Phyre2

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Description	P77754
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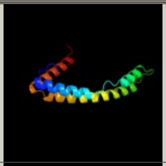
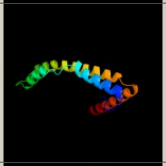
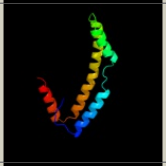
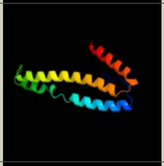
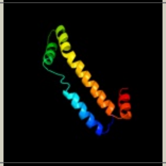
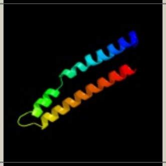
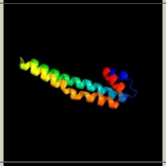
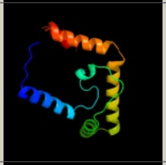
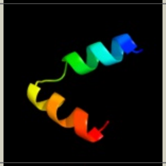
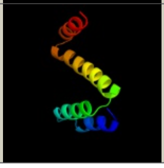
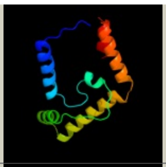
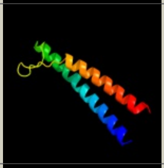
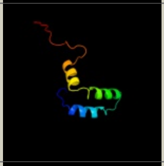
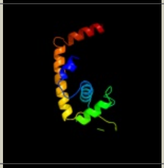
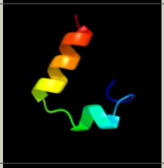
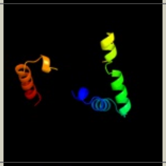
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3itfA_	Alignment		99.9	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic adaptor protein cpxp; **PDBTitle:** structural basis for the inhibitory function of the cpxp adaptor2 protein
2	c3qzcA_	Alignment		99.8	28	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**periplasmic protein cpxp; **PDBTitle:** structure of the periplasmic stress response protein cpxp
3	c3o39A_	Alignment		99.8	93	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**periplasmic protein related to spheroblast formation; **PDBTitle:** crystal structure of spy
4	c3epvB_	Alignment		99.8	12	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**nickel and cobalt resistance protein cnrr; **PDBTitle:** x-ray structure of the metal-sensor cnrx in both the apo- and copper-2 bound forms
5	c3oeoD_	Alignment		99.8	99	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**spheroplast protein y; **PDBTitle:** the crystal structure e. coli spy
6	c3layF_	Alignment		98.6	15	**PDB header:**metal binding protein **Chain:** F: **PDB Molecule:**zinc resistance-associated protein; **PDBTitle:** alpha-helical barrel formed by the decamer of the zinc resistance-2 associated protein (stm4172) from salmonella enterica subsp. enterica3 serovar typhimurium str. lt2
7	c3g6iA_	Alignment		86.1	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative outer membrane protein, part of carbohydrate **PDBTitle:** crystal structure of an outer membrane protein, part of a putative2 carbohydrate binding complex (bt_1022) from bacteroides3 thetaiotaomicron vpi-5482 at 1.93 a resolution
8	c2qguA_	Alignment		78.9	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**probable signal peptide protein; **PDBTitle:** three-dimensional structure of the phospholipid-binding protein from2 ralstonia solanacearum q8xv73_ralsq in complex with a phospholipid at3 the resolution 1.53 a. northeast structural genomics consortium4 target rsr89
9	d3cmna1	Alignment		69.8	15	**Fold:**Zincin-like **Superfamily:**Metalloproteases ("zincins"), catalytic domain **Family:**Caur0242-like
10	c2i9lL_	Alignment		59.5	40	**PDB header:**immune system/viral protein **Chain:** L: **PDB Molecule:**virion membrane protein m25; **PDBTitle:** structure of fab 7d11 from a neutralizing antibody against the2 poxvirus l1 protein
11	c2xv9A_	Alignment		52.9	13	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**aba-1a1 repeat unit; **PDBTitle:** the solution structure of aba-1a saturated with oleic acid

12	c3cmnA_	Alignment		48.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative hydrolase; **PDBTitle:** crystal structure of a putative hydrolase with a novel fold2 from chloroflexus aurantiacus
13	c2an7A_	Alignment		43.4	29	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein pard; **PDBTitle:** solution structure of the bacterial antidote pard
14	c3ieeA_	Alignment		41.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative exported protein; **PDBTitle:** crystal structure of hypothetical protein bf3319 from bacteroides2 fragilis (yp_212931.1) from bacteroides fragilis nctc 9343 at 1.70 a3 resolution
15	c2amiA_	Alignment		33.9	25	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**caltractin; **PDBTitle:** solution structure of the calcium-loaded n-terminal sensor2 domain of centrin
16	c2dmxA_	Alignment		32.8	9	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 8; **PDBTitle:** solution structure of the j domain of dnaj homolog2 subfamily b member 8
17	c3oopA_	Alignment		32.4	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**lin2960 protein; **PDBTitle:** the structure of a protein with unknown function from listeria innocua2 clip11262
