






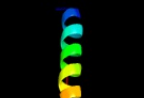

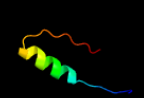

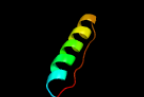



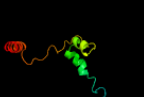









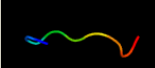
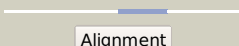

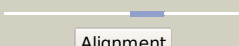

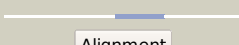
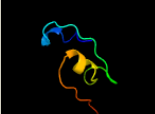
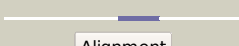
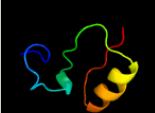

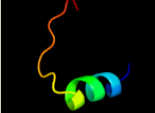



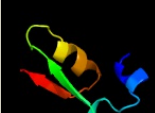
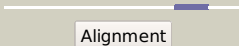
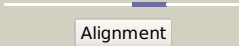
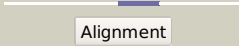
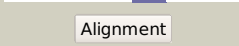

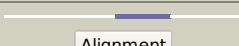
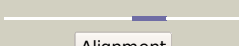



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3189_(-)_3554639_3555259
Date	Thu Aug 8 16:20:38 BST 2019
Unique Job ID	61a7bbca363b2aff

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6fkqB_	 Alignment		100.0	22	PDB header: toxin Chain: B; PDB Molecule: rv1989c (mbct); PDBTitle: crystal structure of the m.tuberculosis mbct-mbca toxin-antitoxin2 complex.
2	c6gw6A_	 Alignment		98.3	23	PDB header: toxin Chain: A; PDB Molecule: res toxin; PDBTitle: structure of the pseudomonas putida res-xre toxin-antitoxin complex
3	c6d0hA_	 Alignment		98.1	20	PDB header: toxin Chain: A; PDB Molecule: part: cog5654 (res domain) toxin; PDBTitle: part: prs adp-ribosylating toxin bound to cognate antitoxin pars
4	d1a9xa3	 Alignment		42.3	23	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
5	c5dotA_	 Alignment		41.0	29	PDB header: ligase Chain: A; PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 apo form
6	c5douC_	 Alignment		39.6	27	PDB header: ligase Chain: C; PDB Molecule: carbamoyl-phosphate synthase [ammonia], mitochondrial; PDBTitle: crystal structure of human carbamoyl phosphate synthetase i (cps1),2 ligand-bound form
7	d1zd3a1	 Alignment		27.0	16	Fold: HAD-like Superfamily: HAD-like Family: YihX-like
8	d1qvia_	 Alignment		25.6	24	Fold: HAD-like Superfamily: HAD-like Family: Hypothetical protein MW1667 (SA1546)
9	c3nvtA_	 Alignment		25.0	22	PDB header: transferase/isomerase Chain: A; PDB Molecule: 3-deoxy-d-arabino-heptulosonate 7-phosphate synthase; PDBTitle: 1.95 angstrom crystal structure of a bifunctional 3-deoxy-7-2 phosphoheptulonate synthase/chorismate mutase (aroa) from listeria3 monocytogenes egd-e
10	c6ghbB_	 Alignment		24.0	18	PDB header: protein binding Chain: B; PDB Molecule: upf0413 protein gk0824; PDBTitle: crystal structure of spx in complex with yjbh (oxidized)
11	d2b0ca1	 Alignment		23.1	17	Fold: HAD-like Superfamily: HAD-like Family: YihX-like

