Phyre2

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Description	P0AGF4
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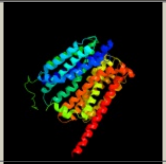
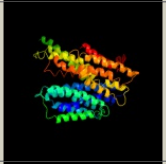
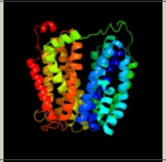
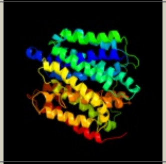
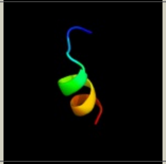
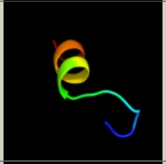
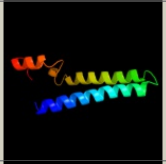
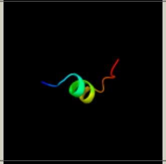
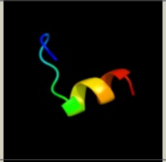
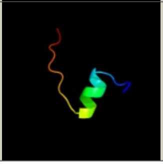
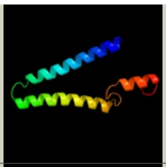
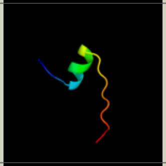
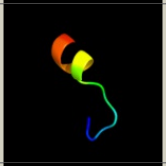
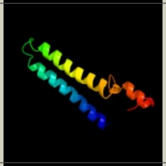
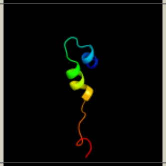
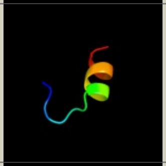
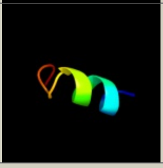
Unique Job ID	e921f1771acff438

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	c3o7pA_	Alignment		99.9	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**l-fucose-proton symporter; **PDBTitle:** crystal structure of the e.coli fucose:proton symporter, fucp (n162a)
3	c2xutC_	Alignment		99.9	10	**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.
4	d1pv7a_	Alignment		99.9	11	**Fold:**MFS general substrate transporter **Superfamily:**MFS general substrate transporter **Family:**LacY-like proton/sugar symporter
5	c2gfpA_	Alignment		99.9	12	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**multidrug resistance protein d; **PDBTitle:** structure of the multidrug transporter emrd from2 escherichia coli
6	d1fs1b1	Alignment		40.9	46	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
7	c3ff5B_	Alignment		34.0	33	**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
8	c3nd0A_	Alignment		28.5	18	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sll0855 protein; **PDBTitle:** x-ray crystal structure of a slow cyanobacterial cl-/h+ antiporter
9	d1fs2b1	Alignment		25.8	35	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
10	c2w85A_	Alignment		25.7	33	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**peroxisomal membrane anchor protein pex14; **PDBTitle:** structure of pex14 in compex with pex19
11	d1nexa1	Alignment		25.5	19	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like

12	c2ht2B_	Alignment		25.3	13	**PDB header:**membrane protein **Chain:** B: **PDB Molecule:**h(+)/cl(-) exchange transporter clca; **PDBTitle:** structure of the escherichia coli clc chloride channel2 y445h mutant and fab complex
13	d2ovra1	Alignment		23.3	33	**Fold:**Skp1 dimerisation domain-like **Superfamily:**Skp1 dimerisation domain-like **Family:**Skp1 dimerisation domain-like
14	c3c9pA_	Alignment		20.3	31	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein sp1917; **PDBTitle:** crystal structure of uncharacterized protein sp1917
15	d1xpja_	Alignment		18.1	39	**Fold:**HAD-like **Superfamily:**HAD-like **Family:**Hypothetical protein VC0232
16	d1kpla_	Alignment		17.9	16	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
17	c2xc7A_	Alignment		17.6	12	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**phosphorylated adapter rna export protein; **PDBTitle:** solution structure of phax-rbd in complex with ssrna
18	d1ofcx1	Alignment		15.0	33	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
19	d1y7oa1	Alignment		14.6	26	**Fold:**ClpP/crotonase **Superfamily:**ClpP/crotonase **Family:**Clp protease, ClpP subunit
20	c2g9pA_	Alignment		13.7	36	**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
21	d1otsa_	Alignment	not modelled	12.7	13	**Fold:**Clc chloride channel **Superfamily:**Clc chloride channel **Family:**Clc chloride channel
22	d2a26a1	Alignment	not modelled	11.5	40	**Fold:**Long alpha-hairpin **Superfamily:**Calcyclin-binding protein-like **Family:**Siah interacting protein N terminal domain-like
23	d1agxa_	Alignment	not modelled	10.6	20	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
