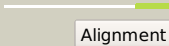
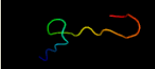
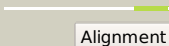
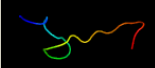
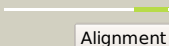
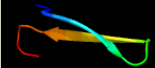
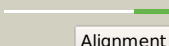
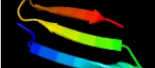
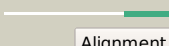
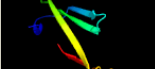
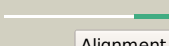

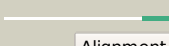
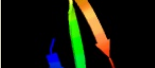
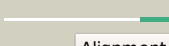
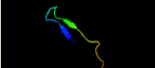
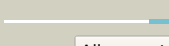




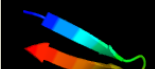
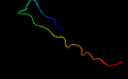
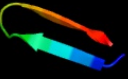
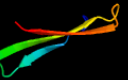
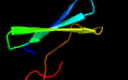



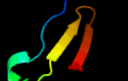



Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD3142c_(-)_3509115_3509543
Date	Thu Aug 8 16:20:32 BST 2019
Unique Job ID	14866f033ce75869

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3luuA_	 Alignment		65.9	32	PDB header: biosynthetic protein Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein with unknown function which belongs to2 pfam duf971 family (afe_2189) from acidithiobacillus ferrooxidans3 atcc 23270 at 1.93 a resolution
2	c2l6pA_	 Alignment		65.4	29	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: phac1, phac2 and phad genes; PDBTitle: nmr solution structure of the protein np_253742.1
3	c2l6nA_	 Alignment		60.4	29	PDB header: structure genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein yp_001092504.1; PDBTitle: nmr solution structure of the protein yp_001092504.1
4	d2auwa2	 Alignment		57.5	23	Fold: NE0471 N-terminal domain-like Superfamily: NE0471 N-terminal domain-like Family: NE0471 N-terminal domain-like
5	c3pbpD_	 Alignment		42.9	17	PDB header: transport protein,structural protein Chain: D: PDB Molecule: nucleoporin nup82; PDBTitle: structure of the yeast heterotrimeric nup82-nup159-nup116 nucleoporin2 complex
6	c2auwB_	 Alignment		42.1	23	PDB header: unknown function Chain: B: PDB Molecule: hypothetical protein ne0471; PDBTitle: crystal structure of putative dna binding protein ne0471 from2 nitrosomonas europaea atcc 19718
7	c5lhxA_	 Alignment		41.9	26	PDB header: structural protein Chain: A: PDB Molecule: serine/threonine-protein kinase plk4; PDBTitle: pb3 domain of drosophila melanogaster plk4 (sak)
8	d1lp9e1	 Alignment		41.0	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
9	d1bd2d1	 Alignment		38.6	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
10	d1j8hd1	 Alignment		36.4	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
11	d3pmga4	 Alignment		35.7	43	Fold: TBP-like Superfamily: Phosphoglucosyltransferase, C-terminal domain Family: Phosphoglucosyltransferase, C-terminal domain

