Phyre^2

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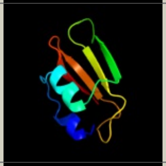
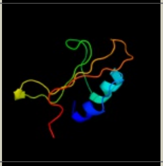
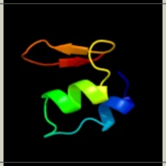
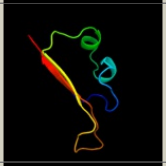
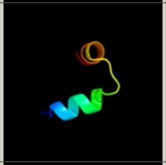
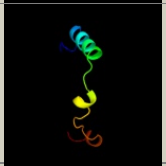
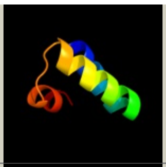
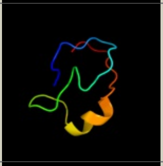
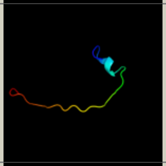
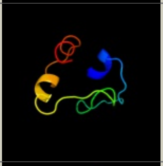
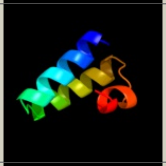
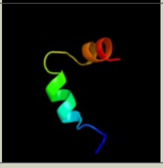
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2kxxA_	Alignment		100.0	97	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**small protein a; **PDBTitle:** nmr structure of escherichia coli bame, a lipoprotein component of the2 beta-barrel assembly machinery complex
2	c2pxgA_	Alignment		99.9	30	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**outer membrane protein; **PDBTitle:** nmr solution structure of omla
3	c3d4eA_	Alignment		97.8	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative beta-lactamase inhibitor protein; **PDBTitle:** crystal structure of putative beta-lactamase inhibitor protein2 (np_721579.1) from streptococcus mutans at 1.40 a resolution
4	d2g2ub1	Alignment		97.0	21	**Fold:**BLIP-like **Superfamily:**beta-lactamase-inhibitor protein, BLIP **Family:**beta-lactamase-inhibitor protein, BLIP
5	c3gmvX_	Alignment		88.6	30	**PDB header:**protein binding **Chain:** X: **PDB Molecule:**beta-lactamase inhibitory protein blip-i; **PDBTitle:** crystal structure of beta-lactamse inhibitory protein-i2 (blip-i) in apo form
6	c3gmxB_	Alignment		88.3	21	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**blp; **PDBTitle:** crystal structure of beta-lactamse inhibitory protein-like2 protein (blp) at 1.05 angstrom resolution
7	d1uw4a_	Alignment		54.9	14	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Smg-4/UPF3
8	c2o1uA_	Alignment		37.7	38	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of full length grp94 with amp-pnp bound
9	c3fmyA_	Alignment		23.2	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**hth-type transcriptional regulator mqsa **PDBTitle:** structure of the c-terminal domain of the e. coli protein2 mqsa (ygit/b3021)
10	c2vgpD_	Alignment		19.7	17	**PDB header:**transferase **Chain:** D: **PDB Molecule:**inner centromere protein a; **PDBTitle:** crystal structure of aurora b kinase in complex with a2 aminothiazole inhibitor
11	d2cwqa1	Alignment		19.2	17	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**TTHA0727-like

12	c2qeuA_	Alignment		18.3	7	**PDB header:**lyase **Chain:** A: **PDB Molecule:**putative carboxymuconolactone decarboxylase; **PDBTitle:** crystal structure of putative carboxymuconolactone decarboxylase2 (yp_555818.1) from burkholderia xenovorans lb400 at 1.65 a resolution
13	c1vliA_	Alignment		17.8	15	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**spore coat polysaccharide biosynthesis protein spse; **PDBTitle:** crystal structure of spore coat polysaccharide biosynthesis protein2 spse (bsu37870) from bacillus subtilis at 2.38 a resolution
14	d1vqop1	Alignment		17.0	11	**Fold:**Ribosomal protein L19 (L19e) **Superfamily:**Ribosomal protein L19 (L19e) **Family:**Ribosomal protein L19 (L19e)
15	d2qqra1	Alignment		17.0	22	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
16	c2wwaJ_	Alignment		16.8	17	**PDB header:**ribosome **Chain:** J: **PDB Molecule:**60s ribosomal protein l19; **PDBTitle:** cryo-em structure of idle yeast ssh1 complex bound to the2 yeast 80s ribosome
17	c2cg9A_	Alignment		16.6	35	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**atp-dependent molecular chaperone hsp82; **PDBTitle:** crystal structure of an hsp90-sba1 closed chaperone complex
18	c4a1cO_	Alignment		16.0	17	**PDB header:**ribosome **Chain:** O: **PDB Molecule:**rpl19; **PDBTitle:** t.thermophila 60s ribosomal subunit in complex with2 initiation factor 6. this file contains 5s rrna,3 5.8s rrna and proteins of molecule 4.
