




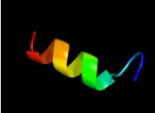







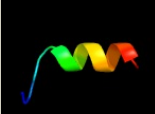

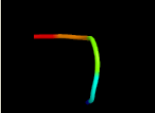



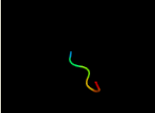


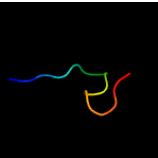
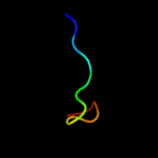
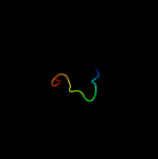



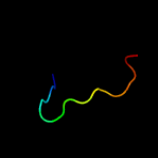
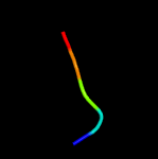
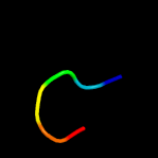


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1616_(-)_1815690_1816088
Date	Fri Aug 2 13:30:21 BST 2019
Unique Job ID	1c4558b4f6246948

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5b46B_	 Alignment		70.8	47	PDB header: oxidoreductase Chain: B: PDB Molecule: 2-oxoacid--ferredoxin oxidoreductase beta subunit; PDBTitle: 2-oxoacid:ferredoxin oxidoreductase 2 from sulfolobus tokodai - ligand2 free form
2	c6n2oB_	 Alignment		55.2	25	PDB header: oxidoreductase Chain: B: PDB Molecule: pyruvate ferredoxin/ flavodoxin oxidoreductase, beta PDBTitle: 2-oxoglutarate:ferredoxin oxidoreductase from magnetococcus marinus2 with 2-oxoglutarate, coenzyme a and succinyl-coa bound
3	c5c4iC_	 Alignment		45.8	20	PDB header: oxidoreductase Chain: C: PDB Molecule: oxalate oxidoreductase subunit beta; PDBTitle: structure of an oxalate oxidoreductase
4	c5i9wC_	 Alignment		39.8	43	PDB header: ligase Chain: C: PDB Molecule: acetophenone carboxylase beta subunit; PDBTitle: crystal structure of the apc core complex
5	c5m45I_	 Alignment		35.8	50	PDB header: ligase Chain: I: PDB Molecule: acetone carboxylase gamma subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus
6	c5yf1A_	 Alignment		28.8	20	PDB header: transferase Chain: A: PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of carnmt1 bound to carnosine and sfg
7	d2c42a2	 Alignment		25.8	20	Fold: Thiamin diphosphate-binding fold (THDP-binding) Superfamily: Thiamin diphosphate-binding fold (THDP-binding) Family: PFOR PP module
8	c2jm2A_	 Alignment		24.7	80	PDB header: hormone/growth factor Chain: A: PDB Molecule: insulin-like growth factor-binding protein 6; PDBTitle: structure of the n-terminal subdomain of insulin-like2 growth factor (igf) binding protein-6 and its interactions3 with igfs
9	c3ju6A_	 Alignment		23.3	33	PDB header: transferase Chain: A: PDB Molecule: arginine kinase; PDBTitle: crystal structure of dimeric arginine kinase in complex with2 ampnpn and arginine
10	c2crcA_	 Alignment		22.3	71	PDB header: ligase Chain: A: PDB Molecule: ubiquitin conjugating enzyme 7 interacting PDBTitle: solution structure of the zf-ranbp domain of the protein2 hbv associated factor
11	c4o9pC_	 Alignment		22.2	24	PDB header: membrane protein Chain: C: PDB Molecule: nad(p) transhydrogenase subunit alpha 2; PDBTitle: crystal structure of thermus thermophilis transhydrogeanse domain ii2 dimer semet derivative

