



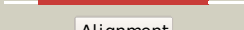

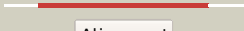








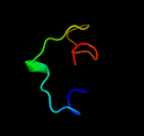
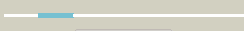
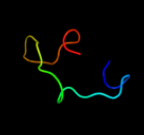



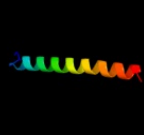


# Phyre2

Email	I.a.kelley@imperial.ac.uk
Description	P42628
Date	Thu Jan 5 12:01:58 GMT 2012
Unique Job ID	6d29287edca19c16

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	<a href="#">c3giaA_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> uncharacterized protein mj0609; <b>PDBTitle:</b> crystal structure of apct transporter
2	<a href="#">c3lrcC_</a>	 Alignment		100.0	14	<b>PDB header:</b> transport protein <b>Chain:</b> C: <b>PDB Molecule:</b> arginine/agmatine antiporter; <b>PDBTitle:</b> structure of e. coli adic (p1)
3	<a href="#">c2jlnA_</a>	 Alignment		99.9	11	<b>PDB header:</b> membrane protein <b>Chain:</b> A: <b>PDB Molecule:</b> mhp1; <b>PDBTitle:</b> structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
4	<a href="#">d2a65a1</a>	 Alignment		99.1	13	<b>Fold:</b> SNF-like <b>Superfamily:</b> SNF-like <b>Family:</b> SNF-like
5	<a href="#">c2xq2A_</a>	 Alignment		99.0	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> structure of the k294a mutant of vsglT
6	<a href="#">c3dh4A_</a>	 Alignment		98.6	10	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> sodium/glucose cotransporter; <b>PDBTitle:</b> crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
7	<a href="#">c2w8aC_</a>	 Alignment		92.3	11	<b>PDB header:</b> membrane protein <b>Chain:</b> C: <b>PDB Molecule:</b> glycine betaine transporter betp; <b>PDBTitle:</b> crystal structure of the sodium-coupled glycine betaine2 symporter betp from corynebacterium glutamicum with bound3 substrate
8	<a href="#">c2f5zK_</a>	 Alignment		30.9	23	<b>PDB header:</b> oxidoreductase/protein binding <b>Chain:</b> K: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component; <b>PDBTitle:</b> crystal structure of human dihydrolipoamide dehydrogenase2 (e3) complexed to the e3-binding domain of human e3-3 binding protein
9	<a href="#">c1zy8M_</a>	 Alignment		30.8	23	<b>PDB header:</b> oxidoreductase <b>Chain:</b> M: <b>PDB Molecule:</b> pyruvate dehydrogenase protein x component; <b>PDBTitle:</b> the crystal structure of dihydrolipoamide dehydrogenase and2 dihydrolipoamide dehydrogenase-binding protein (didomain)3 subcomplex of human pyruvate dehydrogenase complex.
10	<a href="#">c3hfxA_</a>	 Alignment		28.4	12	<b>PDB header:</b> transport protein <b>Chain:</b> A: <b>PDB Molecule:</b> l-carnitine/gamma-butyrobetaine antiporter; <b>PDBTitle:</b> crystal structure of carnitine transporter
11	<a href="#">c2hg5D_</a>	 Alignment		26.8	19	<b>PDB header:</b> membrane protein <b>Chain:</b> D: <b>PDB Molecule:</b> kcsa channel; <b>PDBTitle:</b> cs+ complex of a k channel with an amide to ester substitution in the2 selectivity filter

12	<a href="#">c2eq7C_</a>	Alignment		15.5	24	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> 2-oxoglutarate dehydrogenase e2 component; <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdo
13	<a href="#">c2eq8C_</a>	Alignment		9.5	28	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdp
14	<a href="#">c3eabK_</a>	Alignment		9.2	29	<b>PDB header:</b> cell cycle <b>Chain:</b> K: <b>PDB Molecule:</b> chmp1b; <b>PDBTitle:</b> crystal structure of spastin mit in complex with esct iii
15	<a href="#">c2eq9C_</a>	Alignment		9.0	20	<b>PDB header:</b> oxidoreductase <b>Chain:</b> C: <b>PDB Molecule:</b> pyruvate dehydrogenase complex, dihydrolipoamide <b>PDBTitle:</b> crystal structure of lipoamide dehydrogenase from thermus thermophilus2 hb8 with psbdb
16	<a href="#">dlw85i_</a>	Alignment		9.0	28	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
17	<a href="#">c3dv0L_</a>	Alignment		9.0	28	<b>PDB header:</b> oxidoreductase/transferase <b>Chain:</b> I: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> snapshots of catalysis in the e1 subunit of the pyruvate2 dehydrogenase multi-enzyme complex
18	<a href="#">d2fqma1</a>	Alignment		8.2	29	<b>Fold:</b> Phosphoprotein oligomerization domain-like <b>Superfamily:</b> Phosphoprotein oligomerization domain-like <b>Family:</b> Phosphoprotein oligomerization domain-like
19	<a href="#">c1w3dA_</a>	Alignment		8.0	28	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> dihydrolipoyllysine-residue acetyltransferase <b>PDBTitle:</b> nmr structure of the peripheral-subunit binding domain of2 bacillus stearothermophilus e2p
20	<a href="#">d2cyua1</a>	Alignment		8.0	20	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
21	<a href="#">dlw4ha1</a>	Alignment	not modelled	7.9	20	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
22	<a href="#">dlbala_</a>	Alignment	not modelled	7.3	20	<b>Fold:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Superfamily:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex <b>Family:</b> Peripheral subunit-binding domain of 2-oxo acid dehydrogenase complex
23	<a href="#">c1w4kA_</a>	Alignment	not modelled	6.8	24	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> pyruvate dehydrogenase e2; <b>PDBTitle:</b> peripheral-subunit binding domains from mesophilic, 2 thermophilic, and hyperthermophilic bacteria fold by3 ultrafast, apparently two-state transitions
24	<a href="#">c1z9iA_</a>	Alignment	not modelled	6.8	15	<b>PDB header:</b> transferase <b>Chain:</b> A: <b>PDB Molecule:</b> epidermal growth factor receptor; <b>PDBTitle:</b> a structural model for the membrane-bound form of the2 juxtamembrane domain of the epidermal growth factor3 receptor
25	<a href="#">c2z3xC_</a>	Alignment	not modelled	6.2	43	<b>PDB header:</b> dna binding protein/dna <b>Chain:</b> C: <b>PDB Molecule:</b> small, acid-soluble spore protein c; <b>PDBTitle:</b> structure of a protein-dna complex essential for dna2 protection in spore of bacillus species