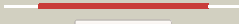

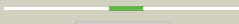
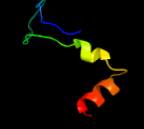





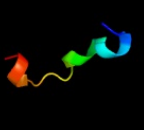



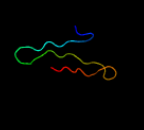



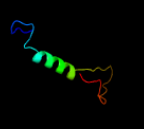




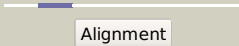





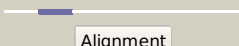

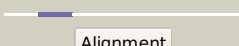

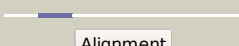

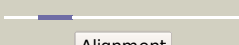






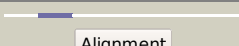

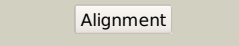

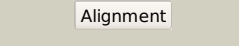





Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2403c_(ppR)_2700545_2701300
Date	Wed Aug 7 12:50:01 BST 2019
Unique Job ID	f5eb8910e95a6bc3

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4esqA_	 Alignment		100.0	22	PDB header: transferase Chain: A: PDB Molecule: serine/threonine protein kinase; PDBTitle: crystal structure of the extracellular domain of pknh from2 mycobacterium tuberculosis
2	c3lo3E_	 Alignment		54.2	18	PDB header: structure genomics, unknown function Chain: E: PDB Molecule: uncharacterized conserved protein; PDBTitle: the crystal structure of a conserved functionally unknown protein from2 colwellia psychrerythraea 34h.
3	d2fiua1	 Alignment		45.6	29	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Atu0297-like
4	c5uz5C_	 Alignment		24.2	9	PDB header: nuclear protein/rna Chain: C: PDB Molecule: u1 small nuclear ribonucleoprotein a,tap tag; PDBTitle: s. cerevisiae u1 snrnp
5	c2b3gB_	 Alignment		14.6	17	PDB header: replication Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: p53n (fragment 33-60) bound to rpa70n
6	c3dcaC_	 Alignment		13.8	11	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: rpa0582; PDBTitle: crystal structure of the rpa0582- protein of unknown2 function from rhodopseudomonas palustris- a structural3 genomics target
7	d1jaea1	 Alignment		13.5	27	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
8	c3i08D_	 Alignment		13.3	12	PDB header: signaling protein Chain: D: PDB Molecule: neurogenic locus notch homolog protein 1; PDBTitle: crystal structure of the s1-cleaved notch1 negative2 regulatory region (nrr)
9	d1zata2	 Alignment		12.6	18	Fold: L,D-transpeptidase pre-catalytic domain-like Superfamily: L,D-transpeptidase pre-catalytic domain-like Family: L,D-transpeptidase pre-catalytic domain-like
10	c5mx2r_	 Alignment		11.7	56	PDB header: oxidoreductase Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
11	c5tisir_	 Alignment		11.1	56	PDB header: photosynthesis Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex

12	c5kair_	 Alignment		11.1	56	PDB header: electron transport Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: nh3-bound rt xfel structure of photosystem ii 500 ms after the 2nd2 illumination (2f) at 2.8 a resolution
13	c5tisR_	 Alignment		11.1	56	PDB header: photosynthesis Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: room temperature xfel structure of the native, doubly-illuminated2 photosystem ii complex
14	c4pj0r_	 Alignment		11.0	56	PDB header: oxidoreductase, electron transport Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
15	c5mx2R_	 Alignment		10.8	56	PDB header: oxidoreductase Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: photosystem ii depleted of the mn4cao5 cluster at 2.55 a resolution
16	c4ub8R_	 Alignment		10.8	56	PDB header: electron transport, photosynthesis Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: native structure of photosystem ii (dataset-2) by a femtosecond x-ray2 laser
17	c5kafR_	 Alignment		10.8	56	PDB header: electron transport Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: rt xfel structure of photosystem ii in the dark state at 3.0 a2 resolution
18	c5ws5R_	 Alignment		10.8	56	PDB header: photosynthesis Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: native xfel structure of photosystem ii (preflash dark dataset)
19	c5ws6R_	 Alignment		10.8	56	PDB header: photosynthesis Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: native xfel structure of photosystem ii (preflash two-flash dataset)
20	c5gthR_	 Alignment		10.8	56	PDB header: photosynthesis Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: native xfel structure of photosystem ii (dark dataset)
21	c5gtiR_	 Alignment	not modelled	10.8	56	PDB header: photosynthesis Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: native xfel structure of photosystem ii (two flash dataset)
22	c4ub6R_	 Alignment	not modelled	10.8	56	PDB header: electron transport, photosynthesis Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: native structure of photosystem ii (dataset-1) by a femtosecond x-ray2 laser
23	c4il6R_	 Alignment	not modelled	10.8	56	PDB header: electron transport Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: structure of sr-substituted photosystem ii
24	c4pj0R_	 Alignment	not modelled	10.8	56	PDB header: oxidoreductase, electron transport Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: structure of t.elongatus photosystem ii, rows of dimers crystal2 packing
25	d1g94a1	 Alignment	not modelled	10.5	29	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
26	d1r2za1	 Alignment	not modelled	10.1	18	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
27	d1tdza1	 Alignment	not modelled	9.4	20	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
28	c5kafr_	 Alignment	not modelled	9.3	56	PDB header: electron transport Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: rt xfel structure of photosystem ii in the dark state at 3.0 a2 resolution
29	c2chaA	 Alignment	not modelled	9.1	12	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: conserved protein mth639;

29	c3c0nA	Alignment	not modelled	9.1	12	PDBTitle: crystal structure of a conserved protein (mth639) from2 methanobacterium thermoautotrophicum
30	d1k82a1	Alignment	not modelled	8.9	18	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
31	c5kaiR	Alignment	not modelled	7.8	56	PDB header: electron transport Chain: R: PDB Molecule: photosystem ii protein y; PDBTitle: nh3-bound rt xfel structure of photosystem ii 500 ms after the 2nd2 illumination (2f) at 2.8 a resolution
32	c2n8fA	Alignment	not modelled	7.7	63	PDB header: toxin Chain: A: PDB Molecule: spider toxin pi-hexatoxin-hi1a; PDBTitle: chemical shift assignments and structure calculation of spider toxin2 pi-hexatoxin-hi1a
33	d1k3xa1	Alignment	not modelled	6.8	14	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
34	d2hkja1	Alignment	not modelled	6.4	5	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Topoisomerase VI-B subunit middle domain
35	c2ly4B	Alignment	not modelled	5.8	18	PDB header: nuclear protein/antitumour protein Chain: B: PDB Molecule: cellular tumor antigen p53; PDBTitle: hmgb1-facilitated p53 dna binding occurs via hmg-box/p532 transactivation domain interaction and is regulated by the acidic3 tail
36	d1hx0a1	Alignment	not modelled	5.8	29	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
37	d3dhpA1	Alignment	not modelled	5.6	24	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain Family: alpha-Amylases, C-terminal beta-sheet domain
38	d1ee8a1	Alignment	not modelled	5.4	16	Fold: S13-like H2TH domain Superfamily: S13-like H2TH domain Family: Middle domain of MutM-like DNA repair proteins
39	c6ehil	Alignment	not modelled	5.4	7	PDB header: dna binding protein Chain: I: PDB Molecule: nuclease nuct; PDBTitle: nuct from helicobacter pylori