12	c3l2eB_	Alignment		20.3	33	PDB header: transferase Chain: B; PDB Molecule: glycoamine kinase beta chain; PDBTitle: glycoamine kinase, alpha-beta heterodimer from marine worm2 namalycastis sp.
13	c3zqjF_	Alignment		18.2	38	PDB header: dna binding protein Chain: F; PDB Molecule: uvrbc system protein a; PDBTitle: mycobacterium tuberculosis uvra
14	d1crka2	Alignment		17.6	33	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
15	c1i0eD_	Alignment		17.1	33	PDB header: transferase Chain: D; PDB Molecule: creatine kinase,m chain; PDBTitle: crystal structure of creatine kinase from human muscle
16	c3na7A_	Alignment		17.0	67	PDB header: gene regulation, chaperone Chain: A; PDB Molecule: hp0958; PDBTitle: 2.2 angstrom structure of the hp0958 protein from helicobacter pylori2 ccug 17874
17	d1vd4a_	Alignment		15.9	38	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
18	c2a45L_	Alignment		15.7	38	PDB header: hydrolase/hydrolase inhibitor Chain: L; PDB Molecule: fibrinogen gamma chain; PDBTitle: crystal structure of the complex between thrombin and the central "e"2 region of fibrin
19	c2y0fD_	Alignment		15.5	80	PDB header: oxidoreductase Chain: D; PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: structure of gcpe (ispg) from thermus thermophilus hb27
20	c1nuiA_	Alignment		15.3	50	PDB header: replication Chain: A; PDB Molecule: dna primase/helicase; PDBTitle: crystal structure of the primase fragment of bacteriophage t7 primase-2 helicase protein
21	d2dlqa2	Alignment	not modelled	15.3	57	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
22	d1u6ra2	Alignment	not modelled	14.8	31	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
23	c1r19A_	Alignment	not modelled	14.7	38	PDB header: transferase Chain: A; PDB Molecule: arginine kinase; PDBTitle: crystal structure of creatine-adi arginine kinase ternary2 complex
24	d1g0wa2	Alignment	not modelled	14.7	46	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
25	d1qh4a2	Alignment	not modelled	14.7	46	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
26	d1m15a2	Alignment	not modelled	14.5	38	Fold: Glutamine synthetase/guanido kinase Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
27	c2n1pA_	Alignment	not modelled	14.0	24	PDB header: viral protein Chain: A; PDB Molecule: non-structural protein 5b, ns5b; PDBTitle: structure of the c-terminal membrane domain of hcv ns5b protein
28	c5x62A_	Alignment	not modelled	13.7	40	PDB header: transferase Chain: A; PDB Molecule: carnosine n-methyltransferase; PDBTitle: crystal structure of a carnosine n-methyltransferase bound by adohcy
						Fold: Glutamine synthetase/guanido kinase

