Phyre^2

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Description	RVBD3711c_(dnaQ)_4155918_4156907
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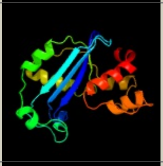
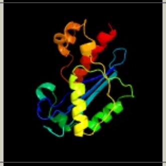
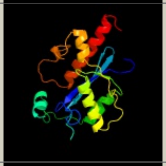
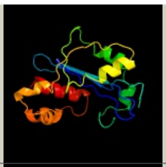
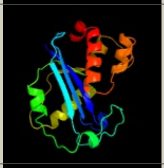
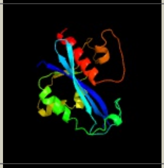
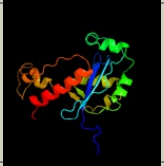
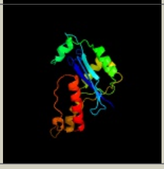
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2qxfa1	Alignment		100.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
2	c4rg8A_	Alignment		100.0	26	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exonuclease i; **PDBTitle:** structural and biochemical studies of a moderately thermophilic2 exonuclease i from methylocaldum szegediense
3	c2p1jB_	Alignment		100.0	25	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii polc-type; **PDBTitle:** crystal structure of a polc-type dna polymerase iii exonuclease domain2 from thermotoga maritima
4	c5fkvD_	Alignment		100.0	26	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase iii epsilon; **PDBTitle:** cryo-em structure of the e. coli replicative dna polymerase complex2 bound to dna (dna polymerase iii alpha, beta, epsilon, tau complex)
5	d1y97a1	Alignment		100.0	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
6	c1zbhA_	Alignment		100.0	18	**PDB header:**hydrolase/rna **Chain:** A: **PDB Molecule:**3'-5' exonuclease eri1; **PDBTitle:** 3'-end specific recognition of histone mrna stem-loop by 3'-2 exonuclease
7	d2f96a1	Alignment		100.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
8	c3cm6A_	Alignment		100.0	18	**PDB header:**hydrolase, apoptosis **Chain:** A: **PDB Molecule:**cell death-related nuclease 4; **PDBTitle:** crystal structure of cell-death related nuclease 4 (crn-4)2 bound with er
9	d2guia1	Alignment		100.0	28	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
10	c3u6fA_	Alignment		100.0	19	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**three prime repair exonuclease 1; **PDBTitle:** mouse trex1 d200n mutant
11	c2xriA_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**eri1 exoribonuclease 3; **PDBTitle:** crystal structure of human eri1 exoribonuclease 3

12	c1zbuB_	Alignment		100.0	18	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3'-5' exonuclease eri1; **PDBTitle:** crystal structure of full-length 3'-exonuclease
13	d3b6oa1	Alignment		100.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
14	c5z9xA_	Alignment		100.0	20	**PDB header:**plant protein/rna **Chain:** A: **PDB Molecule:**small rna degrading nuclease 1; **PDBTitle:** arabidopsis small rna degrading nuclease 1 in complex with an rna2 substrate
15	d1j9aa_	Alignment		100.0	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
16	c3tr8A_	Alignment		100.0	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** structure of an oligoribonuclease (orn) from coxiella burnetii
17	d1w0ha_	Alignment		100.0	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
18	c5l80B_	Alignment		100.0	16	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**maternal protein exuperantia,maternal protein exuperantia; **PDBTitle:** structure of exuperantia exo-like and sam-like domains
19	c2is3B_	Alignment		100.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease t; **PDBTitle:** crystal structure of escherichia coli rnase t
20	c6n6jB_	Alignment		100.0	15	**PDB header:**rna binding protein/rna **Chain:** B: **PDB Molecule:**rna exonuclease 2 homolog,small fragment nuclease; **PDBTitle:** human rexo2 bound to paa
21	c4wbqA_	Alignment	not modelled	100.0	15	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**qde-2-interacting protein; **PDBTitle:** crystal structure of the exonuclease domain of qip (qde-2 interacting2 protein) solved by native-sad phasing.
