Phyre^2

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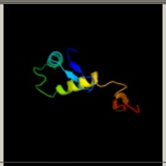
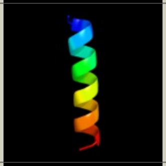
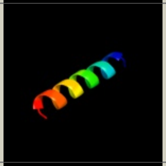
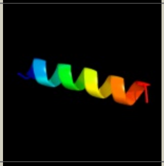
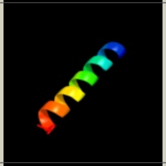
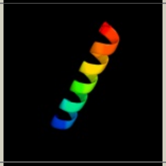
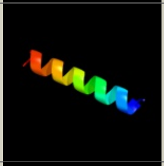
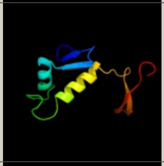
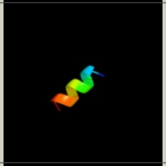
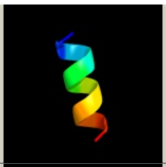
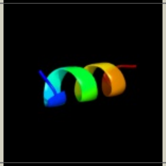
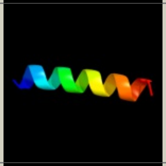
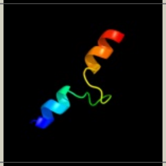
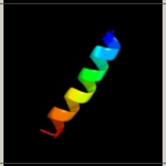
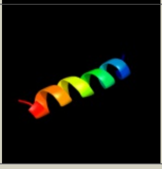
Description	P11865
Date	Thu Jan 5 11:32:53 GMT 2012
Unique Job ID	a57d615ed6f44897

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1tf5a1	Alignment		39.8	16	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
2	c2ccfA_	Alignment		35.1	63	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** antiparallel configuration of pli e20s
3	c2cceA_	Alignment		34.8	63	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** parallel configuration of pli e20s
4	c2cceB_	Alignment		34.8	63	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** parallel configuration of pli e20s
5	c1unyA_	Alignment		33.3	52	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
6	c2rjiB_	Alignment		32.6	33	**PDB header:**protein transport, cell invasion **Chain:** B: **PDB Molecule:**erythrocyte binding antigen 175; **PDBTitle:** malarial eba-175 region vi crystallographic structure2 reveals a kix-like binding interface
7	c1unzB_	Alignment		30.3	52	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
8	c1unzA_	Alignment		30.3	52	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
9	d1nkta1	Alignment		29.0	19	**Fold:**Pre-protein crosslinking domain of SecA **Superfamily:**Pre-protein crosslinking domain of SecA **Family:**Pre-protein crosslinking domain of SecA
10	c1unvA_	Alignment		18.8	58	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
11	c1unvB_	Alignment		18.7	58	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles

12	c1u9gA_	Alignment		18.7	58	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(8)l(9)
13	c1u9gB_	Alignment		18.7	58	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(8)l(9)
14	d2co7b2	Alignment		15.7	22	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
15	c1envA_	Alignment		15.3	46	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hiv-1 envelope protein chimera consisting of a fragment of **PDBTitle:** atomic structure of the ectodomain from hiv-1 gp41
16	c1gcmA_	Alignment		14.7	58	**PDB header:**transcription regulation **Chain:** A: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
17	d1twfc1	Alignment		14.6	50	**Fold:**DCoH-like **Superfamily:**RBP11-like subunits of RNA polymerase **Family:**RNA polymerase alpha subunit dimerisation domain
18	c2ag3A_	Alignment		14.5	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**gcn4-pli; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: substitution of the k(15)-l(16) amide with a triazole
19	c1gclA_	Alignment		14.4	58	**PDB header:**leucine zipper **Chain:** A: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
20	c1gclB_	Alignment		14.4	58	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
21	c1gclC_	Alignment	not modelled	14.4	58	**PDB header:**leucine zipper **Chain:** C: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
22	c1gclD_	Alignment	not modelled	14.4	58	**PDB header:**leucine zipper **Chain:** D: **PDB Molecule:**gcn4; **PDBTitle:** gcn4 leucine zipper core mutant p-li
23	c1w5iA_	Alignment	not modelled	13.2	58	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** aba does not affect topology of pli.
24	c1uo2A_	Alignment	not modelled	13.2	58	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
25	c1uo2B_	Alignment	not modelled	12.4	58	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
26	c1w5iB_	Alignment	not modelled	12.4	58	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** aba does not affect topology of pli.
27	c1unyB_	Alignment	not modelled	12.2	61	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
28	c1uo1A_	Alignment	not modelled	12.0	58	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
						PDB header:four helix bundle

