Phyre^2

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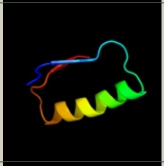
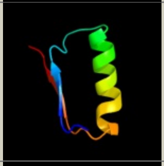
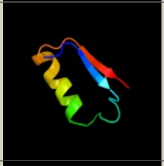
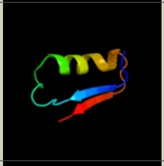
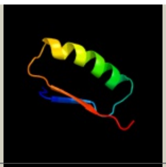
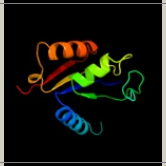
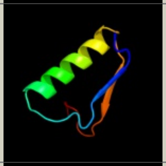
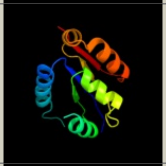
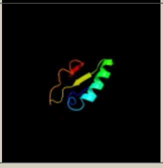
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ezkB_	Alignment		99.9	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**dna packaging protein gp17; **PDBTitle:** bacteriophage t4 gp17 motor assembly based on crystal2 structures and cryo-em reconstructions
2	c2o0hA_	Alignment		99.1	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dna packaging protein gp17; **PDBTitle:** t4 gp17 atpase domain mutant complexed with atp
3	c3c6aA_	Alignment		96.0	10	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**terminase large subunit; **PDBTitle:** crystal structure of the rb49 gp17 nuclease domain
4	c2wbnA_	Alignment		91.0	11	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**terminase large subunit; **PDBTitle:** crystal structure of the g2p (large terminase) nuclease2 domain from the bacteriophage spp1
5	c3llmB_	Alignment		81.5	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase a; **PDBTitle:** crystal structure analysis of a rna helicase
6	c2f55C_	Alignment		72.3	17	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**polyprotein; **PDBTitle:** two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
7	c1cu1B_	Alignment		71.9	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
8	c1a1vA_	Alignment		69.1	18	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
9	d1a1va1	Alignment		68.9	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
10	c3l9oA_	Alignment		53.4	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome
11	c2xgjA_	Alignment		53.1	8	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** structure of mtr4, a dexh helicase involved in nuclear rna2 processing and surveillance

12	c3kx2A_	Alignment		50.8	25	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna **PDBTitle:** crystal structure of prp43p in complex with adp
13	c3dkpA_	Alignment		47.3	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx52; **PDBTitle:** human dead-box rna-helicase ddx52, conserved domain i in complex with2 adp
14	d1yksa1	Alignment		46.3	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
15	c2qeqA_	Alignment		46.1	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit; **PDBTitle:** crystal structure of kunjin virus ns3 helicase
16	d1tf5a3	Alignment		45.8	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
17	c2jlrA_	Alignment		44.9	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease subunit ns3; **PDBTitle:** dengue virus 4 ns3 helicase in complex with amppnp
18	c1ymfA_	Alignment		44.3	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**genome polyprotein [contains: flavivirin **PDBTitle:** crystal structure of yellow fever virus ns3 helicase2 complexed with adp
19	c3ly5A_	Alignment		43.5	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx18; **PDBTitle:** ddx18 dead-domain
20	d1eiwa_	Alignment		43.0	17	**Fold:**Flavodoxin-like **Superfamily:**Hypothetical protein MTH538 **Family:**Hypothetical protein MTH538
21	d1qwga_	Alignment	not modelled	42.6	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
22	d1rifa_	Alignment	not modelled	37.7	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**DNA helicase UvsW
23	c2z83A_	Alignment	not modelled	36.9	13	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**helicase/nucleoside triphosphatase; **PDBTitle:** crystal structure of catalytic domain of japanese2 encephalitis virus ns3 helicase/nucleoside triphosphatase3 at a resolution 1.8
24	d2nu7b1	Alignment	not modelled	36.9	22	**Fold:**Flavodoxin-like **Superfamily:**Succinyl-CoA synthetase domains **Family:**Succinyl-CoA synthetase domains
25	c2wv9A_	Alignment	not modelled	36.7	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns2b regulatory subunit, flavivirin **PDBTitle:** crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
26	c2va8A_	Alignment	not modelled	34.3	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
27	d1vhxa_	Alignment	not modelled	32.6	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**Putative Holliday junction resolvase RuvX
28	c1qfqB_	Alignment	not modelled	30.7	38	**PDB header:**transcription/rna **Chain:** B: **PDB Molecule:**36-mer n-terminal peptide of the n protein; **PDBTitle:** bacteriophage lambda n-protein-nutboxb-rna complex