24	c3mmyF_	Alignment	not modelled	10.3	46	**PDB header:**nuclear protein **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
25	c1cirA_	Alignment	not modelled	10.2	30	**PDB header:**serine protease inhibitor **Chain:** A: **PDB Molecule:**chymotrypsin inhibitor 2; **PDBTitle:** complex of two fragments of ci2 [(1-40)(dot)(41-64)]
26	c2p1nD_	Alignment	not modelled	9.7	33	**PDB header:**signaling protein **Chain:** D: **PDB Molecule:**skp1-like protein 1a; **PDBTitle:** mechanism of auxin perception by the tir1 ubiqutin ligase
27	c1egpA_	Alignment	not modelled	9.4	31	**PDB header:**proteinase inhibitor **Chain:** A: **PDB Molecule:**eglin-c; **PDBTitle:** proteinase inhibitor eglin c with hydrolysed reactive center
28	d2p7vb1	Alignment	not modelled	9.2	22	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
						PDB header:transferase

29	c1pzmB_	Alignment	not modelled	8.7	19	**Chain:** B: **PDB Molecule:**hypoxanthine-guanine phosphoribosyltransferase; **PDBTitle:** crystal structure of hgprt-ase from leishmania tarentolae in complex2 with gmp
30	c1ysmA_	Alignment	not modelled	8.6	36	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcyclin-binding protein; **PDBTitle:** nmr structure of n-terminal domain (residues 1-77) of siah-2 interacting protein.
31	d1ysma1	Alignment	not modelled	8.6	36	**Fold:**Long alpha-hairpin **Superfamily:**Calcyclin-binding protein-like **Family:**Siah interacting protein N terminal domain-like
32	c2f9jP_	Alignment	not modelled	8.6	35	**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
33	c1nexC_	Alignment	not modelled	8.6	19	**PDB header:**ligase, cell cycle **Chain:** C: **PDB Molecule:**centromere dna-binding protein complex cbf3 **PDBTitle:** crystal structure of scskp1-sccdc4-cpd peptide complex
34	d1hh1a_	Alignment	not modelled	8.5	36	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Hjc-like
35	d2j85a1	Alignment	not modelled	8.5	14	**Fold:**STIV B116-like **Superfamily:**STIV B116-like **Family:**STIV B116-like
36	d1g9sa_	Alignment	not modelled	8.5	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
37	d1fsga_	Alignment	not modelled	8.4	33	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
38	d1x9na2	Alignment	not modelled	8.4	15	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**DNA ligase/mRNA capping enzyme postcatalytic domain
39	d1pzma_	Alignment	not modelled	8.3	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
40	c3nxkE_	Alignment	not modelled	8.1	7	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**cytoplasmic l-asparaginase; **PDBTitle:** crystal structure of probable cytoplasmic l-asparaginase from2 campylobacter jejuni
41	d2hkja1	Alignment	not modelled	7.6	22	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Topoisomerase VI-B subunit middle domain
42	d2ipqx1	Alignment	not modelled	7.5	19	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**STY4665 C-terminal domain-like
43	d1b78a_	Alignment	not modelled	7.3	18	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
44	c2wltA_	Alignment	not modelled	7.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** the crystal structure of helicobacter pylori l-asparaginase2 at 1.4 a resolution
45	c3qnqD_	Alignment	not modelled	7.1	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
46	c2jbhA_	Alignment	not modelled	7.0	25	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphoribosyltransferase domain-containing protein 1; **PDBTitle:** human phosphoribosyl transferase domain containing 1
47	d1xjsa_	Alignment	not modelled	6.9	14	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
48	d1zq1a2	Alignment	not modelled	6.9	19	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
49	d1wmib1	Alignment	not modelled	6.9	25	**Fold:**Non-globular all-alpha subunits of globular proteins **Superfamily:**RelB-like **Family:**RelB-like
50	c2inpD_	Alignment	not modelled	6.9	33	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**phenol hydroxylase component phl; **PDBTitle:** structure of the phenol hydroxylase-regulatory protein2 complex
