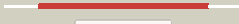



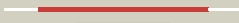
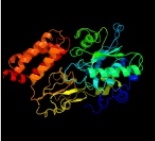













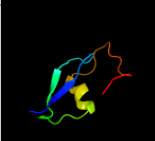

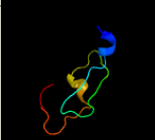


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3150_(nuoF)_3515409_3516746
Date	Thu Aug 8 16:20:33 BST 2019
Unique Job ID	86feaf0b8b01c40c

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2fugA_	 Alignment		100.0	51	PDB header: oxidoreductase Chain: A: PDB Molecule: nadh-quinone oxidoreductase chain 1; PDBTitle: crystal structure of the hydrophilic domain of respiratory complex i2 from thermus thermophilus
2	c6q9gD_	 Alignment		100.0	44	PDB header: oxidoreductase Chain: D: PDB Molecule: nadh-quinone oxidoreductase subunit f; PDBTitle: crystal structure of reduced aquifex aeolicus nadh-quinone2 oxidoreductase subunits nuoE g129d and nuoF bound to nadh
3	c5lc5F_	 Alignment		100.0	46	PDB header: oxidoreductase Chain: F: PDB Molecule: nadh dehydrogenase [ubiquinone] flavoprotein 1, PDBTitle: structure of mammalian respiratory complex i, class2
4	c5xf9E_	 Alignment		100.0	39	PDB header: oxidoreductase Chain: E: PDB Molecule: nad-reducing hydrogenase; PDBTitle: crystal structure of nad+-reducing [nife]-hydrogenase in the air-2 oxidized state
5	d2fug12	 Alignment		100.0	56	Fold: Nqo1 FMN-binding domain-like Superfamily: Nqo1 FMN-binding domain-like Family: Nqo1 FMN-binding domain-like
6	c4p6vA_	 Alignment		100.0	16	PDB header: oxidoreductase Chain: A: PDB Molecule: na(+)-translocating nadh-quinone reductase subunit a; PDBTitle: crystal structure of the na+-translocating nadh:ubiquinone2 oxidoreductase from vibrio cholerae
7	d2fug11	 Alignment		100.0	42	Fold: Bromodomain-like Superfamily: Nqo1C-terminal domain-like Family: Nqo1C-terminal domain-like
8	d2fug13	 Alignment		99.9	52	Fold: beta-Grasp (ubiquitin-like) Superfamily: Nqo1 middle domain-like Family: Nqo1 middle domain-like
9	c2w8iG_	 Alignment		95.4	18	PDB header: membrane protein Chain: G: PDB Molecule: putative outer membrane lipoprotein wza; PDBTitle: crystal structure of wza24-345.
10	c2j58G_	 Alignment		94.6	18	PDB header: membrane protein Chain: G: PDB Molecule: outer membrane lipoprotein wza; PDBTitle: the structure of wza
11	c3p42D_	 Alignment		90.4	18	PDB header: unknown function Chain: D: PDB Molecule: predicted protein; PDBTitle: structure of gfcc (ymcb), protein encoded by the e. coli group 42 capsule operon

