











Phyre2

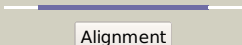
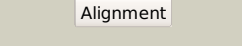
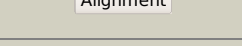
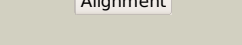
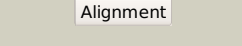
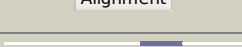
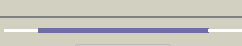
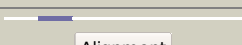
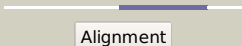

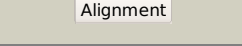
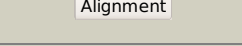
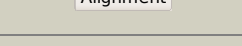
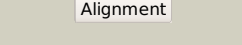
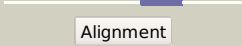

Email	mdejesus@rockefeller.edu
Description	RVBD1976c (-)_2218852_2219259
Date	Mon Aug 5 13:25:07 BST 2019
Unique Job ID	30ff82052bdf82f

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5mq9A_	 Alignment		100.0	24	PDB header: translation Chain: A: PDB Molecule: uncharacterized protein yacp; PDBTitle: crystal structure of rae1 (yacp) from bacillus subtilis (w164l mutant)
2	d1cmwa2	 Alignment		97.6	25	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
3	c1cmwA_	 Alignment		97.4	25	PDB header: transferase Chain: A: PDB Molecule: protein (dna polymerase i); PDBTitle: crystal structure of taq dna-polymerase shows a new orientation for2 the structure-specific nuclease domain
4	c3zddA_	 Alignment		97.4	23	PDB header: hydrolase/dna Chain: A: PDB Molecule: protein xni; PDBTitle: structure of e. coli exoix in complex with the palindromic 5ov62 oligonucleotide and potassium
5	c6c34A_	 Alignment		97.3	18	PDB header: dna binding protein Chain: A: PDB Molecule: 5'-3' exonuclease; PDBTitle: mycobacterium smegmatis dna flap endonuclease mutant d125n
6	c1ut8B_	 Alignment		97.2	15	PDB header: hydrolase Chain: B: PDB Molecule: exodeoxyribonuclease; PDBTitle: divalent metal ions (zinc) bound to t5 5'-exonuclease
7	d1tfra2	 Alignment		97.0	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
8	d1xo1a2	 Alignment		96.9	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
9	c3v32B_	 Alignment		95.9	23	PDB header: hydrolase Chain: B: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 n-terminal conserved domain
10	c3v33A_	 Alignment		95.6	20	PDB header: hydrolase Chain: A: PDB Molecule: ribonuclease zc3h12a; PDBTitle: crystal structure of mcpi1 conserved domain with zinc-finger motif
11	c3ix7A_	 Alignment		94.6	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ttha0540; PDBTitle: crystal structure of a domain of functionally unknown protein from2 thermus thermophilus hb8

