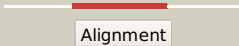
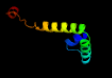


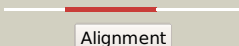
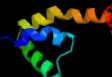
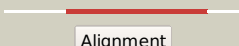
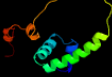
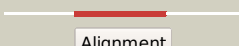
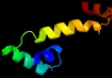
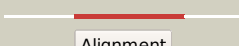

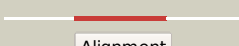




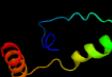

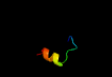


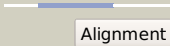
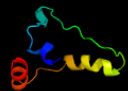
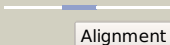

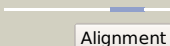

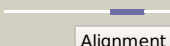

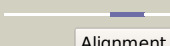

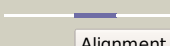

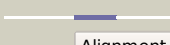

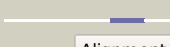



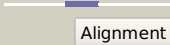
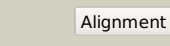
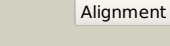
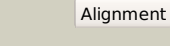
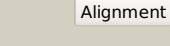
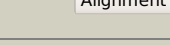
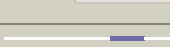



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1222_(-)_1365350_1365814
Date	Wed Jul 31 22:05:31 BST 2019
Unique Job ID	44f48ff21c6584d6

Detailed template
information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5wuqD_	 Alignment		99.4	15	PDB header: metal binding protein Chain: D: PDB Molecule: anti-sigma-w factor rsiw; PDBTitle: crystal structure of sigw in complex with its anti-sigma rsiw, a zinc2 binding form
2	c5frhA_	 Alignment		99.4	14	PDB header: transcription Chain: A: PDB Molecule: anti-sigma factor rsra; PDBTitle: solution structure of oxidised rsra
3	c3hugJ_	 Alignment		99.4	22	PDB header: transcription/membrane protein Chain: J: PDB Molecule: probable conserved membrane protein; PDBTitle: crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
4	c2z2sD_	 Alignment		99.4	22	PDB header: transcription Chain: D: PDB Molecule: anti-sigma factor chrr, transcriptional activator chrr; PDBTitle: crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
5	c3vdoB_	 Alignment		99.2	10	PDB header: dna binding protein/protein binding Chain: B: PDB Molecule: anti-sigma-k factor rska; PDBTitle: structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
6	c6in7A_	 Alignment		98.7	15	PDB header: transcription Chain: A: PDB Molecule: sigma factor algu negative regulatory protein; PDBTitle: crystal structure of algu in complex with muca(cyto)
7	c1or7C_	 Alignment		97.3	16	PDB header: transcription Chain: C: PDB Molecule: sigma-e factor negative regulatory protein; PDBTitle: crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
8	d1or7c_	 Alignment		97.3	16	Fold: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Superfamily: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA Family: N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
9	c3n6qF_	 Alignment		25.1	13	PDB header: oxidoreductase Chain: F: PDB Molecule: yghz aldo-keto reductase; PDBTitle: crystal structure of yghz from e. coli
10	d2ou3a1	 Alignment		24.5	24	Fold: TerB-like Superfamily: TerB-like Family: COG3793-like
11	c2jxuA_	 Alignment		24.3	13	PDB header: unknown function Chain: A: PDB Molecule: terb; PDBTitle: nmr solution structure of kp-terb, a tellurite resistance2 protein from klebsiella pneumoniae

