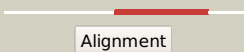
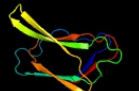




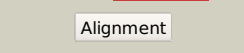
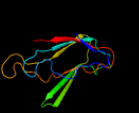


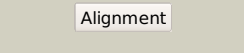

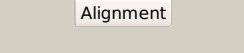


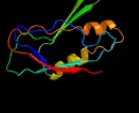
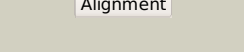

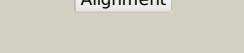
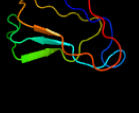
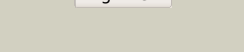














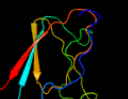







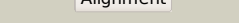


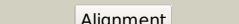



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD2227_(-)_2500939_2501640
Date	Mon Aug 5 13:25:36 BST 2019
Unique Job ID	a55e2ec291b83d4d

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3dkqB_	 Alignment		98.8	30	PDB header: oxidoreductase Chain: B: PDB Molecule: pkhd-type hydroxylase sba1_3634; PDBTitle: crystal structure of putative oxygenase (yp_001051978.1) from <i>Shewanella baltica</i> os155 at 2.26 Å resolution
2	c6f0wA_	 Alignment		98.3	20	PDB header: oxidoreductase Chain: A: PDB Molecule: hif prolyl hydroxylase; PDBTitle: prolyl hydroxylase in complex with hypoxia inducible factor oxygen2 degradation domain peptide fragment from <i>Trichoplax adhaerens</i>
3	c4iw3J_	 Alignment		98.1	18	PDB header: metal binding protein/translation Chain: J: PDB Molecule: putative uncharacterized protein; PDBTitle: crystal structure of a <i>Pseudomonas putida</i> prolyl-4-hydroxylase (p4h)2 in complex with elongation factor tu (ef-tu)
4	c5c5tB_	 Alignment		98.1	19	PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase; PDBTitle: the crystal structure of viral collagen prolyl hydroxylase vcpH from <i>Paramecium bursaria</i> chloroella virus-1 - 20g complex
5	c2jijA_	 Alignment		97.9	23	PDB header: hydrolase Chain: A: PDB Molecule: prolyl-4 hydroxylase; PDBTitle: crystal structure of the apo form of <i>Chlamydomonas reinhardtii</i> prolyl-4 hydroxylase type I
6	c2g19A_	 Alignment		97.8	20	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: cellular oxygen sensing: crystal structure of hypoxia-inducible factor2 prolyl hydroxylase (phd2)
7	c6ax6B_	 Alignment		97.7	20	PDB header: oxidoreductase Chain: B: PDB Molecule: procollagen lysyl hydroxylase and glycosyltransferase; PDBTitle: the crystal structure of a lysyl hydroxylase from <i>Acanthamoeba</i> polyphaga mimivirus
8	c3itqB_	 Alignment		97.5	19	PDB header: oxidoreductase Chain: B: PDB Molecule: prolyl 4-hydroxylase, alpha subunit domain protein; PDBTitle: crystal structure of a prolyl 4-hydroxylase from <i>Bacillus anthracis</i>
9	c3ouiA_	 Alignment		96.8	17	PDB header: oxidoreductase Chain: A: PDB Molecule: egl nine homolog 1; PDBTitle: phd2-r717 with 40787422
10	c6fxyA_	 Alignment		96.5	21	PDB header: transferase Chain: A: PDB Molecule: procollagen-lysine,2-oxoglutarate 5-dioxygenase 3; PDBTitle: crystal structure of full-length human lysyl hydroxylase lh3 -2 cocrystal with Fe2+, Mn2+, UDP-gal - structure from long-wavelength3 s-sad
11	c6n1fD_	 Alignment		96.5	27	PDB header: oxidoreductase Chain: D: PDB Molecule: oxidoreductase, 20g-fe(ii) oxygenase family; PDBTitle: crystal structure of oxidoreductase, 20g-fe(ii) oxygenase family, from <i>Burkholderia pseudomallei</i>

