Phyre2

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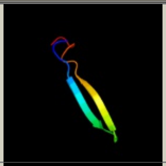
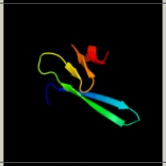
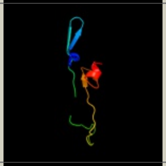
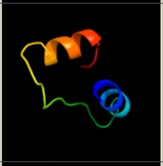
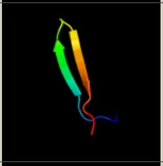
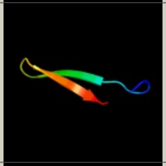
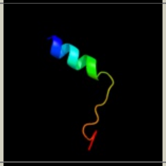
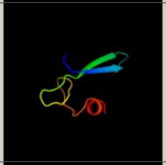
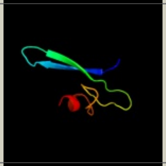
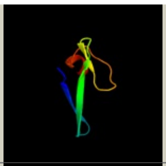
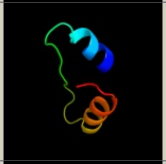
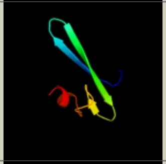
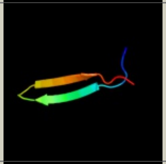
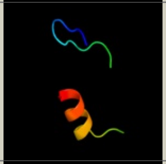
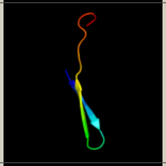
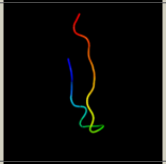
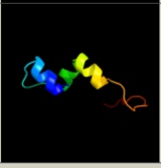
Description	P07010
Date	Thu Jan 5 10:59:57 GMT 2012
Unique Job ID	ce70540e8a0836d8

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3hizB_	Alignment		35.8	20	**PDB header:**transferase/oncoprotein **Chain:** B: **PDB Molecule:**phosphatidylinositol 3-kinase regulatory subunit **PDBTitle:** crystal structure of p110alpha h1047r mutant in complex with2 nish2 of p85alpha
2	d2shpa2	Alignment		31.7	26	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
3	d2eyva1	Alignment		30.2	26	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
4	d1nzja_	Alignment		21.6	37	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
5	d2izva2	Alignment		20.7	32	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
6	d1rpya_	Alignment		20.5	15	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
7	c3rrwB_	Alignment		19.6	23	**PDB header:**plant protein **Chain:** B: **PDB Molecule:**thylakoid lumenal 29 kda protein, chloroplastic; **PDBTitle:** crystal structure of the tl29 protein from arabidopsis thaliana
8	d1lc0a2	Alignment		17.3	67	**Fold:**FwdE/GAPDH domain-like **Superfamily:**Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain **Family:**Biliverdin reductase
9	d1a81e1	Alignment		15.5	25	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
10	c2lctA_	Alignment		14.9	21	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**proto-oncogene vav; **PDBTitle:** solution structure of the vav1 sh2 domain complexed with a syk-derived2 doubly phosphorylated peptide
11	c2k7cA_	Alignment		14.6	45	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** nmr structure of mg2+-bound cabp1 c-domain

