Phyre^2

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Description	P39393
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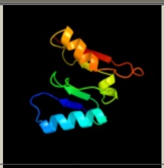
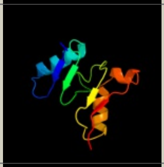
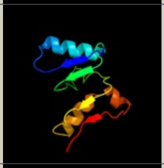
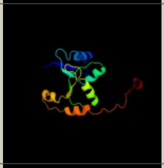
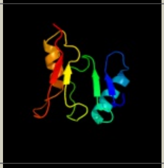
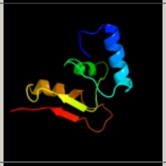
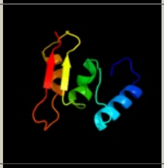
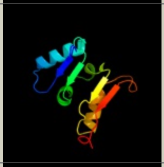
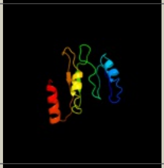
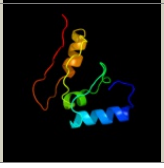
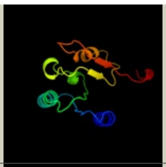
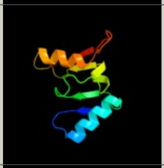
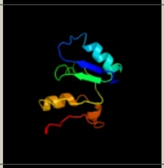
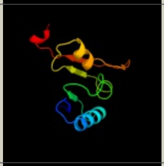
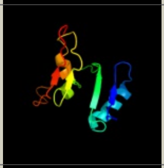
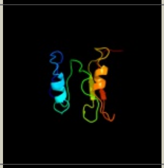
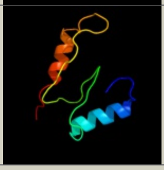
Unique Job ID	59cfd90441049a96

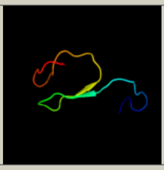
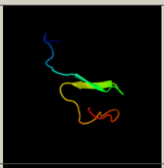
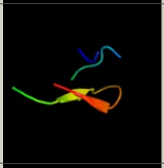
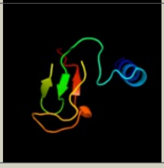
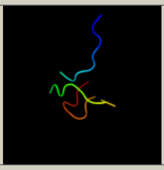
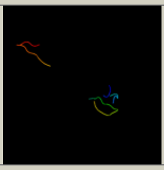
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2v1xB_	Alignment		99.5	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent dna helicase q1; **PDBTitle:** crystal structure of human recq-like dna helicase
2	d2p6ra4	Alignment		99.4	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
3	c1oywA_	Alignment		99.4	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase; **PDBTitle:** structure of the recq catalytic core
4	d1oywa3	Alignment		99.3	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
5	c3rc8A_	Alignment		99.3	15	**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
6	c2db3D_	Alignment		99.3	13	**PDB header:**hydrolase/rna **Chain:** D: **PDB Molecule:**atp-dependent rna helicase vasa; **PDBTitle:** structural basis for rna unwinding by the dead-box protein2 drosophila vasa
7	c2xgjA_	Alignment		99.3	19	**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
8	c4a4zA_	Alignment		99.2	21	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**antiviral helicase ski2; **PDBTitle:** crystal structure of the s. cerevisiae dexh helicase ski2 bound to2 amppnp
9	c2i4iA_	Alignment		99.2	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx3x; **PDBTitle:** crystal structure of human dead-box rna helicase ddx3x
10	c1gm5A_	Alignment		99.2	13	**PDB header:**helicase **Chain:** A: **PDB Molecule:**recg; **PDBTitle:** structure of recg bound to three-way dna junction
11	c3l9oA_	Alignment		99.2	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dob1; **PDBTitle:** crystal structure of mtr4, a co-factor of the nuclear exosome

12	d2eyqa5	Alignment		99.2	19	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
13	c1hv8B_	Alignment		99.2	14	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**putative atp-dependent rna helicase mj0669; **PDBTitle:** crystal structure of a dead box protein from the2 hyperthermophile methanococcus jannaschii
14	c3fhtA_	Alignment		99.1	17	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** crystal structure of human dbp5 in complex with amppnp and rna
15	c3i32A_	Alignment		99.1	15	**PDB header:**rna binding protein,hydrolase **Chain:** A: **PDB Molecule:**heat resistant rna dependent atpase; **PDBTitle:** dimeric structure of a hera helicase fragment including the c-terminal2 reca domain, the dimerization domain, and the rna binding domain
16	c1s2mA_	Alignment		99.1	16	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**putative atp-dependent rna helicase dhh1; **PDBTitle:** crystal structure of the dead box protein dhh1p
17	c2hxyC_	Alignment		99.1	13	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**probable atp-dependent rna helicase ddx48; **PDBTitle:** crystal structure of human apo-eif4aiii
18	d1gm5a4	Alignment		99.0	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
19	c1xtkA_	Alignment		99.0	14	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**probable atp-dependent rna helicase p47; **PDBTitle:** structure of decd to dead mutation of human uap56
20	c2zj2A_	Alignment		99.0	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative ski2-type helicase; **PDBTitle:** archaeal dna helicase hjm apo state in form 1
