Phyre2

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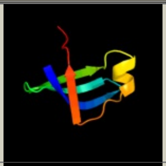
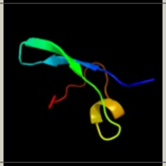
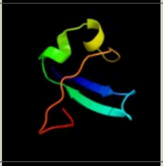
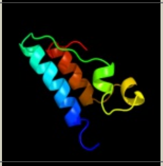
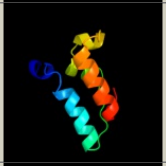
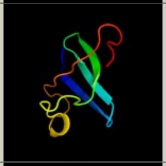
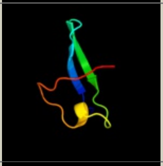
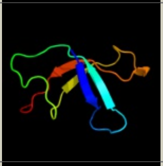
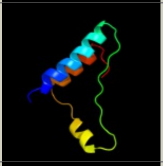
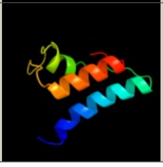
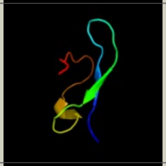
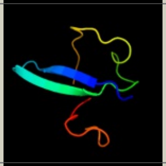
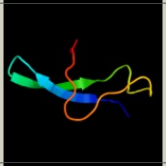
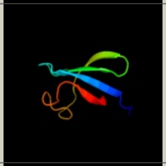
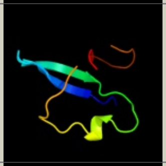
Unique Job ID	601b1508541f07d7

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3i4oA_	Alignment		91.6	20	**PDB header:**translation **Chain:** A: **PDB Molecule:**translation initiation factor if-1; **PDBTitle:** crystal structure of translation initiation factor 1 from2 mycobacterium tuberculosis
2	c1zn1L_	Alignment		87.1	17	**PDB header:**biosynthetic/structural protein/rna **Chain:** L: **PDB Molecule:**30s ribosomal protein s12; **PDBTitle:** coordinates of rrf fitted into cryo-em map of the 70s post-2 termination complex
3	c3fovA_	Alignment		87.0	28	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0102 protein rpa0323; **PDBTitle:** crystal structure of protein rpa0323 of unknown function from2 rhodopseudomonas palustris
4	c2oqkA_	Alignment		86.8	31	**PDB header:**translation **Chain:** A: **PDB Molecule:**putative translation initiation factor eif-1a; **PDBTitle:** crystal structure of putative cryptosporidium parvum translation2 initiation factor eif-1a
5	c1xdoB_	Alignment		85.1	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of escherichia coli polyphosphate kinase
6	d2o8ra4	Alignment		84.2	21	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
7	d1ah9a_	Alignment		83.8	21	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
8	d2uubl1	Alignment		83.5	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
9	d1d7qa_	Alignment		83.0	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
10	d1xdpa4	Alignment		82.7	19	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
11	c2o8rA_	Alignment		77.0	21	**PDB header:**transferase **Chain:** A: **PDB Molecule:**polyphosphate kinase; **PDBTitle:** crystal structure of polyphosphate kinase from2 porphyromonas gingivalis

12	d1jt8a_	Alignment		75.0	13	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
13	d2qall1	Alignment		74.9	17	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
14	c2zkql_	Alignment		72.0	21	**PDB header:**ribosomal protein/rna **Chain:** L: **PDB Molecule:** **PDBTitle:** structure of a mammalian ribosomal 40s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
15	c1s1hL_	Alignment		70.3	24	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**40s ribosomal protein s23; **PDBTitle:** structure of the ribosomal 80s-eef2-sordarin complex from2 yeast obtained by docking atomic models for rna and protein3 components into a 11.7 a cryo-em map. this file, 1s1h,4 contains 40s subunit. the 60s ribosomal subunit is in file5 1s1i.
16	d1i94l_	Alignment		69.3	26	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
17	c3m9bK_	Alignment		68.6	27	**PDB header:**chaperone **Chain:** K: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of the amino terminal coiled coil domain and the2 inter domain of the mycobacterium tuberculosis proteasomal atpase mpa
18	c2xzmL_	Alignment		68.5	15	**PDB header:**ribosome **Chain:** L: **PDB Molecule:**40s ribosomal protein s12; **PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1
19	c2vldA_	Alignment		66.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**upf0286 protein pyrab01260; **PDBTitle:** crystal structure of a repair endonuclease from pyrococcus2 abyssi
20	c3m0zD_	Alignment		62.1	38	**PDB header:**lyase **Chain:** D: **PDB Molecule:**putative aldolase; **PDBTitle:** crystal structure of putative aldolase from klebsiella2 pneumoniae.