12	d2fdia1	 Alignment		94.8	18	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: AlkB-like
13	c4nhyC	 Alignment		93.8	20	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: C: PDB Molecule: 2-oxoglutarate and iron-dependent oxygenase domain- PDBTitle: crystal structure of human ogfod1, 2-oxoglutarate and iron-dependent2 oxygenase domain containing 1, in complex with pyridine-2,4-3 dicarboxylic acid (2,4-pdca)
14	c2iuwA	 Alignment		93.4	12	PDB header: oxidoreductase Chain: A: PDB Molecule: alkylated repair protein alkb homolog 3; PDBTitle: crystal structure of human abh3 in complex with iron ion and 2-2 oxoglutarate
15	d2iuwA1	 Alignment		93.2	14	Fold: Double-stranded beta-helix Superfamily: Clavamate synthase-like Family: AlkB-like
16	c6iuqA	 Alignment		91.4	16	PDB header: oxidoreductase Chain: A: PDB Molecule: prolyl 4-hydroxylase; PDBTitle: crystal structure and expression patterns of prolyl 4-hydroxylases2 from phytophthora capsici
17	c3kt4A	 Alignment		87.6	16	PDB header: oxidoreductase Chain: A: PDB Molecule: pkhd-type hydroxylase tpa1; PDBTitle: crystal structure of tpa1 from saccharomyces cerevisiae, a component2 of the messenger ribonucleoprotein complex
18	c4xaaA	 Alignment		87.1	25	PDB header: oxidoreductase Chain: A: PDB Molecule: putative oxygenase; PDBTitle: crystal structure of avio1 from streptomyces viridochromogenes tue57
19	c4qkbA	 Alignment		87.0	19	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-ketoglutarate-dependent dioxygenase alkb homolog 7, PDBTitle: crystal structure of seleno-methionine labelled human alkbh7 in2 complex with alpha-ketoglutarate and mn(ii)
20	c4nj4A	 Alignment		86.4	15	PDB header: oxidoreductase/oxidoreductase inhibitor Chain: A: PDB Molecule: rna demethylase alkbh5; PDBTitle: crystal structure of human alkbh5
21	c3bvcA	 Alignment	not modelled	79.3	15	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein ism_01780; PDBTitle: crystal structure of uncharacterized protein ism_01780 from2 roseovarius nubinhibens ism
22	c5xoiA	 Alignment	not modelled	78.2	20	PDB header: oxidoreductase Chain: A: PDB Molecule: oxidoreductase, 2og-fe oxygenase family protein, putative, PDBTitle: the structure of osalkbh1
23	c5ylbA	 Alignment	not modelled	76.8	15	PDB header: oxidoreductase Chain: A: PDB Molecule: uncharacterized protein p8a3.02c; PDBTitle: crystal structure of ofd2 from schizosaccharomyces pombe at 1.80 a
24	c3thtB	 Alignment	not modelled	76.2	25	PDB header: oxidoreductase Chain: B: PDB Molecule: alkylated dna repair protein alkb homolog 8; PDBTitle: crystal structure and rna binding properties of the rrm/alkb domains2 in human abh8, an enzyme catalyzing trna hypermodification, northeast3 structural genomics consortium target hr5601b
25	c5erID	 Alignment	not modelled	63.1	20	PDB header: isomerase Chain: D: PDB Molecule: snon,snon; PDBTitle: crystal structure of the epimerase snon in complex with ni2+,2 succinate and nogalamycin ro
26	c3gjbA	 Alignment	not modelled	55.2	24	PDB header: biosynthetic protein Chain: A: PDB Molecule: cytc3; PDBTitle: cytc3 with fe(ii) and alpha-ketoglutarate
27	c3mguA	 Alignment	not modelled	53.2	15	PDB header: oxidoreductase Chain: A: PDB Molecule: pkhd-type hydroxylase tpa1; PDBTitle: structure of s. cerevisiae tpa1 protein, a proline hydroxylase2 modifying ribosomal protein rps23
						PDB header: oxidoreductase/dna