21	c2va8A_	Alignment	not modelled	99.0	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ski2-type helicase; **PDBTitle:** dna repair helicase hel308
22	c2fwrA_	Alignment	not modelled	99.0	14	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad25; **PDBTitle:** structure of archaeoglobus fulgidis xpb
23	c1wp9D_	Alignment	not modelled	99.0	16	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**atp-dependent rna helicase, putative; **PDBTitle:** crystal structure of pyrococcus furiosus hef helicase domain
24	c2z0mA_	Alignment	not modelled	99.0	8	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**337aa long hypothetical atp-dependent rna **PDBTitle:** crystal structure of hypothetical atp-dependent rna2 helicase from sulfolobus tokodaii
25	c3earA_	Alignment	not modelled	99.0	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hera; **PDBTitle:** novel dimerization motif in the dead box rna helicase hera: form 1,2 partial dimer
26	d1s2ma2	Alignment	not modelled	99.0	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
27	d1t5la2	Alignment	not modelled	99.0	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
28	c2vsxA_	Alignment	not modelled	99.0	13	**PDB header:**translation/hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase eif4a; **PDBTitle:** crystal structure of a translation initiation complex

29	c3tmiA_	Alignment	not modelled	99.0	11	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx58; **PDBTitle:** structural basis for rna recognition and activation of rig-i
30	c1c4oA_	Alignment	not modelled	98.9	10	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna nucleotide excision repair enzyme uvrb; **PDBTitle:** crystal structure of the dna nucleotide excision repair enzyme uvrb2 from thermus thermophilus
31	c3i5yA_	Alignment	not modelled	98.9	15	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**atp-dependent rna helicase mss116; **PDBTitle:** structure of mss116p bound to ssrna containing a single 5-bru and amp-2 pnp
32	d2j0sa2	Alignment	not modelled	98.9	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
33	c2fzlA_	Alignment	not modelled	98.9	13	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna repair protein rad25, xpb; **PDBTitle:** structure of c-terminal domain of archaeoglobus fulgidus xpb
34	d1t5ia_	Alignment	not modelled	98.9	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
35	c2eyqA_	Alignment	not modelled	98.9	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**transcription-repair coupling factor; **PDBTitle:** crystal structure of escherichia coli transcription-repair2 coupling factor
36	c3ewsA_	Alignment	not modelled	98.8	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx19b; **PDBTitle:** human dead-box rna-helicase ddx19 in complex with adp
37	c2d7dA_	Alignment	not modelled	98.8	10	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**uvrabc system protein b; **PDBTitle:** structural insights into the cryptic dna dependent atp-ase2 activity of uvrb
38	d1c4oa2	Alignment	not modelled	98.8	10	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
39	d1hv8a2	Alignment	not modelled	98.8	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
40	d1wp9a2	Alignment	not modelled	98.7	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
41	c2hjvB_	Alignment	not modelled	98.7	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase dbpa; **PDBTitle:** structure of the second domain (residues 207-368) of the2 bacillus subtilis yxin protein
42	c3pexA_	Alignment	not modelled	98.7	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** s. cerevisiae dbp5 l327v bound to gle1 h337r and ip6
43	d1fuka_	Alignment	not modelled	98.7	14	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
44	c2jlrA_	Alignment	not modelled	98.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**serine protease subunit ns3; **PDBTitle:** dengue virus 4 ns3 helicase in complex with amppnp
45	c2ocaA_	Alignment	not modelled	98.7	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent dna helicase uvsw; **PDBTitle:** the crystal structure of t4 uvsw
46	c2v6jA_	Alignment	not modelled	98.7	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna helicase; **PDBTitle:** kokobera virus helicase: mutant met47thr
