Phyre^2

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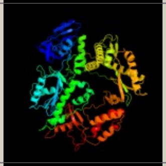
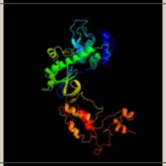
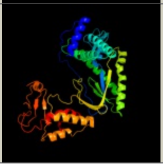
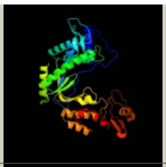
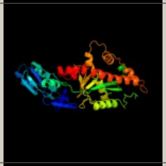
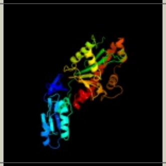
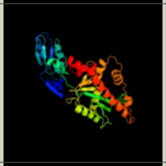
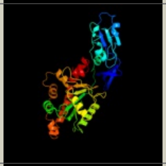
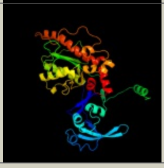
Description	P21189
Date	Thu Jan 5 11:38:01 GMT 2012
Unique Job ID	6b5e9bca3885544a

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c1q8iA_	Alignment		100.0	100	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase ii; **PDBTitle:** crystal structure of escherichia coli dna polymerase ii
2	c3iayA_	Alignment		100.0	22	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase delta catalytic subunit; **PDBTitle:** ternary complex of dna polymerase delta
3	c2gv9B_	Alignment		100.0	22	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the herpes simplex virus type 1 dna polymerase
4	c2vwkA_	Alignment		100.0	25	**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
5	c1d5aA_	Alignment		100.0	25	**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
6	c2dtuA_	Alignment		100.0	20	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** crystal structure of the beta hairpin loop deletion variant2 of rb69 gp43 in complex with dna containing an abasic site3 analog
7	c1s5jA_	Alignment		100.0	19	**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
8	d1tgoa2	Alignment		100.0	29	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
9	d1ih7a2	Alignment		100.0	22	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
10	d1wn7a2	Alignment		100.0	29	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
11	d1d5aa2	Alignment		100.0	29	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I

12	d1qhta2	Alignment		100.0	29	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
13	d1q8ia2	Alignment		100.0	100	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
14	d1q8ia1	Alignment		100.0	100	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
15	d1s5ja2	Alignment		100.0	23	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
16	d1qhta1	Alignment		100.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
17	d1tgoa1	Alignment		100.0	19	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
18	d1wn7a1	Alignment		100.0	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
19	d1d5aa1	Alignment		100.0	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
20	d1s5ja1	Alignment		100.0	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
21	d1ih7a1	Alignment	not modelled	100.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
22	d1noya_	Alignment	not modelled	100.0	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
23	c2ex3l_	Alignment	not modelled	99.9	17	**PDB header:**transferase/replication **Chain:** I: **PDB Molecule:**dna polymerase; **PDBTitle:** bacteriophage phi29 dna polymerase bound to terminal protein
24	d1x9ma1	Alignment	not modelled	99.7	14	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
25	d2py5a2	Alignment	not modelled	99.6	18	**Fold:**DNA/RNA polymerases **Superfamily:**DNA/RNA polymerases **Family:**DNA polymerase I
26	c2kzzA_	Alignment	not modelled	98.4	18	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**protein (dna polymerase i); **PDBTitle:** klenow fragment with normal substrate and zinc only
27	c1tk0A_	Alignment	not modelled	98.2	18	**PDB header:**transferase/electron transport/dna **Chain:** A: **PDB Molecule:**dna polymerase; **PDBTitle:** t7 dna polymerase ternary complex with 8 oxo guanosine and2 ddctp at the insertion site
28	d2qxfa1	Alignment	not modelled	98.1	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
29	d2guia1	Alignment	not modelled	97.8	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like

