Phyre2

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Description	Q46909
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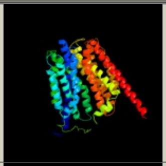
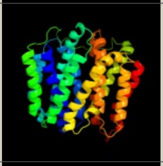
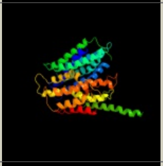
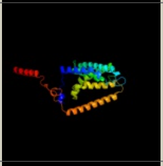
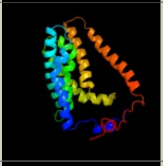
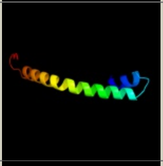
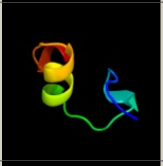
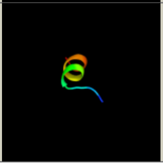
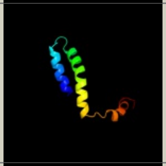
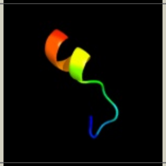
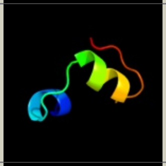
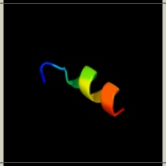
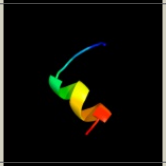
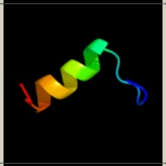
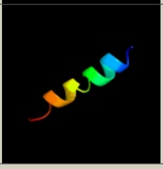
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1pw4a_	Alignment		100.0	12	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**Glycerol-3-phosphate transporter
2	d1pv7a_	Alignment		100.0	10	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
3	c3o7pA_	Alignment		100.0	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
4	c2gfpA_	Alignment		99.9	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
5	c2xutC_	Alignment		99.9	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**proton/peptide symporter family protein; **PDBTitle:** crystal structure of a proton dependent oligopeptide (pot)2 family transporter.
6	c3b9yA_	Alignment		70.4	10	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**ammonium transporter family rh-like protein; **PDBTitle:** crystal structure of the nitrosomonas europaea rh protein
7	c3hd6A_	Alignment		60.8	9	**PDB header:**membrane protein, transport protein **Chain:** A: **PDB Molecule:**ammonium transporter rh type c; **PDBTitle:** crystal structure of the human rhesus glycoprotein rhcg
8	c3qnqD_	Alignment		52.8	13	**PDB header:**membrane protein, transport protein **Chain:** D: **PDB Molecule:**pts system, cellobiose-specific iic component; **PDBTitle:** crystal structure of the transporter chbc, the iic component from the2 n,n'-diacetylchitobiose-specific phosphotransferase system
9	c3pvpA_	Alignment		27.3	21	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
10	d1fs1b1	Alignment		26.9	8	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
11	d1fs2b1	Alignment		21.1	8	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like

12	c3ff5B_	Alignment		19.9	12	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**peroxisomal biogenesis factor 14; **PDBTitle:** crystal structure of the conserved n-terminal domain of the2 peroxisomal matrix-protein-import receptor, pex14p
13	c2jlnA_	Alignment		18.0	10	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**mhp1; **PDBTitle:** structure of mhp1, a nucleobase-cation-symport-1 family2 transporter
14	c3c9pA_	Alignment		17.3	23	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
15	d1j1va_	Alignment		16.8	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
16	d1nexa1	Alignment		16.2	0	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
17	c2g9pA_	Alignment		15.0	29	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**antimicrobial peptide latarcin 2a; **PDBTitle:** nmr structure of a novel antimicrobial peptide, latarcin 2a,2 from spider (lachesana tarabaevi) venom
18	d2ovra1	Alignment		14.5	8	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
19	c2w85A_	Alignment		13.0	10	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19
20	c3hkzY_	Alignment		13.0	16	**PDB header:**transferase **Chain:** Y: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
21	c2p1nD_	Alignment	not modelled	12.9	15	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
22	d1l8qa1	Alignment	not modelled	12.9	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