19	d2af7a1	Alignment		15.6	15	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
20	c3gn5B_	Alignment		15.2	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**hth-type transcriptional regulator mqsa (ygit/b3021); **PDBTitle:** structure of the e. coli protein mqsa (ygit/b3021)
21	c2rfuA_	Alignment	not modelled	15.1	21	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**influenza b hemagglutinin (ha); **PDBTitle:** crystal structure of influenza b virus hemagglutinin in complex with2 lstc receptor analog
22	d1g3nc2	Alignment	not modelled	14.6	27	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Cyclin
23	c2kfsA_	Alignment	not modelled	14.2	13	**PDB header:**dna-binding protein **Chain:** A: **PDB Molecule:**conserved hypothetical regulatory protein; **PDBTitle:** nmr structure of rv2175c
24	c1q40C_	Alignment	not modelled	13.4	23	**PDB header:**translation **Chain:** C: **PDB Molecule:**mrna transport regulator mtr2; **PDBTitle:** crystal structure of the c. albicans mtr2-mex67 m domain complex
25	d1vlia1	Alignment	not modelled	13.3	15	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
26	c2zkrp_	Alignment	not modelled	12.8	19	**PDB header:**ribosomal protein/rna **Chain:** P: **PDB Molecule:**rna expansion segment es31 part i; **PDBTitle:** structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
27	d1q42a_	Alignment	not modelled	12.4	23	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**NTF2-like
28	c3qqiB_	Alignment	not modelled	11.9	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the ha1 receptor binding domain of h22 hemagglutinin

29	c3mlhA_	Alignment	not modelled	11.7	26	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin; **PDBTitle:** crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain
30	d1jsda_	Alignment	not modelled	11.7	26	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
31	d2visc_	Alignment	not modelled	11.7	39	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
32	d1rd8a_	Alignment	not modelled	11.6	26	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
33	c2iopD_	Alignment	not modelled	11.3	47	**PDB header:**chaperone **Chain:** D: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** crystal structure of full-length htpg, the escherichia coli2 hsp90, bound to adp
34	c3iz5T_	Alignment	not modelled	11.1	19	**PDB header:**ribosome **Chain:** T: **PDB Molecule:**60s ribosomal protein l19 (l19e); **PDBTitle:** localization of the large subunit ribosomal proteins into a 5.5 a2 cryo-em map of triticum aestivum translating 80s ribosome
35	d2zdra1	Alignment	not modelled	11.0	22	**Fold:**beta-clip **Superfamily:**AFP III-like domain **Family:**AFP III-like domain
36	c3eykA_	Alignment	not modelled	10.7	39	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**hemagglutinin ha1 chain; **PDBTitle:** structure of influenza haemagglutinin in complex with an2 inhibitor of membrane fusion
37	d1ijwc_	Alignment	not modelled	10.7	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
38	d2ofya1	Alignment	not modelled	10.5	20	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
39	d1rvxa_	Alignment	not modelled	10.3	26	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
40	d1rv0h_	Alignment	not modelled	10.3	26	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
41	d2ibxa1	Alignment	not modelled	10.1	17	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
42	d1mqma_	Alignment	not modelled	10.0	39	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
43	d2viua_	Alignment	not modelled	10.0	39	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
44	d1hcra_	Alignment	not modelled	9.4	30	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Recombinase DNA-binding domain
45	d1jmca1	Alignment	not modelled	9.2	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Single strand DNA-binding domain, SSB
46	c1p8cD_	Alignment	not modelled	9.2	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** crystal structure of tm1620 (apc4843) from thermotoga2 maritima
47	c3i71B_	Alignment	not modelled	9.0	36	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ethanolamine utilization protein eutk; **PDBTitle:** ethanolamine utilization microcompartment shell subunit, eutk c-2 terminal domain