12	d1fqva1	 Alignment		22.5	20	Fold: F-box domain Superfamily: F-box domain Family: F-box domain
13	d1x4ka2	 Alignment		22.3	44	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
14	c2pkeA	 Alignment		22.1	11	PDB header: hydrolase Chain: A: PDB Molecule: haloacid delahogenase-like family hydrolase; PDBTitle: crystal structure of haloacid delahogenase-like family hydrolase2 (np_639141.1) from xanthomonas campestris at 1.81 a resolution
15	d1a9xa4	 Alignment		21.9	19	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
16	d2fpwa1	 Alignment		21.6	20	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like
17	c4jyrG	 Alignment		18.4	17	PDB header: hydrolase Chain: G: PDB Molecule: d,d-heptose 1,7-bisphosphate phosphatase; PDBTitle: crystal structure of d,d-heptose 1,7-bisphosphate phosphatase from2 burkholderia thailandensis
18	c2hcuA	 Alignment		17.6	24	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: crystal structure of smu.1381 (or leud) from streptococcus mutans
19	c1m6vE	 Alignment		17.5	18	PDB header: ligase Chain: E: PDB Molecule: carbamoyl phosphate synthetase large chain; PDBTitle: crystal structure of the g359f (small subunit) point mutant of2 carbamoyl phosphate synthetase
20	d2g80a1	 Alignment		17.3	17	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
21	c5y4gA	 Alignment	not modelled	15.8	16	PDB header: transferase Chain: A: PDB Molecule: ampb3; PDBTitle: apo structure of ampb3
22	c3vbaE	 Alignment	not modelled	15.4	19	PDB header: lyase Chain: E: PDB Molecule: isopropylmalate/citramalate isomerase small subunit; PDBTitle: crystal structure of methanogen 3-isopropylmalate isomerase small2 subunit
23	c3i28A	 Alignment	not modelled	13.7	17	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase 2; PDBTitle: crystal structure of soluble epoxide hydrolase
24	c3q3wB	 Alignment	not modelled	13.6	29	PDB header: transferase Chain: B: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: isopropylmalate isomerase small subunit from campylobacter jejuni.
25	c2pkpA	 Alignment	not modelled	13.2	29	PDB header: lyase Chain: A: PDB Molecule: homoaconitase small subunit; PDBTitle: crystal structure of 3-isopropylmalate dehydratase (leud)2 from methanocaldococcus jannaschii dsm2661 (mj1271)
26	c5e27B	 Alignment	not modelled	12.6	24	PDB header: cell adhesion Chain: B: PDB Molecule: resuscitation-promoting factor rpfb; PDBTitle: the structure of resuscitation promoting factor b from m. tuberculosis2 reveals unexpected ubiquitin-like domains
27	c3h5jA	 Alignment	not modelled	12.5	24	PDB header: lyase Chain: A: PDB Molecule: 3-isopropylmalate dehydratase small subunit; PDBTitle: leud_1-168 small subunit of isopropylmalate isomerase (rv2987c) from2 mycobacterium tuberculosis
						Fold: Ferredoxin-like