22	c5cy4C_	Alignment	not modelled	100.0	18	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**oligoribonuclease; **PDBTitle:** crystal structure of an oligoribonuclease from acinetobacter baumannii
23	d2igia1	Alignment	not modelled	100.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
24	c6n6dA_	Alignment	not modelled	100.0	18	**PDB header:**rna binding protein/rna **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** vibrio cholerae oligoribonuclease bound to pag
25	c2gbzA_	Alignment	not modelled	100.0	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** the crystal structure of xc847 from xanthomonas campestris: a 3-52 oligoribonuclease of dnaq fold family with a novel opposingly-shifted3 helix
26	c6a4dA_	Alignment	not modelled	100.0	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** pnp-tmp bound oligoribonuclease (orn) from colwellia psychrerythraea2 strain 34h
27	c4fzxC_	Alignment	not modelled	99.9	27	**PDB header:**hydrolase/dna **Chain:** C: **PDB Molecule:**exodeoxyribonuclease 10; **PDBTitle:** exonuclease x in complex with 3' overhanging duplex dna
28	d1wlja_	Alignment	not modelled	99.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease

29	c2ebuA_	Alignment	not modelled	99.7	15	**PDB header:**replication **Chain:** A: **PDB Molecule:**replication factor c subunit 1; **PDBTitle:** solution structure of the brct domain from human2 replication factor c large subunit 1
30	d1l7ba_	Alignment	not modelled	99.7	26	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**DNA ligase
31	d1uoca_	Alignment	not modelled	99.7	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
32	c4czwA_	Alignment	not modelled	99.6	17	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**pab-dependent poly(a)-specific ribonuclease subunit pan2; **PDBTitle:** structure of the neurospora crassa pan2 catalytic unit (protease and2 nuclease domain)
33	d2d5ra1	Alignment	not modelled	99.5	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
34	c2p51A_	Alignment	not modelled	99.5	18	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**spcc18.06c protein; **PDBTitle:** crystal structure of the s. pombe pop2p deadenylation subunit
35	c4gmjB_	Alignment	not modelled	99.4	14	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**ccr4-not transcription complex subunit 7; **PDBTitle:** structure of human not1 mif4g domain co-crystallized with caf1
36	c4q8jA_	Alignment	not modelled	99.4	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pab-dependent poly(a)-specific ribonuclease subunit pan2; **PDBTitle:** structure of the saccharomyces cerevisiae pan2-pan3 core complex
37	c2cokA_	Alignment	not modelled	99.4	9	**PDB header:**transferase **Chain:** A: **PDB Molecule:**poly [adp-ribose] polymerase-1; **PDBTitle:** solution structure of brct domain of poly(adp-ribose)2 polymerase-1
38	c4hecB_	Alignment	not modelled	99.3	18	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of a putative uncharacterized protein from2 mycobacterium tuberculosis
39	c2kzzA_	Alignment	not modelled	99.3	16	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** klenow fragment with normal substrate and zinc only
40	d1kfsa1	Alignment	not modelled	99.3	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
41	d1x9ma1	Alignment	not modelled	99.1	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
42	d1tgoa1	Alignment	not modelled	99.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
43	d1wn7a1	Alignment	not modelled	99.1	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
44	d1qhta1	Alignment	not modelled	99.1	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
45	c5dkuB_	Alignment	not modelled	99.1	15	**PDB header:**transferase **Chain:** B: **PDB Molecule:**prex dna polymerase; **PDBTitle:** c-terminal his tagged appol exonuclease mutant
46	c3d45B_	Alignment	not modelled	99.0	22	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of mouse parn in complex with m7gpppg
47	d1d5aa1	Alignment	not modelled	99.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
48	c1njzA_	Alignment	not modelled	99.0	20	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase i; **PDBTitle:** cytosine-thymine mismatch at the polymerase active site
49	c2a1sC_	Alignment	not modelled	99.0	22	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**poly(a)-specific ribonuclease parn; **PDBTitle:** crystal structure of native parn nuclease domain
50	c2d8mA_	Alignment	not modelled	99.0	19	**PDB header:**dna binding protein **Chain:** A: **PDB Molecule:**dna-repair protein xrcc1; **PDBTitle:** solution structure of the first brct domain of dna-repair2 protein xrcc1