18	c2x5qA_	Alignment		24.9	35	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**sso1986; **PDBTitle:** crystal structure of hypothetical protein sso1986 from2 sulfolobus solfataricus p2
19	d1q44a_	Alignment		23.7	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
20	d1pcfa_	Alignment		22.9	33	**Fold:**ssDNA-binding transcriptional regulator domain **Superfamily:**ssDNA-binding transcriptional regulator domain **Family:**Transcriptional coactivator PC4 C-terminal domain
21	d1eh1a_	Alignment	not modelled	22.2	10	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
22	c1zd1B_	Alignment	not modelled	22.2	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**sulfotransferase 4a1; **PDBTitle:** human sulfortransferase sult4a1
23	d1g3ma_	Alignment	not modelled	22.1	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
24	d1wova1	Alignment	not modelled	22.0	17	**Fold:**Heme oxygenase-like **Superfamily:**Heme oxygenase-like **Family:**Eukaryotic type heme oxygenase
25	d1akha_	Alignment	not modelled	21.7	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
26	c2kz5A_	Alignment	not modelled	21.5	15	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor nf-e2 45 kda subunit; **PDBTitle:** solution nmr structure of transcription factor nf-e2 subunit's dna2 binding domain from homo sapiens, northeast structural genomics3 consortium target hr4653b
27	d1wh7a_	Alignment	not modelled	20.9	24	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
28	c2crjA_	Alignment	not modelled	20.9	15	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**swi/snf-related matrix-associated actin- **PDBTitle:** solution structure of the hmg domain of mouse hmg domain2 protein hmgx2
						PDB header:transcription/dna

29	c2xsdC_	Alignment	not modelled	20.7	11	**Chain:** C: **PDB Molecule:**pou domain, class 3, transcription factor 1; **PDBTitle:** crystal structure of the dimeric oct-6 (pou3f1) pou domain2 bound to palindromic more dna
30	c2k5jB_	Alignment	not modelled	19.8	9	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yiif; **PDBTitle:** solution structure of protein yiif from shigella flexneri2 serotype 5b (strain 8401) . northeast structural genomics3 consortium target sft1
31	c2kqxA_	Alignment	not modelled	19.4	10	**PDB header:**chaperone binding protein **Chain:** A: **PDB Molecule:**curved dna-binding protein; **PDBTitle:** nmr structure of the j-domain (residues 2-72) in the2 escherichia coli cbpa
32	d3d1kb1	Alignment	not modelled	19.3	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
33	c2ctoA_	Alignment	not modelled	18.7	17	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**novel protein; **PDBTitle:** solution structure of the hmg box like domain from human2 hypothetical protein flj14904
34	c2eqzA_	Alignment	not modelled	18.7	6	**PDB header:**transcription **Chain:** A: **PDB Molecule:**high mobility group protein b3; **PDBTitle:** solution structure of the first hmg-box domain from high2 mobility group protein b3
35	c3rh3A_	Alignment	not modelled	18.5	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized duf3829-like protein; **PDBTitle:** crystal structure of an uncharacterized duf3829-like protein (bt_1908)2 from bacteroides thetaiotaomicron vpi-5482 at 2.10 a resolution
36	d1ek8a_	Alignment	not modelled	18.3	9	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
37	d1is1a_	Alignment	not modelled	18.3	10	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
38	d1i94m_	Alignment	not modelled	17.9	15	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
39	d1j99a_	Alignment	not modelled	17.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
40	c2k19A_	Alignment	not modelled	17.8	22	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**putative piscicolin 126 immunity protein; **PDBTitle:** nmr solution structure of pisi
41	d1jebb_	Alignment	not modelled	17.3	38	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
42	c2da4A_	Alignment	not modelled	16.9	9	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein dkfzp686k21156; **PDBTitle:** solution structure of the homeobox domain of the2 hypothetical protein, dkfzp686k21156
43	c3fghA_	Alignment	not modelled	16.7	13	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor a, mitochondrial; **PDBTitle:** human mitochondrial transcription factor a box b