51	d2csba1	Alignment	not modelled	6.8	29	**Fold:**SAM domain-like **Superfamily:**RuvA domain 2-like **Family:**Topoisomerase V repeat domain
52	d1ee8a1	Alignment	not modelled	6.8	31	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
53	d1nnsa_	Alignment	not modelled	6.7	13	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
54	d1cjba_	Alignment	not modelled	6.7	32	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
						PDB header:dna binding protein/dna **Chain:** A: **PDB Molecule:**chromosomal replication initiator protein

55	c3pvpA_	Alignment	not modelled	6.7	8	dnaa; **PDBTitle:** structure of mycobacterium tuberculosis dnaa-dbd in complex with box22 dna
56	c3d8lB_	Alignment	not modelled	6.6	53	**PDB header:**viral protein **Chain:** B: **PDB Molecule:**orf12; **PDBTitle:** crystal structure of orf12 from the lactococcus lactis bacteriophage2 p2
57	d1wfza_	Alignment	not modelled	6.5	27	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
58	d4pgaa_	Alignment	not modelled	6.4	29	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
59	d1j1va_	Alignment	not modelled	6.4	12	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
60	d3bzka3	Alignment	not modelled	6.4	27	**Fold:**Tex N-terminal region-like **Superfamily:**Tex N-terminal region-like **Family:**Tex N-terminal region-like
61	c2kjyA_	Alignment	not modelled	6.4	45	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**protein phosphatase 1 regulatory subunit 12a; **PDBTitle:** mypt1(658-714)
62	d1pyya2	Alignment	not modelled	6.3	41	**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
63	d1l8qa1	Alignment	not modelled	6.2	11	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**TrpR-like **Family:**Chromosomal replication initiation factor DnaA C-terminal domain IV
64	d1hgxa_	Alignment	not modelled	6.2	19	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
65	d1tdza1	Alignment	not modelled	6.2	25	**Fold:**S13-like H2TH domain **Superfamily:**S13-like H2TH domain **Family:**Middle domain of MutM-like DNA repair proteins
66	c3orgB_	Alignment	not modelled	6.1	17	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**cmclc; **PDBTitle:** crystal structure of a eukaryotic clc transporter
67	c2cfmA_	Alignment	not modelled	6.1	24	**PDB header:**ligase **Chain:** A: **PDB Molecule:**thermostable dna ligase; **PDBTitle:** atp-dependent dna ligase from pyrococcus furiosus
68	d1v7ra_	Alignment	not modelled	6.0	21	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**ITPase (Ham1)
69	c3o7mD_	Alignment	not modelled	6.0	27	**PDB header:**transferase **Chain:** D: **PDB Molecule:**hypoxanthine phosphoribosyltransferase; **PDBTitle:** 1.98 angstrom resolution crystal structure of a hypoxanthine-guanine2 phosphoribosyltransferase (hpt-2) from bacillus anthracis str. 'ames3 ancestor'
70	c2ovqA_	Alignment	not modelled	5.9	33	**PDB header:**transcription/cell cycle **Chain:** A: **PDB Molecule:**s-phase kinase-associated protein 1a; **PDBTitle:** structure of the skp1-fbw7-cyclinedegc complex
71	d1xeqa1	Alignment	not modelled	5.8	50	**Fold:**S15/NS1 RNA-binding domain **Superfamily:**S15/NS1 RNA-binding domain **Family:**N-terminal, RNA-binding domain of nonstructural protein NS1
72	d1rp5a2	Alignment	not modelled	5.8	35	**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
73	c3dh4A_	Alignment	not modelled	5.8	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** crystal structure of sodium/sugar symporter with bound galactose from2 vibrio parahaemolyticus
74	c3bezC_	Alignment	not modelled	5.8	11	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**protease 4; **PDBTitle:** crystal structure of escherichia coli signal peptide peptidase (sppa),2 semet crystals
75	c3p2lD_	Alignment	not modelled	5.8	11	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** crystal structure of atp-dependent clp protease subunit p from2 francisella tularensis
76	d1rsob_	Alignment	not modelled	5.7	35	**Fold:**L27 domain **Superfamily:**L27 domain **Family:**L27 domain
