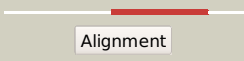

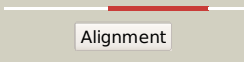

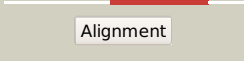
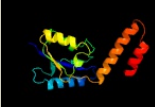
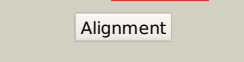

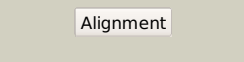

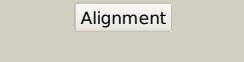

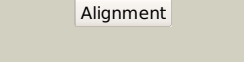

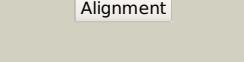

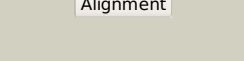

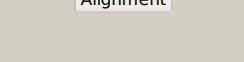

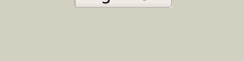



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2886c_(-)_3195555_3196442
Date	Thu Aug 8 16:20:03 BST 2019
Unique Job ID	c53f88c74d8c42eb

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6dgbA_	 Alignment		100.0	54	PDB header: hydrolase Chain: A: PDB Molecule: is607 family transposase is1535; PDBTitle: crystal structure of the c-terminal catalytic domain of is1535 tnpa,2 an is607-like serine recombinase
2	c3lhkA_	 Alignment		99.9	24	PDB header: dna binding protein Chain: A: PDB Molecule: putative dna binding protein mj0014; PDBTitle: crystal structure of putative dna binding protein from2 methanocaldococcus jannaschii.
3	c3lhfC_	 Alignment		99.9	36	PDB header: recombination Chain: C: PDB Molecule: serine recombinase; PDBTitle: the crystal structure of a serine recombinase from sulfolobus2 solfataricus to 2.3a
4	c6dgcA_	 Alignment		99.9	32	PDB header: hydrolase Chain: A: PDB Molecule: isc1926 tnpa c-terminal catalytic domain; PDBTitle: crystal structure of the c-terminal catalytic domain of isc1926 tnpa,2 an is607-like serine recombinase
5	d1gdta2	 Alignment		99.8	23	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
6	c3bvpB_	 Alignment		99.8	19	PDB header: recombination Chain: B: PDB Molecule: tp901-1 integrase; PDBTitle: crystal structure of the n-terminal catalytic domain of tp901-12 integrase
7	c3g13B_	 Alignment		99.8	15	PDB header: recombination Chain: B: PDB Molecule: putative conjugative transposon recombinase; PDBTitle: crystal structure of putative conjugative transposon recombinase from2 clostridium difficile
8	c3guvA_	 Alignment		99.8	17	PDB header: recombination Chain: A: PDB Molecule: site-specific recombinase, resolvase family protein; PDBTitle: crystal structure of a resolvase family site-specific recombinase from2 streptococcus pneumoniae
9	c2gm4B_	 Alignment		99.8	24	PDB header: recombination, dna Chain: B: PDB Molecule: transposon gamma-delta resolvase; PDBTitle: an activated, tetrameric gamma-delta resolvase: hin chimaera bound to2 cleaved dna
10	d2gm4a2	 Alignment		99.8	24	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
11	c2mhcA_	 Alignment		99.7	19	PDB header: recombination Chain: A: PDB Molecule: tnpx; PDBTitle: nmr structure of the catalytic domain of the large serine resolvase2 tnpX