21	d1hr0w_	Alignment	not modelled	59.7	24	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
22	c2a5hC_	Alignment	not modelled	57.9	19	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**l-lysine 2,3-aminomutase; **PDBTitle:** 2.1 angstrom x-ray crystal structure of lysine-2,3-aminomutase from2 clostridium subterminale sb4, with michaelis analog (l-alpha-lysine3 external aldimine form of pyridoxal-5'-phosphate).
23	c2dgyA_	Alignment	not modelled	53.5	12	**PDB header:**translation **Chain:** A: **PDB Molecule:**mgc11102 protein; **PDBTitle:** solution structure of the eukaryotic initiation factor 1a2 in mgc11102 protein
24	d1v0wa2	Alignment	not modelled	49.1	17	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Phospholipase D
25	d1u0la1	Alignment	not modelled	45.8	16	**Fold:**OB-fold **Superfamily:**Nucleic acid-binding proteins **Family:**Cold shock DNA-binding domain-like
26	c3fp9E_	Alignment	not modelled	43.3	26	**PDB header:**hydrolase **Chain:** E: **PDB Molecule:**proteasome-associated atpase; **PDBTitle:** crystal structure of intern domain of proteasome-associated2 atpase, mycobacterium tuberculosis
27	d2ebfx2	Alignment	not modelled	42.6	20	**Fold:**EreA/ChaN-like **Superfamily:**EreA/ChaN-like **Family:**PMT domain-like
28	c1pk8D_	Alignment	not modelled	41.6	19	**PDB header:**membrane protein **Chain:** D: **PDB Molecule:**rat synapsin i; **PDBTitle:** crystal structure of rat synapsin i c domain complexed to2 ca.atp

29	d2ga5a1	Alignment	not modelled	34.5	23	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
30	d1ekga_	Alignment	not modelled	32.7	28	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
31	c3muxB_	Alignment	not modelled	31.6	33	**PDB header:**lyase **Chain:** B: **PDB Molecule:**putative 4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** the crystal structure of a putative 4-hydroxy-2-oxoglutarate aldolase2 from bacillus anthracis to 1.45a
32	c3m6yA_	Alignment	not modelled	29.3	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**4-hydroxy-2-oxoglutarate aldolase; **PDBTitle:** structure of 4-hydroxy-2-oxoglutarate aldolase from bacillus cereus at2 1.45 a resolution.
33	c2qs7D_	Alignment	not modelled	26.2	32	**PDB header:**oxidoreductase **Chain:** D: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative oxidoreductase of the dsre/dsrf-like2 family (sso1126) from sulfolobus solfataricus p2 at 2.09 a resolution
34	c2pd2A_	Alignment	not modelled	25.8	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein st0148; **PDBTitle:** crystal structure of (st0148) conserved hypothetical from sulfolobus2 tokodaii strain7
35	d2p97a1	Alignment	not modelled	25.6	10	**Fold:**Metallo-hydrolase/oxidoreductase **Superfamily:**Metallo-hydrolase/oxidoreductase **Family:**Ava3068-like
36	c1nm3B_	Alignment	not modelled	24.2	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**protein hi0572; **PDBTitle:** crystal structure of heamophilus influenza hybrid-prx5
37	d1i7na2	Alignment	not modelled	23.5	15	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
38	d2cv4a1	Alignment	not modelled	21.1	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
39	d1byra_	Alignment	not modelled	20.6	24	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Nuclease
40	c1yjxD_	Alignment	not modelled	20.1	19	**PDB header:**isomerase, hydrolase **Chain:** D: **PDB Molecule:**phosphoglycerate mutase 1; **PDBTitle:** crystal structure of human b type phosphoglycerate mutase
41	c3m9pA_	Alignment	not modelled	19.6	13	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**male-specific lethal 3 homolog; **PDBTitle:** human msl3 chromodomain bound to dna and h4k20me1 peptide
42	c3pnxF_	Alignment	not modelled	19.0	33	**PDB header:**transferase **Chain:** F: **PDB Molecule:**putative sulfurtransferase dsre; **PDBTitle:** crystal structure of a putative sulfurtransferase dsre (swol_2425)2 from syntrophomonas wolfei str. goettingen at 1.92 a resolution
43	c2r2dC_	Alignment	not modelled	18.9	15	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**zn-dependent hydrolases; **PDBTitle:** structure of a quorum-quenching lactonase (aiib) from agrobacterium2 tumefaciens
44	c3s9xA_	Alignment	not modelled	18.6	22	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**asch domain; **PDBTitle:** high resolution crystal structure of asch domain from lactobacillus2 crispatus jv v101
45	d2rdea2	Alignment	not modelled	18.5	11	**Fold:**Split barrel-like **Superfamily:**PilZ domain-like **Family:**PilZ domain-associated domain
46	d1e32a1	Alignment	not modelled	17.7	19	**Fold:**Double psi beta-barrel **Superfamily:**ADC-like **Family:**Cdc48 N-terminal domain-like
47	d2okfa1	Alignment	not modelled	17.2	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XisH-like
48	d1jx7a_	Alignment	not modelled	17.2	13	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
49	d1xdpa3	Alignment	not modelled	17.1	14	**Fold:**Phospholipase D/nuclease **Superfamily:**Phospholipase D/nuclease **Family:**Polyphosphate kinase C-terminal domain
50	c3dnxA_	Alignment	not modelled	16.9	29	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein spo1766; **PDBTitle:** spo1766 protein of unknown function from silicibacter pomeroyi.