47	c2p6nA_	Alignment	not modelled	98.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase ddx41; **PDBTitle:** human dead-box rna helicase ddx41, helicase domain
48	d1jr6a_	Alignment	not modelled	98.6	7	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
49	c2p6uA_	Alignment	not modelled	98.6	12	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**afuhel308 helicase; **PDBTitle:** apo structure of the hel308 superfamily 2 helicase
50	d2fwra1	Alignment	not modelled	98.6	15	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
51	d2g2ja1	Alignment	not modelled	98.6	16	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
52	c3oiyB_	Alignment	not modelled	98.6	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**reverse gyrase helicase domain; **PDBTitle:** helicase domain of reverse gyrase from thermotoga maritima
53	c2vbcA_	Alignment	not modelled	98.5	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**dengue 4 ns3 full-length protein; **PDBTitle:** crystal structure of the ns3 protease-helicase from dengue2 virus
54	d1tf5a4	Alignment	not modelled	98.5	12	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain

55	c3tbkA_	Alignment	not modelled	98.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rig-i helicase domain; **PDBTitle:** mouse rig-i atpase domain
56	c3kx2A_	Alignment	not modelled	98.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pre-mrna-splicing factor atp-dependent rna **PDBTitle:** crystal structure of prp43p in complex with adp
57	c3bxzA_	Alignment	not modelled	98.4	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**preprotein translocase subunit seca; **PDBTitle:** crystal structure of the isolated dead motor domains from2 escherichia coli seca
58	c2jgnB_	Alignment	not modelled	98.4	11	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**atp-dependent rna helicase ddx3x; **PDBTitle:** ddx3 helicase domain
59	c2kbfA_	Alignment	not modelled	98.4	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**atp-dependent rna helicase dbp5; **PDBTitle:** solution structure of carboxyl-terminal domain of dbp5p
60	c2wv9A_	Alignment	not modelled	98.3	12	**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
61	d1a1va2	Alignment	not modelled	98.3	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
62	c2z83A_	Alignment	not modelled	98.2	9	**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
63	c1gl9B_	Alignment	not modelled	98.2	19	**PDB header:**topoisomerase **Chain:** B: **PDB Molecule:**reverse gyrase; **PDBTitle:** archaeoglobus fulgidus reverse gyrase complexed with adpnp
64	d1gkub2	Alignment	not modelled	98.0	18	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Helicase-like "domain" of reverse gyrase
65	c1ymfA_	Alignment	not modelled	98.0	5	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**genome polyprotein [contains: flavivirin **PDBTitle:** crystal structure of yellow fever virus ns3 helicase2 complexed with adp
66	d2bmfa2	Alignment	not modelled	97.9	6	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
67	c1a1vA_	Alignment	not modelled	97.8	11	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**protein (ns3 protein); **PDBTitle:** hepatitis c virus ns3 helicase domain complexed with single2 stranded sdna
68	c2qeqA_	Alignment	not modelled	97.7	4	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**flavivirin protease ns3 catalytic subunit; **PDBTitle:** crystal structure of kunjin virus ns3 helicase
69	c3h1tA_	Alignment	not modelled	97.7	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**type i site-specific restriction-modification **PDBTitle:** the fragment structure of a putative hsdr subunit of a type2 i restriction enzyme from vibrio vulnificus yj016
70	c2w74B_	Alignment	not modelled	97.5	13	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**type i restriction enzyme ecor124ii r protein; **PDBTitle:** mutant (k220r) of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
71	c2f55C_	Alignment	not modelled	96.9	5	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**polyprotein; **PDBTitle:** two hepatitis c virus ns3 helicase domains complexed with2 the same strand of dna
72	d8ohma2	Alignment	not modelled	96.8	23	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