12	c4bqqB_	Alignment		99.7	17	PDB header: hydrolase Chain: B: PDB Molecule: integrase; PDBTitle: protein crystal structure of the n-terminal and recombinase domains of2 the streptomyces temperate phage serine recombinase, fc31 integrase.
13	c3ploX_	Alignment		99.6	17	PDB header: recombination Chain: X: PDB Molecule: dna-invertase; PDBTitle: crystal structure of the fis-independent mutant of gin
14	d2rsla_	Alignment		99.6	24	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
15	c3pkzK_	Alignment		99.6	24	PDB header: recombination Chain: K: PDB Molecule: recombinase sin; PDBTitle: structural basis for catalytic activation of a serine recombinase
16	c2r0qF_	Alignment		99.5	21	PDB header: recombination/dna Chain: F: PDB Molecule: putative transposon tn552 dna-invertase bin3; PDBTitle: crystal structure of a serine recombinase- dna regulatory2 complex
17	c4m6fA_	Alignment		99.5	20	PDB header: hydrolase/dna Chain: A: PDB Molecule: dna-invertase; PDBTitle: dimer of the g-segment invertase bound to a dna substrate
18	d1hx7a_	Alignment		99.5	26	Fold: Resolvase-like Superfamily: Resolvase-like Family: gamma,delta resolvase, catalytic domain
19	d1pm6a_	Alignment		82.7	28	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
20	d1rh6a_	Alignment		73.5	30	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: Excisionase-like
21	d1zl0a2	Alignment	not modelled	70.5	17	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
22	c4i92A_	Alignment	not modelled	66.5	35	PDB header: viral protein Chain: A: PDB Molecule: receptor binding protein; PDBTitle: structure of the rbp from lactococcal phage 1358 in complex with 22 glcnac molecules
23	c4j2nB_	Alignment	not modelled	66.2	19	PDB header: viral protein Chain: B: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
24	c4j2nA_	Alignment	not modelled	66.1	19	PDB header: viral protein Chain: A: PDB Molecule: gp37; PDBTitle: crystal structure of mycobacteriophage pukovnik xis
25	d1ewqa2	Alignment	not modelled	62.0	15	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: ABC transporter ATPase domain-like
26	c6r6kB_	Alignment	not modelled	51.6	18	PDB header: protein transport Chain: B: PDB Molecule: abc transporter substrate-binding protein; PDBTitle: structure of a fpvc mutant from pseudomonas aeruginosa
27	c3gp4B_	Alignment	not modelled	49.9	24	PDB header: transcription regulator Chain: B: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of putative merr family transcriptional regulator2 from listeria monocytogenes
28	c3ndnC_	Alignment	not modelled	49.7	20	PDB header: lyase Chain: C: PDB Molecule: o-succinylhomoserine sulfhydrylase; PDBTitle: crystal structure of o-succinylhomoserine sulfhydrylase from2 mycobacterium tuberculosis covalently bound to pyridoxal-5-phosphate
29	d2bccqa2	Alignment	not modelled	49.1	29	Fold: SAM domain-like Superfamily: PsbU/PolX domain-like