51	d2inba1	Alignment	not modelled	16.4	20	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**XisH-like
52	d1o12a1	Alignment	not modelled	15.2	21	**Fold:**Composite domain of metallo-dependent hydrolases **Superfamily:**Composite domain of metallo-dependent hydrolases **Family:**N-acetylglucosamine-6-phosphate deacetylase, NagA
53	c3h43F_	Alignment	not modelled	14.9	17	**PDB header:**hydrolase **Chain:** F: **PDB Molecule:**proteasome-activating nucleotidase; **PDBTitle:** n-terminal domain of the proteasome-activating nucleotidase2 of methanocaldococcus jannaschii
54	c3m9qA_	Alignment	not modelled	14.8	9	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein male-specific lethal-3; **PDBTitle:** drosophila msl3 chromodomain

55	c2br6A_	Alignment	not modelled	14.7	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**aiia-like protein; **PDBTitle:** crystal structure of quorum-quenching n-acyl homoserine2 lactone lactonase
56	d1g94a2	Alignment	not modelled	14.7	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
57	c3dcyA_	Alignment	not modelled	13.7	19	**PDB header:**apoptosis regulator **Chain:** A: **PDB Molecule:**regulator protein; **PDBTitle:** crystal structure a tp53-induced glycolysis and apoptosis2 regulator protein from homo sapiens.
58	d2fqla1	Alignment	not modelled	12.8	19	**Fold:**N domain of copper amine oxidase-like **Superfamily:**Frataxin/Nqo15-like **Family:**Frataxin-like
59	c3o27B_	Alignment	not modelled	12.6	19	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** the crystal structure of c68 from the hybrid virus-plasmid pssvx
60	d1l1sa_	Alignment	not modelled	11.5	20	**Fold:**DsrEFH-like **Superfamily:**DsrEFH-like **Family:**DsrEF-like
61	c3tinA_	Alignment	not modelled	11.5	33	**PDB header:**ligase **Chain:** A: **PDB Molecule:**ttl protein; **PDBTitle:** tubulin tyrosine ligase
62	d1pk8a2	Alignment	not modelled	11.4	23	**Fold:**ATP-grasp **Superfamily:**Glutathione synthetase ATP-binding domain-like **Family:**Synapsin C-terminal domain
63	c2wg6L_	Alignment	not modelled	11.4	16	**PDB header:**transcription,hydrolase **Chain:** L: **PDB Molecule:**general control protein gcn4, **PDBTitle:** proteasome-activating nucleotidase (pan) n-domain (57-134)2 from archaeoglobus fulgidus fused to gcn4, p61a mutant
64	c2fb6A_	Alignment	not modelled	11.0	30	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**conserved hypothetical protein; **PDBTitle:** structure of conserved protein of unknown function bt1422 from2 bacteroides thetaiotaomicron
65	c2wagA_	Alignment	not modelled	10.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**lysozyme, putative; **PDBTitle:** the structure of a family 25 glycosyl hydrolase from2 bacillus anthracis.
66	c2qpqC_	Alignment	not modelled	10.5	13	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**protein bug27; **PDBTitle:** structure of bug27 from bordetella pertussis
67	d1qnia1	Alignment	not modelled	10.3	15	**Fold:**Cupredoxin-like **Superfamily:**Cupredoxins **Family:**Nitrosocyanin
68	c3e9eB_	Alignment	not modelled	10.0	9	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**zgc:56074; **PDBTitle:** structure of full-length h11a mutant form of tigar from danio rerio
69	c3aj3A_	Alignment	not modelled	10.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**4-pyridoxolactonase; **PDBTitle:** crystal structure of selenomethionine substituted 4-pyridoxolactonase2 from mesorhizobium loti
70	c3i38H_	Alignment	not modelled	9.9	17	**PDB header:**chaperone **Chain:** H: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
71	c2rcnA_	Alignment	not modelled	9.6	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of the ribosomal interacting gtpase yjeq from the2 enterobacterial species salmonella typhimurium.