28	c3btzA_	Alignment	not modelled	46.7	16	Chain: A: PDB Molecule: alpha-ketoglutarate-dependent dioxygenase alkB homolog 2; PDBTitle: crystal structure of human abh2 cross-linked to dsdna
29	c5aycA_	Alignment	not modelled	42.0	19	PDB header: transferase Chain: A: PDB Molecule: 4-o-beta-d-mannosyl-d-glucose phosphorylase; PDBTitle: crystal structure of ruminococcus albus 4-o-beta-d-mannosyl-d-glucose2 phosphorylase (ramp1) in complexes with sulfate and 4-o-beta-d-3 mannosyl-d-glucose
30	c3watA_	Alignment	not modelled	23.0	19	PDB header: transferase Chain: A: PDB Molecule: 4-o-beta-d-mannosyl-d-glucose phosphorylase; PDBTitle: crystal structure of 4-o-beta-d-mannosyl-d-glucose phosphorylase mgp2 complexed with man+glc
31	d1r8ja2	Alignment	not modelled	17.9	22	Fold: Flavodoxin-like Superfamily: CheY-like Family: N-terminal domain of the circadian clock protein KaiA
32	c4lt5A_	Alignment	not modelled	16.6	21	PDB header: oxidoreductase/dna Chain: A: PDB Molecule: naegleria tet-like dioxygenase; PDBTitle: structure of a naegleria tet-like dioxygenase in complex with 5-2 methylcytosine dna
33	d2eiaa1	Alignment	not modelled	16.1	16	Fold: Acyl carrier protein-like Superfamily: Retrovirus capsid dimerization domain-like Family: Retrovirus capsid protein C-terminal domain
34	c4xabA_	Alignment	not modelled	16.0	18	PDB header: oxidoreductase Chain: A: PDB Molecule: evdo2; PDBTitle: crystal structure of evdo2 from micromonospora carbonacea var.2 aurantiaca
35	c4p29A_	Alignment	not modelled	15.6	13	PDB header: protein binding Chain: A: PDB Molecule: lpoa; PDBTitle: crystal structure of the lpoa n-terminal domain from haemophilus2 influenzae
36	d2dsma1	Alignment	not modelled	13.8	29	Fold: Yqal-like Superfamily: Yqal-like Family: Yqal-like
37	c5oetB_	Alignment	not modelled	13.0	16	PDB header: ligase Chain: B: PDB Molecule: glutathione synthetase-like effector 30 (gpa-gss30-apo); PDBTitle: the structure of a glutathione synthetase like-effector (gss30) from2 globodera pallida in apoform.
38	c4xvvB_	Alignment	not modelled	12.8	28	PDB header: chaperone Chain: B: PDB Molecule: acid stress chaperone hdeb; PDBTitle: crystal structure of an acid stress chaperone hdeb (kpn_03484) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 1.70 a3 resolution
39	c1xexB_	Alignment	not modelled	12.7	14	PDB header: cell cycle Chain: B: PDB Molecule: smc protein; PDBTitle: structural biochemistry of atp-driven dimerization and dna2 stimulated activation of smc atpases.
40	c2rrnA_	Alignment	not modelled	11.8	27	PDB header: protein transport Chain: A: PDB Molecule: probable secdf protein-export membrane protein; PDBTitle: solution structure of secdf periplasmic domain p4
41	c5zm4B_	Alignment	not modelled	11.4	16	PDB header: oxidoreductase Chain: B: PDB Molecule: dioxygenase anda; PDBTitle: fe(ii)/(alpha)ketoglutarate-dependent dioxygenase anda with2 preandiloid c
42	c3j3ah_	Alignment	not modelled	10.3	29	PDB header: ribosome Chain: H: PDB Molecule: 40s ribosomal protein s7; PDBTitle: structure of the human 40s ribosomal proteins
43	c5e6wA_	Alignment	not modelled	10.2	14	PDB header: cell adhesion Chain: A: PDB Molecule: integrin beta-2; PDBTitle: re-refinement of the crystal structure of the plexin-semaphorin-2 integrin domain/hybrid domain/i-egf1 segment from the human integrin3 b2 subunit
44	d2bzea1	Alignment	not modelled	9.6	17	Fold: SH3-like barrel Superfamily: Plus3-like Family: Plus3
45	c3qzFD_	Alignment	not modelled	9.2	29	PDB header: viral protein Chain: D: PDB Molecule: replicase polyprotein 1ab; PDBTitle: structure of the c-terminal domain of nsp4 from feline coronavirus
46	c5gj9A_	Alignment	not modelled	9.2	14	PDB header: oxidoreductase Chain: A: PDB Molecule: 1-aminocyclopropane-1-carboxylate oxidase 2; PDBTitle: crystal structure of arabidopsis thaliana aco2 in complex with poa
47	c5j92B_	Alignment	not modelled	9.0	12	PDB header: oxidoreductase Chain: B: PDB Molecule: putative alpha kg dependent 2,4-d dioxygenase; PDBTitle: crystal structure of a putative alpha-ketoglutarate dependent 2,4-d2 dioxygenase from burkholderia xenovorans
48	d1jswa_	Alignment	not modelled	8.8	31	Fold: L-aspartase-like Superfamily: L-aspartase-like Family: L-aspartase/fumarase
49	c5mg3F_	Alignment	not modelled	8.4	27	PDB header: chaperone Chain: F: PDB Molecule: protein translocase subunit secf; PDBTitle: em fitted model of bacterial holo-translocon
50	d2pw6a1	Alignment	not modelled	8.3	17	Fold: Phosphorylase/hydrolase-like Superfamily: LigB-like Family: LigB-like
51	d1wgya_	Alignment	not modelled	8.3	16	Fold: beta-Grasp (ubiquitin-like) Superfamily: Ubiquitin-like Family: Ras-binding domain, RBD
52	d1vi2a2	Alignment	not modelled	8.3	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like