						Family: DnaQ-like 3'-5' exonuclease
30	d1y97a1	Alignment	not modelled	97.8	22	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
31	c1njzA_	Alignment	not modelled	97.7	13	**PDB header:**transferase/dna **Chain:** A: **PDB Molecule:**dna polymerase i; **PDBTitle:** cytosine-thymine mismatch at the polymerase active site
32	d1kfsa1	Alignment	not modelled	97.6	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
33	d2f96a1	Alignment	not modelled	97.6	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
34	d1wlja_	Alignment	not modelled	96.6	13	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
35	c2e6mA_	Alignment	not modelled	96.5	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**werner syndrome atp-dependent helicase homolog; **PDBTitle:** structure of mouse werner exonuclease domain
36	d1yt3a3	Alignment	not modelled	96.4	15	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
37	c3u6fA_	Alignment	not modelled	96.1	21	**PDB header:**hydrolase/dna **Chain:** A: **PDB Molecule:**three prime repair exonuclease 1; **PDBTitle:** mouse trex1 d200n mutant
38	c2p1jB_	Alignment	not modelled	95.8	27	**PDB header:**transferase **Chain:** B: **PDB Molecule:**dna polymerase iii polc-type; **PDBTitle:** crystal structure of a polc-type dna polymerase iii2 exonuclease domain from thermotoga maritima
39	c2is3B_	Alignment	not modelled	95.5	24	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**ribonuclease t; **PDBTitle:** crystal structure of escherichia coli rnase t
40	c3tr8A_	Alignment	not modelled	95.4	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**oligoribonuclease; **PDBTitle:** structure of an oligoribonuclease (orn) from coxiella burnetii
41	d1w0ha_	Alignment	not modelled	95.4	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
42	d2py5a1	Alignment	not modelled	95.3	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
43	d2igia1	Alignment	not modelled	94.6	20	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
44	d2hhva1	Alignment	not modelled	94.3	11	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
45	d3b6oa1	Alignment	not modelled	94.3	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
46	c2xriA_	Alignment	not modelled	93.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**eri1 exoribonuclease 3; **PDBTitle:** crystal structure of human eri1 exoribonuclease 3
47	c2gbzA_	Alignment	not modelled	93.6	17	**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
48	c4ktqA_	Alignment	not modelled	93.3	20	**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
49	d1j9aa_	Alignment	not modelled	93.2	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
50	d2hbka2	Alignment	not modelled	92.4	21	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
51	c1yt3A_	Alignment	not modelled	92.2	14	**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
52	c2hbkA_	Alignment	not modelled	90.8	21	**PDB header:**hydrolase, gene regulation **Chain:** A: **PDB Molecule:**exosome complex exonuclease rrp6; **PDBTitle:** structure of the yeast nuclear exosome component, rrp6p,2 reveals an interplay between the active site and the hrdc3 domain; protein in complex with mn
53	d1vk0a_	Alignment	not modelled	88.8	16	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**DnaQ-like 3'-5' exonuclease
54	c3ikmD_	Alignment	not modelled	80.1	21	**PDB header:**transferase **Chain:** D: **PDB Molecule:**dna polymerase subunit gamma-1; **PDBTitle:** crystal structure of human mitochondrial dna polymerase2 holoenzyme
55	c1zbhA_	Alignment	not modelled	78.7	17	**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

56	c3cymA_	Alignment	not modelled	69.9	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein bad_0989; **PDBTitle:** crystal structure of protein bad_0989 from bifidobacterium2 adolescentis
57	c1zbuB_	Alignment	not modelled	62.0	17	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**3'-5' exonuclease eri1; **PDBTitle:** crystal structure of full-length 3'-exonuclease
58	c3sahA_	Alignment	not modelled	52.6	16	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**exosome component 10; **PDBTitle:** crystal structure of the human rrp6 catalytic domain with y436a2 mutation in the catalytic site
59	c3fniA_	Alignment	not modelled	49.1	11	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative diflavin flavoprotein a 3; **PDBTitle:** crystal structure of a diflavin flavoprotein a3 (all3895) from nostoc2 sp., northeast structural genomics consortium target nsr431a
60	d1uoca_	Alignment	not modelled	44.0	17	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
61	c1q7tA_	Alignment	not modelled	30.5	18	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**hypothetical protein rv1170; **PDBTitle:** rv1170 (mshb) from mycobacterium tuberculosis
62	c3cm6A_	Alignment	not modelled	27.0	17	**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
63	d1q74a_	Alignment	not modelled	26.9	17	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
64	d1n71a_	Alignment	not modelled	21.8	23	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
65	c3f8kA_	Alignment	not modelled	18.0	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein acetyltransferase; **PDBTitle:** crystal structure of protein acetyltransferase (pat) from2 sulfolobus solfataricus
66	d1wdua_	Alignment	not modelled	17.5	27	**Fold:**DNase I-like **Superfamily:**DNase I-like **Family:**DNase I-like
67	c1g2cS_	Alignment	not modelled	17.1	38	**PDB header:**viral protein **Chain:** S: **PDB Molecule:**fusion protein (f); **PDBTitle:** human respiratory syncytial virus fusion protein core
68	d1bo4a_	Alignment	not modelled	16.4	26	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
69	c1bo4A_	Alignment	not modelled	16.4	26	**PDB header:**transferase **Chain:** A: **PDB Molecule:**protein (serratia marcescens aminoglycoside-3-n- **PDBTitle:** crystal structure of a gcn5-related n-acetyltransferase: serratia2 marescens aminoglycoside 3-n-acetyltransferase
70	c3zquA_	Alignment	not modelled	16.3	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**probable aromatic acid decarboxylase; **PDBTitle:** structure of a probable aromatic acid decarboxylase
71	d1uana_	Alignment	not modelled	16.0	20	**Fold:**LmbE-like **Superfamily:**LmbE-like **Family:**LmbE-like
72	c2ixdB_	Alignment	not modelled	15.4	8	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**lmbe-related protein; **PDBTitle:** crystal structure of the putative deacetylase bc1534 from2 bacilus cereus
73	d1gx1a_	Alignment	not modelled	15.1	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
74	c3gjzB_	Alignment	not modelled	15.0	16	**PDB header:**immune system **Chain:** B: **PDB Molecule:**microcin immunity protein mccf; **PDBTitle:** crystal structure of microcin immunity protein mccf from bacillus2 anthracis str. ames
75	d1iv3a_	Alignment	not modelled	14.1	18	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
76	d1t0aa_	Alignment	not modelled	13.8	22	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
77	d1vh8a_	Alignment	not modelled	13.6	16	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
78	c3re3B_	Alignment	not modelled	13.5	19	**PDB header:**lyase **Chain:** B: **PDB Molecule:**2-c-methyl-d-erythritol 2,4-cyclodiphosphate synthase; **PDBTitle:** crystal structure of 2-c-methyl-d-erythritol 2,4-cyclodiphosphate2 synthase from francisella tularensis
79	d1y9wa1	Alignment	not modelled	13.4	22	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
80	d1rfza_	Alignment	not modelled	13.0	39	**Fold:**YutG-like **Superfamily:**YutG-like **Family:**YutG-like
81	c3i9sA_	Alignment	not modelled	12.3	11	**PDB header:**transferase **Chain:** A: **PDB Molecule:**integron cassette protein; **PDBTitle:** structure from the mobile metagenome of v.cholerae. integron2 cassette protein vch_cass6
						PDB header:circadian clock protein