12	d2cdea1	Alignment		34.6	31	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
13	d1kfia4	Alignment		32.5	29	Fold: TBP-like Superfamily: Phosphoglucomutase, C-terminal domain Family: Phosphoglucomutase, C-terminal domain
14	c4g6tA_	Alignment		30.2	16	PDB header: chaperone Chain: A: PDB Molecule: type iii chaperone protein shca; PDBTitle: structure of the hopa1-scha chaperone-effector complex
15	c3k8rA_	Alignment		30.1	24	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of protein of unknown function (yp_427503.1) from2 rhodospirillum rubrum atcc 11170 at 2.75 a resolution
16	d1kgcd1	Alignment		29.0	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
17	c5xcxB_	Alignment		28.3	28	PDB header: immune system Chain: B: PDB Molecule: vl-sarah(s37c) chimera; PDBTitle: crystal structure of ts2/16 fv-clasp fragment
18	c5ix9A_	Alignment		27.2	21	PDB header: antifreeze protein, cell adhesion Chain: A: PDB Molecule: antifreeze protein; PDBTitle: cell surface anchoring domain
19	c2ldmA_	Alignment		27.2	33	PDB header: transcription/protein binding Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: solution structure of human phf20 tudor2 domain bound to a p53 segment2 containing a dimethyllysine analog p53k370me2
20	d2esvd1	Alignment		26.1	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
21	d1h5ba_	Alignment	not modelled	24.0	30	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
22	d2qqsa2	Alignment	not modelled	22.9	47	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
23	d1qrnd1	Alignment	not modelled	22.7	32	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
24	d2ak4d1	Alignment	not modelled	21.3	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
25	c2ol3A_	Alignment	not modelled	21.2	27	PDB header: immune system Chain: A: PDB Molecule: bm3.3 t-cell receptor alpha-chain; PDBTitle: crystal structure of bm3.3 scfv tcr in complex with pbm8-h-2kbm8 mhc2 class i molecule
26	c4kq7B_	Alignment	not modelled	19.9	20	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: hypothetical protein; PDBTitle: crystal structure of a duf2961 family protein (bacuni_00161) from2 bacteroides uniformis atcc 8492 at 1.62 a resolution
27	c3p8dB_	Alignment	not modelled	19.0	33	PDB header: protein binding Chain: B: PDB Molecule: medulloblastoma antigen mu-mb-50.72; PDBTitle: crystal structure of the second tudor domain of human phf20 (homodimer2 form)
28	d1jyoa_	Alignment	not modelled	18.5	20	Fold: Secretion chaperone-like Superfamily: Type III secretory system chaperone-like Family: Type III secretory system chaperone
						PDB header: immune system

29	c5xcqB_	Alignment	not modelled	17.4	21	Chain: B: PDB Molecule: vi-sarah(m24c) chimera; PDBTitle: crystal structure of p20.1 fv-clasp fragment with its antigen peptide
30	d1mbya_	Alignment	not modelled	17.0	26	Fold: Polo-box domain Superfamily: Polo-box domain Family: Swapped Polo-box domain
31	d1i9ea_	Alignment	not modelled	16.8	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
32	c2equA_	Alignment	not modelled	16.6	22	PDB header: protein binding Chain: A: PDB Molecule: phd finger protein 20-like 1; PDBTitle: solution structure of the tudor domain of phd finger2 protein 20-like 1
33	d1u3hb1	Alignment	not modelled	16.5	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
34	d1w7ja1	Alignment	not modelled	15.5	27	Fold: SH3-like barrel Superfamily: Myosin S1 fragment, N-terminal domain Family: Myosin S1 fragment, N-terminal domain
35	c4m8aA_	Alignment	not modelled	15.4	26	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: crystal structure of thermotoga maritima ftsh periplasmic domain
36	d2qgra2	Alignment	not modelled	15.4	47	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
37	c5zu4B_	Alignment	not modelled	15.1	20	PDB header: antitumor protein Chain: B: PDB Molecule: natterin-like protein; PDBTitle: crystal structure of lamprey immune protein
38	c5fu5A_	Alignment	not modelled	15.0	25	PDB header: sugar binding protein Chain: A: PDB Molecule: cbm77-rfpl; PDBTitle: the complexity of the ruminococcus flavefaciens cellulosome2 reflects an expansion in glycan recognition
39	d2fug31	Alignment	not modelled	14.6	8	Fold: Double psi beta-barrel Superfamily: ADC-like Family: Formate dehydrogenase/DMSO reductase, C-terminal domain
40	c4by2C_	Alignment	not modelled	14.4	12	PDB header: structural protein Chain: C: PDB Molecule: anastral spindle 2, sas 4; PDBTitle: sas-4 (dcpap) tcp domain in complex with a proline rich motif of ana22 (dstil) of drosophila melanogaster
41	d1fo0a_	Alignment	not modelled	14.2	27	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
42	c2x8nA_	Alignment	not modelled	14.1	19	PDB header: structural genomics Chain: A: PDB Molecule: cv0863; PDBTitle: solution nmr structure of uncharacterized protein cv0863 from2 chromobacterium violaceum. northeast structural genomics target3 (nesg) target cvt3. ocsb target cv0863.
43	c4uc4A_	Alignment	not modelled	14.0	14	PDB header: replication Chain: A: PDB Molecule: lysine-specific demethylase 4b; PDBTitle: crystal structure of hybrid tudor domain of human lysine demethylase2 kdm4b
44	d1prt1	Alignment	not modelled	13.8	20	Fold: OB-fold Superfamily: Bacterial enterotoxins Family: Bacterial AB5 toxins, B-subunits
45	c6hhkB_	Alignment	not modelled	13.7	21	PDB header: viral protein Chain: B: PDB Molecule: gp105; PDBTitle: structure of gp105 of listeria bacteriophage a511
46	d2bnqd1	Alignment	not modelled	13.4	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
47	c4chjA_	Alignment	not modelled	12.8	36	PDB header: cell cycle Chain: A: PDB Molecule: imc sub-compartment protein isp3; PDBTitle: structure of inner membrane complex (imc) sub-compartment2 protein 3 (isp3) from toxoplasma gondii
48	d1b88a_	Alignment	not modelled	12.3	24	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
49	c3tgoD_	Alignment	not modelled	12.3	14	PDB header: membrane protein Chain: D: PDB Molecule: lipoprotein 34; PDBTitle: crystal structure of the e. coli bamcd complex
50	d1aoga2	Alignment	not modelled	12.0	13	Fold: FAD/NAD(P)-binding domain Superfamily: FAD/NAD(P)-binding domain Family: FAD/NAD-linked reductases, N-terminal and central domains
51	d1tvda_	Alignment	not modelled	11.8	22	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
52	c3mb2j_	Alignment	not modelled	11.8	29	PDB header: isomerase Chain: j: PDB Molecule: 4-oxalocrotonate tautomerase family enzyme - beta subunit; PDBTitle: kinetic and structural characterization of a heterohexamer 4-2 oxalocrotonate tautomerase from chloroflexus aurantiacus j-10-fl:3 implications for functional and structural diversity in the4 tautomerase superfamily
53	c4gvbB_	Alignment	not modelled	11.7	17	PDB header: toxin Chain: B: PDB Molecule: kp6 killer toxin subunit beta; PDBTitle: crystal structure of the virally encoded antifungal protein, kp6,2 heterodimer
54	c3qiiA_	Alignment	not modelled	11.3	33	PDB header: transcription regulator Chain: A: PDB Molecule: phd finger protein 20; PDBTitle: crystal structure of tudor domain 2 of human phd finger protein 20

