










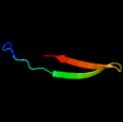
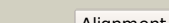
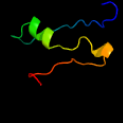
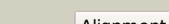


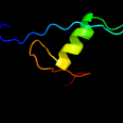



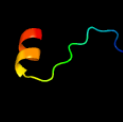
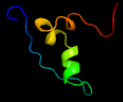
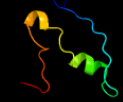
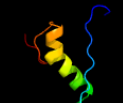
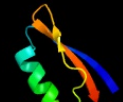
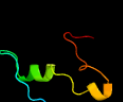



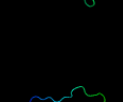


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0316 (-) _384535_385149
Date	Tue Jul 23 14:50:38 BST 2019
Unique Job ID	f822e8a3d4fb1fd1

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1mlia_	 Alignment		100.0	26	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Muconalactone isomerase, MLI
2	c3znul_	 Alignment		100.0	38	PDB header: lyase Chain: I: PDB Molecule: 5-chloromuconolactone dehalogenase; PDBTitle: crystal structure of clcf in crystal form 2
3	d1s7ia_	 Alignment		68.2	22	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: DGPF domain (Pfam 04946)
4	c4lbhA_	 Alignment		66.0	22	PDB header: lyase Chain: A: PDB Molecule: 5-chloro-2-hydroxyhydroquinone dehydrochlorinase (tftg); PDBTitle: 5-chloro-2-hydroxyhydroquinone dehydrochlorinase (tftg) from2 burkholderia phenoliruptrix ac1100: apo-form
5	d2cfxa2	 Alignment		57.9	9	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
6	d1vpra1	 Alignment		39.3	43	Fold: Lipocalins Superfamily: Lipocalins Family: Dinoflagellate luciferase repeat
7	d8ruca2	 Alignment		39.1	28	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
8	d1mwqa_	 Alignment		37.0	14	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Ycil-like
9	d1gk8a2	 Alignment		36.2	28	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
10	d1bxna2	 Alignment		35.4	23	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
11	c2n3zA_	 Alignment		34.7	15	PDB header: structural genomics, de novo protein Chain: A: PDB Molecule: or446; PDBTitle: solution nmr structure of de novo designed protein, rossmann2x2 fold,2 northeast structural genomics consortium (nesg) target or446

12	d1rbla2	Alignment		34.2	31	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
13	d1bwva2	Alignment		31.9	23	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
14	d1svda2	Alignment		31.3	26	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
15	d1p9qc3	Alignment		24.3	16	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain
16	c1bwvA_	Alignment		23.9	23	PDB header: lyase Chain: A: PDB Molecule: protein (ribulose bisphosphate carboxylase); PDBTitle: activated ribulose 1,5-bisphosphate carboxylase/oxygenase (rubisco)2 complexed with the reaction intermediate analogue 2-carboxyarabinitol3 1,5-bisphosphate
17	c3we7A_	Alignment		23.5	18	PDB header: hydrolase Chain: A: PDB Molecule: putative uncharacterized protein ph0499; PDBTitle: crystal structure of diacetylchitobiose deacetylase from pyrococcus2 horikoshii
18	c5bmoB_	Alignment		20.0	23	PDB header: hydrolase Chain: B: PDB Molecule: putative uncharacterized protein Inmx; PDBTitle: Inmx protein, a putative glcnac-pi de-n-acetylase from streptomyces2 atroolivaceus
19	d1wdda2	Alignment		18.3	31	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
20	c4exqA_	Alignment		16.2	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase (upd) from2 burkholderia thailandensis e264
21	c5cqaA_	Alignment	not modelled	16.2	21	PDB header: lyase Chain: A: PDB Molecule: 4-oxalmesaconate hydratase; PDBTitle: crystal structure of galb, the 4-carboxy-2-hydroxymuconate hydratase,2 from pseudomonas putida kt2440
22	d1q7sa_	Alignment	not modelled	16.2	23	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
23	d1geha2	Alignment	not modelled	15.6	19	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
24	d1x1na1	Alignment	not modelled	15.5	21	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
25	d1t95a3	Alignment	not modelled	15.4	16	Fold: Ferredoxin-like Superfamily: EF-G C-terminal domain-like Family: Hypothetical protein AF0491, C-terminal domain
26	c4oi6A_	Alignment	not modelled	13.9	9	PDB header: metal binding protein Chain: A: PDB Molecule: nickel responsive protein; PDBTitle: crystal structure analysis of nickel-bound form sco4226 from2 streptomyces coelicolor a3(2)
27	c2zv3E_	Alignment	not modelled	13.6	15	PDB header: hydrolase Chain: E: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of project mj0051 from methanocaldococcus2 jannaschii dsm 2661
28	d1tz7a1	Alignment	not modelled	13.5	24	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
						PDB header: transferase