82	c2e1nA_	Alignment	not modelled	12.1	7	**Chain:** A: **PDB Molecule:**pex; **PDBTitle:** crystal structure of the cyanobacterium circadian clock modifier pex
83	d1o6ca_	Alignment	not modelled	12.0	15	**Fold:**UDP-Glycosyltransferase/glycogen phosphorylase **Superfamily:**UDP-Glycosyltransferase/glycogen phosphorylase **Family:**UDP-N-acetylglucosamine 2-epimerase
84	c2wvmA_	Alignment	not modelled	11.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**mannosyl-3-phosphoglycerate synthase; **PDBTitle:** h309a mutant of mannosyl-3-phosphoglycerate synthase from2 thermus thermophilus hb27 in complex with3 gdp-alpha-d-mannose and mg(ii)
85	c2xppB_	Alignment	not modelled	11.6	75	**PDB header:**transcription **Chain:** B: **PDB Molecule:**chromatin structure modulator; **PDBTitle:** crystal structure of a spt6-iws1(spn1) complex from2 encephalitozoon cuniculi, form iii
86	d1w55a2	Alignment	not modelled	11.5	14	**Fold:**Bacillus chorismate mutase-like **Superfamily:**IpsF-like **Family:**IpsF-like
87	c3bf4B_	Alignment	not modelled	11.1	26	**PDB header:**unknown function **Chain:** B: **PDB Molecule:**ethyl tert-butyl ether degradation ethd protein; **PDBTitle:** crystal structure of an ethd-like protein (reut_b5694) from ralstonia2 eutropha jmp134 at 2.10 a resolution
88	d1s3za_	Alignment	not modelled	11.0	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
89	c3tebA_	Alignment	not modelled	10.6	29	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**endonuclease/exonuclease/phosphatase; **PDBTitle:** endonuclease/exonuclease/phosphatase family protein from leptotrichia2 buccalis c-1013-b
90	d1q2ya_	Alignment	not modelled	10.1	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
91	d1ghea_	Alignment	not modelled	9.9	15	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
92	d1r57a_	Alignment	not modelled	9.9	10	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT
93	c3hlyA_	Alignment	not modelled	9.8	13	**PDB header:**flavoprotein **Chain:** A: **PDB Molecule:**flavodoxin-like domain; **PDBTitle:** crystal structure of the flavodoxin-like domain from2 synechococcus sp q5mzp6_synp6 protein. northeast structural3 genomics consortium target snr135d.
94	d1a6db2	Alignment	not modelled	9.7	11	**Fold:**The "swivelling" beta/beta/alpha domain **Superfamily:**GroEL apical domain-like **Family:**Group II chaperonin (CCT, TRIC), apical domain
95	c3qd8M_	Alignment	not modelled	9.7	11	**PDB header:**metal binding protein **Chain:** M: **PDB Molecule:**probable bacterioferritin bfrb; **PDBTitle:** crystal structure of mycobacterium tuberculosis bfrb
96	d2auna2	Alignment	not modelled	9.5	22	**Fold:**Flavodoxin-like **Superfamily:**Class I glutamine amidotransferase-like **Family:**LD-carboxypeptidase A N-terminal domain-like
97	d2i09a2	Alignment	not modelled	8.9	14	**Fold:**DeoB insert domain-like **Superfamily:**DeoB insert domain-like **Family:**DeoB insert domain-like
98	d2d5ra1	Alignment	not modelled	8.9	23	**Fold:**Ribonuclease H-like motif **Superfamily:**Ribonuclease H-like **Family:**CAF1-like ribonuclease
99	d2beia1	Alignment	not modelled	8.5	11	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**N-acetyl transferase, NAT