29	d1vrpa2	Alignment	not modelled	13.6	38	Superfamily: Glutamine synthetase/guanido kinase Family: Guanido kinase catalytic domain
30	c1wcoN	Alignment	not modelled	13.6	50	PDB header: peptide/antibiotic Chain: N: PDB Molecule: nisin z; PDBTitle: the solution structure of the nisin-lipid ii complex
31	d1x4la2	Alignment	not modelled	13.4	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
32	d1k82a3	Alignment	not modelled	13.3	36	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
33	c1qk1H	Alignment	not modelled	13.3	31	PDB header: transferase (creatine kinase) Chain: H: PDB Molecule: creatine kinase, ubiquitous mitochondrial; PDBTitle: crystal structure of human ubiquitous mitochondrial creatine kinase
34	c6fh2A	Alignment	not modelled	13.1	31	PDB header: signaling protein Chain: A: PDB Molecule: protein-arginine kinase; PDBTitle: protein arginine kinase mcsb in the amp-pn-bound state
35	d1ee8a3	Alignment	not modelled	13.0	24	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
36	c4iloA	Alignment	not modelled	13.0	29	PDB header: unknown function Chain: A: PDB Molecule: ct398; PDBTitle: 2.12a resolution structure of ct398 from chlamydia trachomatis
37	c3noyA	Alignment	not modelled	12.9	80	PDB header: oxidoreductase Chain: A: PDB Molecule: 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase; PDBTitle: crystal structure of ispg (gcpe)
38	c3a44D	Alignment	not modelled	12.7	50	PDB header: metal binding protein Chain: D: PDB Molecule: hydrogenase nickel incorporation protein hypa; PDBTitle: crystal structure of hypa in the dimeric form
39	d1k18a	Alignment	not modelled	12.6	75	Fold: Zinc finger domain of DNA polymerase-alpha Superfamily: Zinc finger domain of DNA polymerase-alpha Family: Zinc finger domain of DNA polymerase-alpha
40	d1k3xa3	Alignment	not modelled	12.4	36	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
41	c3hkzP	Alignment	not modelled	12.3	60	PDB header: transferase Chain: P: PDB Molecule: dna-directed rna polymerase subunit p; PDBTitle: the x-ray crystal structure of rna polymerase from archaea
42	c3b08H	Alignment	not modelled	12.3	71	PDB header: signaling protein/metal binding protein Chain: H: PDB Molecule: ranbp-type and c3hc4-type zinc finger-containing protein 1; PDBTitle: crystal structure of the mouse hoil1-l-nzf in complex with linear di-2 ubiquitin
43	c5o9zN	Alignment	not modelled	12.2	38	PDB header: splicing Chain: N: PDB Molecule: zinc finger matr-in-type protein 2; PDBTitle: cryo-em structure of a pre-catalytic human spliceosome primed for 2 activation (b complex)
44	c2bx9J	Alignment	not modelled	12.0	67	PDB header: transcription regulation Chain: J: PDB Molecule: tryptophan rna-binding attenuator protein-inhibitory PDBTitle: crystal structure of b.subtilis anti-trap protein, an2 antagonist of trap-rna interactions
45	d1dgsa1	Alignment	not modelled	11.9	57	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: NAD+-dependent DNA ligase, domain 3
46	c1vw4W	Alignment	not modelled	11.8	80	PDB header: ribosome Chain: W: PDB Molecule: 54s ribosomal protein l32, mitochondrial; PDBTitle: structure of the yeast mitochondrial large ribosomal subunit
47	d1l1ta3	Alignment	not modelled	11.7	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
48	c5fywW	Alignment	not modelled	11.6	33	PDB header: transcription Chain: W: PDB Molecule: transcription initiation factor iie subunit alpha; PDBTitle: transcription initiation complex structures elucidate dna opening (oc)
49	c1x31D	Alignment	not modelled	11.6	57	PDB header: oxidoreductase Chain: D: PDB Molecule: sarcosine oxidase delta subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from 2 corynebacterium sp. u-96
50	d1tdza3	Alignment	not modelled	11.2	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
51	c2kveA	Alignment	not modelled	11.1	43	PDB header: hormone Chain: A: PDB Molecule: mesencephalic astrocyte-derived neurotrophic factor; PDBTitle: c-terminal domain of mesencephalic astrocyte-derived neurotrophic2 factor (manf)
52	c6cipD	Alignment	not modelled	11.0	20	PDB header: oxidoreductase Chain: D: PDB Molecule: pyruvate-ferredoxin oxidoreductase; PDBTitle: pyruvate:ferredoxin oxidoreductase from moorella thermoacetica with 2 acetyl-tpp bound
53	c4esjA	Alignment	not modelled	10.7	50	PDB header: hydrolase/dna Chain: A: PDB Molecule: type-2 restriction enzyme dpni; PDBTitle: restriction endonuclease dpni in complex with target dna
54	c2c3vA	Alignment	not modelled	10.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: pyruvate-ferredoxin oxidoreductase;