23	c2f9jP_	Alignment	not modelled	11.8	13	**PDB header:**rna binding protein **Chain:** P: **PDB Molecule:**splicing factor 3b subunit 1; **PDBTitle:** 3.0 angstrom resolution structure of a y22m mutant of the spliceosomal2 protein p14 bound to a region of sf3b155
24	d1xwya1	Alignment	not modelled	9.2	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
25	d1xpja_	Alignment	not modelled	8.9	11	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
26	c3hkzZ_	Alignment	not modelled	8.9	16	**PDB header:**transferase **Chain:** Z: **PDB Molecule:**dna-directed rna polymerase subunit 13; **PDBTitle:** the x-ray crystal structure of rna polymerase from archaea
27	d1ymga1	Alignment	not modelled	8.5	2	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
28	c1ymgA_	Alignment	not modelled	8.5	2	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**lens fiber major intrinsic protein; **PDBTitle:** the channel architecture of aquaporin o at 2.2 angstrom resolution
						PDB header:nuclear protein

29	c3mmyF_	Alignment	not modelled	8.4	14	**Chain:** F: **PDB Molecule:**nuclear pore complex protein nup98; **PDBTitle:** structural and functional analysis of the interaction between the2 nucleoporin nup98 and the mrna export factor rae1
30	c3m91B_	Alignment	not modelled	8.2	25	**PDB header:**hydrolase regulator **Chain:** B: **PDB Molecule:**prokaryotic ubiquitin-like protein pup; **PDBTitle:** crystal structure of the prokaryotic ubiquitin-like protein (pup)2 complexed with the amino terminal coiled coil of the mycobacterium3 tuberculosis proteasomal atpase mpa
31	d1xeqa1	Alignment	not modelled	8.2	40	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**N-terminal, RNA-binding domain of nonstructural protein NS1
32	c2vpzG_	Alignment	not modelled	7.9	19	**PDB header:**oxidoreductase **Chain:** G: **PDB Molecule:**hypothetical membrane spanning protein; **PDBTitle:** polysulfide reductase native structure
33	c2y0sJ_	Alignment	not modelled	7.7	11	**PDB header:**transferase **Chain:** J: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
34	c2y0sQ_	Alignment	not modelled	7.7	11	**PDB header:**transferase **Chain:** Q: **PDB Molecule:**rna polymerase subunit 13; **PDBTitle:** crystal structure of sulfolobus shibatae rna polymerase in2 p21 space group
35	c3r66A_	Alignment	not modelled	7.7	40	**PDB header:**viral protein/antiviral protein **Chain:** A: **PDB Molecule:**non-structural protein 1; **PDBTitle:** crystal structure of human isg15 in complex with ns1 n-terminal region2 from influenza virus b, northeast structural genomics consortium3 target ids hx6481, hr2873, and or2
36	d2a1la1	Alignment	not modelled	7.6	7	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Phoshatidylinositol transfer protein, PITP
37	d1rsob_	Alignment	not modelled	7.5	13	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
38	c3m9dI_	Alignment	not modelled	7.2	20	**PDB header:**chaperone **Chain:** I: **PDB Molecule:**prokaryotic ubiquitin-like protein pup; **PDBTitle:** crystal structure of the prokaryotic ubiquintin-like protein pup2 complexed with the hexameric proteasomal atpase mpa which includes3 the amino terminal coiled coil domain and the inter domain
39	c1egpA_	Alignment	not modelled	7.1	20	**PDB header:**proteinase inhibitor **Chain:** A: **PDB Molecule:**eglin-c; **PDBTitle:** proteinase inhibitor eglin c with hydrolysed reactive center
40	c2l16A_	Alignment	not modelled	7.1	11	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatad; **PDBTitle:** solution structure of bacillus subtilits tatad protein in dpc micelles
41	c2waqQ_	Alignment	not modelled	7.0	11	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
42	c2rddB_	Alignment	not modelled	6.8	6	**PDB header:**membrane protein/transport protein **Chain:** B: **PDB Molecule:**upf0092 membrane protein yajc; **PDBTitle:** x-ray crystal structure of acrb in complex with a novel2 transmembrane helix.
