Phyre2

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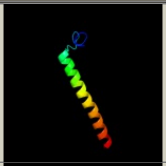
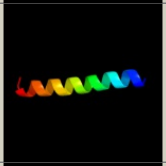
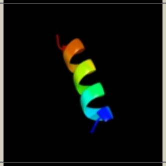
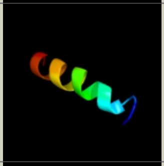
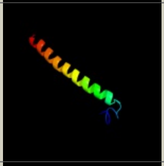
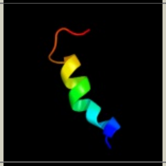
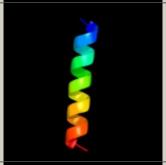
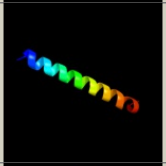
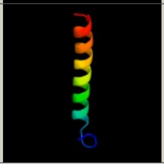
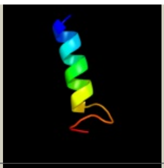
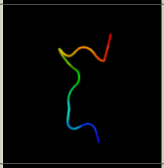
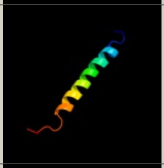
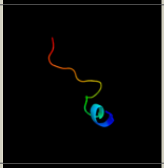
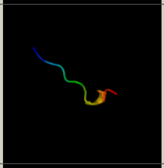
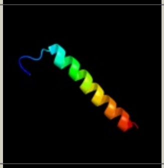
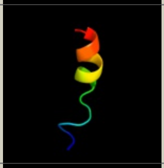
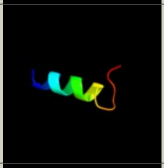
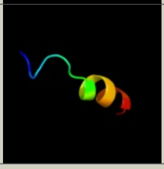
Description	P0AFM9
Date	Thu Jan 5 11:26:48 GMT 2012
Unique Job ID	42b08a00809a53b3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d3bzka3	Alignment		52.2	16	**Fold:**Tex N-terminal region-like **Superfamily:**Tex N-terminal region-like **Family:**Tex N-terminal region-like
2	c1aq5C_	Alignment		48.3	24	**PDB header:**coiled-coil **Chain:** C: **PDB Molecule:**cartilage matrix protein; **PDBTitle:** high-resolution solution nmr structure of the trimeric coiled-coil2 domain of chicken cartilage matrix protein, 20 structures
3	c2xdjF_	Alignment		40.9	31	**PDB header:**unknown function **Chain:** F: **PDB Molecule:**uncharacterized protein ybgf; **PDBTitle:** crystal structure of the n-terminal domain of e.coli ybgf
4	d1e52a_	Alignment		40.6	22	**Fold:**Long alpha-hairpin **Superfamily:**C-terminal UvrC-binding domain of UvrB **Family:**C-terminal UvrC-binding domain of UvrB
5	c2oceA_	Alignment		36.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein pa5201; **PDBTitle:** crystal structure of tex family protein pa5201 from2 pseudomonas aeruginosa
6	c2pnvA_	Alignment		32.1	23	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**small conductance calcium-activated potassium **PDBTitle:** crystal structure of the leucine zipper domain of small-2 conductance ca2+-activated k+ (skca) channel from rattus3 norvegicus
7	d1nkzb_	Alignment		24.9	37	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
8	d1jb0i_	Alignment		24.4	18	**Fold:**Single transmembrane helix **Superfamily:**Subunit VIII of photosystem I reaction centre, PsaI **Family:**Subunit VIII of photosystem I reaction centre, PsaI
9	c2oqqB_	Alignment		23.1	24	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor hy5; **PDBTitle:** crystal structure of hy5 leucine zipper homodimer from2 arabidopsis thaliana
10	c3okqA_	Alignment		23.0	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**bud site selection protein 6; **PDBTitle:** crystal structure of a core domain of yeast actin nucleation cofactor2 bud6
11	d1wrda1	Alignment		22.6	17	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain

12	c1b9uA_	Alignment		20.8	32	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein (atp synthase); **PDBTitle:** membrane domain of the subunit b of the e.coli atp synthase
13	d1pfta_	Alignment		20.7	50	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
14	c3mk7F_	Alignment		20.2	21	**PDB header:**oxidoreductase **Chain:** F: **PDB Molecule:**cytochrome c oxidase, cbb3-type, subunit p; **PDBTitle:** the structure of cbb3 cytochrome oxidase
15	c3ixzB_	Alignment		20.2	28	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**potassium-transporting atpase subunit beta; **PDBTitle:** pig gastric h+/k+-atpase complexed with aluminium fluoride
16	d1dl6a_	Alignment		20.1	25	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
17	d1wr6a1	Alignment		19.4	17	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
18	c3bz1y_	Alignment		18.8	47	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii protein y; **PDBTitle:** crystal structure of cyanobacterial photosystem ii (part 12 of 2). this file contains first monomer of psii dimer
19	c2d96A_	Alignment		18.6	32	**PDB header:**transcription **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p100 subunit; **PDBTitle:** solution structure of the death domain of nuclear factor nf-2 kappa-b p100
20	c3arcy_	Alignment		18.1	47	**PDB header:**electron transport, photosynthesis **Chain:** Y: **PDB Molecule:**protein ycf12; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
21	c3arcY_	Alignment	not modelled	18.1	47	**PDB header:**electron transport, photosynthesis **Chain:** Y: **PDB Molecule:**protein ycf12; **PDBTitle:** crystal structure of oxygen-evolving photosystem ii at 1.9 angstrom2 resolution
22	d1nu9c2	Alignment	not modelled	17.8	40	**Fold:**immunoglobulin/albumin-binding domain-like **Superfamily:**Staphylocoagulase **Family:**Staphylocoagulase
23	c1a92B_	Alignment	not modelled	17.6	24	**PDB header:**leucine zipper **Chain:** B: **PDB Molecule:**delta antigen; **PDBTitle:** oligomerization domain of hepatitis delta antigen
24	c3a0hy_	Alignment	not modelled	17.1	47	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
25	c3a0hY_	Alignment	not modelled	17.1	47	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of i-substituted photosystem ii complex
26	c3m06F_	Alignment	not modelled	16.9	14	**PDB header:**protein binding **Chain:** F: **PDB Molecule:**tnf receptor-associated factor 2; **PDBTitle:** crystal structure of traf2
27	c3ls1A_	Alignment	not modelled	14.8	12	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
28	d1g7oa1	Alignment	not modelled	14.5	14	**Fold:**GST C-terminal domain-like **Superfamily:**GST C-terminal domain-like **Family:**Glutathione S-transferase (GST), C-terminal domain
						Fold: Spectrin repeat-like

29	d1o3xa_	Alignment	not modelled	14.3	24	**Superfamily:**GAT-like domain **Family:**GAT domain
30	d1bf5a1	Alignment	not modelled	14.2	17	**Fold:**STAT-like **Superfamily:**STAT **Family:**STAT
31	c2jgoB_	Alignment	not modelled	14.2	30	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
32	c3ljmC_	Alignment	not modelled	14.2	30	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
33	c3ljmB_	Alignment	not modelled	14.2	30	**PDB header:**de novo protein **Chain:** B: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
34	c2jgoC_	Alignment	not modelled	14.2	30	**PDB header:**de novo protein **Chain:** C: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
35	c2jgoA_	Alignment	not modelled	14.2	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l9c; **PDBTitle:** stucture of the arsenated de novo designed peptide coil ser2 l9c
36	c3ljmA_	Alignment	not modelled	14.2	30	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**coil ser l9c; **PDBTitle:** structure of de novo designed apo peptide coil ser l9c
37	c3efdK_	Alignment	not modelled	14.1	27	**PDB header:**immune system **Chain:** K: **PDB Molecule:**kcsa; **PDBTitle:** the crystal structure of the cytoplasmic domain of kcsa
38	c3b37A_	Alignment	not modelled	14.1	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aminopeptidase n; **PDBTitle:** crystal structure of e. coli aminopeptidase n in complex with tyrosine
39	c3a0by_	Alignment	not modelled	13.8	47	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
40	c2d99A_	Alignment	not modelled	13.6	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-048, a gtf2i domain in human2 cdna
41	c2e3lA_	Alignment	not modelled	13.5	25	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor gtf2ird2 beta; **PDBTitle:** solution structure of rsgi ruh-068, a gtf2i domain in human2 cdna
42	c2dn5A_	Alignment	not modelled	13.1	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-057, a gtf2i domain in human2 cdna
43	c2dbfA_	Alignment	not modelled	12.9	33	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**nuclear factor nf-kappa-b p105 subunit; **PDBTitle:** solution structure of the death domain in human nuclear2 factor nf-kappa-b p105 subunit
44	c2dzrA_	Alignment	not modelled	12.6	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-067, a gtf2i domain in human2 cdna
45	c2dzqA_	Alignment	not modelled	12.5	42	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i repeat domain- **PDBTitle:** solution structure of rsgi ruh-066, a gtf2i domain in human2 cdna
46	c1cosA_	Alignment	not modelled	12.2	30	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
47	c1cosC_	Alignment	not modelled	12.2	30	**PDB header:**alpha-helical bundle **Chain:** C: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
48	c1cosB_	Alignment	not modelled	12.2	30	**PDB header:**alpha-helical bundle **Chain:** B: **PDB Molecule:**coiled serine; **PDBTitle:** crystal structure of a synthetic triple-stranded alpha-2 helical bundle