12	d1gvea_	 Alignment		22.8	16	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
13	c6h0jA_	 Alignment		21.4	18	PDB header: protein binding Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: a1-type acp domain from module 5 of mlsA1
14	c6gc1A_	 Alignment		20.0	20	PDB header: unknown function Chain: A: PDB Molecule: nhl repeat-containing protein 2; PDBTitle: crystal structure of trx-like and nhl repeat containing domains of 2 human nhlrc2
15	d2f8aa1	 Alignment		19.4	5	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
16	c4tr3A_	 Alignment		18.2	15	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
17	c5ze4A_	 Alignment		17.4	22	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase, chloroplastic; PDBTitle: the structure of holo- structure of dhad complex with [2fe-2s] cluster
18	c5oynB_	 Alignment		16.2	15	PDB header: lyase Chain: B: PDB Molecule: dehydratase, ilvd/edd family; PDBTitle: crystal structure of d-xylonate dehydratase in holo-form
19	c3lwaA_	 Alignment		15.6	35	PDB header: isomerase Chain: A: PDB Molecule: secreted thiol-disulfide isomerase; PDBTitle: the crystal structure of a secreted thiol-disulfide isomerase from 2 corynebacterium glutamicum to 1.75a
20	d1or5a_	 Alignment		15.1	6	Fold: Acyl carrier protein-like Superfamily: ACP-like Family: Acyl-carrier protein (ACP)
21	d2v4ja1	 Alignment	not modelled	14.6	42	Fold: Ferredoxin-like Superfamily: 4Fe-4S ferredoxins Family: Ferredoxin domains from multidomain proteins
22	c3n2tA_	 Alignment	not modelled	14.2	16	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxidoreductase; PDBTitle: structure of the glycerol dehydrogenase akr11b4 from gluconobacter 2 oxydans
23	c2wfbA_	 Alignment	not modelled	13.7	38	PDB header: biosynthetic protein Chain: A: PDB Molecule: putative uncharacterized protein orp; PDBTitle: high resolution structure of the apo form of the orange 2 protein (orp) from desulfovibrio gigas
24	c2ju2A_	 Alignment	not modelled	13.3	41	PDB header: transferase Chain: A: PDB Molecule: erythronolide synthase; PDBTitle: minimized mean solution structure of the acyl carrier 2 protein domain from module 2 of 6-deoxyerythronolide b3 synthase (debs)
25	d1z6na1	 Alignment	not modelled	13.1	19	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Thioltransferase
26	c4xk2A_	 Alignment	not modelled	12.6	23	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo/keto reductase; PDBTitle: crystal structure of aldo-keto reductase from polaromonas sp. js666
27	d1wjva1	 Alignment	not modelled	12.4	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: C2HC finger
28	c4fyuB_	 Alignment	not modelled	12.2	15	PDB header: oxidoreductase Chain: B: PDB Molecule: thioredoxin; PDBTitle: crystal structure of thioredoxin from wuchereria bancrofti at 2.02 angstrom