29	c5m6qA_	Alignment	not modelled	12.3	36	Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of kutzneria albida transglutaminase
30	d1eswa_	Alignment	not modelled	11.5	15	Fold: TIM beta/alpha-barrel Superfamily: (Trans)glycosidases Family: Amylase, catalytic domain
31	c3mlhA_	Alignment	not modelled	11.3	28	PDB header: viral protein Chain: A: PDB Molecule: hemagglutinin; PDBTitle: crystal structure of the 2009 h1n1 influenza virus hemagglutinin2 receptor-binding domain
32	c2ixdB_	Alignment	not modelled	11.2	21	PDB header: hydrolase Chain: B: PDB Molecule: lmbe-related protein; PDBTitle: crystal structure of the putative deacetylase bc1534 from bacillus2 cereus
33	d1iyjb4	Alignment	not modelled	11.0	45	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Single strand DNA-binding domain, SSB
34	c2e1aD_	Alignment	not modelled	10.8	22	PDB header: transcription Chain: D: PDB Molecule: 75aa long hypothetical regulatory protein asnc; PDBTitle: crystal structure of ffrp-dm1
35	c2wzoA_	Alignment	not modelled	10.7	22	PDB header: cell cycle Chain: A: PDB Molecule: transforming growth factor beta regulator 1; PDBTitle: the structure of the fyr domain
36	c3c8dA_	Alignment	not modelled	10.7	14	PDB header: hydrolase Chain: A: PDB Molecule: enterochelin esterase; PDBTitle: crystal structure of the enterobactin esterase fes from2 shigella flexneri in the presence of 2,3-di-hydroxy-n-3 benzoyl-glycine
37	c3w66A_	Alignment	not modelled	10.3	19	PDB header: metal transport Chain: A: PDB Molecule: magnetosome protein mamm; PDBTitle: mamm-ctd d249a and h285a
38	c5zx1A_	Alignment	not modelled	9.9	28	PDB header: transcription Chain: A: PDB Molecule: ent; PDBTitle: crystal structure of ent domain from t. brucei
39	d1t1ja_	Alignment	not modelled	9.6	24	Fold: Flavodoxin-like Superfamily: N-(deoxy)ribosyltransferase-like Family: Hypothetical protein PA1492
40	d1vqod1	Alignment	not modelled	9.1	25	Fold: RL5-like Superfamily: RL5-like Family: Ribosomal protein L5
41	c3g36D_	Alignment	not modelled	9.0	35	PDB header: nuclear protein Chain: D: PDB Molecule: protein dpy-30 homolog; PDBTitle: crystal structure of the human dpy-30-like c-terminal domain
42	d2puza1	Alignment	not modelled	9.0	23	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
43	c2m09A_	Alignment	not modelled	8.9	13	PDB header: transcription Chain: A: PDB Molecule: splicing factor 1; PDBTitle: structure, phosphorylation and u2af65 binding of the nterminal domain2 of splicing factor 1 during 3 splice site recognition
44	d1xbwa_	Alignment	not modelled	8.7	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: PG130-like
45	c2vsaA_	Alignment	not modelled	8.7	25	PDB header: toxin Chain: A: PDB Molecule: mosquitocidal toxin; PDBTitle: structure and mode of action of a mosquitocidal holotoxin
46	c3ez1A_	Alignment	not modelled	8.2	22	PDB header: transferase Chain: A: PDB Molecule: aminotransferase mocr family; PDBTitle: crystal structure of putative aminotransferase (mocr family)2 (yp_604413.1) from deinococcus geothermalis dsm 11300 at 2.60 a3 resolution
47	c4ogeA_	Alignment	not modelled	8.1	12	PDB header: hydrolase Chain: A: PDB Molecule: hnh endonuclease domain protein; PDBTitle: crystal structure of the type ii-c cas9 enzyme from actinomyces2 naeslundii
48	c5macD_	Alignment	not modelled	8.1	16	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
49	c3zm8A_	Alignment	not modelled	8.0	23	PDB header: hydrolase Chain: A: PDB Molecule: gh26 endo-beta-1,4-mannanase; PDBTitle: crystal structure of podospora anserina gh26-cbm352 beta-(1,4)-mannanase
50	d2ikba1	Alignment	not modelled	8.0	63	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: NMB1012-like
51	d1vzia1	Alignment	not modelled	7.9	25	Fold: Immunoglobulin-like beta-sandwich Superfamily: Superoxide reductase-like Family: Superoxide reductase-like
52	d2q09a1	Alignment	not modelled	7.9	35	Fold: Composite domain of metallo-dependent hydrolases Superfamily: Composite domain of metallo-dependent hydrolases Family: Imidazolonepropionase-like
53	c1gehE_	Alignment	not modelled	7.8	19	PDB header: lyase Chain: E: PDB Molecule: ribulose-1,5-bisphosphate carboxylase/oxygenase; PDBTitle: crystal structure of archaeal rubisco (ribulose 1,5-bisphosphate2 carboxylase/oxygenase)
54	c2djwF_	Alignment	not modelled	7.6	16	PDB header: unknown function Chain: F: PDB Molecule: probable transcriptional regulator, asnc family; PDBTitle: crystal structure of ttha0845 from thermus thermophilus

						hb8
55	d1dfxa1	Alignment	not modelled	7.5	33	Fold: Immunoglobulin-like beta-sandwich Superfamily: Superoxide reductase-like Family: Superoxide reductase-like
56	c3cyvA	Alignment	not modelled	7.1	13	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: crystal structure of uroporphyrinogen decarboxylase from <i>Shigella flexneri</i> : new insights into its catalytic mechanism
57	c3j1zP	Alignment	not modelled	6.9	9	PDB header: metal transport Chain: P: PDB Molecule: cation efflux family protein; PDBTitle: inward-facing conformation of the zinc transporter YiiP revealed by 2 cryo-electron microscopy
58	d2nr7a1	Alignment	not modelled	6.8	38	Fold: Lysozyme-like Superfamily: Lysozyme-like Family: NMB1012-like
59	c5ho5D	Alignment	not modelled	6.7	15	PDB header: metal transport Chain: D: PDB Molecule: magnetosome protein Mamb; PDBTitle: mamb
60	c5vfkA	Alignment	not modelled	6.6	29	PDB header: unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of an archaeal Duf61 family protein Sso0941
61	c2d3kA	Alignment	not modelled	6.6	20	PDB header: hydrolase Chain: A: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: structural study on project ID PH1539 from <i>Pyrococcus horikoshii</i> OT3
62	d1r3sa	Alignment	not modelled	6.6	11	Fold: TIM beta/alpha-barrel Superfamily: UROD/MetE-like Family: Uroporphyrinogen decarboxylase, UROD
63	c1rcxH	Alignment	not modelled	6.6	28	PDB header: lyase (carbon-carbon) Chain: H: PDB Molecule: ribulose biphosphate carboxylase/oxygenase; PDBTitle: non-activated spinach Rubisco in complex with its substrate 2-ribulose-1,5-bisphosphate
64	c6c23C	Alignment	not modelled	6.4	26	PDB header: gene regulation Chain: C: PDB Molecule: histone-lysine N-methyltransferase Ezh2; PDBTitle: cryo-EM structure of PRC2 bound to cofactors Aebp2 and Jarid2 in the 2 compact active state
65	c4f15D	Alignment	not modelled	6.2	28	PDB header: immune system Chain: D: PDB Molecule: hemagglutinin; PDBTitle: molecular basis of infectivity of 2009 pandemic H1N1 influenza A2 viruses
66	c5nhuJ	Alignment	not modelled	6.1	38	PDB header: hydrolase Chain: J: PDB Molecule: agap008004-pa; PDBTitle: human alpha-thrombin complexed with Anopheles gambiae Ce52 anticoagulant
67	d1s0pa	Alignment	not modelled	6.1	45	Fold: N-terminal domain of adenylyl cyclase associated protein, CAP Superfamily: N-terminal domain of adenylyl cyclase associated protein, CAP Family: N-terminal domain of adenylyl cyclase associated protein, CAP
68	c4fayC	Alignment	not modelled	6.0	20	PDB header: glycerol-binding protein Chain: C: PDB Molecule: microcompartments protein; PDBTitle: crystal structure of a trimeric bacterial microcompartment shell 2 protein PduB with glycerol metabolites
69	d2d69a2	Alignment	not modelled	5.9	18	Fold: Ferredoxin-like Superfamily: RuBisCO, large subunit, small (N-terminal) domain Family: Ribulose 1,5-bisphosphate carboxylase-oxygenase
70	d1rka	Alignment	not modelled	5.9	15	Fold: Peptidyl-tRNA hydrolase II Superfamily: Peptidyl-tRNA hydrolase II Family: Peptidyl-tRNA hydrolase II
71	c6hpfA	Alignment	not modelled	5.9	19	PDB header: hydrolase Chain: A: PDB Molecule: endo-beta-mannanase; PDBTitle: structure of inactive E165Q mutant of fungal non-CBM carrying Gh262 endo-beta-mannanase from <i>Yunnania penicillata</i> in complex with alpha-6,2-3,6,1-di-galactosyl-mannotriose
72	c5nhuL	Alignment	not modelled	5.9	75	PDB header: hydrolase Chain: I: PDB Molecule: agap008004-pa; PDBTitle: human alpha-thrombin complexed with Anopheles gambiae Ce52 anticoagulant
73	c1jpkA	Alignment	not modelled	5.8	11	PDB header: lyase Chain: A: PDB Molecule: uroporphyrinogen decarboxylase; PDBTitle: gly156asp mutant of human UROD, human uroporphyrinogen III decarboxylase
74	c5iohB	Alignment	not modelled	5.7	33	PDB header: hydrolase/protein binding Chain: B: PDB Molecule: cell division cycle-associated protein 2; PDBTitle: Repoman-pp1a (protein phosphatase 1, alpha isoform) holoenzyme complex
75	c1xtyD	Alignment	not modelled	5.7	18	PDB header: hydrolase Chain: D: PDB Molecule: peptidyl-trna hydrolase; PDBTitle: crystal structure of <i>Sulfolobus solfataricus</i> peptidyl-trna hydrolase
76	d2cyya2	Alignment	not modelled	5.6	16	Fold: Ferredoxin-like Superfamily: Dimeric alpha+beta barrel Family: Lrp/AsnC-like transcriptional regulator C-terminal domain
77	d3bypa1	Alignment	not modelled	5.6	19	Fold: Alpha-lytic protease prodomain-like Superfamily: Cation efflux protein cytoplasmic domain-like Family: Cation efflux protein cytoplasmic domain-like
78	c6qekB	Alignment	not modelled	5.5	18	PDB header: transport protein Chain: B: PDB Molecule: magnetosome protein; PDBTitle: putative membrane transporter, magnetosome protein Mamm Ctd2 [desulfamplus magnetovallimortis bw-1]
79	c2zztA	Alignment	not modelled	5.4	12	PDB header: transport protein Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of the cytosolic domain of the cation 2 diffusion facilitator family protein
						Fold: alpha/beta-Hydrolases

80	d3c8da2	Alignment	not modelled	5.4	14	Superfamily: alpha/beta-Hydrolases Family: Carboxylesterase
81	d1sdwa1	Alignment	not modelled	5.2	15	Fold: Nucleoplasmin-like/MP (viral coat and capsid proteins) Superfamily: PHM/PNGase F Family: Peptidylglycine alpha-hydroxylating monooxygenase, PHM
82	d1k4ia_	Alignment	not modelled	5.2	18	Fold: YrdC/RibB Superfamily: YrdC/RibB Family: 3,4-dihydroxy-2-butanone 4-phosphate synthase, DHBP synthase, RibB
83	c5j28C_	Alignment	not modelled	5.2	33	PDB header: hydrolase/protein binding Chain: C: PDB Molecule: antigen ki-67; PDBTitle: ki67-pp1g (protein phosphatase 1, gamma isoform) holoenzyme complex
84	c3di4A_	Alignment	not modelled	5.2	24	PDB header: metal binding protein Chain: A: PDB Molecule: uncharacterized protein duf1989; PDBTitle: crystal structure of a duf1989 family protein (spo0365) from2 silicibacter pomeroyi dss-3 at 1.60 a resolution
85	d1uzhc1	Alignment	not modelled	5.1	30	Fold: RuBisCO, small subunit Superfamily: RuBisCO, small subunit Family: RuBisCO, small subunit
86	c3oruA_	Alignment	not modelled	5.1	14	PDB header: metal binding protein Chain: A: PDB Molecule: duf1989 family protein; PDBTitle: crystal structure of a duf1989 family protein (tm1040_0329) from2 silicibacter sp. tm1040 at 1.11 a resolution