

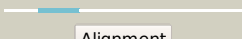
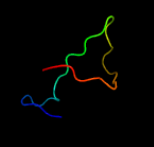
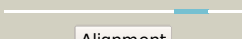
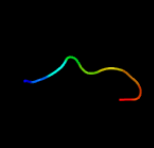

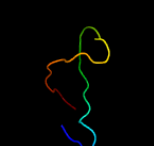



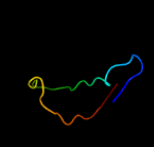

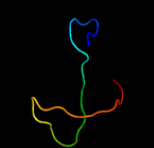

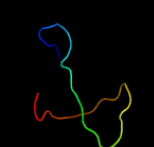



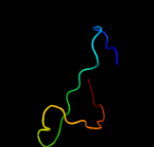


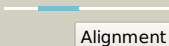
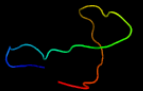
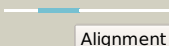
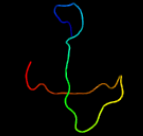
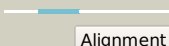

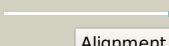
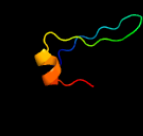
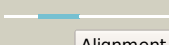



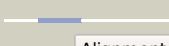
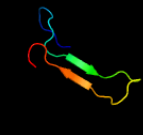
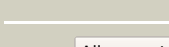
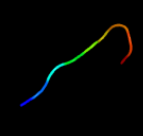

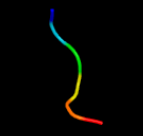
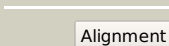
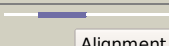


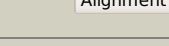
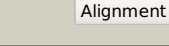
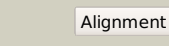
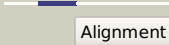
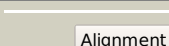


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2598 (-) _2926996_2927490
Date	Wed Aug 7 12:50:23 BST 2019
Unique Job ID	bdbb21672b21542e

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2prda_	 Alignment		39.6	16	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
2	c5teaF_	 Alignment		39.1	19	PDB header: hydrolase Chain: F: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of an inorganic pyrophosphatase from neisseria2 gonorrhoeae
3	c5wxkA_	 Alignment		38.0	44	PDB header: transferase Chain: A: PDB Molecule: earp; PDBTitle: earp bound with domain i of ef-p
4	c2uxsA_	 Alignment		37.6	13	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: 2.7a crystal structure of inorganic pyrophosphatase (rv3628)2 from mycobacterium tuberculosis at ph 7.5
5	d1qeza_	 Alignment		36.9	16	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
6	d1udea_	 Alignment		36.1	6	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
7	c3d63B_	 Alignment		35.8	19	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from burkholderia2 pseudomallei
8	c6n1cB_	 Alignment		35.7	13	PDB header: hydrolase Chain: B: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from legionella2 pneumophila philadelphia 1
9	c3fq3H_	 Alignment		35.3	13	PDB header: hydrolase Chain: H: PDB Molecule: inorganic pyrophosphatase;bacterial/archaeal inorganic PDBTitle: crystal structure of inorganic phosphatase from brucella melitensis
10	c3ld3A_	 Alignment		34.2	13	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic phosphatase from anaplasma2 phagocytophilum at 1.75a resolution
11	c3emjL_	 Alignment		34.1	16	PDB header: hydrolase Chain: L: PDB Molecule: inorganic pyrophosphatase; PDBTitle: 2.2 a crystal structure of inorganic pyrophosphatase from2 rickettsia prowazekii (p21 form)

12	c4lugA_	 Alignment		34.1	16	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase ppa1 from arabidopsis2 thaliana
13	c3tr4C_	 Alignment		33.8	16	PDB header: hydrolase Chain: C: PDB Molecule: inorganic pyrophosphatase; PDBTitle: structure of an inorganic pyrophosphatase (ppa) from coxiella burnetii
14	c1ygzC_	 Alignment		32.8	19	PDB header: hydrolase Chain: C: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from helicobacter2 pylori
15	c5ii6A_	 Alignment		32.6	14	PDB header: cell adhesion Chain: A: PDB Molecule: zona pellucida sperm-binding protein 2; PDBTitle: crystal structure of the zp-n1 domain of mouse sperm receptor zp2 at2 0.95 a resolution
16	c3lo0A_	 Alignment		32.2	13	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of inorganic pyrophosphatase from2 ehrlichia chaffeensis
17	d1i40a_	 Alignment		31.4	19	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
18	d2fug71	 Alignment		24.1	21	Fold: N domain of copper amine oxidase-like Superfamily: Frataxin/Nqo15-like Family: Nqo15-like
19	c3iwdC_	 Alignment		20.8	33	PDB header: lyase Chain: C: PDB Molecule: s-adenosylmethionine decarboxylase; PDBTitle: t. maritima adometdc complex with 5'-deoxy-5'-dimethyl thioadenosine
20	c5nv8A_	 Alignment		17.4	50	PDB header: transferase Chain: A: PDB Molecule: ef-p arginine 32 rhamnosyl-transferase; PDBTitle: structural basis for earp-mediated arginine glycosylation of2 translation elongation factor ef-p
21	d2fmma1	 Alignment	not modelled	15.6	86	Fold: SH3-like barrel Superfamily: Chromo domain-like Family: Chromo domain
22	d2dbsa1	 Alignment	not modelled	14.2	24	Fold: TTHC002-like Superfamily: TTHC002-like Family: TTHC002-like
23	c5wrtB_	 Alignment	not modelled	12.6	16	PDB header: hydrolase Chain: B: PDB Molecule: soluble inorganic pyrophosphatase; PDBTitle: crystal structure of type i inorganic pyrophosphatase from toxoplasma2 gondii.
24	c5c5zA_	 Alignment	not modelled	10.5	26	PDB header: hydrolase Chain: A: PDB Molecule: glutamyl-trna amidotransferase; PDBTitle: crystal structure analysis of c4763, a uropathogenic e. coli-specific2 protein
25	c6gzua_	 Alignment	not modelled	9.3	50	PDB header: transferase Chain: A: PDB Molecule: conserved membrane protein; PDBTitle: structure of chlamydia abortus effector protein chladub
26	c4lubA_	 Alignment	not modelled	9.0	18	PDB header: lyase Chain: A: PDB Molecule: putative prephenate dehydratase; PDBTitle: x-ray structure of prephenate dehydratase from streptococcus mutans
27	d1twla_	 Alignment	not modelled	8.9	7	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
28	d2hja1	 Alignment	not modelled	8.8	27	Fold: dsRBD-like Superfamily: YcfA/nrd intein domain Family: Ykff-like
29	c2hja	 Alignment	not modelled	8.8	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical protein ykff;