43	d1f15a_	Alignment	not modelled	6.7	17	**Fold:**Nucleoplasmin-like/VP (viral coat and capsid proteins) **Superfamily:**Positive stranded ssRNA viruses **Family:**Bromoviridae-like VP
44	d2p7vb1	Alignment	not modelled	6.7	6	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
45	c1cirA_	Alignment	not modelled	6.7	17	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** complex of two fragments of ci2 [(1-40)(dot)(41-64)]
46	d1j4na_	Alignment	not modelled	6.6	6	**Fold:**Aquaporin-like **Superfamily:**Aquaporin-like **Family:**Aquaporin-like
47	d1t27a_	Alignment	not modelled	6.6	7	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Phoshatidylinositol transfer protein, PITP
48	d1ofcx1	Alignment	not modelled	6.6	0	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
49	c2diiA_	Alignment	not modelled	6.6	5	**PDB header:**transcription **Chain:** A: **PDB Molecule:**tfiih basal transcription factor complex p62 **PDBTitle:** solution structure of the bsd domain of human tfiih basal2 transcription factor complex p62 subunit
50	c1nexC_	Alignment	not modelled	6.5	0	**PDB header:**ligase, cell cycle **Chain:** C: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
51	d1xjsa_	Alignment	not modelled	6.5	7	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
52	c1dgrW_	Alignment	not modelled	6.5	6	**PDB header:**plant protein **Chain:** W: **PDB Molecule:**canavalin; **PDBTitle:** refined crystal structure of canavalin from jack bean
53	d2j85a1	Alignment	not modelled	6.4	15	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like

54	c3gg7A_	Alignment	not modelled	6.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized metalloprotein; **PDBTitle:** crystal structure of an uncharacterized metalloprotein from2 deinococcus radiodurans
55	d2ppxa1	Alignment	not modelled	6.4	4	**Fold:**lambda repressor-like DNA-binding domains **Superfamily:**lambda repressor-like DNA-binding domains **Family:**SinR domain-like
56	c2ppxA_	Alignment	not modelled	6.4	4	**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
57	c2kz6A_	Alignment	not modelled	6.3	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of protein cv0426 from chromobacterium violaceum,2 northeast structural genomics consortium (nesg) target cvt2
58	d2ocda1	Alignment	not modelled	6.3	5	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
59	d1jmxa1	Alignment	not modelled	6.2	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
60	d2diia1	Alignment	not modelled	6.2	5	**Fold:**BSD domain-like **Superfamily:**BSD domain-like **Family:**BSD domain
61	d1j6oa_	Alignment	not modelled	6.1	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
62	c3h00A_	Alignment	not modelled	6.1	20	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** structure of the c-terminal domain of a putative hiv-1 gp412 fusion intermediate
63	c2kdcC_	Alignment	not modelled	5.8	11	**PDB header:**transferase **Chain:** C: **PDB Molecule:**diacylglycerol kinase; **PDBTitle:** nmr solution structure of e. coli diacylglycerol kinase2 (dagk) in dpc micelles
64	c2wb1Q_	Alignment	not modelled	5.6	11	**PDB header:**transcription **Chain:** Q: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
65	c3bs3A_	Alignment	not modelled	5.6	17	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**putative dna-binding protein; **PDBTitle:** crystal structure of a putative dna-binding protein from bacteroides2 fragilis
66	d1agxa_	Alignment	not modelled	5.6	20	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
67	d1pbya1	Alignment	not modelled	5.5	8	**Fold:**Cytochrome c **Superfamily:**Cytochrome c **Family:**Quinohemoprotein amine dehydrogenase A chain, domains 1 and 2
68	c3rkoK_	Alignment	not modelled	5.4	14	**PDB header:**oxidoreductase **Chain:** K: **PDB Molecule:**nadh-quinone oxidoreductase subunit k; **PDBTitle:** crystal structure of the membrane domain of respiratory complex i from2 e. coli at 3.0 angstrom resolution
69	c2wwbA_	Alignment	not modelled	5.4	11	**PDB header:**ribosome **Chain:** A: **PDB Molecule:**protein transport protein sec61 subunit alpha isoform 1; **PDBTitle:** cryo-em structure of the mammalian sec61 complex bound to the2 actively translating wheat germ 80s ribosome
70	c2ci2I_	Alignment	not modelled	5.3	17	**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
71	d1vola2	Alignment	not modelled	5.2	6	**Fold:**Cyclin-like **Superfamily:**Cyclin-like **Family:**Transcription factor IIB (TFIIB), core domain
72	c2wb1J_	Alignment	not modelled	5.2	11	**PDB header:**transcription **Chain:** J: **PDB Molecule:**dna-directed rna polymerase rpo13 subunit; **PDBTitle:** the complete structure of the archaeal 13-subunit dna-2 directed rna polymerase
73	d1zzma1	Alignment	not modelled	5.2	11	**Fold:**TIM beta/alpha-barrel **Superfamily:**Metallo-dependent hydrolases **Family:**TatD Mg-dependent DNase-like
74	d1to2i_	Alignment	not modelled	5.1	17	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
75	d1csei_	Alignment	not modelled	5.1	17	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
76	d1ypci_	Alignment	not modelled	5.1	21	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors