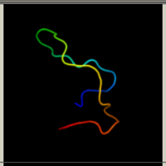
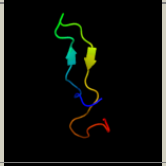
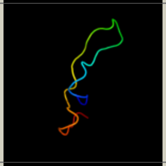
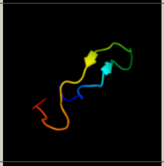
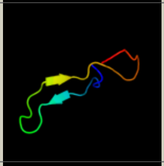
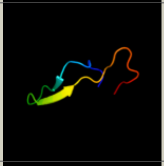
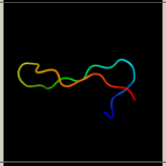
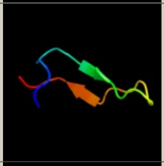
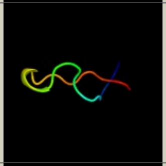
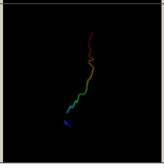
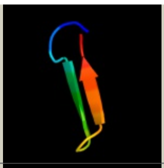
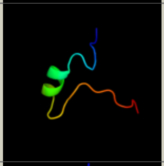
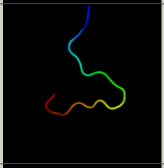
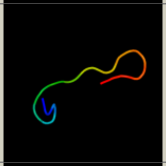
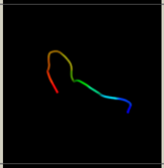
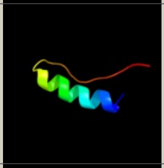
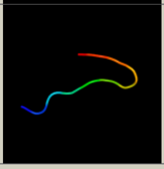
Phyre2

Email	l.a.kelley@imperial.ac.uk
Description	P0ACW4
Date	Thu Jan 5 11:19:16 GMT 2012
Unique Job ID	5a0cf00443445036

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tiha_	Alignment		81.2	35	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
2	d1pjua1	Alignment		80.7	39	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
3	d1fyba1	Alignment		80.1	39	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
4	d4sgbi_	Alignment		77.6	35	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
5	d1oyvi_	Alignment		71.6	39	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
6	c1fybA_	Alignment		69.3	39	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**proteinase inhibitor; **PDBTitle:** solution structure of c1-t1, a two-domain proteinase2 inhibitor derived from the circular precursor protein na-3 propi from nicotiana alata
7	d1ce3a_	Alignment		50.6	41	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
8	d1pjua2	Alignment		35.9	45	**Fold:**Plant proteinase inhibitors **Superfamily:**Plant proteinase inhibitors **Family:**Plant proteinase inhibitors
9	c2d3jA_	Alignment		13.3	40	**PDB header:**signaling protein inhibitor **Chain:** A: **PDB Molecule:**wnt inhibitory factor-1; **PDBTitle:** nmr structure of the wif domain from human wif-1
10	c2e3eA_	Alignment		12.5	38	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**defensin, mutant def-bbb; **PDBTitle:** nmr structure of def-bbb, a mutant of anopheles defensin2 def-aaa
11	d2jnaa1	Alignment		11.9	30	**Fold:**Dodecin subunit-like **Superfamily:**YdgH-like **Family:**YdgH-like

12	c2e2fA_	Alignment		10.2	40	**PDB header:**antifungal protein **Chain:** A: **PDB Molecule:**diapausin; **PDBTitle:** solution structure of dsp
13	d1zuea1	Alignment		9.6	56	**Fold:**Defensin-like **Superfamily:**Defensin-like **Family:**Defensin
14	c1xfeA_	Alignment		9.5	35	**PDB header:**lipid transport, endocytosis/exocytosis **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** solution structure of the la7-egfa pair from the ldl2 receptor
15	d2cupa2	Alignment		9.5	40	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**LIM domain
16	d1e43a1	Alignment		8.3	55	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
17	d1bgva2	Alignment		8.2	31	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
18	d1ud2a1	Alignment		8.2	55	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
19	d2d3na1	Alignment		8.0	55	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
20	d2gjpa1	Alignment		7.8	45	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
21	d1eoka_	Alignment	not modelled	7.3	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Type II chitinase
22	c1ozbI_	Alignment	not modelled	6.1	67	**PDB header:**protein transport **Chain:** I: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of secb complexed with seca c-terminus
23	d1ozbi_	Alignment	not modelled	6.1	67	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
24	c1ozbJ_	Alignment	not modelled	6.1	67	**PDB header:**protein transport **Chain:** J: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of secb complexed with seca c-terminus
25	c1d2jA_	Alignment	not modelled	6.0	26	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor; **PDBTitle:** ldl receptor ligand-binding module 6
26	d1hvxa1	Alignment	not modelled	5.9	55	**Fold:**Glycosyl hydrolase domain **Superfamily:**Glycosyl hydrolase domain **Family:**alpha-Amylases, C-terminal beta-sheet domain
27	c4a1eT_	Alignment	not modelled	5.9	36	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**rpl24; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna, 5.8s rrna3 and proteins of molecule 1
28	d1v9la2	Alignment	not modelled	5.8	19	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
						Fold: Knottins (small inhibitors, toxins, lectins)

29	d1g26a_	Alignment	not modelled	5.7	38	**Superfamily:**Granulin repeat **Family:**Granulin repeat
30	c2i1pA_	Alignment	not modelled	5.7	43	**PDB header:**ligand binding protein **Chain:** A: **PDB Molecule:**low-density lipoprotein receptor-related protein **PDBTitle:** solution structure of the twelfth cysteine-rich ligand-2 binding repeat in rat megalin
31	d1euza2	Alignment	not modelled	5.6	27	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
32	d1hwxa2	Alignment	not modelled	5.6	19	**Fold:**Aminoacid dehydrogenase-like, N-terminal domain **Superfamily:**Aminoacid dehydrogenase-like, N-terminal domain **Family:**Aminoacid dehydrogenases
33	d1tm6a_	Alignment	not modelled	5.5	67	**Fold:**Sec-C motif **Superfamily:**Sec-C motif **Family:**Sec-C motif
34	c1tm6A_	Alignment	not modelled	5.5	67	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** nmr structure of the free zinc binding c-terminal domain of2 seca