49	d1wmub_	Alignment	not modelled	12.0	18	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
50	c3a0bY_	Alignment	not modelled	11.0	47	**PDB header:**electron transport **Chain:** Y: **PDB Molecule:**photosystem ii reaction center protein ycf12; **PDBTitle:** crystal structure of br-substituted photosystem ii complex
51	d1q60a_	Alignment	not modelled	10.8	42	**Fold:**GTF2I-like repeat **Superfamily:**GTF2I-like repeat **Family:**GTF2I-like repeat
52	c2ed2A_	Alignment	not modelled	10.8	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-069, a gtf2i domain in human2 cdna
53	d1zkea1	Alignment	not modelled	10.5	38	**Fold:**ROP-like **Superfamily:**HP1531-like **Family:**HP1531-like
54	d1f6ga_	Alignment	not modelled	10.5	21	**Fold:**Voltage-gated potassium channels **Superfamily:**Voltage-gated potassium channels **Family:**Voltage-gated potassium channels

55	c2dn4A_	Alignment	not modelled	10.4	50	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-060, a gtf2i domain in human2 cdna
56	c1coiA_	Alignment	not modelled	10.4	25	**PDB header:**alpha-helical bundle **Chain:** A: **PDB Molecule:**coil-vald; **PDBTitle:** designed trimeric coiled coil-vald
57	c3c18B_	Alignment	not modelled	10.3	12	**PDB header:**transferase **Chain:** B: **PDB Molecule:**nucleotidyltransferase-like protein; **PDBTitle:** crystal structure of nucleotidyltransferase-like protein2 (zp_00538802.1) from exiguobacterium sibiricum 255-15 at 1.90 a3 resolution
58	c3b8eB_	Alignment	not modelled	10.1	28	**PDB header:**hydrolase/transport protein **Chain:** B: **PDB Molecule:**sodium/potassium-transporting atpase subunit **PDBTitle:** crystal structure of the sodium-potassium pump
59	c1ci6B_	Alignment	not modelled	10.1	19	**PDB header:**transcription **Chain:** B: **PDB Molecule:**transcription factor c/ebp beta; **PDBTitle:** transcription factor atf4-c/ebp beta bzip heterodimer
60	c1by0A_	Alignment	not modelled	10.0	24	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
61	d1ijdb_	Alignment	not modelled	9.9	39	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits
62	c2ejeA_	Alignment	not modelled	9.3	33	**PDB header:**transcription **Chain:** A: **PDB Molecule:**general transcription factor ii-i; **PDBTitle:** solution structure of rsgi ruh-071, a gtf2i domain in human2 cdna
63	c3bmbB_	Alignment	not modelled	8.8	19	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**regulator of nucleoside diphosphate kinase; **PDBTitle:** crystal structure of a new rna polymerase interacting2 protein
64	c3eabD_	Alignment	not modelled	8.7	15	**PDB header:**cell cycle **Chain:** D: **PDB Molecule:**spastin; **PDBTitle:** crystal structure of spastin mit in complex with escrt iii
65	d1wmga_	Alignment	not modelled	8.2	47	**Fold:**DEATH domain **Superfamily:**DEATH domain **Family:**DEATH domain, DD
66	d1mlda2	Alignment	not modelled	8.1	18	**Fold:**LDH C-terminal domain-like **Superfamily:**LDH C-terminal domain-like **Family:**Lactate & malate dehydrogenases, C-terminal domain
67	c2d3kA_	Alignment	not modelled	7.8	23	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** structural study on project id ph1539 from pyrococcus2 horikoshii ot3
68	c3sb1B_	Alignment	not modelled	7.6	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**hydrogenase expression protein; **PDBTitle:** hydrogenase expression protein huph from thiobacillus denitrificans2 atcc 25259
69	c3r45C_	Alignment	not modelled	7.6	30	**PDB header:**nuclear protein **Chain:** C: **PDB Molecule:**holliday junction recognition protein; **PDBTitle:** structure of a cenp-a-histone h4 heterodimer in complex with chaperone2 hjurp
70	c1xtyD_	Alignment	not modelled	7.6	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** crystal structure of sulfolobus solfataricus peptidyl-trna2 hydrolase
71	d2ay0a1	Alignment	not modelled	7.5	33	**Fold:**Ribbon-helix-helix **Superfamily:**Ribbon-helix-helix **Family:**PutA pre-N-terminal region-like
72	d1ab4a_	Alignment	not modelled	7.3	24	**Fold:**Type II DNA topoisomerase **Superfamily:**Type II DNA topoisomerase **Family:**Type II DNA topoisomerase
73	c3m6nA_	Alignment	not modelled	7.3	16	**PDB header:**lyase **Chain:** A: **PDB Molecule:**rpff protein; **PDBTitle:** crystal structure of rpff