12	c2izoA_	Alignment		94.4	16	PDB header: hydrolase Chain: A; PDB Molecule: flap structure-specific endonuclease; PDBTitle: structure of an archaeal pcna1-pcna2-fen1 complex
13	d1ul1x2	Alignment		93.7	18	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
14	c2hwwC_	Alignment		93.1	20	PDB header: rna binding protein Chain: C; PDB Molecule: telomerase-binding protein est1a; PDBTitle: structure of pin domain of human smg6
15	c1b43A_	Alignment		92.2	31	PDB header: transferase Chain: A; PDB Molecule: protein (fen-1); PDBTitle: fen-1 from p. furiosus
16	d1o4wa_	Alignment		91.9	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
17	c5jppd_	Alignment		91.7	33	PDB header: ribosome Chain: D; PDB Molecule: wd40 domain proteins; PDBTitle: cryo-em structure of the 90s pre-ribosome
18	c1a77A_	Alignment		90.5	25	PDB header: 5'-3' exo/endo nuclease Chain: A; PDB Molecule: flap endonuclease-1 protein; PDBTitle: flap endonuclease-1 from methanococcus jannaschii
19	c2ihnA_	Alignment		90.3	18	PDB header: hydrolase/dna Chain: A; PDB Molecule: ribonuclease h; PDBTitle: co-crystal of bacteriophage t4 rnase h with a fork dna2 substrate
20	c4wa8A_	Alignment		89.9	18	PDB header: hydrolase Chain: A; PDB Molecule: flap endonuclease 1; PDBTitle: methanopyrus kandleri fen-1 nuclease
21	c5yz4A_	Alignment	not modelled	89.2	34	PDB header: hydrolase Chain: A; PDB Molecule: rrna-processing protein fcf1; PDBTitle: structure of the pin domain endonuclease utp24
22	c3q8lA_	Alignment	not modelled	89.0	21	PDB header: hydrolase/dna Chain: A; PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of human flap endonuclease fen1 (wt) in complex with2 substrate 5'-flap dna, sm3+, and k+
23	c1ul1Y_	Alignment	not modelled	88.0	18	PDB header: hydrolase/dna binding protein Chain: Y; PDB Molecule: flap endonuclease-1; PDBTitle: crystal structure of the human fen1-pcna complex
24	c4mj7B_	Alignment	not modelled	88.0	22	PDB header: rna binding protein Chain: B; PDB Molecule: rrna-processing protein utp23; PDBTitle: crystal structure of the pin domain of saccharomyces cerevisiae utp23
25	c1rxvA_	Alignment	not modelled	87.0	28	PDB header: hydrolase/dna Chain: A; PDB Molecule: flap structure-specific endonuclease; PDBTitle: crystal structure of a. fulgidus fen-1 bound to dna
26	c3i8oA_	Alignment	not modelled	79.9	18	PDB header: rna binding protein Chain: A; PDB Molecule: kh domain-containing protein mj1533; PDBTitle: a domain of a functionally unknown protein from methanocaldococcus2 jannaschii dsm 2661.
27	c4q0rB_	Alignment	not modelled	65.2	19	PDB header: hydrolase/dna Chain: B; PDB Molecule: dna repair protein rad2; PDBTitle: the catalytic core of rad2 (complex i)
28	c3qeaZ_	Alignment	not modelled	61.3	14	PDB header: hydrolase/dna Chain: Z; PDB Molecule: exonuclease 1; PDBTitle: crystal structure of human exonuclease 1 exo1 (wt) in complex with dna2 (complex ii)
						Fold: PIN domain-like