54	c2c3yA	Alignment	not modelled	10.8	20	PDBTitle: crystal structure of the radical form of2 pyruvate:ferredoxin oxidoreductase from desulfovibrio3 africanus PDB header: transferase
55	c3jq3A	Alignment	not modelled	10.6	23	Chain: A; PDB Molecule: lombricine kinase; PDBTitle: crystal structure of lombricine kinase, complexed with substrate adp
56	d1nuia2	Alignment	not modelled	10.5	43	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: DNA primase zinc finger
57	d1r2za3	Alignment	not modelled	10.3	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: C-terminal, Zn-finger domain of MutM-like DNA repair proteins
58	d1m3va1	Alignment	not modelled	10.2	45	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
59	c2opfA	Alignment	not modelled	9.8	44	PDB header: hydrolase/dna Chain: A; PDB Molecule: endonuclease viii; PDBTitle: crystal structure of the dna repair enzyme endonuclease-viii (nei)2 from e. coli (r252a) in complex with ap-site containing dna substrate
60	c2kdxA	Alignment	not modelled	9.6	33	PDB header: metal-binding protein Chain: A; PDB Molecule: hydrogenase/urease nickel incorporation protein PDBTitle: solution structure of hypa protein
61	d1pfta	Alignment	not modelled	9.2	50	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
62	c5y06A	Alignment	not modelled	9.0	57	PDB header: unknown function Chain: A; PDB Molecule: msmeg_4306; PDBTitle: structural characterization of msmeg_4306 from mycobacterium smegmatis
63	d1dxsa	Alignment	not modelled	9.0	67	Fold: SAM domain-like Superfamily: SAM/Pointed domain Family: SAM (sterile alpha motif) domain
64	c2epqA	Alignment	not modelled	8.8	33	PDB header: transcription Chain: A; PDB Molecule: poz-, at hook-, and zinc finger-containing PDBTitle: solution structure of the third zinc finger domain of zinc2 finger protein 278
65	d1dl6a	Alignment	not modelled	8.7	22	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
66	d1nj8a3	Alignment	not modelled	8.4	31	Fold: Class II aaRS and biotin synthetases Superfamily: Class II aaRS and biotin synthetases Family: Class II aminoacyl-tRNA synthetase (aaRS)-like, catalytic domain
67	c4v195	Alignment	not modelled	8.3	80	PDB header: ribosome Chain: 5; PDB Molecule: mitoribosomal protein bl32m, mrpl32; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
68	d1h7va	Alignment	not modelled	8.3	33	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
69	c6o9lQ	Alignment	not modelled	8.2	38	PDB header: transcription/dna Chain: Q; PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the closed state
70	c6o3pA	Alignment	not modelled	8.1	67	PDB header: hydrolase Chain: A; PDB Molecule: peroxisomal nadh pyrophosphatase nudt12; PDBTitle: crystal structure of the catalytic domain of mouse nudt12 in complex2 with amp and 3 mg2+ ions
71	c2f5qA	Alignment	not modelled	8.1	44	PDB header: hydrolase/dna Chain: A; PDB Molecule: formamidopyrimidine-dna glycosidase; PDBTitle: catalytically inactive (e3q) mutm crosslinked to oxog:c2 containing dna cc2
72	c4wo8A	Alignment	not modelled	8.1	38	PDB header: transferase Chain: A; PDB Molecule: taurocyamine kinase; PDBTitle: the substrate-free duplicated taurocyamine kinase from schistosoma2 mansoni
73	c2mrfA	Alignment	not modelled	8.0	50	PDB header: ligase Chain: A; PDB Molecule: e3 ubiquitin-protein ligase rad18; PDBTitle: nmr structure of the ubiquitin-binding zinc finger (ubz) domain from2 human rad18
74	c3zywB	Alignment	not modelled	8.0	31	PDB header: metal binding protein Chain: B; PDB Molecule: glutaredoxin-3; PDBTitle: crystal structure of the first glutaredoxin domain of human2 glutaredoxin 3 (glrx3)
75	d1ywsa1	Alignment	not modelled	8.0	67	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
76	c2vf7B	Alignment	not modelled	7.9	38	PDB header: dna binding protein Chain: B; PDB Molecule: excinuclease abc, subunit a.; PDBTitle: crystal structure of uvra2 from deinococcus radiodurans
77	c3rpfC	Alignment	not modelled	7.9	43	PDB header: transferase Chain: C; PDB Molecule: molybdopterin converting factor, subunit 1 (moad); PDBTitle: protein-protein complex of subunit 1 and 2 of molybdopterin-converting2 factor from helicobacter pylori 26695
78	c5y4uA	Alignment	not modelled	7.8	28	PDB header: oxidoreductase Chain: A; PDB Molecule: monothiol glutaredoxin-3; PDBTitle: crystal structure of grx domain of grx3 from saccharomyces cerevisiae
79	c2k5cA	Alignment	not modelled	7.8	57	PDB header: metal binding protein Chain: A; PDB Molecule: uncharacterized protein pf0385; PDBTitle: nmr structure for pf0385
						PDB header: oxidoreductase