44	c2zvpX_	Alignment	not modelled	16.4	23	**PDB header:**transferase **Chain:** X: **PDB Molecule:**tyrosine-ester sulfotransferase; **PDBTitle:** crystal structure of mouse cytosolic sulfotransferase msult1d1 complex2 with pap and p-nitrophenol
45	c3lf9A_	Alignment	not modelled	16.0	9	**PDB header:**immune system **Chain:** A: **PDB Molecule:**4e10_d0_1is1a_001_c (t161); **PDBTitle:** crystal structure of hiv epitope-scaffold 4e10_d0_1is1a_001_c
46	c2h8kA_	Alignment	not modelled	15.9	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sult1c3 splice variant d; **PDBTitle:** human sulfotranferase sult1c3 in complex with pap
47	c3d1nK_	Alignment	not modelled	15.8	22	**PDB header:**transcription regulator/dna **Chain:** K: **PDB Molecule:**pou domain, class 6, transcription factor 1; **PDBTitle:** structure of human brn-5 transcription factor in complex2 with corticotrophin-releasing hormone gene promoter
48	d2uubm1	Alignment	not modelled	15.7	16	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Ribosomal protein S13
49	d1wqga1	Alignment	not modelled	15.5	7	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
50	d1lwma_	Alignment	not modelled	15.1	13	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
51	d2sasa_	Alignment	not modelled	14.9	35	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
52	d1pq9a_	Alignment	not modelled	14.9	14	**Fold:**Nuclear receptor ligand-binding domain **Superfamily:**Nuclear receptor ligand-binding domain **Family:**Nuclear receptor ligand-binding domain
53	c1o6uA_	Alignment	not modelled	14.7	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sec14-like protein 2; **PDBTitle:** the crystal structure of human supernatant protein factor
54	d1lvaa3	Alignment	not modelled	14.4	18	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB

55	d1v63a_	Alignment	not modelled	14.3	12	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
56	d1dd5a_	Alignment	not modelled	14.1	10	**Fold:**RRF/tRNA synthetase additional domain-like **Superfamily:**Ribosome recycling factor, RRF **Family:**Ribosome recycling factor, RRF
57	d1qpwb_	Alignment	not modelled	13.9	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
58	c1y698_	Alignment	not modelled	13.7	7	**PDB header:**ribosome **Chain:** 8: **PDB Molecule:**ribosome recycling factor; **PDBTitle:** rrf domain i in complex with the 50s ribosomal subunit from2 deinococcus radiodurans
59	d1h8ba_	Alignment	not modelled	13.7	14	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**EF-hand modules in multidomain proteins
60	c2zrrA_	Alignment	not modelled	13.6	24	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**mundticin ks immunity protein; **PDBTitle:** crystal structure of an immunity protein that contributes2 to the self-protection of bacteriocin-producing3 enterococcus mundtii 15-1a
61	c2e6oA_	Alignment	not modelled	13.6	5	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**hmg box-containing protein 1; **PDBTitle:** solution structure of the hmg box domain from human hmg-box2 transcription factor 1
62	d1q20a_	Alignment	not modelled	13.6	22	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
63	c1j3xA_	Alignment	not modelled	13.2	6	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**high mobility group protein 2; **PDBTitle:** solution structure of the n-terminal domain of the hmgb2
64	d1j3xa_	Alignment	not modelled	13.2	6	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
65	c3ktdC_	Alignment	not modelled	13.2	12	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**prephenate dehydrogenase; **PDBTitle:** crystal structure of a putative prephenate dehydrogenase (cgl0226)2 from corynebacterium glutamicum atcc 13032 at 2.60 a resolution
66	d1olma1	Alignment	not modelled	13.1	24	**Fold:**RuvA C-terminal domain-like **Superfamily:**CRAL/TRIO N-terminal domain **Family:**CRAL/TRIO N-terminal domain
67	d1hsma_	Alignment	not modelled	12.9	10	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
68	c2co9A_	Alignment	not modelled	12.8	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**thymus high mobility group box protein tox; **PDBTitle:** solution structure of the hmg_box domain of thymus high2 mobility group box protein tox from mouse
69	d3proc1	Alignment	not modelled	12.7	23	**Fold:**Alpha-lytic protease prodomain-like **Superfamily:**Alpha-lytic protease prodomain **Family:**Alpha-lytic protease prodomain