29	c2kvcA	Alignment	not modelled	12.1	24	PDB header: unknown function Chain: A: PDB Molecule: putative uncharacterized protein; PDBTitle: solution structure of the mycobacterium tuberculosis protein rv0543c,2 a member of the duf3349 superfamily. seattle structural genomics3 center for infectious disease target mytud.17112.a
30	d1i5ga	Alignment	not modelled	11.4	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
31	c6drfA	Alignment	not modelled	11.4	17	PDB header: signaling protein Chain: A: PDB Molecule: protein rd3; PDBTitle: structure of human retinal degeneration 3(rd3) protein
32	d2db7a1	Alignment	not modelled	10.8	21	Fold: Orange domain-like Superfamily: Orange domain-like Family: Hairy Orange domain
33	c2re2A	Alignment	not modelled	10.5	15	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein ta1041; PDBTitle: crystal structure of a putative iron-molybdenum cofactor (femo-co)2 dinitrogenase (ta1041m) from thermoplasma acidophilum dsm 1728 at3 1.30 a resolution
34	d1jroa1	Alignment	not modelled	10.4	35	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
35	c2he3A	Alignment	not modelled	10.3	5	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)
36	d1tja2	Alignment	not modelled	9.8	20	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: Prokaryotic DksA/TraR C4-type zinc finger
37	c5j84A	Alignment	not modelled	9.5	19	PDB header: lyase Chain: A: PDB Molecule: dihydroxy-acid dehydratase; PDBTitle: crystal structure of l-arabinonate dehydratase in holo-form
38	c5m45l	Alignment	not modelled	9.4	12	PDB header: ligase Chain: I: PDB Molecule: acetone carboxylase gamma subunit; PDBTitle: structure of acetone carboxylase purified from xanthobacter2 autotrophicus
39	c3jb9i	Alignment	not modelled	9.1	10	PDB header: rna binding protein/rna Chain: I: PDB Molecule: small nuclear ribonucleoprotein f; PDBTitle: cryo-em structure of the yeast spliceosome at 3.6 angstrom resolution
40	d2fy6a1	Alignment	not modelled	8.9	15	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
41	c2hyxA	Alignment	not modelled	8.8	20	PDB header: unknown function Chain: A: PDB Molecule: protein dipz; PDBTitle: structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
42	c2lusA	Alignment	not modelled	8.7	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: nmr structure of carnoscorpius rotundicauda thioredoxin related2 protein 16 and its role in regulating transcription factor nf-kb3 activity
43	c4i4dA	Alignment	not modelled	8.6	18	PDB header: biosynthetic protein Chain: A: PDB Molecule: peptide synthetase nrps type ii-pcp; PDBTitle: structure of blmi, a type-ii acyl-carrier-protein from streptomyces2 verticillus involved in bleomycin biosynthesis
44	c4f40B	Alignment	not modelled	8.6	16	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f2-alpha synthase/d-arabinose dehydrogenase; PDBTitle: x-ray crystal structure of apo prostaglandin f synthase from2 leishmania major friedlin
45	d1s1pa	Alignment	not modelled	8.5	10	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
46	c5hvcA	Alignment	not modelled	8.5	19	PDB header: transferase Chain: A: PDB Molecule: type i modular polyketide synthase; PDBTitle: solution structure of the apo state of the acyl carrier protein from2 the mlsa2 subunit of the mycolactone polyketide synthase
47	d2cvba1	Alignment	not modelled	8.3	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
48	c4pq1B	Alignment	not modelled	8.1	40	PDB header: oxidoreductase Chain: B: PDB Molecule: putative electron transport related protein; PDBTitle: crystal structure and functional implications of a dsbf homologue from2 corynebacterium diphtheriae
49	c3ewlA	Alignment	not modelled	8.0	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized conserved protein bf1870; PDBTitle: crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
50	d1t3va	Alignment	not modelled	8.0	23	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
51	c2n98A	Alignment	not modelled	8.0	31	PDB header: transport protein Chain: A: PDB Molecule: acyl carrier protein; PDBTitle: solution structure of acyl carrier protein lipid from actinoplanes2 friuliensis
52	d1o8xa	Alignment	not modelled	8.0	5	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
53	c3razA	Alignment	not modelled	7.9	25	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-related protein;