12	c1c4cA_	Alignment		63.0	15	PDB header: oxidoreductase Chain: A: PDB Molecule: protein (fe-only hydrogenase); PDBTitle: binding of exogenously added carbon monoxide at the active2 site of the fe-only hydrogenase (cpi) from clostridium3 pasteurianum
13	c3swrA_	Alignment		48.5	36	PDB header: transferase Chain: A: PDB Molecule: dna (cytosine-5)-methyltransferase 1; PDBTitle: structure of human dnmt1 (601-1600) in complex with sinefungin
14	c3bl5E_	Alignment		47.4	19	PDB header: hydrolase Chain: E: PDB Molecule: queuosine biosynthesis protein quec; PDBTitle: crystal structure of quec from bacillus subtilis: an enzyme2 involved in preq1 biosynthesis
15	c2b76N_	Alignment		42.3	11	PDB header: oxidoreductase Chain: N: PDB Molecule: fumarate reductase iron-sulfur protein; PDBTitle: e. coli quinol fumarate reductase frda e49q mutation
16	c3pt6B_	Alignment		41.7	38	PDB header: transferase/dna Chain: B: PDB Molecule: dna (cytosine-5)-methyltransferase 1; PDBTitle: crystal structure of mouse dnmt1(650-1602) in complex with dna
17	c2bs2E_	Alignment		40.8	22	PDB header: oxidoreductase Chain: E: PDB Molecule: quinol-fumarate reductase iron-sulfur subunit b; PDBTitle: quinol:fumarate reductase from wolinnella succinogenes
18	d2bs2b1	Alignment		40.1	20	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
19	d1kf6b1	Alignment		39.7	13	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
20	c5xmjl_	Alignment		36.8	16	PDB header: electron transport Chain: J: PDB Molecule: succinate dehydrogenase iron-sulfur subunit; PDBTitle: crystal structure of quinol:fumarate reductase from desulfovibrio2 gigas
21	c6ff6A_	Alignment	not modelled	36.7	13	PDB header: de novo protein Chain: A: PDB Molecule: bric1; PDBTitle: crystal structure of novel repeat protein bric1
22	c4tr3A_	Alignment	not modelled	36.4	9	PDB header: oxidoreductase Chain: A: PDB Molecule: type iii iodothyronine deiodinase; PDBTitle: mouse iodothyronine deiodinase 3 catalytic core, semet-labeled active2 site mutant secys->cys
23	c4ijgB_	Alignment	not modelled	34.6	18	PDB header: oxidoreductase Chain: B: PDB Molecule: 5,10-methenyltetrahydromethanopterin hydrogenase; PDBTitle: crystal structure of fe-hydrogenase from methanothermobacter2 marburgensis in complex with toluenesulfonylmethylisocyanide
24	c4uhxA_	Alignment	not modelled	30.9	15	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidase; PDBTitle: human aldehyde oxidase in complex with phthalazine and thioridazine
25	c3cf4A_	Alignment	not modelled	29.6	20	PDB header: oxidoreductase Chain: A: PDB Molecule: acetyl-coa decarboxylase/synthase alpha subunit; PDBTitle: structure of the codh component of the m. barkeri acds complex
26	c5odcC_	Alignment	not modelled	28.1	19	PDB header: oxidoreductase Chain: C: PDB Molecule: heterodisulfide reductase, subunit c; PDBTitle: heterodisulfide reductase / [nife]-hydrogenase complex from2 methanothermococcus thermolithotrophicus at 2.3 a resolution
27	c5xjoF_	Alignment	not modelled	27.7	67	PDB header: transferase/membrane protein Chain: F: PDB Molecule: protein epidermal patterning factor 1; PDBTitle: plant receptor erl1-tmm in complex with peptide epf1
28	c2h89B_	Alignment	not modelled	26.7	13	PDB header: oxidoreductase Chain: B: PDB Molecule: succinate dehydrogenase ip subunit;