29	c1uo1B_	Alignment	not modelled	12.0	58	**Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
30	c1uo0B_	Alignment	not modelled	12.0	58	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
31	c1uo0A_	Alignment	not modelled	12.0	58	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
32	d1hc1a2	Alignment	not modelled	11.6	28	**Fold:**Di-copper centre-containing domain **Superfamily:**Di-copper centre-containing domain **Family:**Hemocyanin middle domain
33	d1m98a1	Alignment	not modelled	11.4	21	**Fold:**Orange carotenoid protein, N-terminal domain **Superfamily:**Orange carotenoid protein, N-terminal domain **Family:**Orange carotenoid protein, N-terminal domain
34	d1b4ub_	Alignment	not modelled	11.3	14	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**LigB-like **Family:**LigB-like
35	c1w5jA_	Alignment	not modelled	11.0	53	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
36	c1w5jC_	Alignment	not modelled	11.0	53	**PDB header:**four helix bundle **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
37	c1w5jB_	Alignment	not modelled	11.0	53	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
38	c1w5jD_	Alignment	not modelled	11.0	53	**PDB header:**four helix bundle **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
39	d3bwuc2	Alignment	not modelled	10.6	17	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
40	c1u9fA_	Alignment	not modelled	9.9	59	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
41	c2g7hA_	Alignment	not modelled	9.9	15	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methylated-dna--protein-cysteine **PDBTitle:** structure of an o6-methylguanine dna methyltransferase from2 methanococcus jannaschii (mj1529)
42	c1i6hC_	Alignment	not modelled	9.8	50	**PDB header:**transcription/dna-rna hybrid **Chain:** C: **PDB Molecule:**dna-directed rna polymerase ii 45kd polypeptide; **PDBTitle:** rna polymerase ii elongation complex
43	c3howC_	Alignment	not modelled	9.8	50	**PDB header:**transcription,transferase/dna/rna hybrid **Chain:** C: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb3; **PDBTitle:** complete rna polymerase ii elongation complex iii with a t-u2 mismatch and a frayed rna 3'-uridine
44	d1llaa2	Alignment	not modelled	9.7	28	**Fold:**Di-copper centre-containing domain **Superfamily:**Di-copper centre-containing domain **Family:**Hemocyanin middle domain
45	c1gcmB_	Alignment	not modelled	9.4	52	**PDB header:**transcription regulation **Chain:** B: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
46	c2eocA_	Alignment	not modelled	9.4	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase 3; **PDBTitle:** solution structure of the wgr domain from human poly [adp-2 ribose] polymerase-3
47	c1gcmC_	Alignment	not modelled	9.0	52	**PDB header:**transcription regulation **Chain:** C: **PDB Molecule:**gcn4p-ii; **PDBTitle:** gcn4 leucine zipper core mutant p-li
48	c1u9fB_	Alignment	not modelled	8.9	59	**PDB header:**transcription **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
49	c1u9fC_	Alignment	not modelled	8.9	59	**PDB header:**transcription **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
50	c2pmzS_	Alignment	not modelled	8.7	32	**PDB header:**translation, transferase **Chain:** S: **PDB Molecule:**dna-directed rna polymerase subunit d; **PDBTitle:** archaeal rna polymerase from sulfolobus solfataricus
51	c3efyB_	Alignment	not modelled	8.2	38	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cif (cell cycle inhibiting factor); **PDBTitle:** structure of the cyclomodulin cif from pathogenic2 escherichia coli
52	c1u9fD_	Alignment	not modelled	8.2	59	**PDB header:**transcription **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** heterocyclic peptide backbone modification in gcn4-pli based coiled2 coils: replacement of k(15)l(16)
53	d1p5va2	Alignment	not modelled	8.0	20	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
54	c1bdfC_	Alignment	not modelled	7.8	40	**PDB header:**nucleotidyltransferase **Chain:** C: **PDB Molecule:**rna polymerase alpha subunit; **PDBTitle:** structure of escherichia coli rna polymerase alpha subunit2 n-terminal domain
55	d1l4ia2	Alignment	not modelled	7.7	15	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain

56	d1xsqa_	Alignment	not modelled	7.5	20	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
57	c3rrrM_	Alignment	not modelled	7.4	78	**PDB header:**viral protein **Chain:** M: **PDB Molecule:**fusion glycoprotein f0; **PDBTitle:** structure of the rsv f protein in the post-fusion conformation
58	c1m98A_	Alignment	not modelled	7.3	21	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**orange carotenoid protein; **PDBTitle:** crystal structure of orange carotenoid protein
59	d2bdra1	Alignment	not modelled	7.2	43	**Fold:**Double-stranded beta-helix **Superfamily:**RmlC-like cupins **Family:**Ureidoglycolate hydrolase AllA
60	c1uo3B_	Alignment	not modelled	7.1	58	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
61	c3h0gO_	Alignment	not modelled	7.1	46	**PDB header:**transcription **Chain:** O: **PDB Molecule:**dna-directed rna polymerase ii subunit rpb3; **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
62	d2j2za2	Alignment	not modelled	7.1	21	**Fold:**C2 domain-like **Superfamily:**Periplasmic chaperone C-domain **Family:**Periplasmic chaperone C-domain
63	c1smyB_	Alignment	not modelled	7.0	50	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna-directed rna polymerase alpha chain; **PDBTitle:** structural basis for transcription regulation by alarmone2 ppgpp
64	c1uo5B_	Alignment	not modelled	6.9	58	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
65	c1uo5A_	Alignment	not modelled	6.9	58	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
66	d1nbwa1	Alignment	not modelled	6.7	35	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**Swiveling domain of dehydratase reactivase alpha subunit **Family:**Swiveling domain of dehydratase reactivase alpha subunit
67	c2k21A_	Alignment	not modelled	6.6	71	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**potassium voltage-gated channel subfamily e **PDBTitle:** nmr structure of human kcne1 in lmpg micelles at ph 6.0 and2 40 degree c
68	c1untA_	Alignment	not modelled	6.3	58	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
69	d1rpya_	Alignment	not modelled	6.3	14	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
70	d1sisa_	Alignment	not modelled	6.2	71	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Short-chain scorpion toxins
71	c1w5kB_	Alignment	not modelled	6.0	47	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
72	c1w5kD_	Alignment	not modelled	6.0	47	**PDB header:**four helix bundle **Chain:** D: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
73	c1w5kC_	Alignment	not modelled	6.0	47	**PDB header:**four helix bundle **Chain:** C: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
74	c1w5kA_	Alignment	not modelled	6.0	47	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** an anti-parallel four helix bundle
75	c2r2vB_	Alignment	not modelled	5.9	50	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**gcn4 leucine zipper; **PDBTitle:** sequence determinants of the topology of the lac repressor2 tetrameric coiled coil
76	c1untB_	Alignment	not modelled	5.9	58	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
77	d1bcoa1	Alignment	not modelled	5.8	23	**Fold:**mu transposase, C-terminal domain **Superfamily:**mu transposase, C-terminal domain **Family:**mu transposase, C-terminal domain
78	c1unuB_	Alignment	not modelled	5.5	42	**PDB header:**four helix bundle **Chain:** B: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
79	c1unuA_	Alignment	not modelled	5.5	42	**PDB header:**four helix bundle **Chain:** A: **PDB Molecule:**general control protein gcn4; **PDBTitle:** structure based engineering of internal molecular surfaces2 of four helix bundles
80	d1ugla_	Alignment	not modelled	5.5	100	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Plant defensins