48	c2ivfA_	Alignment	not modelled	8.8	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ethylbenzene dehydrogenase alpha-subunit; **PDBTitle:** ethylbenzene dehydrogenase from aromatoleum aromaticum
49	d1jsma_	Alignment	not modelled	8.8	21	**Fold:**Viral protein domain **Superfamily:**Viral protein domain **Family:**Influenza hemagglutinin headpiece
50	c2o1wB_	Alignment	not modelled	8.8	50	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin; **PDBTitle:** structure of n-terminal plus middle domains (n+m) of grp94
51	d1zbra1	Alignment	not modelled	8.6	19	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
52	c2wr2B_	Alignment	not modelled	8.5	26	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**hemagglutinin; **PDBTitle:** structure of influenza h2 avian hemagglutinin with avian2 receptor
53	d1vkea_	Alignment	not modelled	8.1	20	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
54	c2ppxA_	Alignment	not modelled	8.0	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein atu1735; **PDBTitle:** crystal structure of a hth xre-family like protein from agrobacterium2 tumefaciens
55	d2ppxa1	Alignment	not modelled	8.0	21	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like

56	d2hqva1	Alignment	not modelled	8.0	11	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**ChuX-like
57	d1dwma_	Alignment	not modelled	7.9	27	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
58	d1nr3a_	Alignment	not modelled	7.9	33	**Fold:**DNA-binding protein Tfx **Superfamily:**DNA-binding protein Tfx **Family:**DNA-binding protein Tfx
59	c3rdyA_	Alignment	not modelled	7.9	9	**PDB header:**hydrolase inhibitor **Chain:** A: **PDB Molecule:**bwi-1=protease inhibitor/trypsin inhibitor; **PDBTitle:** crystal structure of buckwheat trypsin inhibitor rbti at 1.84 angstrom2 resolution
60	d1bw6a_	Alignment	not modelled	7.6	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Centromere-binding
61	c3ct5A_	Alignment	not modelled	7.4	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**morphogenesis protein 1; **PDBTitle:** crystal and cryoem structural studies of a cell wall degrading enzyme2 in the bacteriophage phi29 tail
62	d1yqga1	Alignment	not modelled	7.2	16	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
63	d2v9va2	Alignment	not modelled	7.1	13	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**C-terminal fragment of elongation factor SelB
64	c3beyC_	Alignment	not modelled	7.1	19	**PDB header:**structural genomics, unknown function **Chain:** C: **PDB Molecule:**conserved protein o27018; **PDBTitle:** crystal structure of the protein o27018 from methanobacterium2 thermoautotrophicum. northeast structural genomics consortium target3 tt217
65	d1iiea_	Alignment	not modelled	7.0	33	**Fold:**Class II MHC-associated invariant chain ectoplasmic trimerization domain **Superfamily:**Class II MHC-associated invariant chain ectoplasmic trimerization domain **Family:**Class II MHC-associated invariant chain ectoplasmic trimerization domain
66	c2ci2I_	Alignment	not modelled	6.9	5	**PDB header:**proteinase inhibitor (chymotrypsin) **Chain:** I: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** crystal and molecular structure of the serine proteinase2 inhibitor ci-2 from barley seeds
67	d2snii_	Alignment	not modelled	6.9	5	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
68	d1ypci_	Alignment	not modelled	6.8	5	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
69	d1to2i_	Alignment	not modelled	6.8	5	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
70	c2hl7A_	Alignment	not modelled	6.7	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**cytochrome c-type biogenesis protein ccmh; **PDBTitle:** crystal structure of the periplasmic domain of ccmh from pseudomonas2 aeruginosa
71	c1ha0A_	Alignment	not modelled	6.5	39	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**protein (hemagglutinin precursor); **PDBTitle:** hemagglutinin precursor ha0
72	d2j0pa1	Alignment	not modelled	6.2	14	**Fold:**Heme iron utilization protein-like **Superfamily:**Heme iron utilization protein-like **Family:**HemS/ChuS-like
73	d1j8ba_	Alignment	not modelled	6.1	30	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