53	c3l2aA	Alignment	not modelled	7.9	23	PDBTitle: the crystal structure of thioredoxin-related protein from neisseria2 meningitidis serogroup b PDB header: transferase
54	c5w1sM	Alignment	not modelled	7.8	24	Chain: M: PDB Molecule: protein trar; PDBTitle: x-ray crystal structure of escherichia coli rna polymerase and trar2 complex
55	c3vthA	Alignment	not modelled	7.8	30	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation factor; PDBTitle: crystal structure of full-length hypf in the phosphate-and2 nucleotide-bound form
56	d1o73a	Alignment	not modelled	7.5	10	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
57	c2l22A	Alignment	not modelled	7.4	19	PDB header: biosynthetic protein Chain: A: PDB Molecule: mupirocin didomain acyl carrier protein; PDBTitle: mupirocin didomain acp
58	c4g9iA	Alignment	not modelled	7.4	30	PDB header: transferase Chain: A: PDB Molecule: hydrogenase maturation protein hypf; PDBTitle: crystal structure of t.kodakarensis hypf
59	d2hzab1	Alignment	not modelled	7.2	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
60	c3cynC	Alignment	not modelled	7.1	5	PDB header: oxidoreductase Chain: C: PDB Molecule: probable glutathione peroxidase 8; PDBTitle: the structure of human gpx8
61	c4ca3A	Alignment	not modelled	7.1	28	PDB header: ribosomal protein Chain: A: PDB Molecule: hybrid polyketide synthase-non ribosomal peptide PDBTitle: solution structure of streptomyces virginiae vira acp5b
62	c3ha9A	Alignment	not modelled	7.0	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized thioredoxin-like protein; PDBTitle: the 1.7a crystal structure of a thioredoxin-like protein from2 aeropyrum pernix
63	c2qtdA	Alignment	not modelled	6.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein mj0327; PDBTitle: crystal structure of a putative dinitrogenase (mj0327) from2 methanocaldococcus jannaschii dsm at 1.70 a resolution
64	c5camC	Alignment	not modelled	6.9	4	PDB header: transcription Chain: C: PDB Molecule: pupr protein; PDBTitle: crystal structure of the cytoplasmic domain of the pseudomonas putida2 anti-sigma factor pupr (semet)
65	d1hw6a	Alignment	not modelled	6.8	19	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
66	d2hzaa1	Alignment	not modelled	6.7	29	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
67	c3b73A	Alignment	not modelled	6.6	27	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: phih1 repressor-like protein; PDBTitle: crystal structure of the phih1 repressor-like protein from haloarcula2 marismortui
68	c2ywiA	Alignment	not modelled	6.5	10	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: hypothetical conserved protein; PDBTitle: crystal structure of uncharacterized conserved protein from2 geobacillus kaustophilus
69	c2p31B	Alignment	not modelled	6.5	10	PDB header: oxidoreductase Chain: B: PDB Molecule: glutathione peroxidase 7; PDBTitle: crystal structure of human glutathione peroxidase 7
70	d1n62a1	Alignment	not modelled	6.3	20	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
71	c6nd4a	Alignment	not modelled	6.2	13	PDB header: ribosome Chain: A: PDB Molecule: mpp10; PDBTitle: conformational switches control early maturation of the eukaryotic2 small ribosomal subunit
72	c3b3dA	Alignment	not modelled	6.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: putative morphine dehydrogenase; PDBTitle: b.subtilis ytbe
73	d1pz1a	Alignment	not modelled	6.2	16	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
74	c2lo2A	Alignment	not modelled	6.1	56	PDB header: transcription Chain: A: PDB Molecule: saga-associated factor 11; PDBTitle: solution structure of sgf11(63-99) zinc finger domain
75	c3s9fA	Alignment	not modelled	6.1	15	PDB header: electron transport Chain: A: PDB Molecule: tryparedoxin; PDBTitle: the structure of tryparedoxin i from leishmania major
76	c2bmx8	Alignment	not modelled	6.0	18	PDB header: oxidoreductase Chain: B: PDB Molecule: alkyl hydroperoxidase c; PDBTitle: mycobacterium tuberculosis ahpc
77	c3gwnA	Alignment	not modelled	5.8	9	PDB header: oxidoreductase Chain: A: PDB Molecule: probable fad-linked sulfhydryl oxidase r596; PDBTitle: crystal structure of the fad binding domain from mimivirus sulfhydryl2 oxidase r596
78	d2bmx1	Alignment	not modelled	5.8	20	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: Glutathione peroxidase-like
79	d2bj7a1	Alignment	not modelled	5.7	50	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like