53	c2d40C	Alignment	not modelled	8.3	10	PDB header: oxidoreductase Chain: C: PDB Molecule: putative gentisate 1,2-dioxygenase; PDBTitle: crystal structure of z3393 from escherichia coli o157:h7
54	d1vh0a	Alignment	not modelled	8.2	26	Fold: alpha/beta knot Superfamily: alpha/beta knot Family: YbeA-like
55	c5u7gB	Alignment	not modelled	8.2	29	PDB header: transferase Chain: B: PDB Molecule: creb-binding protein; PDBTitle: crystal structure of the catalytic core of cbp
56	c3brgC	Alignment	not modelled	8.1	19	PDB header: dna binding protein/dna Chain: C: PDB Molecule: recombining binding protein suppressor of hairless; PDBTitle: csl (rbp-jk) bound to dna
57	d1s9ca1	Alignment	not modelled	8.1	60	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
58	c1eiaA	Alignment	not modelled	7.7	24	PDB header: viral protein Chain: A: PDB Molecule: eiav capsid protein p26; PDBTitle: x-ray crystal structure of equine infectious anemia virus2 (eiav) capsid protein p26
59	c4bhwB	Alignment	not modelled	7.4	29	PDB header: transferase Chain: B: PDB Molecule: histone acetyltransferase p300; PDBTitle: structural basis for autoinhibition of the acetyltransferase activity2 of p300
60	c3biyA	Alignment	not modelled	7.3	29	PDB header: transferase Chain: A: PDB Molecule: histone acetyltransferase p300; PDBTitle: crystal structure of p300 histone acetyltransferase domain in complex2 with a bisubstrate inhibitor, lys-coa
61	d1nvta2	Alignment	not modelled	7.2	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
62	c5b58T	Alignment	not modelled	7.1	33	PDB header: metal binding protein Chain: T: PDB Molecule: putative hemin transport system, substrate-binding protein; PDBTitle: inward-facing conformation of abc heme importer bhuv in complex with2 periplasmic heme binding protein bhut from burkholderia cenocepacia
63	c2k1cA	Alignment	not modelled	7.1	22	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: capsid protein p24; PDBTitle: nmr structure of the c-terminal domain of hiv-1 capsid in complex with2 peptide inhibitor
64	c6ff48	Alignment	not modelled	6.9	29	PDB header: splicing Chain: 8: PDB Molecule: splicing factor 3b subunit 2; PDBTitle: human bact spliceosome core structure
65	c2mhcA	Alignment	not modelled	6.9	20	PDB header: protein binding Chain: A: PDB Molecule: penicillin-binding protein activator lpoa; PDBTitle: e. coli lpoa n-terminal domain
66	d1w6ka2	Alignment	not modelled	6.8	21	Fold: alpha/alpha toroid Superfamily: Terpenoid cyclases/Protein prenyltransferases Family: Terpene synthases
67	c3hsbB	Alignment	not modelled	6.8	24	PDB header: rna binding protein/rna Chain: B: PDB Molecule: protein hfq; PDBTitle: crystal structure of ymah (hfq) from bacillus subtilis in complex with2 an rna aptamer
68	c3o14B	Alignment	not modelled	6.6	21	PDB header: gene regulation Chain: B: PDB Molecule: anti-ecsfactor, chrr; PDBTitle: crystal structure of an anti-ecsfactor, chrr (maqu_0586) from2 marinobacter aquaeolei vt8 at 1.70 a resolution
69	c2xuvB	Alignment	not modelled	6.6	35	PDB header: unknown function Chain: B: PDB Molecule: hdeb; PDBTitle: the structure of hdeb
70	c4mdyA	Alignment	not modelled	6.5	18	PDB header: transport protein Chain: A: PDB Molecule: periplasmic binding protein; PDBTitle: crystal structure of periplasmic solute binding protein from2 mycobacterium smegmatis str. mc2 155
71	c6hwiA	Alignment	not modelled	6.5	18	PDB header: viral protein Chain: A: PDB Molecule: gag-pro-pol polyprotein; PDBTitle: immature m-pmv capsid hexamer structure in intact virus particles
72	d1npya2	Alignment	not modelled	6.5	17	Fold: Aminoacid dehydrogenase-like, N-terminal domain Superfamily: Aminoacid dehydrogenase-like, N-terminal domain Family: Shikimate dehydrogenase-like
73	c4cbzA	Alignment	not modelled	6.4	15	PDB header: signaling protein Chain: A: PDB Molecule: protein jagged-1; PDBTitle: notch ligand, jagged-1, contains an n-terminal c2 domain
74	d1pn2a2	Alignment	not modelled	6.2	50	Fold: Thioesterase/thiol ester dehydrase-isomerase Superfamily: Thioesterase/thiol ester dehydrase-isomerase Family: MaoC-like
75	d3brda1	Alignment	not modelled	6.2	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: E set domains Family: NF-kappa-B/REL/DORSAL transcription factors, C-terminal domain
76	d1zeeal	Alignment	not modelled	6.0	16	Fold: Indolic compounds 2,3-dioxygenase-like Superfamily: Indolic compounds 2,3-dioxygenase-like Family: Indoleamine 2,3-dioxygenase-like
77	d2d40a1	Alignment	not modelled	5.8	11	Fold: Double-stranded beta-helix Superfamily: RmIC-like cupins Family: Gentisate 1,2-dioxygenase-like
78	d1kq1a	Alignment	not modelled	5.7	43	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Pleiotropic translational regulator Hfq PDB header: oxidoreductase

