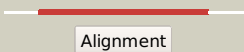

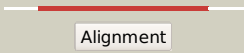

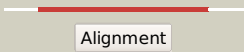

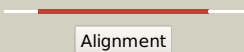

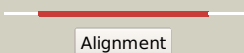

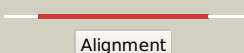


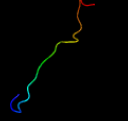
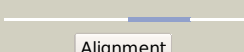
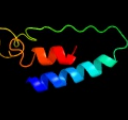
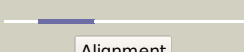

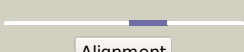
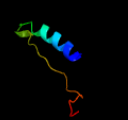
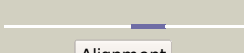
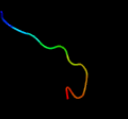



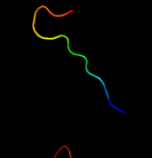
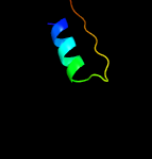
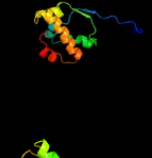


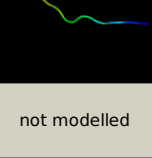


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2728c (-)_3040776_3041471
Date	Wed Aug 7 12:50:38 BST 2019
Unique Job ID	2aa675c51da89447

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3vsjB_	 Alignment		100.0	15	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-amino-5-chlorophenol 1,6-dioxygenase beta subunit; PDBTitle: crystal structure of 1,6-apd (2-animophenol-1,6-dioxygenase) complexed2 with intermediate products
2	c3vsjA_	 Alignment		100.0	13	PDB header: oxidoreductase Chain: A: PDB Molecule: 2-amino-5-chlorophenol 1,6-dioxygenase alpha subunit; PDBTitle: crystal structure of 1,6-apd (2-animophenol-1,6-dioxygenase) complexed2 with intermediate products
3	d1b4ub_	 Alignment		100.0	12	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
4	c3wrbB_	 Alignment		100.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: gallate dioxygenase; PDBTitle: crystal structure of the anaerobic h124f desb-gallate complex
5	c3bd0D_	 Alignment		99.9	15	PDB header: peptide binding protein Chain: D: PDB Molecule: protein memo1; PDBTitle: crystal structure of memo, form ii
6	d2pw6a1	 Alignment		99.8	12	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
7	d1a73a_	 Alignment		22.8	30	Fold: His-Me finger endonucleases Superfamily: His-Me finger endonucleases Family: Intron-encoded homing endonucleases
8	c3wrwE_	 Alignment		22.6	14	PDB header: transferase Chain: E: PDB Molecule: tm-1 protein; PDBTitle: crystal structure of the n-terminal domain of resistance protein
9	c4uplC_	 Alignment		19.1	24	PDB header: hydrolase Chain: C: PDB Molecule: sulfatase family protein; PDBTitle: dimeric sulfatase spas2 from silicibacter pomeroyi
10	d1y6va1	 Alignment		11.8	18	Fold: Alkaline phosphatase-like Superfamily: Alkaline phosphatase-like Family: Alkaline phosphatase
11	c4s1nA_	 Alignment		11.7	23	PDB header: transferase Chain: A: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: the crystal structure of phosphoribosylglycinamide formyltransferase2 from streptococcus pneumoniae tigr4