						PDBTitle: avian respiratory complex ii with malonate bound
29	d1nekbl	Alignment	not modelled	26.1	21	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Fumarate reductase/Succinate dehydrogenase iron-sulfur protein, C-terminal domain
30	d1i5na_	Alignment	not modelled	25.4	13	Fold: Four-helical up-and-down bundle Superfamily: Histidine-containing phosphotransfer domain, HPT domain Family: Chemotaxis protein CheA P1 domain
31	c5xkjF_	Alignment	not modelled	23.5	56	PDB header: transferase/membrane protein/hormone Chain: F: PDB Molecule: protein epidermal patterning factor 2; PDBTitle: crystal structure of plant receptor erl1-tmm in complex with epf2
32	d2pg3a1	Alignment	not modelled	23.0	44	Fold: Adenine nucleotide alpha hydrolase-like Superfamily: Adenine nucleotide alpha hydrolases-like Family: N-type ATP pyrophosphatases
33	c4pziA_	Alignment	not modelled	21.9	36	PDB header: transcription/dna Chain: A: PDB Molecule: histone-lysine n-methyltransferase 2b; PDBTitle: zinc finger region of ml12 in complex with cpg dna
34	c1ogpD_	Alignment	not modelled	21.5	30	PDB header: oxidoreductase Chain: D: PDB Molecule: sulfite oxidase; PDBTitle: the crystal structure of plant sulfite oxidase provides2 insight into sulfite oxidation in plants and animals
35	c3kyiA_	Alignment	not modelled	21.1	15	PDB header: transferase Chain: A: PDB Molecule: putative histidine protein kinase; PDBTitle: crystal structure of the phosphorylated p1 domain of chea3 in complex2 with chey6 from r. sphaeroides
36	c4d4wA_	Alignment	not modelled	20.6	45	PDB header: transcription Chain: A: PDB Molecule: methyl-cpg-binding domain protein 1; PDBTitle: solution structure of human mbd1 cxxc1 domain
37	c4hp1C_	Alignment	not modelled	20.2	45	PDB header: dna binding protein/dna Chain: C: PDB Molecule: loc100036628 protein; PDBTitle: crystal structure of tet3 in complex with a non-cpg dsdna
38	c1nekB_	Alignment	not modelled	20.0	16	PDB header: oxidoreductase/electron transport Chain: B: PDB Molecule: succinate dehydrogenase iron-sulfur protein; PDBTitle: complex ii (succinate dehydrogenase) from e. coli with2 ubiquinone bound
39	c6dlwl_	Alignment	not modelled	19.7	26	PDB header: immune system Chain: I: PDB Molecule: complement component c9; PDBTitle: complement component polyc9
40	c1gthD_	Alignment	not modelled	19.0	13	PDB header: oxidoreductase Chain: D: PDB Molecule: dihydropyrimidine dehydrogenase; PDBTitle: dihydropyrimidine dehydrogenase (dpd) from pig, ternary complex with2 nadph and 5-iodouracil
41	c3s9fA_	Alignment	not modelled	18.8	33	PDB header: electron transport Chain: A: PDB Molecule: tryparedoxin; PDBTitle: the structure of tryparedoxin i from leishmania major
42	c1ffuA_	Alignment	not modelled	18.6	10	PDB header: hydrolase Chain: A: PDB Molecule: cuts, iron-sulfur protein of carbon monoxide PDBTitle: carbon monoxide dehydrogenase from hydrogenophaga2 pseudoflava which lacks the mo-pyranopterin moiety of the3 molybdenum cofactor
43	c5fmwS_	Alignment	not modelled	18.5	26	PDB header: structural protein Chain: S: PDB Molecule: polyc9; PDBTitle: the poly-c9 component of the complement membrane attack complex
44	d1o8xa_	Alignment	not modelled	18.3	26	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
45	d1uufa1	Alignment	not modelled	18.2	45	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
46	c5w9qA_	Alignment	not modelled	17.9	36	PDB header: dna binding protein/dna Chain: A: PDB Molecule: methyl-cpg-binding domain protein 1; PDBTitle: zinc finger region of mbd1 in complex with cpg dna
47	c2lusA_	Alignment	not modelled	17.9	35	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: nmr structure of carcinoscorpius rotundicauda thioredoxin related2 protein 16 and its role in regulating transcription factor nf-kb3 activity
48	c2lp4A_	Alignment	not modelled	17.7	14	PDB header: transferase/signaling protein Chain: A: PDB Molecule: chemotaxis protein chea; PDBTitle: solution structure of p1-chey/p2 complex in bacterial chemotaxis
49	c1dgiA_	Alignment	not modelled	17.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: aldehyde oxidoreductase; PDBTitle: crystal structure of the aldehyde oxidoreductase from2 desulfovibrio desulfuricans atcc 27774
50	c6asdC_	Alignment	not modelled	17.4	45	PDB header: dna binding protein/dna Chain: C: PDB Molecule: methylcytosine dioxygenase tet1; PDBTitle: zinc finger region of human tet1 in complex with cpg dna
51	c5jcaL_	Alignment	not modelled	17.0	16	PDB header: oxidoreductase Chain: L: PDB Molecule: nadh-dependent ferredoxin:nadp oxidoreductase (nfni) PDBTitle: nadp(h) bound nadh-dependent ferredoxin:nadp oxidoreductase (nfni)2 from pyrococcus furiosus
52	c3qmhA_	Alignment	not modelled	16.8	55	PDB header: dna binding protein/dna Chain: A: PDB Molecule: cpg-binding protein; PDBTitle: structural basis of selective binding of non-methylated cpg islands2 (dna-tcga) by the cxxc domain of cfp1
53	c4z3cC_	Alignment	not modelled	16.7	55	PDB header: dna binding protein/dna Chain: C: PDB Molecule: methylcytosine dioxygenase; PDBTitle: zinc finger region of human tet3 in complex with cpg dna