						Family: DNA polymerase beta-like, second domain
30	d1jmsa3	Alignment	not modelled	47.4	43	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
31	c2nvwB_	Alignment	not modelled	45.5	9	PDB header: transcription Chain: B: PDB Molecule: galactose/lactose metabolism regulatory protein PDBTitle: crystal sctecture of transcriptional regulator gal80p from2 kluveromyces lactis
32	c5i44E_	Alignment	not modelled	44.7	24	PDB header: dna binding protein/dna Chain: E: PDB Molecule: chromosome-anchoring protein raca; PDBTitle: structure of raca-dna complex; p21 form
33	c4yztA_	Alignment	not modelled	44.6	20	PDB header: hydrolase Chain: A: PDB Molecule: cellulose hydrolase; PDBTitle: crystal structure of a tri-modular gh5 (subfamily 4) endo-beta-1, 4-2 glucanase from bacillus licheniformis complexed with celotetraose
34	d2fmpa2	Alignment	not modelled	42.5	21	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
35	c4e5sC_	Alignment	not modelled	42.3	15	PDB header: hydrolase Chain: C: PDB Molecule: mcclike protein (ba_5613); PDBTitle: crystal structure of mcclike protein (ba_5613) from bacillus2 anthracis str. ames
36	d2auna2	Alignment	not modelled	41.7	14	Fold: Flavodoxin-like Superfamily: Class I glutamine amidotransferase-like Family: LD-carboxypeptidase A N-terminal domain-like
37	c3hjtB_	Alignment	not modelled	41.3	11	PDB header: cell adhesion, transport protein Chain: B: PDB Molecule: lmb; PDBTitle: structure of laminin binding protein (lmb) of streptococcus agalactiae2 a bifunctional protein with adhesin and metal transporting activity
38	c1nvmB_	Alignment	not modelled	41.2	21	PDB header: lyase/oxidoreductase Chain: B: PDB Molecule: acetaldehyde dehydrogenase (acylating); PDBTitle: crystal structure of a bifunctional aldolase-dehydrogenase :2 sequestering a reactive and volatile intermediate
39	d2vana1	Alignment	not modelled	41.0	21	Fold: SAM domain-like Superfamily: PsbU/PoIX domain-like Family: DNA polymerase beta-like, second domain
40	c1zrsB_	Alignment	not modelled	40.5	16	PDB header: hydrolase Chain: B: PDB Molecule: hypothetical protein; PDBTitle: wild-type ld-carboxypeptidase
41	c5d88A_	Alignment	not modelled	39.9	20	PDB header: hydrolase Chain: A: PDB Molecule: predicted protease of the collagenase family; PDBTitle: the structure of the u32 peptidase mk0906
42	c3crnA_	Alignment	not modelled	39.0	12	PDB header: signaling protein Chain: A: PDB Molecule: response regulator receiver domain protein, chey-like; PDBTitle: crystal structure of response regulator receiver domain protein (chey-2 like) from methanospirillum hungatei jf-1
43	d2ctza1	Alignment	not modelled	38.4	16	Fold: PLP-dependent transferase-like Superfamily: PLP-dependent transferases Family: Cystathionine synthase-like
44	d1v6ta_	Alignment	not modelled	36.8	26	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
45	d1pq4a_	Alignment	not modelled	36.3	10	Fold: Chelatase-like Superfamily: "Helical backbone" metal receptor Family: TroA-like
46	d1t6ca1	Alignment	not modelled	36.2	18	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
47	c5ijgB_	Alignment	not modelled	35.3	13	PDB header: hydrolase Chain: B: PDB Molecule: cys/met metabolism pyridoxal-phosphate-dependent enzyme; PDBTitle: crystal structure of o-acetylhomoserine sulfhydrylase from brucella2 melitensis at 2.0 a resolution
48	c1z4hA_	Alignment	not modelled	35.0	21	PDB header: protein binding, dna binding protein Chain: A: PDB Molecule: tor inhibition protein; PDBTitle: the response regulator tori belongs to a new family of2 atypical excisionase
49	c6amaO_	Alignment	not modelled	34.9	21	PDB header: dna binding protein/dna Chain: O: PDB Molecule: putative dna-binding protein; PDBTitle: structure of s. coelicolor/s. venezuelae bldc-smea-ssfa complex to2 3.09 angstrom
50	d1u6za2	Alignment	not modelled	34.3	10	Fold: Ribonuclease H-like motif Superfamily: Actin-like ATPase domain Family: Ppx/GppA phosphatase
51	c5f1yA_	Alignment	not modelled	34.2	13	PDB header: hydrolase Chain: A: PDB Molecule: mccc family protein; PDBTitle: crystal structure of ba3275, the member of s66 family of serine2 peptidases
52	c4r24B_	Alignment	not modelled	33.2	14	PDB header: transcription/dna Chain: B: PDB Molecule: hth-type transcriptional regulator tnra; PDBTitle: complete dissection of b. subtilis nitrogen homeostatic circuitry
53	c1ng7A_	Alignment	not modelled	33.0	14	PDB header: viral protein Chain: A: PDB Molecule: genome polyprotein [core protein p3a]; PDBTitle: the solution structure of the soluble domain of poliovirus2 3a protein
54	d1ng7a_	Alignment	not modelled	33.0	14	Fold: Soluble domain of poliovirus core protein 3a Superfamily: Soluble domain of poliovirus core protein 3a Family: Soluble domain of poliovirus core protein 3a