72	d2gjpa2	Alignment	not modelled	9.3	6	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
73	d1ea9c3	Alignment	not modelled	8.9	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain
74	d1s98a_	Alignment	not modelled	8.9	11	**Fold:**HesB-like domain **Superfamily:**HesB-like domain **Family:**HesB-like domain
75	d1t62a_	Alignment	not modelled	8.5	28	**Fold:**PUA domain-like **Superfamily:**PUA domain-like **Family:**Hypothetical protein EF3133
76	c2vpmB_	Alignment	not modelled	8.5	21	**PDB header:**ligase **Chain:** B: **PDB Molecule:**trypanothione synthetase; **PDBTitle:** trypanothione synthetase
77	c1u0lB_	Alignment	not modelled	8.4	16	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable gtpase engc; **PDBTitle:** crystal structure of yjeq from thermotoga maritima
78	d1nm3a2	Alignment	not modelled	8.4	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
79	d1pkla1	Alignment	not modelled	7.8	21	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
80	c1wn4A_	Alignment	not modelled	7.7	36	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**vontr protein; **PDBTitle:** nmr structure of vontr
81	d1ua7a2	Alignment	not modelled	7.5	7	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**Amylase, catalytic domain

82	d1a3xa1	Alignment	not modelled	7.4	27	**Fold:**PK beta-barrel domain-like **Superfamily:**PK beta-barrel domain-like **Family:**Pyruvate kinase beta-barrel domain
83	d3e9va1	Alignment	not modelled	7.3	18	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
84	c3dhuC_	Alignment	not modelled	7.0	12	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**alpha-amylase; **PDBTitle:** crystal structure of an alpha-amylase from lactobacillus2 plantarum
85	c2yv5A_	Alignment	not modelled	7.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**yjeq protein; **PDBTitle:** crystal structure of yjeq from aquifex aeolicus
86	c3bmwA_	Alignment	not modelled	6.7	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**cyclomaltodextrin glucanotransferase; **PDBTitle:** cyclodextrin glycosyl transferase from thermoanerobacterium2 thermosulfurigenes em1 mutant s77p complexed with a maltoheptaose3 inhibitor
87	c1bplA_	Alignment	not modelled	6.6	9	**PDB header:**glycosyltransferase **Chain:** A: **PDB Molecule:**alpha-1,4-glucan-4-glucanohydrolase; **PDBTitle:** glycosyltransferase
88	d1lkxa_	Alignment	not modelled	6.4	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Motor proteins
89	d1zbsa2	Alignment	not modelled	6.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**BadF/BadG/BcrA/BcrD-like
90	d1cw0a_	Alignment	not modelled	6.3	16	**Fold:**Restriction endonuclease-like **Superfamily:**Restriction endonuclease-like **Family:**Very short patch repair (VSR) endonuclease
91	c2zfnA_	Alignment	not modelled	6.2	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** self-acetylation mediated histone h3 lysine 56 acetylation by rtt109
92	c3d35A_	Alignment	not modelled	6.2	40	**PDB header:**transferase **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** crystal structure of rtt109-ac-coa complex
93	d2z15a1	Alignment	not modelled	5.9	14	**Fold:**BTG domain-like **Superfamily:**BTG domain-like **Family:**BTG domain-like
94	c3i38L_	Alignment	not modelled	5.9	18	**PDB header:**chaperone **Chain:** L: **PDB Molecule:**putative chaperone dnaj; **PDBTitle:** structure of a putative chaperone protein dnaj from klebsiella2 pneumoniae subsp. pneumoniae mgh 78578
95	c3cz7A_	Alignment	not modelled	5.9	40	**PDB header:**replication **Chain:** A: **PDB Molecule:**regulator of ty1 transposition protein 109; **PDBTitle:** molecular basis for the autoregulation of the protein acetyl2 transferase rtt109
96	c1i7nA_	Alignment	not modelled	5.8	15	**PDB header:**neuropeptide **Chain:** A: **PDB Molecule:**synapsin ii; **PDBTitle:** crystal structure analysis of the c domain of synapsin ii2 from rat brain
97	c1ud8A_	Alignment	not modelled	5.8	0	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**amylase; **PDBTitle:** crystal structure of amyk38 with lithium ion
98	c1sg3A_	Alignment	not modelled	5.8	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**allantoicase; **PDBTitle:** structure of allantoicase
99	c2nw0B_	Alignment	not modelled	5.7	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**plyb; **PDBTitle:** crystal structure of a lysin