54	c2jyiA	Alignment	not modelled	16.3	55	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein hrx; PDBTitle: solution structure of mll cxxc domain
55	d1ogpa2	Alignment	not modelled	16.2	28	Fold: Oxidoreductase molybdopterin-binding domain Superfamily: Oxidoreductase molybdopterin-binding domain Family: Oxidoreductase molybdopterin-binding domain
56	d1z6na1	Alignment	not modelled	15.8	22	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
57	d1cdoa1	Alignment	not modelled	15.7	36	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
58	c5w9sC	Alignment	not modelled	15.6	36	PDB header: dna binding protein/dna Chain: C: PDB Molecule: cxxc-type zinc finger protein 5; PDBTitle: zinc finger of human cxxc5 in complex with cpg dna
59	d1gtea1	Alignment	not modelled	15.4	14	Fold: Globin-like Superfamily: alpha-helical ferredoxin Family: Dihydropyrimidine dehydrogenase, N-terminal domain
60	d1zxia1	Alignment	not modelled	15.3	15	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
61	c5d6sB	Alignment	not modelled	15.2	27	PDB header: oxidoreductase Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: structure of epoxyqueuosine reductase from streptococcus thermophilus.
62	c3nsjA	Alignment	not modelled	15.0	21	PDB header: immune system Chain: A: PDB Molecule: perforin-1; PDBTitle: the x-ray crystal structure of lymphocyte perforin
63	c2jrza	Alignment	not modelled	14.4	14	PDB header: oxidoreductase Chain: A: PDB Molecule: histone demethylase jarid1c; PDBTitle: solution structure of the bright/arid domain from the human2 jarid1c protein.
64	c2j2sA	Alignment	not modelled	14.0	55	PDB header: transcription regulation Chain: A: PDB Molecule: zinc finger protein hrx; PDBTitle: solution structure of the nonmethyl-cpg-binding cxxc domain of the2 leukaemia-associated mll histone methyltransferase
65	c3f46A	Alignment	not modelled	13.7	17	PDB header: oxidoreductase Chain: A: PDB Molecule: 5,10-methenyltetrahydromethanopterin hydrogenase; PDBTitle: the crystal structure of c176a mutated [fe]-hydrogenase (hmd)2 holoenzyme from methanocaldococcus jannaschii
66	c4hpgE	Alignment	not modelled	13.3	34	PDB header: protein transport Chain: E: PDB Molecule: atg31; PDBTitle: crystal structure of the atg17-atg31-atg29 complex
67	c6fosD	Alignment	not modelled	13.3	10	PDB header: photosynthesis Chain: D: PDB Molecule: photosystem i p700 chlorophyll a apoprotein a2; PDBTitle: cyanidioschyzon merolae photosystem i
68	c2bm0A	Alignment	not modelled	13.3	16	PDB header: elongation factor Chain: A: PDB Molecule: elongation factor g; PDBTitle: ribosomal elongation factor g (ef-g) fusidic acid resistant mutant2 t84a
69	c2he3A	Alignment	not modelled	12.9	14	PDB header: oxidoreductase Chain: A: PDB Molecule: glutathione peroxidase 2; PDBTitle: crystal structure of the selenocysteine to cysteine mutant of human2 glutathione peroxidase 2 (gpx2)
70	d1i5ga	Alignment	not modelled	12.9	26	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
71	c4ex8A	Alignment	not modelled	12.6	19	PDB header: ligase Chain: A: PDB Molecule: alna; PDBTitle: crystal structure of the prealnumycin c-glycosynthasealna
72	d1kx9b	Alignment	not modelled	12.2	17	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
73	c5d0bB	Alignment	not modelled	12.2	36	PDB header: oxidoreductase/rna Chain: B: PDB Molecule: epoxyqueuosine reductase; PDBTitle: crystal structure of epoxyqueuosine reductase with a trna-tyr2 epoxyqueuosine-modified trna stem loop
74	d1n8va	Alignment	not modelled	11.9	17	Fold: alpha-alpha superhelix Superfamily: Chemosensory protein Csp2 Family: Chemosensory protein Csp2
75	c3thdD	Alignment	not modelled	11.7	26	PDB header: hydrolase Chain: D: PDB Molecule: beta-galactosidase; PDBTitle: crystal structure of human beta-galactosidase in complex with 1-2 deoxygalactonojirimycin
76	c3jz4C	Alignment	not modelled	11.6	11	PDB header: oxidoreductase Chain: C: PDB Molecule: succinate-semialdehyde dehydrogenase [nadp+]; PDBTitle: crystal structure of e. coli nadp dependent enzyme
77	d2gtga1	Alignment	not modelled	11.4	13	Fold: Sapoin-like Superfamily: Sapoin Family: NKL-like
78	c2ds8A	Alignment	not modelled	11.1	35	PDB header: metal binding protein, protein binding Chain: A: PDB Molecule: atp-dependent clp protease atp-binding subunit PDBTitle: structure of the zbd-xb complex
79	c5ikfB	Alignment	not modelled	11.0	33	PDB header: transcription Chain: B: PDB Molecule: cryptic loci regulator protein 1; PDBTitle: crystal structure of the c-terminal domain of the mit1 nucleosome2 remodeler in complex with clr1
						PDB header: oxidoreductase Chain: B: PDB Molecule: putative nad-dependent aldehyde