51	c5okiA_	Alignment	not modelled	98.9	15	**PDB header:**replication **Chain:** A: **PDB Molecule:**dna polymerase epsilon catalytic subunit a; **PDBTitle:** crystal structure of the ctf18-1-8 module from ctf18-rfc in complex2 with a 63 kda fragment of dna polymerase epsilon
52	c1tk0A_	Alignment	not modelled	98.9	24	**PDB header:**transferase/electron transport/dna **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** t7 dna polymerase ternary complex with 8 oxo guanosine and ddctp at2 the insertion site
53	d2hhva1	Alignment	not modelled	98.9	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
54	c4m8oA_	Alignment	not modelled	98.9	14	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase epsilon catalytic subunit a; **PDBTitle:** ternary complex of dna polymerase epsilon with an incoming datp

55	c6r5kA_	Alignment	not modelled	98.8	17	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**pan2-pan3 deadenylation complex catalytic subunit pan2; **PDBTitle:** cryo-em structure of a poly(a) rnp bound to the pan2-pan3 deadenylase
56	c6fwkB_	Alignment	not modelled	98.8	17	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**dna polymerase epsilon catalytic subunit a; **PDBTitle:** the crystal structure of pol2core-m644g in complex with dna and an2 incoming nucleotide
57	c5zo4B_	Alignment	not modelled	98.8	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**putative 3'-5' exonuclease family protein; **PDBTitle:** inactive state of the nuclease
58	c4bmcA_	Alignment	not modelled	98.7	14	**PDB header:**replication **Chain:** A: **PDB Molecule:**s-m checkpoint control protein rad4; **PDBTitle:** crystal structure of s.pombe rad4 brct1,2
59	c2couA_	Alignment	not modelled	98.7	12	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**ect2 protein; **PDBTitle:** solution structure of the second brct domain of epithelial2 cell transforming 2
60	c3l3eA_	Alignment	not modelled	98.7	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna topoisomerase 2-binding protein 1; **PDBTitle:** crystal structure of the sixth brct domain of human topbp1
61	c2xnkA_	Alignment	not modelled	98.7	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**dna topoisomerase 2-binding protein 1; **PDBTitle:** structure and function of the rad9-binding region of the dna damage2 checkpoint adaptor topbp1
62	c2vwkA_	Alignment	not modelled	98.7	15	**PDB header:**dna replication **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** uracil recognition in archaeal dna polymerases captured by2 x-ray crystallography. v93q polymerase variant
63	c4x0pB_	Alignment	not modelled	98.7	9	**PDB header:**transferase/dna **Chain:** B: **PDB Molecule:**dna polymerase theta; **PDBTitle:** ternary complex of human dna polymerase theta c-terminal domain2 binding ddatp opposite a tetrahydrofuran ap site analog
64	c2gv9B_	Alignment	not modelled	98.7	13	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase
65	c5mdnB_	Alignment	not modelled	98.7	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase; **PDBTitle:** structure of the family b dna polymerase from the hyperthermophilic2 archaeon pyrobaculum calidifontis
66	c1d5aA_	Alignment	not modelled	98.7	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (dna polymerase); **PDBTitle:** crystal structure of an archaebacterial dna polymerase2 d.tok. deposition of second native structure at 2.43 angstrom
67	c2gv9A_	Alignment	not modelled	98.7	12	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase
68	c3ef0A_	Alignment	not modelled	98.6	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase; **PDBTitle:** the structure of fcp1, an essential rna polymerase ii ctd phosphatase
69	c4n40A_	Alignment	not modelled	98.6	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**protein ect2; **PDBTitle:** crystal structure of human epithelial cell-transforming sequence 22 protein
70	c3iayA_	Alignment	not modelled	98.5	19	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit; **PDBTitle:** ternary complex of dna polymerase delta
71	c3ef1A_	Alignment	not modelled	98.5	11	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**rna polymerase ii subunit a c-terminal domain phosphatase; **PDBTitle:** the structure of fcp1, an essential rna polymerase ii ctd phosphatase
72	d1q8ia1	Alignment	not modelled	98.5	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
73	d1cdza_	Alignment	not modelled	98.5	11	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**DNA-repair protein XRCC1
74	d1wf6a_	Alignment	not modelled	98.5	16	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**DNA topoisomerase II binding protein 1, TopBP1
75	c3ii6Y_	Alignment	not modelled	98.5	15	**PDB header:**ligase/dna binding protein **Chain:** Y: **PDB Molecule:**dna ligase 4; **PDBTitle:** structure of human xrcc4 in complex with the tandem brct2 domains of dna ligaseiv.
