Phyre^2

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Description	P37002
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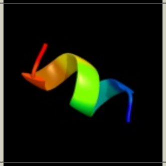
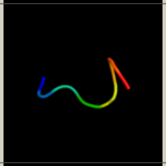
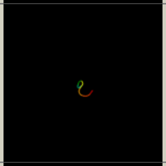
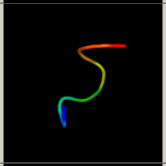
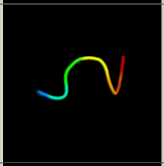
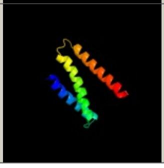
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1m2zE_	Alignment		14.2	33	**PDB header:**hormone/hormone activator **Chain:** E: **PDB Molecule:**nuclear receptor coactivator 2; **PDBTitle:** crystal structure of a dimer complex of the human2 glucocorticoid receptor ligand-binding domain bound to3 dexamethasone and a tif2 coactivator motif
2	c3gn8C_	Alignment		11.4	33	**PDB header:**hormone/hormone activator **Chain:** C: **PDB Molecule:**nuclear receptor coactivator 2; **PDBTitle:** x-ray crystal structure of ancgr2 in complex with2 dexamethasone
3	c3gn8E_	Alignment		10.7	33	**PDB header:**hormone/hormone activator **Chain:** E: **PDB Molecule:**nuclear receptor coactivator 2; **PDBTitle:** x-ray crystal structure of ancgr2 in complex with2 dexamethasone
4	c1m2zB_	Alignment		9.6	33	**PDB header:**hormone/hormone activator **Chain:** B: **PDB Molecule:**nuclear receptor coactivator 2; **PDBTitle:** crystal structure of a dimer complex of the human2 glucocorticoid receptor ligand-binding domain bound to3 dexamethasone and a tif2 coactivator motif
5	c2xokG_	Alignment		8.9	38	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma, mitochondrial; **PDBTitle:** refined structure of yeast f1c10 atpase complex to 3 a2 resolution
6	c2qe7G_	Alignment		6.5	25	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**atp synthase subunit gamma; **PDBTitle:** crystal structure of the f1-atpase from the thermoalkaliphilic2 bacterium bacillus sp. ta2.a1
7	d2jdig1	Alignment		6.4	38	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
8	d1fs0g_	Alignment		6.2	63	**Fold:**Pyruvate kinase C-terminal domain-like **Superfamily:**ATP synthase (F1-ATPase), gamma subunit **Family:**ATP synthase (F1-ATPase), gamma subunit
9	d1u7ga_	Alignment		6.2	14	**Fold:**Ammonium transporter **Superfamily:**Ammonium transporter **Family:**Ammonium transporter

10	d1sxda_	Alignment		5.7	8	**Fold:**SAM domain-like **Superfamily:**SAM/Pointed domain **Family:**Pointed domain