29	d1a77a2	Alignment	not modelled	58.6	26	Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
30	c5f4hF	Alignment	not modelled	55.2	13	PDB header: hydrolase Chain: F: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
31	d1y82a1	Alignment	not modelled	50.1	14	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
32	c2zktB	Alignment	not modelled	48.4	17	PDB header: isomerase Chain: B: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: structure of ph0037 protein from pyrococcus horikoshii
33	c5ywwA	Alignment	not modelled	45.6	13	PDB header: hydrolase Chain: A: PDB Molecule: nucleotide binding protein pinc; PDBTitle: archael ruvb-like holiday junction helicase
34	d1o98a2	Alignment	not modelled	44.3	20	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, catalytic domain
35	d1rxwa2	Alignment	not modelled	40.6	21	Fold: PIN domain-like Superfamily: PIN domain-like Family: 5' to 3' exonuclease catalytic domain
36	d1pkla3	Alignment	not modelled	27.1	24	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
37	c5t9jB	Alignment	not modelled	26.7	23	PDB header: hydrolase Chain: B: PDB Molecule: flap endonuclease gen homolog 1; PDBTitle: crystal structure of human gen1 in complex with holliday junction dna2 in the upper interface
38	c2ayxA	Alignment	not modelled	24.4	10	PDB header: transferase Chain: A: PDB Molecule: sensor kinase protein rcsc; PDBTitle: solution structure of the e.coli rcsc c-terminus (residues2700-949) containing linker region and phosphoreceiver3 domain
39	c3m8yC	Alignment	not modelled	24.2	13	PDB header: isomerase Chain: C: PDB Molecule: phosphopentomutase; PDBTitle: phosphopentomutase from bacillus cereus after glucose-1,6-bisphosphate2 activation
40	c2i09A	Alignment	not modelled	23.6	13	PDB header: isomerase Chain: A: PDB Molecule: phosphopentomutase; PDBTitle: crystal structure of putative phosphopentomutase from streptococcus2 mutans
41	c3qoyA	Alignment	not modelled	22.4	15	PDB header: ribosomal protein Chain: A: PDB Molecule: 50s ribosomal protein l1; PDBTitle: crystal structure of ribosomal protein l1 from aquifex aeolicus
42	c3hdvB	Alignment	not modelled	20.2	18	PDB header: transcription regulator Chain: B: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator receiver protein from2 pseudomonas putida
43	d1liua3	Alignment	not modelled	20.1	15	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
44	d1e0ta3	Alignment	not modelled	19.6	21	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
45	c3lxqB	Alignment	not modelled	19.3	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein vp1736; PDBTitle: the crystal structure of a protein in the alkaline phosphatase2 superfamily from vibrio parahaemolyticus to 1.95a
46	c4o1iA	Alignment	not modelled	19.2	13	PDB header: transcription regulator Chain: A: PDB Molecule: transcriptional regulatory protein; PDBTitle: crystal structure of the regulatory domain of mtbglNr
47	d2g50a3	Alignment	not modelled	19.1	18	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
48	c4my4A	Alignment	not modelled	19.0	15	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of phosphoglycerate mutase from staphylococcus2 aureus.
49	d1a3xa3	Alignment	not modelled	17.7	18	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
50	d1yioa2	Alignment	not modelled	17.4	20	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
51	c3tb4A	Alignment	not modelled	16.9	15	PDB header: hydrolase Chain: A: PDB Molecule: vibriobactin-specific isochorismatase; PDBTitle: crystal structure of the isc domain of vibb
52	c6m8oA	Alignment	not modelled	16.0	14	PDB header: signaling protein Chain: A: PDB Molecule: dna-binding response regulator; PDBTitle: crystal structure of the receiver domain of lytr from staphylococcus2 aureus
53	c1o98A	Alignment	not modelled	16.0	21	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent PDBTitle: 1.4a crystal structure of phosphoglycerate mutase from2 bacillus stearothermophilus complexed with3 2-phosphoglycerate
54	d1p49a	Alignment	not modelled	15.7	17	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
55	c3bboD	Alignment	not modelled	15.6	20	PDB header: ribosome Chain: D: PDB Molecule: ribosomal protein l1; PDBTitle: homology model for the spinach chloroplast 50s subunit fitted to 9.4a2 cryo-em map of the 70s chlororibosome