74	d1k25a2	Alignment	not modelled	6.1	8	**Fold:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Superfamily:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain **Family:**Penicillin-binding protein 2x (pbp-2x), c-terminal domain
75	c1tinA_	Alignment	not modelled	6.0	13	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**trypsin inhibitor v; **PDBTitle:** three-dimensional structure in solution of cucurbita maxima2 trypsin inhibitor-v determined by nmr spectroscopy
76	c1y4sA_	Alignment	not modelled	6.0	57	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**chaperone protein htpg; **PDBTitle:** conformation rearrangement of heat shock protein 90 upon2 adp binding
77	c2kw0A_	Alignment	not modelled	6.0	6	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**ccmh protein; **PDBTitle:** solution structure of n-terminal domain of ccmh from escherichia.coli
78	c3f6wE_	Alignment	not modelled	5.9	50	**PDB header:**dna binding protein **Chain:** E: **PDB Molecule:**xre-family like protein; **PDBTitle:** xre-family like protein from pseudomonas syringae pv. tomato str.2 dc3000
79	c1vbwA_	Alignment	not modelled	5.9	7	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**trypsin inhibitor bgit; **PDBTitle:** crystal structure of bitter gourd trypsin inhibitor
80	d2ahra1	Alignment	not modelled	5.7	16	**Fold:**6-phosphogluconate dehydrogenase C-terminal domain-like **Superfamily:**6-phosphogluconate dehydrogenase C-terminal domain-like **Family:**ProC C-terminal domain-like
						Fold: Skp1 dimerisation domain-like

81	d2ovra1	Alignment	not modelled	5.7	14	**Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
82	c3pehB_	Alignment	not modelled	5.6	43	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**endoplasmin homolog; **PDBTitle:** crystal structure of the n-terminal domain of an hsp90 from plasmodium2 falciparum, pfl1070c in the presence of a thienopyrimidine derivative
83	c2eblA_	Alignment	not modelled	5.5	36	**PDB header:**transcription **Chain:** A: **PDB Molecule:**coup transcription factor 1; **PDBTitle:** solution structure of the zinc finger, c4-type domain of2 human coup transcription factor 1
84	d1pugb_	Alignment	not modelled	5.5	20	**Fold:**YbaB-like **Superfamily:**YbaB-like **Family:**YbaB-like
85	c2xsdC_	Alignment	not modelled	5.5	42	**PDB header:**transcription/dna **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
86	d1vkeb_	Alignment	not modelled	5.5	20	**Fold:**AhpD-like **Superfamily:**AhpD-like **Family:**CMD-like
87	d1fs2b1	Alignment	not modelled	5.4	14	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
88	d1okga3	Alignment	not modelled	5.4	28	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**3-mercaptopyruvate sulfurtransferase, C-terminal domain
89	d2cmua1	Alignment	not modelled	5.3	19	**Fold:**Pentein, beta/alpha-propeller **Superfamily:**Pentein **Family:**Porphyromonas-type peptidylarginine deiminase
90	c2wstE_	Alignment	not modelled	5.1	27	**PDB header:**viral protein **Chain:** E: **PDB Molecule:**putative fiber protein; **PDBTitle:** head domain of porcine adenovirus type 4 nadc-1 isolate2 fibre
91	c2qzbB_	Alignment	not modelled	5.1	20	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein yfey; **PDBTitle:** crystal structure of the uncharacterized protein yfey from escherichia2 coli
92	d3dxoa1	Alignment	not modelled	5.1	16	**Fold:**Cystatin-like **Superfamily:**NTF2-like **Family:**Atu0744-like
93	c3fldA_	Alignment	not modelled	5.1	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**protein trai; **PDBTitle:** crystal structure of the trai c-terminal domain
94	c3fljA_	Alignment	not modelled	5.1	13	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein conserved in bacteria with a **PDBTitle:** crystal structure of uncharacterized protein conserved in bacteria2 with a cystatin-like fold (yp_168589.1) from silicibacter pomeroyi3 dss-3 at 2.00 a resolution
95	d2hanb1	Alignment	not modelled	5.1	36	**Fold:**Glucocorticoid receptor-like (DNA-binding domain) **Superfamily:**Glucocorticoid receptor-like (DNA-binding domain) **Family:**Nuclear receptor
96	c3cpnA_	Alignment	not modelled	5.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**beta-xylosidase, family 43 glycosyl hydrolase; **PDBTitle:** crystal structure of beta-xylosidase, family 43 glycosyl2 hydrolase from clostridium acetobutylicum