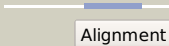



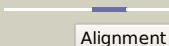





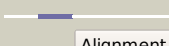

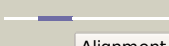











Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0455c (-)_545378_545824
Date	Tue Jul 23 14:50:53 BST 2019
Unique Job ID	cabaff286fe0fb44

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4oo2D_	 Alignment		28.4	27	PDB header: oxidoreductase Chain: D: PDB Molecule: chlorophenol-4-monooxygenase; PDBTitle: streptomyces globisporus c-1027 fad dependent (s)-3-chloro-β-2 tyrosine-s-sgcc2 c-5 hydroxylase sgcc apo form
2	c1r8jB_	 Alignment		19.3	25	PDB header: circadian clock protein Chain: B: PDB Molecule: kaia; PDBTitle: crystal structure of circadian clock protein kaia from2 synechococcus elongatus
3	c4h9kA_	 Alignment		15.3	75	PDB header: hydrolase Chain: A: PDB Molecule: hog cholera virus; PDBTitle: crystal structure of cleavage site mutant of npro of classical swine2 fever virus.
4	c3hwcD_	 Alignment		15.1	21	PDB header: oxidoreductase Chain: D: PDB Molecule: chlorophenol-4-monooxygenase component 2; PDBTitle: crystal structure of chlorophenol 4-monooxygenase (tftd) of2 burkholderia cepacia ac1100
5	c6eb0A_	 Alignment		14.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxyphenylacetate 3-monooxygenase, oxygenase subunit; PDBTitle: structure of 4-hydroxyphenylacetate 3-monooxygenase (hpb), oxygenase2 component from escherichia coli
6	c1eq8C_	 Alignment		11.3	53	PDB header: signaling protein Chain: C: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
7	c1eq8A_	 Alignment		11.3	53	PDB header: signaling protein Chain: A: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
8	c1eq8E_	 Alignment		11.3	53	PDB header: signaling protein Chain: E: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
9	c1eq8B_	 Alignment		11.3	53	PDB header: signaling protein Chain: B: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
10	c1eq8D_	 Alignment		11.3	53	PDB header: signaling protein Chain: D: PDB Molecule: acetylcholine receptor protein; PDBTitle: three-dimensional structure of the pentameric helical2 bundle of the acetylcholine receptor m2 transmembrane3 segment
11	c1a11A_	 Alignment		11.1	53	PDB header: acetylcholine receptor Chain: A: PDB Molecule: acetylcholine receptor m2; PDBTitle: nmr structure of membrane spanning segment 2 of the2 acetylcholine receptor in dpc micelles, 10 structures

12	c4rv2A_	Alignment		10.9	10	PDB header: lyase Chain: A: PDB Molecule: upf0336 protein msmeg_1340/msmei_1302; PDBTitle: crystal structure of (3r)-hydroxyacyl-ACP dehydratase hadab hetero-2 dimer from mycobacterium smegmatis
13	c5n6yC_	Alignment		10.3	24	PDB header: oxidoreductase Chain: C: PDB Molecule: nitrogenase vanadium-iron protein delta chain; PDBTitle: azotobacter vinelandii vanadium nitrogenase
14	d1fi6a_	Alignment		9.9	20	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)
15	d2ghvc1	Alignment		9.1	22	Fold: SARS receptor-binding domain-like Superfamily: SARS receptor-binding domain-like Family: SARS receptor-binding domain-like
16	c3p4hA_	Alignment		8.9	22	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent dna ligase, n-terminal domain protein; PDBTitle: structures of archaeal members of the ligd 3'-phosphoesterase dna2 repair enzyme superfamily
17	d1l5ia_	Alignment		8.2	29	Fold: Origin of replication-binding domain, RBD-like Superfamily: Origin of replication-binding domain, RBD-like Family: DNA-binding domain of REP protein
18	c1ii0A_	Alignment		8.1	35	PDB header: hydrolase Chain: A: PDB Molecule: arsenical pump-driving atpase; PDBTitle: crystal structure of the escherichia coli arsenite-translocating2 atpase
19	d1rh2a_	Alignment		7.5	13	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Interferons/interleukin-10 (IL-10)
20	c5l0lB_	Alignment		7.5	41	PDB header: unknown function Chain: B: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of uncharacterized protein lpg0439
21	c1u8vA_	Alignment	not modelled	7.2	24	PDB header: lyase, isomerase Chain: A: PDB Molecule: gamma-aminobutyrate metabolism dehydratase/isomerase; PDBTitle: crystal structure of 4-hydroxybutyryl-coa dehydratase from clostridium2 aminobutyricum: radical catalysis involving a [4fe-4s] cluster and3 flavin
22	c3p43A_	Alignment	not modelled	7.2	25	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: structure and activities of archaeal members of the ligd 3'2 phosphoesterase dna repair enzyme superfamily
23	c6f0kA_	Alignment	not modelled	7.2	16	PDB header: membrane protein Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: alternative complex iii
24	c5t42A_	Alignment	not modelled	7.2	22	PDB header: viral protein Chain: A: PDB Molecule: envelope glycoprotein; PDBTitle: structure of the ebola virus envelope protein mper/tm domain and its2 interaction with the fusion loop explains their fusion activity
25	c4g5eD_	Alignment	not modelled	7.1	22	PDB header: oxidoreductase Chain: D: PDB Molecule: 2,4,6-trichlorophenol 4-monoxygenase; PDBTitle: 2,4,6-trichlorophenol 4-monoxygenase
26	c2khnA_	Alignment	not modelled	6.9	20	PDB header: signaling protein Chain: A: PDB Molecule: intersectin-1; PDBTitle: nmr solution structure of the eh 1 domain from human2 intersectin-1 protein. northeast structural genomics3 consortium target hr3646e.
27	c3zfnA_	Alignment	not modelled	6.8	71	PDB header: hydrolase Chain: A: PDB Molecule: n-terminal protease npro; PDBTitle: crystal structure of product-like, processed n-terminal protease npro
						PDB header: hydrolase/viral protein Chain: E: PDB Molecule: spike glycoprotein;