56	c5t3yA	 Alignment	not modelled	15.5	25	PDB header: signaling protein Chain: A: PDB Molecule: two-component system response regulator; PDBTitle: solution structure of response regulator protein from burkholderia2 multivorans
57	c3lteH	 Alignment	not modelled	15.5	16	PDB header: transcription Chain: H: PDB Molecule: response regulator; PDBTitle: crystal structure of response regulator (signal receiver domain) from2 bermanella marisubri
58	d1pcva	 Alignment	not modelled	15.4	57	Fold: Osmotin, thaumatin-like protein Superfamily: Osmotin, thaumatin-like protein Family: Osmotin, thaumatin-like protein
59	d1v96a1	 Alignment	not modelled	15.3	17	Fold: PIN domain-like Superfamily: PIN domain-like Family: PIN domain
60	c3oryA	 Alignment	not modelled	15.1	21	PDB header: hydrolase Chain: A: PDB Molecule: flap endonuclease 1; PDBTitle: crystal structure of flap endonuclease 1 from hyperthermophilic2 archaeon desulfurococcus amylolyticus
61	c3igzB	 Alignment	not modelled	15.0	21	PDB header: isomerase Chain: B: PDB Molecule: cofactor-independent phosphoglycerate mutase; PDBTitle: crystal structures of leishmania mexicana phosphoglycerate2 mutase at low cobalt concentration
62	c2gyc2	 Alignment	not modelled	15.0	22	PDB header: ribosome Chain: 2: PDB Molecule: 50s ribosomal protein l1; PDBTitle: structure of the 50s subunit of a secm-stalled e. coli ribosome2 complex obtained by fitting atomic models for rna and protein3 components into cryo-em map emd-1143
63	d1d8wa	 Alignment	not modelled	14.7	37	Fold: TIM beta/alpha-barrel Superfamily: Xylose isomerase-like Family: L-rhamnose isomerase
64	d1du5a	 Alignment	not modelled	14.4	57	Fold: Osmotin, thaumatin-like protein Superfamily: Osmotin, thaumatin-like protein Family: Osmotin, thaumatin-like protein
65	d1auka	 Alignment	not modelled	14.0	16	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
66	c2rdmB	 Alignment	not modelled	13.9	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein from2 sinorhizobium medicae wsm419
67	c2ahnA	 Alignment	not modelled	13.7	57	PDB header: allergen Chain: A: PDB Molecule: thaumatin-like protein; PDBTitle: high resolution structure of a cherry allergen pru av 2
68	c3hheA	 Alignment	not modelled	13.5	10	PDB header: isomerase Chain: A: PDB Molecule: ribose-5-phosphate isomerase a; PDBTitle: crystal structure of ribose-5-phosphate isomerase a from bartonella2 henselae
69	d1fsua	 Alignment	not modelled	12.8	8	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
70	d1hdha	 Alignment	not modelled	12.7	25	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Arylsulfatase
71	c5cnqA	 Alignment	not modelled	12.3	17	PDB header: replication Chain: A: PDB Molecule: nuclease-like protein; PDBTitle: crystal structure of the holliday junction-resolving enzyme gen1 (wt)2 in complex with product dna, mg2+ and mn2+ ions
72	c5vpuA	 Alignment	not modelled	12.0	17	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: crystal structure of 2,3-bisphosphoglycerate-independent2 phosphoglycerate mutase bound to 3-phosphoglycerate, from3 acinetobacter baumannii
73	d1auna	 Alignment	not modelled	11.8	43	Fold: Osmotin, thaumatin-like protein Superfamily: Osmotin, thaumatin-like protein Family: Osmotin, thaumatin-like protein
74	c3qtgA	 Alignment	not modelled	11.8	11	PDB header: transferase Chain: A: PDB Molecule: pyruvate kinase; PDBTitle: crystal structure of pyruvate kinase from pyrobaculum aerophilum
75	c3p14C	 Alignment	not modelled	11.6	41	PDB header: isomerase Chain: C: PDB Molecule: l-rhamnose isomerase; PDBTitle: crystal structure of l-rhamnose isomerase with a novel high thermo-2 stability from bacillus halodurans
76	c5k4pA	 Alignment	not modelled	11.6	20	PDB header: transferase Chain: A: PDB Molecule: probable phosphatidylethanolamine transferase mcr-1; PDBTitle: catalytic domain of mcr-1 phosphoethanolamine transferase
77	c5kgmA	 Alignment	not modelled	11.6	25	PDB header: isomerase Chain: A: PDB Molecule: 2,3-bisphosphoglycerate-independent phosphoglycerate PDBTitle: 2.95a resolution structure of apo independent phosphoglycerate mutase2 from c. elegans (monoclinic form)
78	c5fgnA	 Alignment	not modelled	11.5	20	PDB header: transferase,hydrolase Chain: A: PDB Molecule: lipooligosaccharide phosphoethanolamine transferase a; PDBTitle: integral membrane protein lipooligosaccharide phosphoethanolamine2 transferase a (epta) from neisseria meningitidis
79	c6a82A	 Alignment	not modelled	11.5	32	PDB header: transferase Chain: A: PDB Molecule: phosphoethanolamine transferase eptc; PDBTitle: crystal structure of the c-terminal periplasmic domain of eceptc from2 escherichia coli