79	c2eo2A	Alignment	not modelled	5.6	37	Chain: A: PDB Molecule: adult male hypothalamus cdna, riken full-length PDBTitle: solution structure of the insertion region (510-573) of2 fthfs domain from mouse methylenetetrahydrofolate3 dehydrogenase (nadp+ dependent) 1-like protein
80	c4p9gA	Alignment	not modelled	5.5	11	PDB header: oxidoreductase Chain: A: PDB Molecule: 2,4'-dihydroxyacetophenone dioxygenase; PDBTitle: structure of the 2,4'-dihydroxyacetophenone dioxygenase from2 alcaligenes sp.
81	d1zvfa1	Alignment	not modelled	5.5	17	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
82	c1x65A	Alignment	not modelled	5.4	22	PDB header: rna binding protein Chain: A: PDB Molecule: unr protein; PDBTitle: solution structure of the third cold-shock domain of the human2 kiaa0885 protein (unr protein)
83	c3fbtB	Alignment	not modelled	5.2	13	PDB header: oxidoreductase, lyase Chain: B: PDB Molecule: chorismate mutase and shikimate 5-dehydrogenase fusion PDBTitle: crystal structure of a chorismate mutase/shikimate 5-dehydrogenase2 fusion protein from clostridium acetobutylicum
84	c4y91L	Alignment	not modelled	5.2	36	PDB header: rna binding protein/rna Chain: L: PDB Molecule: rna-binding protein hfq; PDBTitle: crystal structure of a thermotoga maritima hfq homolog
85	c4hgvC	Alignment	not modelled	5.1	37	PDB header: lyase Chain: C: PDB Molecule: fumarate hydratase class ii; PDBTitle: crystal structure of a fumarate hydratase
86	c5xzsA	Alignment	not modelled	5.1	29	PDB header: transcription Chain: A: PDB Molecule: histone acetyltransferase p300; PDBTitle: cryo-em structure of p300
87	d1u1sa1	Alignment	not modelled	5.1	27	Fold: Sm-like fold Superfamily: Sm-like ribonucleoproteins Family: Pleiotropic translational regulator Hfq
88	c2zxkB	Alignment	not modelled	5.1	31	PDB header: oxidoreductase Chain: B: PDB Molecule: red chlorophyll catabolite reductase, PDBTitle: crystal structure of semet-red chlorophyll catabolite2 reductase
89	c3echC	Alignment	not modelled	5.1	63	PDB header: transcription, transcription regulation Chain: C: PDB Molecule: 25-mer fragment of protein armr; PDBTitle: the marr-family repressor mexr in complex with its antirepressor armr
90	c2ba1B	Alignment	not modelled	5.1	23	PDB header: rna binding protein Chain: B: PDB Molecule: archaeal exosome rna binding protein csl4; PDBTitle: archaeal exosome core
91	c1pn2D	Alignment	not modelled	5.0	50	PDB header: lyase Chain: D: PDB Molecule: peroxisomal hydratase-dehydrogenase-epimerase; PDBTitle: crystal structure analysis of the selenomethionine labelled2 2-enoyl-coa hydratase 2 domain of candida tropicalis3 multifunctional enzyme type 2