74	d1kqfb2	Alignment	not modelled	7.1	25	**Fold:**Single transmembrane helix **Superfamily:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor **Family:**Iron-sulfur subunit of formate dehydrogenase N, transmembrane anchor
75	c3ilwA_	Alignment	not modelled	6.9	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna gyrase subunit a; **PDBTitle:** structure of dna gyrase subunit a n-terminal domain
76	d1x79a_	Alignment	not modelled	6.9	23	**Fold:**Spectrin repeat-like **Superfamily:**GAT-like domain **Family:**GAT domain
77	d1t3wa_	Alignment	not modelled	6.5	30	**Fold:**DNA primase DnaG, C-terminal domain **Superfamily:**DNA primase DnaG, C-terminal domain **Family:**DNA primase DnaG, C-terminal domain
78	c2vmlD_	Alignment	not modelled	6.4	29	**PDB header:**photosynthesis **Chain:** D: **PDB Molecule:**phycocyanin beta chain; **PDBTitle:** the monoclinic structure of phycocyanin from gloeobacter2 violaceus
79	c3pp5A_	Alignment	not modelled	6.3	17	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**brk1; **PDBTitle:** high-resolution structure of the trimeric scar/wave complex precursor2 brk1
80	d2clyc1	Alignment	not modelled	6.2	13	**Fold:**Mitochondrial ATP synthase coupling factor 6 **Superfamily:**Mitochondrial ATP synthase coupling factor 6 **Family:**Mitochondrial ATP synthase coupling factor 6

81	c2o7hF_	Alignment	not modelled	6.1	16	**PDB header:**transcription **Chain:** F: **PDB Molecule:**general control protein gcn4; **PDBTitle:** crystal structure of trimeric coiled coil gcn4 leucine zipper
82	c2ergA_	Alignment	not modelled	6.0	19	**PDB header:**transcription activator/dna **Chain:** A: **PDB Molecule:**regulatory protein leu3; **PDBTitle:** crystal structure of leu3 dna-binding domain with a single2 h50c mutation complexed with a 15mer dna duplex
83	c3m0dC_	Alignment	not modelled	5.8	13	**PDB header:**signaling protein **Chain:** C: **PDB Molecule:**tnf receptor-associated factor 1; **PDBTitle:** crystal structure of the traf1:traf2:ciap2 complex
84	c3hroA_	Alignment	not modelled	5.8	26	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transient receptor potential (trp) channel **PDBTitle:** crystal structure of a c-terminal coiled coil domain of2 transient receptor potential (trp) channel subfamily p3 member 2 (trpp2, polycystic kidney disease 2)
85	d3ehbb2	Alignment	not modelled	5.8	7	**Fold:**Transmembrane helix hairpin **Superfamily:**Cytochrome c oxidase subunit II-like, transmembrane region **Family:**Cytochrome c oxidase subunit II-like, transmembrane region
86	c3hrxD_	Alignment	not modelled	5.7	13	**PDB header:**lyase **Chain:** D: **PDB Molecule:**probable enoyl-coa hydratase; **PDBTitle:** crystal structure of phenylacetic acid degradation protein paag
87	c2ba2A_	Alignment	not modelled	5.6	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical upf0134 protein mpn010; **PDBTitle:** crystal structure of the duf16 domain of mpn010 from2 mycoplasma pneumoniae
88	c2voyE_	Alignment	not modelled	5.6	20	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
89	c2hbpA_	Alignment	not modelled	5.6	14	**PDB header:**endocytosis, protein binding **Chain:** A: **PDB Molecule:**cytoskeleton assembly control protein sla1; **PDBTitle:** solution structure of sla1 homology domain 1
90	d2p90a1	Alignment	not modelled	5.5	22	**Fold:**Phosphorylase/hydrolase-like **Superfamily:**Cgl1923-like **Family:**Cgl1923-like
91	c2inrA_	Alignment	not modelled	5.5	27	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** crystal structure of a 59 kda fragment of topoisomerase iv subunit a2 (grla) from staphylococcus aureus
92	c3p8cE_	Alignment	not modelled	5.5	30	**PDB header:**protein binding **Chain:** E: **PDB Molecule:**probable protein brick1; **PDBTitle:** structure and control of the actin regulatory wave complex
93	d1in4a1	Alignment	not modelled	5.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Helicase DNA-binding domain
94	d2h8fb1	Alignment	not modelled	5.4	13	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
95	c2novD_	Alignment	not modelled	5.0	25	**PDB header:**isomerase **Chain:** D: **PDB Molecule:**dna topoisomerase 4 subunit a; **PDBTitle:** breakage-reunion domain of s.pneumoniae topo iv: crystal2 structure of a gram-positive quinolone target