70	c2gwhA_	Alignment	not modelled	12.7	22	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1c2; **PDBTitle:** human sulfotranferase sult1c2 in complex with pap and2 pentachlorophenol
71	c1wnmA_	Alignment	not modelled	12.7	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fibroin-modulator binding-protein-1; **PDBTitle:** nmr structure of fmbp-1 tandem repeat 2 in 30%(v/v) tfe2 solution
72	d1hbrb_	Alignment	not modelled	12.5	31	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
73	d1wh5a_	Alignment	not modelled	12.5	14	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
74	d1a9we_	Alignment	not modelled	12.2	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
75	d1ckta_	Alignment	not modelled	12.2	6	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
76	c3ls1A_	Alignment	not modelled	11.6	9	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**sll1638 protein; **PDBTitle:** crystal structure of cyanobacterial psbq from synechocystis2 sp. pcc 6803 complexed with zn2+
77	d1gyxa_	Alignment	not modelled	11.3	21	**Fold:**Tautomerase/MIF **Superfamily:**Tautomerase/MIF **Family:**4-oxalocrotonate tautomerase-like
78	d1v65a_	Alignment	not modelled	11.3	17	**Fold:**KRAB domain (Kruppel-associated box) **Superfamily:**KRAB domain (Kruppel-associated box) **Family:**KRAB domain (Kruppel-associated box)
79	d3bfxa1	Alignment	not modelled	11.3	17	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
80	c1wz6A_	Alignment	not modelled	11.3	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**hmg-box transcription factor bbx; **PDBTitle:** solution structure of the hmg_box domain of murine bobby2 sox homolog
						Fold: Globin-like

81	d1a4fb_	Alignment	not modelled	11.2	23	**Superfamily:**Globin-like **Family:**Globins
82	c2ctrA_	Alignment	not modelled	11.1	14	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**dnaj homolog subfamily b member 9; **PDBTitle:** solution structure of j-domain from human dnaj subfamily b2 member 9
83	d2h8fb1	Alignment	not modelled	11.1	23	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
84	c2d7lA_	Alignment	not modelled	11.0	13	**PDB header:**gene regulation, dna binding protein **Chain:** A: **PDB Molecule:**wd repeat and hmg-box dna binding protein 1; **PDBTitle:** solution structure of the hmg box domain from human wd2 repeat and hmg-box dna binding protein 1
85	d1k99a_	Alignment	not modelled	10.5	22	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
86	d1i11a_	Alignment	not modelled	10.4	6	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
87	d1xv1a_	Alignment	not modelled	10.2	27	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
88	d1ijwc_	Alignment	not modelled	10.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
89	d1ls6a_	Alignment	not modelled	10.1	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
90	c3u3oA_	Alignment	not modelled	10.1	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**sulfotransferase 1a1; **PDBTitle:** crystal structure of human sult1a1 bound to pap and two 3-cyano-7-2 hydroxycoumarin
91	d2p81a1	Alignment	not modelled	10.1	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
92	d1sknp_	Alignment	not modelled	10.0	21	**Fold:**A DNA-binding domain in eukaryotic transcription factors **Superfamily:**A DNA-binding domain in eukaryotic transcription factors **Family:**A DNA-binding domain in eukaryotic transcription factors
93	d1v4wb_	Alignment	not modelled	10.0	15	**Fold:**Globin-like **Superfamily:**Globin-like **Family:**Globins
94	d1fmja_	Alignment	not modelled	10.0	20	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**PAPS sulfotransferase
95	c2cs1A_	Alignment	not modelled	9.8	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**pms1 protein homolog 1; **PDBTitle:** solution structure of the hmg domain of human dna mismatch2 repair protein
96	d1s7ea1	Alignment	not modelled	9.7	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Homeodomain
97	c1hmfA_	Alignment	not modelled	9.4	9	**PDB header:**dna-binding **Chain:** A: **PDB Molecule:**high mobility group protein fragment-b; **PDBTitle:** structure of the hmg box motif in the b-domain of hmg1
98	d1hmfa_	Alignment	not modelled	9.4	9	**Fold:**HMG-box **Superfamily:**HMG-box **Family:**HMG-box
99	c2yulA_	Alignment	not modelled	9.4	18	**PDB header:**transcription **Chain:** A: **PDB Molecule:**transcription factor sox-17; **PDBTitle:** solution structure of the hmg box of human transcription2 factor sox-17