76	c3ktfB_	Alignment	not modelled	98.5	12	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**microcephalin; **PDBTitle:** structure of the n-terminal brct domain of human microcephalin2 (mcph1).
77	c5c0xK_	Alignment	not modelled	98.5	16	**PDB header:**hydrolase/rna **Chain:** K: **PDB Molecule:**exosome complex exonuclease rrp6; **PDBTitle:** structure of a 12-subunit nuclear exosome complex bound to structured2 rna
78	c2e2wA_	Alignment	not modelled	98.4	16	**PDB header:**ligase **Chain:** A: **PDB Molecule:**dna ligase 4; **PDBTitle:** solution structure of the first brct domain of human dna2 ligase iv
79	c1yt3A_	Alignment	not modelled	98.4	18	**PDB header:**hydrolase,translation **Chain:** A: **PDB Molecule:**ribonuclease d; **PDBTitle:** crystal structure of escherichia coli rnase d, an2 exoribonuclease involved in structured rna processing

80	c4bmdA_	Alignment	not modelled	98.4	18	**PDB header:**replication **Chain:** A: **PDB Molecule:**s-m checkpoint control protein rad4; **PDBTitle:** crystal structure of s.pombe rad4 brct3,4
81	c4xviA_	Alignment	not modelled	98.4	7	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase nu; **PDBTitle:** binary complex of human polymerase nu and dna with the finger domain2 ajar
82	c5n2hA_	Alignment	not modelled	98.4	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** structure of the e9 dna polymerase exonuclease deficient mutant2 (d166a+e168a) from vaccinia virus
83	d1ih7a1	Alignment	not modelled	98.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
84	c4fydA_	Alignment	not modelled	98.4	11	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase alpha catalytic subunit a; **PDBTitle:** crystal structure of yeast dna polymerase alpha bound to dna/rna and2 dgtp
85	d1t15a2	Alignment	not modelled	98.3	14	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**BRCT domain
86	c2ebwA_	Alignment	not modelled	98.3	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** solution structure of the brct domain from human dna repair2 protein rev1
87	d1noya_	Alignment	not modelled	98.3	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
88	c3ueoB_	Alignment	not modelled	98.3	13	**PDB header:**peptide binding protein **Chain:** B: **PDB Molecule:**dna topoisomerase 2-binding protein 1; **PDBTitle:** crystal structure of topbp1 brct4/5 domains in complex with a phospho-2 peptide
89	c4ktqA_	Alignment	not modelled	98.3	19	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (large fragment of dna polymerase i); **PDBTitle:** binary complex of the large fragment of dna polymerase i2 from t. aquaticus bound to a primer/template dna
90	c5exrG_	Alignment	not modelled	98.3	16	**PDB header:**replication **Chain:** G: **PDB Molecule:**dna polymerase alpha catalytic subunit; **PDBTitle:** crystal structure of human primosome
91	d1kzyc1	Alignment	not modelled	98.3	12	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**53BP1
92	c4oo1J_	Alignment	not modelled	98.3	16	**PDB header:**hydrolase/rna **Chain:** J: **PDB Molecule:**exosome complex exonuclease rrp6; **PDBTitle:** structure of an rrp6-rna exosome complex bound to poly(a) rna
93	d1yt3a3	Alignment	not modelled	98.2	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
94	c1q8iA_	Alignment	not modelled	98.2	20	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii; **PDBTitle:** crystal structure of escherichia coli dna polymerase ii
95	d1l0ba1	Alignment	not modelled	98.2	15	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**BRCT domain
96	c3cymA_	Alignment	not modelled	98.2	20	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989; **PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
97	c2vxcA_	Alignment	not modelled	98.1	13	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**dna repair protein rhp9; **PDBTitle:** structure of the crb2-brct2 domain complex with phosphopeptide.