80	c2v3bB	Alignment	not modelled	7.7	25	Chain: B: PDB Molecule: rubredoxin 2; PDBTitle: crystal structure of the electron transfer complex rubredoxin -2 rubredoxin reductase from pseudomonas aeruginosa.
81	c3mjhd	Alignment	not modelled	7.7	57	PDB header: protein transport Chain: D: PDB Molecule: early endosome antigen 1; PDBTitle: crystal structure of human rab5a in complex with the c2h2 zinc finger2 of eea1
82	c4ce45	Alignment	not modelled	7.6	80	PDB header: ribosome Chain: 5: PDB Molecule: mrpl32; PDBTitle: 39s large subunit of the porcine mitochondrial ribosome
83	d2cu8a1	Alignment	not modelled	7.6	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
84	c2kn9A	Alignment	not modelled	7.5	25	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin; PDBTitle: solution structure of zinc-substituted rubredoxin b (rv3250c) from mycobacterium tuberculosis. seattle structural genomics center for infectious disease target mytud.01635.a
85	d2ct1a1	Alignment	not modelled	7.5	38	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
86	d1qcva	Alignment	not modelled	7.4	42	Fold: Rubredoxin-like Superfamily: Rubredoxin-like Family: Rubredoxin
87	d1hk8a	Alignment	not modelled	7.4	50	Fold: PFL-like glycol radical enzymes Superfamily: PFL-like glycol radical enzymes Family: Class III anaerobic ribonucleotide reductase NRDD subunit
88	c1hk8A	Alignment	not modelled	7.4	50	PDB header: oxidoreductase Chain: A: PDB Molecule: anaerobic ribonucleotide-triphosphate reductase; PDBTitle: structural basis for allosteric substrate specificity regulation in class iii ribonucleotide reductases: nrdd in complex with dgtp
89	d1wiia	Alignment	not modelled	7.4	44	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Putative zinc binding domain
90	c2kkhA	Alignment	not modelled	7.4	22	PDB header: metal transport Chain: A: PDB Molecule: putative heavy metal transporter; PDBTitle: structure of the zinc binding domain of the atpase hma4
91	d1wgea1	Alignment	not modelled	7.4	67	Fold: Rubredoxin-like Superfamily: CSL zinc finger Family: CSL zinc finger
92	c1ee8A	Alignment	not modelled	7.4	67	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermophilus hb8
93	c5ywrB	Alignment	not modelled	7.3	44	PDB header: signaling protein Chain: B: PDB Molecule: e3 ubiquitin-protein ligase znrf1; PDBTitle: crystal structure of ring e3 ligase znrf1 in complex with ube2n2 (ubc13)
94	d1qypa	Alignment	not modelled	7.3	56	Fold: Rubredoxin-like Superfamily: Zinc beta-ribbon Family: Transcriptional factor domain
95	c2en8A	Alignment	not modelled	7.3	29	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 224; PDBTitle: solution structure of the c2h2 type zinc finger (region 171-2 203) of human zinc finger protein 224
96	c5iy9Q	Alignment	not modelled	7.2	38	PDB header: transcription, transferase/dna/rna Chain: Q: PDB Molecule: general transcription factor iie subunit 1; PDBTitle: human holo-pic in the initial transcribing state (no iis)
97	d2fiya1	Alignment	not modelled	7.0	71	Fold: FdhE-like Superfamily: FdhE-like Family: FdhE-like
98	d1p6ta2	Alignment	not modelled	6.8	44	Fold: Ferredoxin-like Superfamily: HMA, heavy metal-associated domain Family: HMA, heavy metal-associated domain
99	c1s24A	Alignment	not modelled	6.8	33	PDB header: electron transport Chain: A: PDB Molecule: rubredoxin 2; PDBTitle: rubredoxin domain ii from pseudomonas oleovorans