12	d2oq1a1	Alignment		12.7	19	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
13	d1j09a2	Alignment		12.4	49	**Fold:**Adenine nucleotide alpha hydrolase-like **Superfamily:**Nucleotidylyl transferase **Family:**Class I aminoacyl-tRNA synthetases (RS), catalytic domain
14	c1k9aB_	Alignment		12.1	33	**PDB header:**transferase **Chain:** B: **PDB Molecule:**carboxyl-terminal src kinase; **PDBTitle:** crystal structure analysis of full-length carboxyl-terminal2 src kinase at 2.5 a resolution
15	c2vifA_	Alignment		11.1	18	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**suppressor of cytokine signalling 6; **PDBTitle:** crystal structure of socs6 sh2 domain in complex with a c-kit2 phosphopeptide
16	d1ifqa_	Alignment		10.4	38	**Fold:**Profilin-like **Superfamily:**SNARE-like **Family:**Synatpobrevin N-terminal domain
17	c2eo6A_	Alignment		10.3	9	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**b-cell linker protein; **PDBTitle:** solution structure of the sh2 domain from mouse b-cell2 linker protein blnk
18	c2cr4A_	Alignment		9.7	41	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding protein 2; **PDBTitle:** solution structure of the sh2 domain of human sh3bp2 protein
19	c2x8rE_	Alignment		9.0	22	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**glycosyl hydrolase; **PDBTitle:** the structure of a family gh25 lysozyme from aspergillus2 fumigatus
20	d1wj5a_	Alignment		8.9	23	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**An Obfc1 domain
21	c3aiiA_	Alignment	not modelled	8.2	56	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutamyl-trna synthetase; **PDBTitle:** archaeal non-discriminating glutamyl-trna synthetase from2 methanothermobacter thermautotrophicus
22	d1a81a1	Alignment	not modelled	7.6	35	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
23	d2c9wa2	Alignment	not modelled	7.5	23	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
24	c2fo0A_	Alignment	not modelled	7.4	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**proto-oncogene tyrosine-protein kinase abl1 (1b isoform); **PDBTitle:** organization of the sh3-sh2 unit in active and inactive forms of the2 c-abl tyrosine kinase
25	c3bv8A_	Alignment	not modelled	7.4	28	**PDB header:**transferase **Chain:** A: **PDB Molecule:**tetrahydrodipicolinate acetyltransferase; **PDBTitle:** crystal structure of the n-terminal domain of tetrahydrodipicolinate2 acetyltransferase from staphylococcus aureus
26	c1exdA_	Alignment	not modelled	7.2	33	**PDB header:**ligase/rna **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of a tight-binding glutamine trna bound2 to glutamine aminoacyl trna synthetase
27	c2c9wA_	Alignment	not modelled	7.1	23	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**suppressor of cytokine signaling 2; **PDBTitle:** crystal structure of socs-2 in complex with elongin-b and2 elongin-c at 1.9a resolution
28	c2dx0B_	Alignment	not modelled	6.9	30	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**phospholipase c, gamma 2; **PDBTitle:** crystal structure of the n-terminal sh2 domain of mouse2

						phospholipase c-gamma 2
29	c3i3tG_	Alignment	not modelled	6.7	32	**PDB header:**hydrolase **Chain:** G: **PDB Molecule:**ubiquitin carboxyl-terminal hydrolase 21; **PDBTitle:** crystal structure of covalent ubiquitin-usp21 complex
30	d1bbua1	Alignment	not modelled	6.6	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Anticodon-binding domain
31	c2hz7A_	Alignment	not modelled	6.4	50	**PDB header:**ligase **Chain:** A: **PDB Molecule:**glutaminyl-trna synthetase; **PDBTitle:** crystal structure of the glutaminyl-trna synthetase from2 deinococcus radiodurans
32	d1a81e2	Alignment	not modelled	6.3	35	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
33	c3k0zB_	Alignment	not modelled	6.1	18	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative polyketide cyclase; **PDBTitle:** crystal structure of putative polyketide cyclase (np_977253.1) from2 bacillus cereus atcc 10987 at 1.91 a resolution
34	d2adca1	Alignment	not modelled	6.0	24	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
35	c2eyzA_	Alignment	not modelled	6.0	40	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**v-crk sarcoma virus ct10 oncogene homolog **PDBTitle:** ct10-regulated kinase isoform ii
36	c2el8A_	Alignment	not modelled	5.9	22	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**signal-transducing adaptor protein 2; **PDBTitle:** solution structure of the human stap2 sh2 domain
37	c2nw0B_	Alignment	not modelled	5.8	31	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**plyb; **PDBTitle:** crystal structure of a lysin
38	c1rqqC_	Alignment	not modelled	5.7	15	**PDB header:**transferase/signaling protein **Chain:** C: **PDB Molecule:**adaptor protein aps; **PDBTitle:** crystal structure of the insulin receptor kinase in complex2 with the sh2 domain of aps
39	d1jfxa_	Alignment	not modelled	5.5	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**1,4-beta-N-acetylmuraminidase
40	d2ah2a2	Alignment	not modelled	5.4	19	**Fold:**6-bladed beta-propeller **Superfamily:**Sialidases **Family:**Sialidases (neuraminidases)
41	d1nbfa_	Alignment	not modelled	5.3	31	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Ubiquitin carboxyl-terminal hydrolase, UCH
42	d2g0ta1	Alignment	not modelled	5.2	52	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nitrogenase iron protein-like