55	c3cx3A_	Alignment	not modelled	32.9	11	PDB header: metal binding protein Chain: A: PDB Molecule: lipoprotein; PDBTitle: crystal structure analysis of the streptococcus pneumoniae2 adcaii protein
56	c4h1hB_	Alignment	not modelled	32.8	19	PDB header: hydrolase Chain: B: PDB Molecule: lmo1638 protein; PDBTitle: crystal structure of mccf homolog from listeria monocytogenes egd-e
57	c2vz4A_	Alignment	not modelled	32.4	17	PDB header: transcription Chain: A: PDB Molecule: hth-type transcriptional activator tipa; PDBTitle: the n-terminal domain of merr-like protein tipal bound to promoter dna
58	c2jmlA_	Alignment	not modelled	32.3	21	PDB header: transcription Chain: A: PDB Molecule: dna binding domain/transcriptional regulator; PDBTitle: solution structure of the n-terminal domain of cara repressor
59	d1nvmB2	Alignment	not modelled	30.4	30	Fold: FwdE/GAPDH domain-like Superfamily: Glyceraldehyde-3-phosphate dehydrogenase-like, C-terminal domain Family: GAPDH-like
60	d2dfaa1	Alignment	not modelled	29.9	29	Fold: 7-stranded beta/alpha barrel Superfamily: Glycoside hydrolase/deacetylase Family: LamB/YcsF-like
61	d1zga1	Alignment	not modelled	29.5	13	Fold: Flavodoxin-like Superfamily: CheY-like Family: CheY-related
62	d1q06a_	Alignment	not modelled	29.5	17	Fold: Putative DNA-binding domain Superfamily: Putative DNA-binding domain Family: DNA-binding N-terminal domain of transcription activators
63	c2cb1A_	Alignment	not modelled	29.1	21	PDB header: lyase Chain: A: PDB Molecule: o-acetyl homoserine sulfhydrylase; PDBTitle: crystal structure of o-acetyl homoserine sulfhydrylase2 from thermus thermophilus hb8, oah2.
64	c1ewrA_	Alignment	not modelled	28.7	14	PDB header: hydrolase Chain: A: PDB Molecule: dna mismatch repair protein muts; PDBTitle: crystal structure of taq muts
65	c2nmpC_	Alignment	not modelled	28.6	18	PDB header: lyase Chain: C: PDB Molecule: cystathionine gamma-lyase; PDBTitle: crystal structure of human cystathionine gamma lyase
66	c4s3rA_	Alignment	not modelled	28.4	6	PDB header: transferase Chain: A: PDB Molecule: 4-alpha-glucanotransferase; PDBTitle: amylomaltase malq from escherichia coli in complex with the pseudo-2 heptasaccharide acarviosine-glucose-acarbose
67	c3c2qA_	Alignment	not modelled	27.6	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of conserved putative lor/sdh protein2 from methanococcus maripaludis s2
68	c1y6uA_	Alignment	not modelled	27.5	7	PDB header: dna binding protein Chain: A: PDB Molecule: excisionase from transposon tn916; PDBTitle: the structure of the excisionase (xis) protein from2 conjugative transposon tn916 provides insights into the3 regulation of heterobivalent tyrosine recombinases
69	c2kg4A_	Alignment	not modelled	26.4	17	PDB header: cell cycle Chain: A: PDB Molecule: growth arrest and dna-damage-inducible protein gadd45 PDBTitle: three-dimensional structure of human gadd45alpha in solution by nmr
70	c2ps3A_	Alignment	not modelled	26.0	11	PDB header: metal transport Chain: A: PDB Molecule: high-affinity zinc uptake system protein znua; PDBTitle: structure and metal binding properties of znua, a periplasmic zinc2 transporter from escherichia coli
71	c2zq0B_	Alignment	not modelled	25.1	12	PDB header: hydrolase Chain: B: PDB Molecule: alpha-glucosidase (alpha-glucosidase sub); PDBTitle: crystal structure of sub complexed with acarbose
72	c6pdmA_	Alignment	not modelled	24.5	15	PDB header: transferase Chain: A: PDB Molecule: protein arginine n-methyltransferase 9; PDBTitle: crystal structure of human protein arginine methyltransferase 92 (prmt9)
73	c2ov3A_	Alignment	not modelled	24.4	14	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein component of an abc type zinc PDBTitle: crystal structure of 138-173 znua deletion mutant plus zinc bound
74	c3htkA_	Alignment	not modelled	23.9	32	PDB header: recombination/replication/ligase Chain: A: PDB Molecule: structural maintenance of chromosomes protein 5; PDBTitle: crystal structure of mms21 and smc5 complex
75	c5xfmD_	Alignment	not modelled	23.7	11	PDB header: hydrolase Chain: D: PDB Molecule: alpha-glucosidase; PDBTitle: crystal structure of beta-arabinopyranosidase
76	c3hh0C_	Alignment	not modelled	23.2	12	PDB header: transcription regulator Chain: C: PDB Molecule: transcriptional regulator, merr family; PDBTitle: crystal structure of a transcriptional regulator, merr family from2 bacillus cereus
77	c3bd1B_	Alignment	not modelled	23.0	33	PDB header: transcription Chain: B: PDB Molecule: cro protein; PDBTitle: structure of the cro protein from putative prophage element xfaso 1 in2 xylella fastidiosa strain ann-1
78	c8icZA_	Alignment	not modelled	22.8	21	PDB header: transferase/dna Chain: A: PDB Molecule: protein (dna polymerase beta (e.c.2.7.7.7)); PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7) complexed with2 seven base pairs of dna; soaked in the presence of datp3 (1 millimolar), mnc12 (5 millimolar), and lithium sulfate4 (75 millimolar)
79	c3q23A_	Alignment	not modelled	22.6	15	PDB header: hydrolase Chain: A: PDB Molecule: ld-carboxypeptidase a;