73	c1z63A_	Alignment	not modelled	96.7	9	**PDB header:**hydrolase/dna complex **Chain:** A: **PDB Molecule:**helicase of the snf2/rad54 hamily; **PDBTitle:** sulfolobus solfataricus swi2/snf2 atpase core in complex2 with dsdna
74	c3mwyW_	Alignment	not modelled	96.7	15	**PDB header:**hydrolase **Chain:** W: **PDB Molecule:**chromo domain-containing protein 1; **PDBTitle:** crystal structure of the chromodomain-atpase portion of the yeast chd12 chromatin remodeler
75	c1z3iX_	Alignment	not modelled	96.5	8	**PDB header:**recombination/dna binding **Chain:** X: **PDB Molecule:**similar to rad54-like; **PDBTitle:** structure of the swi2/snf2 chromatin remodeling domain of eukaryotic2 rad54
76	d1nkta4	Alignment	not modelled	96.3	11	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
77	c3dmqA_	Alignment	not modelled	96.0	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna polymerase-associated protein rapa; **PDBTitle:** crystal structure of rapa, a swi2/snf2 protein that2 recycles rna polymerase during transcription
78	c3crw1_	Alignment	not modelled	95.0	12	**PDB header:**hydrolase **Chain:** 1: **PDB Molecule:**xpd/rad3 related dna helicase; **PDBTitle:** "xpd_apo"
79	c3dl8B_	Alignment	not modelled	94.6	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**protein translocase subunit seca; **PDBTitle:** structure of the complex of aquifex aeolicus secyeg and2 bacillus subtilis seca

80	c2fsgA_	Alignment	not modelled	93.9	13	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** complex seca:atp from escherichia coli
81	c1tf2A_	Alignment	not modelled	93.5	16	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**preprotein translocase seca subunit; **PDBTitle:** crystal structure of seca:adp in an open conformation from2 bacillus subtilis
82	d1z3ix1	Alignment	not modelled	88.4	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
83	d1yksa2	Alignment	not modelled	88.0	8	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**RNA helicase
84	c1cu1B_	Alignment	not modelled	84.1	12	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**protein (protease/helicase ns3); **PDBTitle:** crystal structure of an enzyme complex from hepatitis c2 virus
85	c1yuzB_	Alignment		82.8	11	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**nigerythrin; **PDBTitle:** partially reduced state of nigerythrin
86	d1z5za1	Alignment	not modelled	82.7	13	**Fold:**P-loop containing nucleoside triphosphate hydrolases **Superfamily:**P-loop containing nucleoside triphosphate hydrolases **Family:**Tandem AAA-ATPase domain
87	c2hr5B_	Alignment		82.4	16	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**rubrerythrin; **PDBTitle:** pf1283- rubrerythrin from pyrococcus furiosus iron bound form
88	c3ndjA_	Alignment		80.2	36	**PDB header:**transferase **Chain:** A: **PDB Molecule:**methyltransferase; **PDBTitle:** x-ray structure of a c-3'-methyltransferase in complex with s-2 adenosyl-l-homocysteine and sugar product
89	c1dvbA_	Alignment		79.5	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**rubrerythrin; **PDBTitle:** rubrerythrin
90	c1z5zB_	Alignment	not modelled	78.0	13	**PDB header:**hydrolase/recombination **Chain:** B: **PDB Molecule:**helicase of the snf2/rad54 family; **PDBTitle:** sulfolobus solfataricus swi2/snf2 atpase c-terminal domain
91	c3k7aM_	Alignment		71.8	20	**PDB header:**transcription **Chain:** M: **PDB Molecule:**transcription initiation factor iib; **PDBTitle:** crystal structure of an rna polymerase ii-tfiib complex
92	d1dl6a_	Alignment	not modelled	71.8	19	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
93	d1wffa_	Alignment	not modelled	70.9	22	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
94	c3cngC_	Alignment		68.3	24	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**nudix hydrolase; **PDBTitle:** crystal structure of nudix hydrolase from nitrosomonas europaea
95	c2w00B_	Alignment	not modelled	61.8	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**hsdr; **PDBTitle:** crystal structure of the hsdr subunit of the ecor124i2 restriction enzyme in complex with atp
96	c2gb5B_	Alignment	not modelled	61.0	35	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nadh pyrophosphatase; **PDBTitle:** crystal structure of nadh pyrophosphatase (ec 3.6.1.22) (1790429) from2 escherichia coli k12 at 2.30 a resolution