29	c3ngjC_	Alignment	not modelled	30.6	11	**PDB header:**lyase **Chain:** C: **PDB Molecule:**deoxyribose-phosphate aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 entamoeba histolytica
30	d1ub3a_	Alignment	not modelled	30.3	13	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
31	c3b6eA_	Alignment	not modelled	30.1	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**interferon-induced helicase c domain-containing protein 1; **PDBTitle:** crystal structure of human dech-box rna helicase mda5 (melanoma2 differentiation-associated protein 5), dech-domain
32	c2zj2A_	Alignment	not modelled	29.4	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ski2-type helicase; **PDBTitle:** archaeal dna helicase hjm apo state in form 1
33	d1hv8a1	Alignment	not modelled	26.4	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
34	c2zpaB_	Alignment	not modelled	26.2	18	**PDB header:**transferase **Chain:** B: **PDB Molecule:**uncharacterized protein ypfi; **PDBTitle:** crystal structure of trna(met) cytidine acetyltransferase
35	d1kyqa2	Alignment	not modelled	25.8	22	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
36	d1lrza2	Alignment	not modelled	25.3	18	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**FemXAB nonribosomal peptidyltransferases
37	d1s2ma1	Alignment	not modelled	22.7	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
38	d1kfia3	Alignment	not modelled	22.1	12	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
39	c3oa3A_	Alignment	not modelled	20.7	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**aldolase; **PDBTitle:** crystal structure of a putative deoxyribose-phosphate aldolase from2 coccidioides immitis
40	c4a4zA_	Alignment	not modelled	19.9	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
41	c2ixsB_	Alignment	not modelled	19.7	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sdai restriction endonuclease; **PDBTitle:** structure of sdai restriction endonuclease
42	c3o3nB_	Alignment	not modelled	19.5	13	**PDB header:**lyase **Chain:** B: **PDB Molecule:**beta-subunit 2-hydroxyacyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
43	c1gm5A_	Alignment	not modelled	18.5	13	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
44	d2fz4a1	Alignment	not modelled	18.2	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
45	c3rc8A_	Alignment	not modelled	17.2	17	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase supv3l1, mitochondrial; **PDBTitle:** human mitochondrial helicase suv3 in complex with short rna fragment
46	c2vbcA_	Alignment	not modelled	16.0	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
47	d1o0ya_	Alignment	not modelled	15.9	14	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
48	d1n7ka_	Alignment	not modelled	14.5	8	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
49	d2eyqa3	Alignment	not modelled	14.2	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
50	c3berA_	Alignment	not modelled	14.1	7	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase ddx47; **PDBTitle:** human dead-box rna-helicase ddx47, conserved domain i in complex with2 amp
51	d3pmga3	Alignment	not modelled	12.5	15	**Fold:**Phosphoglucomutase, first 3 domains **Superfamily:**Phosphoglucomutase, first 3 domains **Family:**Phosphoglucomutase, first 3 domains
52	c2p6uA_	Alignment	not modelled	12.4	21	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
53	d1uaaa2	Alignment	not modelled	11.2	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
54	d1gm5a3	Alignment	not modelled	11.1	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate

54	d1gm5a3	Alignment	not modelled	11.1	13	hydrolases **Family:**Tandem AAA-ATPase domain
55	d1uc8a1	Alignment	not modelled	10.3	11	**Fold:**PreATP-grasp domain **Superfamily:**PreATP-grasp domain **Family:**Lysine biosynthesis enzyme LysX, N-terminal domain
56	d1q0ua_	Alignment	not modelled	10.3	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
57	c2v6jA_	Alignment	not modelled	10.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
58	d1mzra_	Alignment	not modelled	9.6	9	**Fold:**TIM beta/alpha-barrel **Superfamily:**NAD(P)-linked oxidoreductase **Family:**Aldo-keto reductases (NADP)
59	d2dl6a1	Alignment	not modelled	9.2	11	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
60	d2htja1	Alignment	not modelled	9.2	7	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**FaeA-like
61	d2g9na1	Alignment	not modelled	8.8	9	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
62	d1wp9a1	Alignment	not modelled	8.6	21	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
63	c3pxiB_	Alignment	not modelled	8.5	12	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**negative regulator of genetic competence clpc/mecb; **PDBTitle:** structure of meca108:clpc
64	d1hxra_	Alignment	not modelled	8.4	5	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
65	d1oywa2	Alignment	not modelled	8.3	24	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
66	c3o3nA_	Alignment	not modelled	8.3	4	**PDB header:**lyase **Chain:** A: **PDB Molecule:**alpha-subunit 2-hydroxyisocaproyl-coa dehydratase; **PDBTitle:** (r)-2-hydroxyisocaproyl-coa dehydratase in complex with its substrate2 (r)-2-hydroxyisocaproyl-coa
67	d1mv5a_	Alignment	not modelled	8.1	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**ABC transporter ATPase domain-like
68	d2p6ra3	Alignment	not modelled	8.1	26	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
69	d1nkta3	Alignment	not modelled	7.9	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
70	d2fu5a1	Alignment	not modelled	7.9	5	**Fold:**Mss4-like **Superfamily:**Mss4-like **Family:**RabGEF Mss4
71	d1gkub1	Alignment	not modelled	7.9	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
72	d1hjra_	Alignment	not modelled	7.9	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**RuvC resolvase
73	c2vl7A_	Alignment	not modelled	7.8	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**xpd; **PDBTitle:** structure of s. tokodaii xpd4
74	c3n6jA_	Alignment	not modelled	7.6	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**mandelate racemase/muconate lactonizing protein; **PDBTitle:** crystal structure of mandelate racemase/muconate lactonizing protein2 from actinobacillus succinogenes 130z
75	d2ckaa1	Alignment	not modelled	7.2	9	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
76	c2ckaA_	Alignment	not modelled	7.2	9	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chromodomain-helicase-dna-binding protein 8; **PDBTitle:** solution structures of the brk domains of the human chromo2 helicase domain 7 and 8, reveals structural similarity3 with gyf domain suggesting a role in protein interaction
77	d2e8aa1	Alignment	not modelled	6.8	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Actin-like ATPase domain **Family:**Actin/HSP70
78	c2chvE_	Alignment	not modelled	6.7	13	**PDB header:**dna-binding protein **Chain:** E: **PDB Molecule:**replication factor c small subunit; **PDBTitle:** replication factor c adpnp complex
79	c3d8bB_	Alignment	not modelled	6.7	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**fidgetin-like protein 1; **PDBTitle:** crystal structure of human fidgetin-like protein 1 in complex with adp
						PDB header:toxin