98	c4q5vA_	Alignment	not modelled	98.1	16	**PDB header:**transferase/dna/rna **Chain:** A: **PDB Molecule:**dna polymerase alpha catalytic subunit; **PDBTitle:** crystal structure of the catalytic core of human dna polymerase alpha2 in ternary complex with an rna-primed dna template and aphidicolin
99	d1t15a1	Alignment	not modelled	98.1	13	**Fold:**BRCT domain **Superfamily:**BRCT domain **Family:**BRCT domain
100	c2e6mA_	Alignment	not modelled	98.1	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**werner syndrome atp-dependent helicase homolog; **PDBTitle:** structure of mouse werner exonuclease domain
101	c4ztuA_	Alignment	not modelled	98.1	20	**PDB header:**dna binding protein/dna **Chain:** A: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** structural basis for processivity and antiviral drug toxicity in human2 mitochondrial dna replicase
102	c1kzyD_	Alignment	not modelled	98.1	11	**PDB header:**dna binding protein, protein binding **Chain:** D: **PDB Molecule:**tumor suppressor p53-binding protein 1; **PDBTitle:** crystal structure of the 53bp1 brct region complexed to2 tumor suppressor p53
103	c4id3B_	Alignment	not modelled	98.1	11	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**dna repair protein rev1; **PDBTitle:** crystal structure of the brct domain of s. cerevisiae rev1
104	c1y98A_	Alignment	not modelled	98.0	14	**PDB header:**antitumor protein **Chain:** A: **PDB Molecule:**breast cancer type 1 susceptibility protein; **PDBTitle:** structure of the brct repeats of brca1 bound to a ctip2 phosphopeptide.
105	c1s5jA_	Alignment	not modelled	98.0	23	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase i; **PDBTitle:** insight in dna replication: the crystal structure of dna2 polymerase b1 from the archaeon sulfolobus solfataricus

106	c2dtuA_	Alignment	not modelled	98.0	15	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the beta hairpin loop deletion variant of rb692 gp43 in complex with dna containing an abasic site analog
107	c2r1zB_	Alignment	not modelled	98.0	13	**PDB header:**antitumor protein **Chain:** B: **PDB Molecule:**brca1-associated ring domain protein 1; **PDBTitle:** crystal structure of the bard1 brct repeat
108	c3l40A_	Alignment	not modelled	97.9	5	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**brct-containing protein 1; **PDBTitle:** crystal structure of s. pombe brc1 brct5-brct6 domains
109	c3al3A_	Alignment	not modelled	97.9	14	**PDB header:**dna binding protein/protein binding **Chain:** A: **PDB Molecule:**dna topoisomerase 2-binding protein 1; **PDBTitle:** crystal structure of topbp1 brct7/8-bach1 peptide complex
110	c2azmB_	Alignment	not modelled	97.8	18	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**mediator of dna damage checkpoint protein 1; **PDBTitle:** crystal structure of the mdc1 brct repeat in complex with2 the histone tail of gamma-h2ax
111	c2jw5A_	Alignment	not modelled	97.8	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**dna polymerase lambda; **PDBTitle:** polymerase lambda brct domain
112	c1l0bA_	Alignment	not modelled	97.8	14	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**brca1; **PDBTitle:** crystal structure of rat brca1 tandem-brct region
113	d2hbka2	Alignment	not modelled	97.7	18	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
114	d1s5ja1	Alignment	not modelled	97.7	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
115	c2hbkA_	Alignment	not modelled	97.6	17	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp6; **PDBTitle:** structure of the yeast nuclear exosome component, rrp6p, reveals an2 interplay between the active site and the hrdc domain; protein in3 complex with mn
116	c6k1dB_	Alignment	not modelled	97.6	21	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**exonuclease 3'-5' domain-containing protein 2; **PDBTitle:** crystal structure of exd2 exonuclease domain soaked in mn and gmp
117	c2coeA_	Alignment	not modelled	97.5	17	**PDB header:**transferase **Chain:** A: **PDB Molecule:**deoxynucleotidyltransferase, terminal variant; **PDBTitle:** solution structure of brct domain of terminal2 deoxynucleotidyltransferase
118	c3t1nA_	Alignment	not modelled	97.5	7	**PDB header:**cell cycle/peptide **Chain:** A: **PDB Molecule:**microcephalin; **PDBTitle:** structure of human microcephalin (mcph1) tandem brct domains in2 complex with a cdc27 phosphopeptide
119	c1z56C_	Alignment	not modelled	97.5	16	**PDB header:**ligase **Chain:** C: **PDB Molecule:**dna ligase iv; **PDBTitle:** co-crystal structure of lif1p-lig4p
120	c4nlbA_	Alignment	not modelled	97.4	14	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**ribosomal rna processing protein 6; **PDBTitle:** crystal structure of the catalytic core of rrp6 from trypanosoma2 brucei