97	d1wfla_	Alignment	not modelled	60.1	22	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
98	d1yuza2	Alignment	not modelled	58.7	13	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
99	c3h0gL_	Alignment	not modelled	55.0	47	**PDB header:**transcription **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii **PDBTitle:** rna polymerase ii from schizosaccharomyces pombe
						Fold: Rubredoxin-like

100	d1nnqa2	Alignment	not modelled	54.6	16	**Superfamily:**Rubredoxin-like **Family:**Rubredoxin
101	d1wg2a_	Alignment	not modelled	54.0	21	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
102	d1pfta_	Alignment	not modelled	53.1	28	**Fold:**Rubredoxin-like **Superfamily:**Zinc beta-ribbon **Family:**Transcriptional factor domain
103	c2ja6L_	Alignment	not modelled	52.6	35	**PDB header:**transferase **Chain:** L: **PDB Molecule:**dna-directed rna polymerases i, ii, and iii 7.7 **PDBTitle:** cpd lesion containing rna polymerase ii elongation complex2 b
104	c1m98A_	Alignment	not modelled	51.4	20	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**orange carotenoid protein; **PDBTitle:** crystal structure of orange carotenoid protein
105	d1wfha_	Alignment	not modelled	51.3	21	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
106	d2j0151	Alignment	not modelled	50.6	20	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
107	c3bvoA_	Alignment	not modelled	48.3	37	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**co-chaperone protein hscb, mitochondrial precursor; **PDBTitle:** crystal structure of human co-chaperone protein hscb
108	c3eswA_	Alignment	not modelled	48.2	47	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptide-n(4)-(n-acetyl-beta-glucosaminyl)asparagine **PDBTitle:** complex of yeast pngase with glcnac2-iac.
109	c1i3ql_	Alignment	not modelled	48.1	40	**PDB header:**transcription **Chain:** I: **PDB Molecule:**dna-directed rna polymerase ii 14.2kd **PDBTitle:** rna polymerase ii crystal form i at 3.1 a resolution
110	d1wfpa_	Alignment	not modelled	47.1	21	**Fold:**AN1-like Zinc finger **Superfamily:**AN1-like Zinc finger **Family:**AN1-like Zinc finger
111	c2pziA_	Alignment	not modelled	46.1	35	**PDB header:**transferase **Chain:** A: **PDB Molecule:**probable serine/threonine-protein kinase pkng; **PDBTitle:** crystal structure of protein kinase pkng from mycobacterium2 tuberculosis in complex with tetrahydrobenzothiophene ax20017
112	d2zjrz1	Alignment	not modelled	45.4	20	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L32p
113	c3pfqA_	Alignment	not modelled	44.5	47	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein kinase c beta type; **PDBTitle:** crystal structure and allosteric activation of protein kinase c beta2 ii
114	c2ysoA_	Alignment	not modelled	40.8	38	**PDB header:**transcription **Chain:** A: **PDB Molecule:**zinc finger protein 95 homolog; **PDBTitle:** solution structure of the c2h2 type zinc finger (region 656-2 688) of human zinc finger protein 95 homolog
115	c2ps3A_	Alignment	not modelled	40.5	11	**PDB header:**metal transport **Chain:** A: **PDB Molecule:**high-affinity zinc uptake system protein znua; **PDBTitle:** structure and metal binding properties of znua, a2 periplasmic zinc transporter from escherichia coli
116	c2kwqA_	Alignment	not modelled	39.3	26	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**protein mcm10 homolog; **PDBTitle:** mcm10 c-terminal dna binding domain
117	c2js4A_	Alignment	not modelled	38.5	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**upf0434 protein bb2007; **PDBTitle:** solution nmr structure of bordetella bronchiseptica protein2 bb2007. northeast structural genomics consortium target3 bor54
118	d1lkoa2	Alignment	not modelled	37.6	13	**Fold:**Rubredoxin-like **Superfamily:**Rubredoxin-like **Family:**Rubredoxin
119	d1jwhc_	Alignment	not modelled	36.8	22	**Fold:**Rubredoxin-like **Superfamily:**Casein kinase II beta subunit **Family:**Casein kinase II beta subunit
120	d2ayja1	Alignment	not modelled	35.9	28	**Fold:**Rubredoxin-like **Superfamily:**Zn-binding ribosomal proteins **Family:**Ribosomal protein L40e