28	d1u8wa_	Alignment	not modelled	12.4	26	Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
29	c4ig4A_	Alignment	not modelled	12.0	30	PDB header: hydrolase Chain: A: PDB Molecule: thermostable nppase; PDBTitle: crystal structure of single mutant thermostable nppase (n86s) from2 geobacillus stearothermophilus
30	c4jb3A_	Alignment	not modelled	11.3	13	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of bt_0970, a had family phosphatase from2 bacteroides thetaiotaomicron vpi-5482, target efi-501083, with bound3 sodium and glycerol, closed lid, ordered loop
31	c4s0mC_	Alignment	not modelled	10.9	19	PDB header: transferase Chain: C: PDB Molecule: nucleoside diphosphate kinase; PDBTitle: crystal structure of nucleoside diphosphate kinase at 1.92 a2 resolution from acinetobacter baumannii
32	c2x4dB_	Alignment	not modelled	10.7	10	PDB header: hydrolase Chain: B: PDB Molecule: phospholysine phosphohistidine inorganic pyrophosphate PDBTitle: crystal structure of human phospholysine phosphohistidine inorganic2 pyrophosphate phosphatase lhpp
33	c5dedA_	Alignment	not modelled	10.4	25	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase yjbm; PDBTitle: crystal structure of the small alarmone synthetase 1 from bacillus2 subtilis bound to its product pppgpp
34	c3qgmC_	Alignment	not modelled	10.0	22	PDB header: hydrolase Chain: C: PDB Molecule: p-nitrophenyl phosphatase (pho2); PDBTitle: p-nitrophenyl phosphatase from archaeoglobus fulgidus
35	c2i6xA_	Alignment	not modelled	10.0	16	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase, haloacid dehalogenase-like family; PDBTitle: the structure of a predicted had-like family hydrolase from2 porphyromonas gingivalis.
36	c4ee7A_	Alignment	not modelled	9.8	19	PDB header: transferase Chain: A: PDB Molecule: prenyltransferase; PDBTitle: crystal structure of the novel phenazine prenyltransferase epzp in2 complex with s-thiolodiphosphate (methylated)
37	d1v7la_	Alignment	not modelled	9.3	19	Fold: The "swivelling" beta/beta/alpha domain Superfamily: LeuD/IvD-like Family: LeuD-like
38	c2g80C_	Alignment	not modelled	9.3	17	PDB header: hydrolase Chain: C: PDB Molecule: protein utr4; PDBTitle: crystal structure of utr4 protein (unknown transcript 4 protein)2 (yel038w) from saccharomyces cerevisiae at 2.28 a resolution
39	d1zs9a1	Alignment	not modelled	9.2	17	Fold: HAD-like Superfamily: HAD-like Family: Enolase-phosphatase E1
40	c2xm5A_	Alignment	not modelled	8.9	28	PDB header: transferase Chain: A: PDB Molecule: cloq; PDBTitle: structural and mechanistic analysis of the magnesium-independent2 aromatic prenyltransferase cloq from the clorobioicin biosynthetic3 pathway
41	c4dfdB_	Alignment	not modelled	8.6	13	PDB header: hydrolase Chain: B: PDB Molecule: putative haloacid dehalogenase-like hydrolase; PDBTitle: crystal structure of had family enzyme bt-2542 (target efi-501088)2 from bacteroides thetaiotaomicron, magnesium complex
42	c1cr6A_	Alignment	not modelled	8.6	16	PDB header: hydrolase Chain: A: PDB Molecule: epoxide hydrolase; PDBTitle: crystal structure of murine soluble epoxide hydrolase2 complexed with cpu inhibitor
43	d1yv9a1	Alignment	not modelled	8.5	22	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
44	d1w0ma_	Alignment	not modelled	8.4	25	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
45	c3l9dA_	Alignment	not modelled	8.3	22	PDB header: transferase Chain: A: PDB Molecule: putative gtp pyrophosphokinase; PDBTitle: the crystal structure of smu.1046c from streptococcus mutans ua159
46	c3ddhA_	Alignment	not modelled	8.2	21	PDB header: hydrolase Chain: A: PDB Molecule: putative haloacid dehalogenase-like family hydrolase; PDBTitle: the structure of a putative haloacid dehalogenase-like family2 hydrolase from bacteroides thetaiotaomicron vpi-5482
47	d1ys9a1	Alignment	not modelled	8.1	13	Fold: HAD-like Superfamily: HAD-like Family: NagD-like
48	c2l0rA_	Alignment	not modelled	8.1	18	PDB header: hydrolase,toxin Chain: A: PDB Molecule: lethal factor; PDBTitle: conformational dynamics of the anthrax lethal factor catalytic center
49	d2d6fa2	Alignment	not modelled	7.8	18	Fold: Glutaminase/Asparaginase Superfamily: Glutaminase/Asparaginase Family: Glutaminase/Asparaginase
50	c6fgkA_	Alignment	not modelled	7.7	19	PDB header: transferase Chain: A: PDB Molecule: gtp pyrophosphokinase ywac; PDBTitle: crystal structure of the small alarmone synthetase 2 from bacillus2 subtilis
51	c2lo9A_	Alignment	not modelled	7.6	46	PDB header: toxin Chain: A: PDB Molecule: mu-conotoxin buiib; PDBTitle: nmr solution structure of mu-contoxin buiib
52	c5ndcD_	Alignment	not modelled	7.5	24	PDB header: oxidoreductase Chain: D: PDB Molecule: methyl-viologen reducing hydrogenase subunit d;