12	c5c2gD	Alignment		11.4	10	PDB header: lyase Chain: D: PDB Molecule: form ii rubisco; PDBTitle: gws1b rubisco: form ii rubisco derived from uncultivated2 gallionellacea species (cabp-bound).
13	c2rusB	Alignment		10.2	11	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: rubisco (ribulose-1,5-bisphosphate carboxylase(/slash) PDBTitle: crystal structure of the ternary complex of ribulose-1,5-bisphosphate2 carboxylase, mg(ii), and activator co2 at 2.3-angstroms resolution
14	c9rubB	Alignment		9.7	11	PDB header: lyase(carbon-carbon) Chain: B: PDB Molecule: ribulose-1,5-bisphosphate carboxylase; PDBTitle: crystal structure of activated ribulose-1,5-bisphosphate carboxylase2 complexed with its substrate, ribulose-1,5-bisphosphate
15	d1ac5a	Alignment		9.6	20	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Serine carboxypeptidase-like
16	d2ihta3	Alignment		9.4	19	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
17	d5rubA1	Alignment		9.2	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
18	c6b1vB	Alignment		8.6	16	PDB header: hydrolase Chain: B: PDB Molecule: iota-carrageenan sulfatase; PDBTitle: crystal structure of ps i-cgsb c78s in complex with i-neocarratetraose
19	c1gxsC	Alignment		7.8	36	PDB header: lyase Chain: C: PDB Molecule: p-(s)-hydroxymandelonitrile lyase chain a; PDBTitle: crystal structure of hydroxynitrile lyase from sorghum2 bicolor in complex with inhibitor benzoic acid: a novel3 cyanogenic enzyme
20	c3p9xB	Alignment		7.7	15	PDB header: transferase Chain: B: PDB Molecule: phosphoribosylglycinamide formyltransferase; PDBTitle: crystal structure of phosphoribosylglycinamide formyltransferase from2 bacillus halodurans
21	c4az3A	Alignment	not modelled	7.5	40	PDB header: hydrolase Chain: A: PDB Molecule: lysosomal protective protein 32 kda chain; PDBTitle: crystal structure of cathepsin a, complexed with 15a
22	c1bcrA	Alignment	not modelled	7.3	36	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: serine carboxypeptidase ii; PDBTitle: complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
23	c3uebD	Alignment	not modelled	7.2	9	PDB header: unknown function Chain: D: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of ton_0450 from thermococcus onnurineus na1
24	c3a52A	Alignment	not modelled	7.2	13	PDB header: hydrolase Chain: A: PDB Molecule: cold-active alkaline phosphatase; PDBTitle: crystal structure of cold-active alkailne phosphatase from2 psychrophile shewanella sp.
25	d1wpxa1	Alignment	not modelled	6.9	27	Fold: alpha/beta-Hydrolases Superfamily: alpha/beta-Hydrolases Family: Serine carboxypeptidase-like
26	c5macD	Alignment	not modelled	6.8	13	PDB header: lyase Chain: D: PDB Molecule: ribulose-1,5-bisphosphate carboxylase-oxygenase type iii; PDBTitle: crystal structure of decameric methanococcoides burtonii rubisco2 complexed with 2-carboxyarabinitol bisphosphate
27	c2x9qA	Alignment	not modelled	6.5	8	PDB header: ligase Chain: A: PDB Molecule: cyclodipeptide synthetase; PDBTitle: structure of the mycobacterium tuberculosis protein, rv2275,2 demonstrates that cyclodipeptide synthetases are related3 to type i trna-synthetases.
						Fold: Thiamin diphosphate-binding fold (THDP-binding)

28	d1ovma3	Alignment	not modelled	6.4	19	Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
29	c2qygC_	Alignment	not modelled	6.0	11	PDB header: unknown function Chain: C: PDB Molecule: ribulose biphosphate carboxylase-like protein 2; PDBTitle: crystal structure of a rubisco-like protein rlp2 from rhodospseudomonas2 palustris
30	d1rbla1	Alignment	not modelled	5.2	15	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
31	d1q5qa_	Alignment	not modelled	5.2	15	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Proteasome subunits
32	c1q5rD_	Alignment	not modelled	5.2	15	PDB header: hydrolase Chain: D: PDB Molecule: proteasome alpha-type subunit 1; PDBTitle: the rhodococcus 20s proteasome with unprocessed pro-peptides
33	d1nvpd1	Alignment	not modelled	5.2	23	Fold: Transcription factor IIA (TFIIA), alpha-helical domain Superfamily: Transcription factor IIA (TFIIA), alpha-helical domain Family: Transcription factor IIA (TFIIA), alpha-helical domain
34	d1geha1	Alignment	not modelled	5.1	11	Fold: TIM beta/alpha-barrel Superfamily: RuBisCo, C-terminal domain Family: RuBisCo, large subunit, C-terminal domain
35	d2djia3	Alignment	not modelled	5.1	27	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: Pyruvate oxidase and decarboxylase PP module
36	c2rm8A_	Alignment	not modelled	5.1	13	PDB header: signaling protein Chain: A: PDB Molecule: sensory rhodopsin ii transducer; PDBTitle: the solution structure of phototactic transducer protein2 httrii linker region from natronomonas pharaonis