80	c5i5fA_	Alignment	not modelled	11.3	17	PDB header: membrane protein Chain: A: PDB Molecule: inner membrane protein yejm; PDBTitle: salmonella global domain 191
81	d1vh3a_	Alignment	not modelled	11.3	14	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: Cytidylyltransferase
82	c3ed4A_	Alignment	not modelled	11.2	21	PDB header: transferase Chain: A: PDB Molecule: arylsulfatase; PDBTitle: crystal structure of putative arylsulfatase from escherichia coli
83	d2i09a1	Alignment	not modelled	11.0	13	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: DeoB catalytic domain-like
84	d2a9pa1	Alignment	not modelled	10.9	9	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
85	d1l7ba_	Alignment	not modelled	10.8	14	Fold: BRCT domain Superfamily: BRCT domain Family: DNA ligase
86	c2w8dB_	Alignment	not modelled	10.4	20	PDB header: transferase Chain: B: PDB Molecule: processed glycerol phosphate lipoteichoic acid synthase 2; PDBTitle: distinct and essential morphogenic functions for wall-and2 lipo-teichoic acids in bacillus subtilis
87	c3b5qB_	Alignment	not modelled	9.9	17	PDB header: hydrolase Chain: B: PDB Molecule: putative sulfatase yidj; PDBTitle: crystal structure of a putative sulfatase (np_810509.1) from2 bacteroides thetaiotaomicron vpi-5482 at 2.40 a resolution
88	c1ew2A_	Alignment	not modelled	9.9	28	PDB header: hydrolase Chain: A: PDB Molecule: phosphatase; PDBTitle: crystal structure of a human phosphatase
89	d1zeda1	Alignment	not modelled	9.9	28	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
90	c4qpjC_	Alignment	not modelled	9.8	11	PDB header: signaling protein/dna binding protein Chain: C: PDB Molecule: cell cycle response regulator ctra; PDBTitle: 2.7 angstrom structure of a phosphotransferase in complex with a2 receiver domain
91	c1t5aB_	Alignment	not modelled	9.8	18	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase, m2 isozyme; PDBTitle: human pyruvate kinase m2
92	c5jyuA_	Alignment	not modelled	9.5	14	PDB header: sigaling protein Chain: A: PDB Molecule: two-component sensor histidine kinase; PDBTitle: nmr structure of pseudo receiver domain of cika from2 thermosynechococcus elongatus
93	c3q3qA_	Alignment	not modelled	9.4	21	PDB header: hydrolase Chain: A: PDB Molecule: alkaline phosphatase; PDBTitle: crystal structure of spap: an novel alkaline phosphatase from2 bacterium sphingomonas sp. strain bsar-1
94	c3ktoA_	Alignment	not modelled	9.1	12	PDB header: transcription regulator Chain: A: PDB Molecule: response regulator receiver protein; PDBTitle: crystal structure of response regulator receiver protein2 from pseudoalteromonas atlantica
95	c3a52A_	Alignment	not modelled	9.1	24	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkaline phosphatase from2 psychrophile shewanella sp.
96	d1ad2a_	Alignment	not modelled	9.1	12	Fold: Ribosomal protein L1 Superfamily: Ribosomal protein L1 Family: Ribosomal protein L1
97	c2l69A_	Alignment	not modelled	9.0	25	PDB header: de novo protein Chain: A: PDB Molecule: rossmann 2x3 fold protein; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
98	c4uopB_	Alignment	not modelled	9.0	16	PDB header: transferase Chain: B: PDB Molecule: lipoteichoic acid primase; PDBTitle: crystal structure of the lipoteichoic acid synthase ltap from listeria2 monocytogenes
99	c4fdiA_	Alignment	not modelled	8.9	25	PDB header: hydrolase Chain: A: PDB Molecule: n-acetylgalactosamine-6-sulfatase; PDBTitle: the molecular basis of mucopolysaccharidosis iv a