29	c2njja_	Alignment	not modelled	6.8	47	PDBTitle: solution nmr structure of protein ykff from escherichia coli.2 northeast structural genomics target er397. PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein;
30	c4q51A_	Alignment	not modelled	7.8	23	PDBTitle: crystal structure of a putative molybdenum cofactor biosynthesis2 protein f from burkholderia cenocepacia j2315
31	c4qlza_	Alignment	not modelled	7.4	16	PDB header: hydrolase, metal binding protein Chain: A: PDB Molecule: sjchgc07024 protein; PDBTitle: the structure of inorganic pyrophosphatase from schistosoma japonicum
32	c6ir8A_	Alignment	not modelled	7.2	20	PDB header: transcription/dna Chain: A: PDB Molecule: oswrky45; PDBTitle: rice wrky/dna complex
33	c5wruA_	Alignment	not modelled	7.1	16	PDB header: hydrolase Chain: A: PDB Molecule: probable inorganic pyrophosphatase; PDBTitle: crystal structure of type i inorganic pyrophosphatase from p2 falciparum
34	c5nnyA_	Alignment	not modelled	6.9	16	PDB header: hydrolase Chain: A: PDB Molecule: wipb; PDBTitle: crystal structure of the phosphatase domain from the legionella2 effector wipb
35	d1e9ga_	Alignment	not modelled	6.8	19	Fold: OB-fold Superfamily: Inorganic pyrophosphatase Family: Inorganic pyrophosphatase
36	c5z6dB_	Alignment	not modelled	6.8	23	PDB header: metal binding protein Chain: B: PDB Molecule: duf1881 domain-containing protein; PDBTitle: crystal structure of abundant perithecial protein (app) from2 neurospora crassa
37	c6h9cA_	Alignment	not modelled	6.7	31	PDB header: virus Chain: A: PDB Molecule: vp4; PDBTitle: cryo-em structure of archaeal extremophilic internal membrane-2 containing haloarcula californiae icosahedral virus 1 (hciv-1) at3 3.74 angstroms resolution.
38	d1nlna_	Alignment	not modelled	6.0	32	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Adenain-like
39	c1vr7A_	Alignment	not modelled	5.8	7	PDB header: lyase Chain: A: PDB Molecule: s-adenosylmethionine decarboxylase proenzyme; PDBTitle: crystal structure of s-adenosylmethionine decarboxylase proenzyme2 (tm0655) from thermotoga maritima at 1.2 a resolution
40	c3j4uj_	Alignment	not modelled	5.8	25	PDB header: virus Chain: J: PDB Molecule: cementing protein; PDBTitle: a new topology of the hk97-like fold revealed in bordetella2 bacteriophage: non-covalent chainmail secured by jellyrolls
41	c6c45A_	Alignment	not modelled	5.7	14	PDB header: hydrolase Chain: A: PDB Molecule: inorganic pyrophosphatase; PDBTitle: crystal structure of human inorganic pyrophosphatase in the p2121212 space group
42	c2l82A_	Alignment	not modelled	5.6	33	PDB header: de novo protein Chain: A: PDB Molecule: designed protein or32; PDBTitle: solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or32
43	c6b4eD_	Alignment	not modelled	5.6	44	PDB header: transport protein Chain: D: PDB Molecule: nucleoporin nup42; PDBTitle: crystal structure of saccharomyces cerevisiae gle1 ctd-nup42 gbm2 complex
44	d2qmwa2	Alignment	not modelled	5.4	12	Fold: Ferredoxin-like Superfamily: ACT-like Family: Phenylalanine metabolism regulatory domain
45	d1vr7a1	Alignment	not modelled	5.4	7	Fold: S-adenosylmethionine decarboxylase Superfamily: S-adenosylmethionine decarboxylase Family: Bacterial S-adenosylmethionine decarboxylase
46	c2jxza_	Alignment	not modelled	5.2	30	PDB header: hormone Chain: A: PDB Molecule: calcitonin; PDBTitle: solution conformation of a non-amyloidogenic analogue of human2 calcitonin in sodium dodecyl sulfate micelles