52	c300cD	Alignment	not modelled	7.3	24	PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
53	c3umgD	Alignment	not modelled	7.5	16	PDB header: hydrolase Chain: D: PDB Molecule: haloacid dehalogenase; PDBTitle: crystal structure of the defluorinating I-2-haloacid dehalogenase2 rha0230
54	d2cupa1	Alignment	not modelled	7.3	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
55	c3cnyA	Alignment	not modelled	7.1	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: inositol catabolism protein iole; PDBTitle: crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcf51 at 1.85 a3 resolution
56	c2qtxL	Alignment	not modelled	7.1	50	PDB header: rna binding protein Chain: L: PDB Molecule: uncharacterized protein mj1435; PDBTitle: crystal structure of an hfq-like protein from methanococcus jannaschii
57	d1x63a1	Alignment	not modelled	6.5	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
58	d1wnaa1	Alignment	not modelled	6.4	24	Fold: TTHA1528-like Superfamily: TTHA1528-like Family: TTHA1528-like
59	c3be3A	Alignment	not modelled	6.3	28	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of a protein belonging to pfam duf16532 from bordetella bronchiseptica
60	c2kzvA	Alignment	not modelled	6.1	20	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution nmr structure of cv_0373(175-257) protein from2 chromobacterium violaceum, northeast structural genomics consortium3 target cvr118a
61	c2h6rG	Alignment	not modelled	6.1	19	PDB header: isomerase Chain: G: PDB Molecule: triosephosphate isomerase; PDBTitle: crystal structure of triosephosphate isomerase (tim) from2 methanocaldococcus jannaschii
62	d1nhkL	Alignment	not modelled	6.1	12	Fold: Ferredoxin-like Superfamily: Nucleoside diphosphate kinase, NDK Family: Nucleoside diphosphate kinase, NDK
63	d1hg3a	Alignment	not modelled	6.1	13	Fold: TIM beta/alpha-barrel Superfamily: Triosephosphate isomerase (TIM) Family: Triosephosphate isomerase (TIM)
64	c1zq1B	Alignment	not modelled	6.0	9	PDB header: lyase Chain: B: PDB Molecule: glutamyl-trna(gln) amidotransferase subunit d; PDBTitle: structure of gatde trna-dependent amidotransferase from2 pyrococcus abyssi
65	c2cftA	Alignment	not modelled	5.9	17	PDB header: phosphatase Chain: A: PDB Molecule: pyridoxal phosphate phosphatase; PDBTitle: crystal structure of human pyridoxal 5'-phosphate2 phosphatase with its substrate
66	c2h90A	Alignment	not modelled	5.8	24	PDB header: oxidoreductase Chain: A: PDB Molecule: xenobiotic reductase a; PDBTitle: xenobiotic reductase a in complex with coumarin
67	c3cnhA	Alignment	not modelled	5.7	23	PDB header: hydrolase Chain: A: PDB Molecule: hydrolase family protein; PDBTitle: crystal structure of predicted hydrolase of haloacid dehalogenase-like2 superfamily (np_295428.1) from deinococcus radiodurans at 1.66 a3 resolution
68	c2locA	Alignment	not modelled	5.7	46	PDB header: toxin Chain: A: PDB Molecule: mu-conotoxin buiib; PDBTitle: conotoxin analogue [d-ala2]buiib
69	c6adqP	Alignment	not modelled	5.7	43	PDB header: electron transport Chain: P: PDB Molecule: prokaryotic respiratory supercomplex associate factor 1 PDBTitle: respiratory complex ciii2civ2sod2 from mycobacterium smegmatis
70	d1w5ra1	Alignment	not modelled	5.5	18	Fold: Cysteine proteinases Superfamily: Cysteine proteinases Family: Arylamine N-acetyltransferase
71	c3ju2A	Alignment	not modelled	5.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein smc04130; PDBTitle: crystal structure of protein smc04130 from sinorhizobium meliloti 1021
72	c2pr7A	Alignment	not modelled	5.4	12	PDB header: hydrolase Chain: A: PDB Molecule: haloacid dehalogenase/epoxide hydrolase family; PDBTitle: crystal structure of uncharacterized protein (np_599989.1) from2 corynebacterium glutamicum atcc 13032 kitasato at 1.44 a resolution
73	d1u7pa	Alignment	not modelled	5.4	16	Fold: HAD-like Superfamily: HAD-like Family: Magnesium-dependent phosphatase-1, Mdp1
74	d1t5ia	Alignment	not modelled	5.2	17	Fold: P-loop containing nucleoside triphosphate hydrolases Superfamily: P-loop containing nucleoside triphosphate hydrolases Family: Tandem AAA-ATPase domain
75	d2o2xa1	Alignment	not modelled	5.2	13	Fold: HAD-like Superfamily: HAD-like Family: Histidinol phosphatase-like