79	c3g23A	Alignment	not modelled	22.6	19	PDBTitle: crystal structure of a ld-carboxypeptidase a (saro_1426) from2 novosphingobium aromaticivorans dsm at 1.89 a resolution PDB header: oxidoreductase
80	c3oqbF	Alignment	not modelled	22.5	19	Chain: F: PDB Molecule: oxidoreductase; PDBTitle: crystal structure of putative oxidoreductase from bradyrhizobium2 japonicum usda 110
81	c3pp5A	Alignment	not modelled	22.3	45	PDB header: structural protein Chain: A: PDB Molecule: brk1; PDBTitle: high-resolution structure of the trimeric scar/wave complex precursor2 brk1
82	c2a93B	Alignment	not modelled	22.3	28	PDB header: leucine zippers Chain: B: PDB Molecule: c-myc-max heterodimeric leucine zipper; PDBTitle: nmr solution structure of the c-myc-max heterodimeric2 leucine zipper, 40 structures
83	c3gx1A	Alignment	not modelled	22.2	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: lin1832 protein; PDBTitle: crystal structure of a domain of lin1832 from listeria innocua
84	c6hmvB	Alignment	not modelled	21.7	10	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-d68 (fusion protein, lvvy mutant)
85	c1kdhA	Alignment	not modelled	21.3	27	PDB header: transferase/dna Chain: A: PDB Molecule: terminal deoxynucleotidyltransferase short PDBTitle: binary complex of murine terminal deoxynucleotidyl2 transferase with a primer single stranded dna
86	c3a24A	Alignment	not modelled	21.2	8	PDB header: hydrolase Chain: A: PDB Molecule: alpha-galactosidase; PDBTitle: crystal structure of bt1871 retaining glycosidase
87	d1s0ya	Alignment	not modelled	21.2	26	Fold: Tautomerase/MIF Superfamily: Tautomerase/MIF Family: 4-oxalocrotonate tautomerase-like
88	c6hqaK	Alignment	not modelled	21.2	29	PDB header: transcription Chain: K: PDB Molecule: subunit (61/68 kda) of tfiid and saga complexes; PDBTitle: molecular structure of promoter-bound yeast tfiid
89	c4r4eA	Alignment	not modelled	21.0	15	PDB header: transcription regulator/dna Chain: A: PDB Molecule: hth-type transcriptional regulator glnr; PDBTitle: structure of glnr-dna complex
90	c3qaoA	Alignment	not modelled	21.0	16	PDB header: transcription regulator Chain: A: PDB Molecule: merr-like transcriptional regulator; PDBTitle: the crystal structure of the n-terminal domain of a merr-like2 transcriptional regulator from listeria monocytogenes egd-e
91	d1a9xa2	Alignment	not modelled	20.7	11	Fold: Methylglyoxal synthase-like Superfamily: Methylglyoxal synthase-like Family: Carbamoyl phosphate synthetase, large subunit allosteric, C-terminal domain
92	c5z6vA	Alignment	not modelled	20.4	19	PDB header: protein transport Chain: A: PDB Molecule: abc-type uncharacterized transport system periplasmic PDBTitle: crystal structure of a substrate-binding protein from rhodothermus2 marinus
93	c3p8cE	Alignment	not modelled	20.4	30	PDB header: protein binding Chain: E: PDB Molecule: probable protein brick1; PDBTitle: structure and control of the actin regulatory wave complex
94	c6hlwB	Alignment	not modelled	20.4	7	PDB header: viral protein Chain: B: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of enterovirus-a71 (fusion protein)
95	c2w9mB	Alignment	not modelled	20.3	14	PDB header: dna replication Chain: B: PDB Molecule: polymerase x; PDBTitle: structure of family x dna polymerase from deinococcus2 radiodurans
96	c1nomA	Alignment	not modelled	20.2	14	PDB header: nucleotidyltransferase Chain: A: PDB Molecule: dna polymerase beta; PDBTitle: dna polymerase beta (pol b) (e.c.2.7.7.7), 31-kd domain; soaked in the2 presence of mncl2 (5 millimolar)
97	c2floA	Alignment	not modelled	19.8	10	PDB header: hydrolase Chain: A: PDB Molecule: exopolyphosphatase; PDBTitle: crystal structure of exopolyphosphatase (ppx) from e. coli o157:h7
98	c3fmfA	Alignment	not modelled	19.3	15	PDB header: ligase Chain: A: PDB Molecule: dethiobiotin synthetase; PDBTitle: crystal structure of mycobacterium tuberculosis dethiobiotin2 synthetase complexed with 7,8 diaminopelargonic acid carbamate
99	c6hltD	Alignment	not modelled	19.3	0	PDB header: viral protein Chain: D: PDB Molecule: genome polyprotein; PDBTitle: crystal structure of human acbd3 gold domain in complex with 3a2 protein of rhinovirus-14 (hrv14)