80	c2r2aB_	Alignment	not modelled	6.7	20	**Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of n-terminal domain of zonular occludens toxin from2 neisseria meningitidis
81	c3fe2B_	Alignment	not modelled	6.6	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx5; **PDBTitle:** human dead-box rna helicase ddx5 (p68), conserved domain i in complex2 with adp
82	d2fwra2	Alignment	not modelled	6.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
83	d1pjqa3	Alignment	not modelled	6.5	28	**Fold:**Siroheme synthase middle domains-like **Superfamily:**Siroheme synthase middle domains-like **Family:**Siroheme synthase middle domains-like
84	d1mzha_	Alignment	not modelled	6.3	15	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
85	d2j0sa1	Alignment	not modelled	6.3	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
86	c2fsgA_	Alignment	not modelled	6.3	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** complex seca:atp from escherichia coli
87	d1fx0b1	Alignment	not modelled	6.2	18	**Fold:**Left-handed superhelix **Superfamily:**C-terminal domain of alpha and beta subunits of F1 ATP synthase **Family:**C-terminal domain of alpha and beta subunits of F1 ATP synthase
88	c3pfiB_	Alignment	not modelled	5.9	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**holliday junction atp-dependent dna helicase ruvb; **PDBTitle:** 2.7 angstrom resolution crystal structure of a probable holliday2 junction dna helicase (ruvb) from campylobacter jejuni subsp. jejuni3 nctc 11168 in complex with adenosine-5'-diphosphate
89	c3iuyB_	Alignment	not modelled	5.7	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**probable atp-dependent rna helicase ddx53; **PDBTitle:** crystal structure of ddx53 dead-box domain
90	d1ir1s_	Alignment	not modelled	5.6	20	**Fold:**RuBisCO, small subunit **Superfamily:**RuBisCO, small subunit **Family:**RuBisCO, small subunit
91	c3o0kB_	Alignment	not modelled	5.4	7	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**aldo/keto reductase; **PDBTitle:** crystal structure of aldo/keto reductase from brucella melitensis
92	c1nsfA_	Alignment	not modelled	5.4	20	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**n-ethylmaleimide sensitive factor; **PDBTitle:** d2 hexamerization domain of n-ethylmaleimide sensitive factor (nsf)
93	d1fvpa_	Alignment	not modelled	5.3	33	**Fold:**TIM beta/alpha-barrel **Superfamily:**Bacterial luciferase-like **Family:**Non-fluorescent flavoprotein (luxF, FP390)
94	d1u83a_	Alignment	not modelled	5.3	12	**Fold:**TIM beta/alpha-barrel **Superfamily:**(2r)-phospho-3-sulfolactate synthase ComA **Family:**(2r)-phospho-3-sulfolactate synthase ComA
95	c1u83A_	Alignment	not modelled	5.3	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**phosphosulfolactate synthase; **PDBTitle:** psl synthase from bacillus subtilis
96	d1nnva_	Alignment	not modelled	5.3	14	**Fold:**Cystatin-like **Superfamily:**Putative dsDNA mimic **Family:**Putative dsDNA mimic
97	c1qhhB_	Alignment	not modelled	5.2	6	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (pcra (subunit)); **PDBTitle:** structure of dna helicase with adpnp
98	d2v0ea1	Alignment	not modelled	5.1	25	**Fold:**GYF/BRK domain-like **Superfamily:**BRK domain-like **Family:**BRK domain-like
99	d2fkia1	Alignment	not modelled	5.1	17	**Fold:**Secretion chaperone-like **Superfamily:**YjbR-like **Family:**YjbR-like