77	d2d6fa2	Alignment	not modelled	5.7	6	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
78	c1wnfA_	Alignment	not modelled	5.6	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**l-asparaginase; **PDBTitle:** crystal structure of ph0066 from pyrococcus horikoshii
79	c1by0A_	Alignment	not modelled	5.6	40	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**protein (hepatitis delta antigen); **PDBTitle:** n-terminal leucine-repeat region of hepatitis delta antigen
80	c3lk2T_	Alignment	not modelled	5.6	37	**PDB header:**protein binding **Chain:** T: **PDB Molecule:**leucine-rich repeat-containing protein 16a; **PDBTitle:** crystal structure of capz bound to the uncapping motif from carmil

81	c2zhhA_	Alignment	not modelled	5.6	8	**PDB header:**transcription **Chain:** A: **PDB Molecule:**redox-sensitive transcriptional activator soxr; **PDBTitle:** crystal structure of soxr
82	d1nh2d1	Alignment	not modelled	5.5	19	**Fold:**Transcription factor IIA (TFIIA), alpha-helical domain **Superfamily:**Transcription factor IIA (TFIIA), alpha-helical domain **Family:**Transcription factor IIA (TFIIA), alpha-helical domain
83	d2ak3a1	Alignment	not modelled	5.4	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Nucleotide and nucleoside kinases
84	c3r66A_	Alignment	not modelled	5.4	50	**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
85	d2ocda1	Alignment	not modelled	5.4	20	**Fold:**Glutaminase/Asparaginase **Superfamily:**Glutaminase/Asparaginase **Family:**Glutaminase/Asparaginase
86	d1u14a_	Alignment	not modelled	5.3	10	**Fold:**Anticodon-binding domain-like **Superfamily:**ITPase-like **Family:**YjjX-like
87	c2yxhB_	Alignment	not modelled	5.3	44	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**mazg-related protein; **PDBTitle:** crystal structure of mazg-related protein from thermotoga maritima
88	c2z7eB_	Alignment	not modelled	5.3	13	**PDB header:**biosynthetic protein **Chain:** B: **PDB Molecule:**nifu-like protein; **PDBTitle:** crystal structure of aquifex aeolicus iscu with bound [2fe-2 2s] cluster
89	d1su0b_	Alignment	not modelled	5.3	23	**Fold:**SufE/NifU **Superfamily:**SufE/NifU **Family:**NifU/IscU domain
90	c1y7oE_	Alignment	not modelled	5.3	23	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**atp-dependent clp protease proteolytic subunit; **PDBTitle:** the structure of streptococcus pneumoniae a153p clpp
91	d1q08a_	Alignment	not modelled	5.2	33	**Fold:**Putative DNA-binding domain **Superfamily:**Putative DNA-binding domain **Family:**DNA-binding N-terminal domain of transcription activators
92	c2jmlA_	Alignment	not modelled	5.2	21	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna binding domain/transcriptional regulator; **PDBTitle:** solution structure of the n-terminal domain of cara repressor
93	d1k25a2	Alignment	not modelled	5.2	24	**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
94	d1j7ja_	Alignment	not modelled	5.1	23	**Fold:**PRTase-like **Superfamily:**PRTase-like **Family:**Phosphoribosyltransferases (PRTases)
95	d1csei_	Alignment	not modelled	5.1	24	**Fold:**CI-2 family of serine protease inhibitors **Superfamily:**CI-2 family of serine protease inhibitors **Family:**CI-2 family of serine protease inhibitors
96	c2bbjB_	Alignment	not modelled	5.1	14	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
97	c1lnlB_	Alignment	not modelled	5.1	14	**PDB header:**oxygen storage/transport **Chain:** B: **PDB Molecule:**hemocyanin; **PDBTitle:** structure of deoxygenated hemocyanin from rapana thomasiana
98	c3oc5A_	Alignment	not modelled	5.1	32	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**toxin coregulated pilus biosynthesis protein f; **PDBTitle:** crystal structure of the vibrio cholerae secreted colonization factor2 tcpf
99	d1jo5a_	Alignment	not modelled	5.0	20	**Fold:**Light-harvesting complex subunits **Superfamily:**Light-harvesting complex subunits **Family:**Light-harvesting complex subunits