</b> hydrolase <b>Chain:</b> B: <b>PDB Molecule:</b> uvrabc system protein c; <b>PDBTitle:</b> crystal structure of the c-terminal half of uvrbc bound to2 its catalytic divalent cation