28	c3sciE_	Alignment	not modelled	6.7	22	PDBTitle: crystal structure of spike protein receptor-binding domain from a2 predicted sars coronavirus human strain complexed with human receptor3 ace2
29	c2kgrA_	Alignment	not modelled	6.6	23	PDB header: protein binding Chain: A; PDB Molecule: intersectin-1; PDBTitle: solution structure of protein itsn1 from homo sapiens.2 northeast structural genomics consortium target hr5524a
30	c3ez6B_	Alignment	not modelled	6.3	31	PDB header: dna binding protein Chain: B; PDB Molecule: plasmid partition protein a; PDBTitle: structure of para- <i>adp</i> complex:tetragonal form
31	d2ezla_	Alignment	not modelled	6.3	13	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Recombinase DNA-binding domain
32	c4qzvB_	Alignment	not modelled	6.2	25	PDB header: hydrolase/viral protein Chain: B; PDB Molecule: spike protein s1; PDBTitle: bat-derived coronavirus hku4 uses mers-cov receptor human cd26 for2 cell entry
33	c5u3mA_	Alignment	not modelled	6.0	80	PDB header: immune system/viral protein Chain: A; PDB Molecule: gp41 mper peptide; PDBTitle: crystal structure of dh511.11p fab in complex with hiv-1 gp41 mper2 peptide
34	c3fiaA_	Alignment	not modelled	5.8	20	PDB header: protein binding Chain: A; PDB Molecule: intersectin-1; PDBTitle: crystal structure of the eh 1 domain from human intersectin-1 protein.2 northeast structural genomics consortium target hr3646e.
35	d2jxca1	Alignment	not modelled	5.8	16	Fold: EF Hand-like Superfamily: EF-hand Family: Eps15 homology domain (EH domain)
36	c2m4mA_	Alignment	not modelled	5.8	18	PDB header: unknown function Chain: A; PDB Molecule: hypothetical protein; PDBTitle: solution structure of the rrm domain of the hypothetical protein2 cagl0m09691g from candida glabrata
37	d1ihua2	Alignment	not modelled	5.8	32	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Nitrogenase iron protein-like
38	c4zv4C_	Alignment	not modelled	5.7	32	PDB header: translation Chain: C; PDB Molecule: tse6; PDBTitle: structure of tse6 in complex with ef-tu
39	d2dk8a1	Alignment	not modelled	5.3	44	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RPO3F domain-like
40	c1javA_	Alignment	not modelled	5.3	80	PDB header: viral protein Chain: A; PDB Molecule: transmembrane glycoprotein (gp41); PDBTitle: average nmr solution structure of the trp-rich peptide of2 hiv gp41 bound to dpc micelles
41	c2aenH_	Alignment	not modelled	5.2	33	PDB header: viral protein Chain: H; PDB Molecule: outer capsid protein vp4, vp8* core; PDBTitle: crystal structure of the rotavirus strain ds-1 vp8* core
42	c2q01A_	Alignment	not modelled	5.1	30	PDB header: isomerase Chain: A; PDB Molecule: uronate isomerase; PDBTitle: crystal structure of glucuronate isomerase from caulobacter crescentus
43	d1t61a2	Alignment	not modelled	5.1	47	Fold: C-type lectin-like Superfamily: C-type lectin-like Family: Noncollagenous (NC1) domain of collagen IV