80	c3vz0B_	Alignment	not modelled	10.9	12	dehydrogenase; PDBTitle: structural insights into cofactor and substrate selection by gox0499
81	c3l0aA_	Alignment	not modelled	10.9	50	PDB header: hydrolase Chain: A: PDB Molecule: putative exonuclease; PDBTitle: crystal structure of putative exonuclease (rer070207002219) from2 eubacterium rectale at 2.19 a resolution
82	d2fzwa1	Alignment	not modelled	10.8	36	Fold: GroES-like Superfamily: GroES-like Family: Alcohol dehydrogenase-like, N-terminal domain
83	c4qwoA_	Alignment	not modelled	10.6	15	PDB header: viral protein Chain: A: PDB Molecule: profilin; PDBTitle: 1.52 angstrom crystal structure of a42r profilin-like protein from2 monkeypox virus zaire-96-i-16
84	c3o2qB_	Alignment	not modelled	10.6	24	PDB header: hydrolase Chain: B: PDB Molecule: rna polymerase ii subunit a c-terminal domain phosphatase PDBTitle: crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
85	c2iu6B_	Alignment	not modelled	10.6	19	PDB header: transferase Chain: B: PDB Molecule: dihydroxyacetone kinase; PDBTitle: regulation of the dha operon of lactococcus lactis
86	d1n62a1	Alignment	not modelled	10.6	15	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
87	c4txdA_	Alignment	not modelled	10.6	38	PDB header: rna binding protein Chain: A: PDB Molecule: csc2; PDBTitle: crystal structure of thermofilum pendens csc2
88	c2o2qA_	Alignment	not modelled	10.5	8	PDB header: oxidoreductase Chain: A: PDB Molecule: formyltetrahydrofolate dehydrogenase; PDBTitle: crystal structure of the c-terminal domain of rat2 10'formyltetrahydrofolate dehydrogenase in complex with nadp
89	d2fa8a1	Alignment	not modelled	10.3	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Selenoprotein W-related
90	c4e8cA_	Alignment	not modelled	10.2	24	PDB header: hydrolase Chain: A: PDB Molecule: glycosyl hydrolase, family 35; PDBTitle: crystal structure of streptococcal beta-galactosidase in complex with2 galactose
91	c3widC_	Alignment	not modelled	10.1	55	PDB header: oxidoreductase Chain: C: PDB Molecule: glucose 1-dehydrogenase; PDBTitle: structure of a glucose dehydrogenase t277f mutant in complex with nadp
92	c1decA_	Alignment	not modelled	10.1	28	PDB header: blood coagulation Chain: A: PDB Molecule: decorsin; PDBTitle: structure of the rgd protein decorsin: conserved motif and distinct2 function in leech proteins that affect blood clotting
93	d1deca_	Alignment	not modelled	10.1	28	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: Leech antihemostatic proteins Family: Hirudin-like
94	c2xexA_	Alignment	not modelled	9.9	16	PDB header: translation Chain: A: PDB Molecule: elongation factor g; PDBTitle: crystal structure of staphylococcus aureus elongation factor2 g
95	c6raoH_	Alignment	not modelled	9.9	16	PDB header: virus like particle Chain: H: PDB Molecule: afp9; PDBTitle: cryo-em structure of the anti-feeding prophage (afp) baseplate, 6-fold2 symmetrised
96	c3ewgA_	Alignment	not modelled	9.8	24	PDB header: transcription Chain: A: PDB Molecule: putative transcription antitermination protein nusg; PDBTitle: crystal structure of the n-terminal domain of nusg (ngn) from2 methanocaldococcus jannaschii
97	c2gk9D_	Alignment	not modelled	9.6	10	PDB header: transferase Chain: D: PDB Molecule: phosphatidylinositol-4-phosphate 5-kinase, type ii, gamma; PDBTitle: human phosphatidylinositol-4-phosphate 5-kinase, type ii, gamma
98	c2ojlB_	Alignment	not modelled	9.6	16	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of q7waf1_borpa from bordetella parapertussis.2 northeast structural genomics target bpr68.
99	c3p04B_	Alignment	not modelled	9.5	18	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized bcr; PDBTitle: crystal structure of the bcr protein from corynebacterium glutamicum.2 northeast structural genomics consortium target cgr8