80	c2hj3A_	Alignment	not modelled	5.7	18	PDB header: oxidoreductase Chain: A: PDB Molecule: sulphydryl oxidase erv1p; PDBTitle: structure of the arabidopsis thaliana erv1 thiol oxidase
81	c1vbjB_	Alignment	not modelled	5.6	12	PDB header: oxidoreductase Chain: B: PDB Molecule: prostaglandin f synthase; PDBTitle: the crystal structure of prostaglandin f synthase from trypanosoma2 brucei
82	c4bmjC_	Alignment	not modelled	5.6	27	PDB header: apoptosis Chain: C: PDB Molecule: tax1-binding protein 1; PDBTitle: structure of the ubz1and2 tandem of the ubiquitin-binding adaptor2 protein tax1bp1
83	d1pyfa_	Alignment	not modelled	5.6	9	Fold: TIM beta/alpha-barrel Superfamily: NAD(P)-linked oxidoreductase Family: Aldo-keto reductases (NADP)
84	c3wbwA_	Alignment	not modelled	5.5	12	PDB header: oxidoreductase Chain: A: PDB Molecule: putative 2,5-diketo-d-gluconic acid reductase; PDBTitle: crystal structure of gox0644 in complex with nadph
85	c2yrmA_	Alignment	not modelled	5.4	33	PDB header: gene regulation Chain: A: PDB Molecule: b-cell lymphoma 6 protein; PDBTitle: solution structure of the 1st zf-c2h2 domain from human b-2 cell lymphoma 6 protein
86	c2kokA_	Alignment	not modelled	5.4	6	PDB header: oxidoreductase Chain: A: PDB Molecule: arsenate reductase; PDBTitle: solution structure of an arsenate reductase (arsc) related protein2 from brucella melitensis. seattle structural genomics center for3 infectious disease target braba.00007.a.
87	c3or5A_	Alignment	not modelled	5.4	20	PDB header: oxidoreductase Chain: A: PDB Molecule: thiol:disulfide interchange protein, thioredoxin family PDBTitle: crystal structure of thiol:disulfide interchange protein, thioredoxin2 family protein from chlorobium tepidum t1s
88	d1t3ba1	Alignment	not modelled	5.3	12	Fold: Thioredoxin fold Superfamily: Thioredoxin-like Family: DsbC/DsbG C-terminal domain-like
89	d1rdua_	Alignment	not modelled	5.2	36	Fold: Ribonuclease H-like motif Superfamily: Nitrogenase accessory factor-like Family: MTH1175-like
90	c2yreA_	Alignment	not modelled	5.2	44	PDB header: protein binding Chain: A: PDB Molecule: f-box only protein 30; PDBTitle: solution structure of the zinc finger domains (1-87) from2 human f-box only protein
91	c3fkfC_	Alignment	not modelled	5.2	11	PDB header: oxidoreductase Chain: C: PDB Molecule: thiol-disulfide oxidoreductase; PDBTitle: thiol-disulfide oxidoreductase from bacteroides fragilis nctc 9343
92	c2bp1C_	Alignment	not modelled	5.2	21	PDB header: oxidoreductase Chain: C: PDB Molecule: afatoxin b1 aldehyde reductase member 2; PDBTitle: structure of the aflatoxin aldehyde reductase in complex with nadph
93	c3krbB_	Alignment	not modelled	5.2	9	PDB header: oxidoreductase Chain: B: PDB Molecule: aldose reductase; PDBTitle: structure of aldose reductase from giardia lamblia at 1.75a resolution
94	c4nsmA_	Alignment	not modelled	5.1	44	PDB header: structural protein Chain: A: PDB Molecule: collagen-like protein sclb; PDBTitle: crystal structure of the streptococcal collagen-like protein 22 globular domain from invasive m3-type group a streptococcus
95	c3ol4B_	Alignment	not modelled	5.1	16	PDB header: unknown function Chain: B: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a putative uncharacterized protein from2 mycobacterium smegmatis, an ortholog of rv0543c
96	d1ffva1	Alignment	not modelled	5.1	23	Fold: CO dehydrogenase ISP C-domain like Superfamily: CO dehydrogenase ISP C-domain like Family: CO dehydrogenase ISP C-domain like
97	c4hbka_	Alignment	not modelled	5.1	12	PDB header: oxidoreductase Chain: A: PDB Molecule: aldo-keto reductase family 1, member b4 (aldose reductase); PDBTitle: structure of the aldose reductase from schistosoma japonicum