55	d1ac6a_	Alignment	not modelled	10.9	29	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
56	d1kj2a_	Alignment	not modelled	10.8	38	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
57	c3aqjQ_	Alignment	not modelled	10.4	40	PDB header: metal binding protein Chain: Q: PDB Molecule: baseplate assembly protein v; PDBTitle: crystal structure of a c-terminal domain of the bacteriophage p2 tail2 spike protein, gpv
58	d1td4a_	Alignment	not modelled	10.3	26	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
59	c6dsIB_	Alignment	not modelled	10.2	28	PDB header: splicing Chain: B: PDB Molecule: consensus engineered intein catc; PDBTitle: consensus engineered intein (cat) with atypical split site
60	c4furD_	Alignment	not modelled	10.0	29	PDB header: hydrolase Chain: D: PDB Molecule: urease subunit gamma 2; PDBTitle: crystal structure of urease subunit gamma 2 from brucella melitensis2 biovar abortus 2308
61	c1yc7B_	Alignment	not modelled	9.7	14	PDB header: immune system Chain: B: PDB Molecule: anti-vsg immunoglobulin heavy chain variable PDBTitle: caban33 vhh fragment against vsg
62	c5edfA_	Alignment	not modelled	9.6	11	PDB header: unknown function Chain: A: PDB Molecule: frpc operon protein; PDBTitle: crystal structure of the selenomethionine-substituted iron-regulated2 protein frpd from neisseria meningitidis
63	d1c5ea_	Alignment	not modelled	9.4	32	Fold: beta-clip Superfamily: Head decoration protein D (gpD, major capsid protein D) Family: Head decoration protein D (gpD, major capsid protein D)
64	d2co3a1	Alignment	not modelled	9.3	47	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
65	d1u3ha1	Alignment	not modelled	9.3	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
66	d2cnza1	Alignment	not modelled	8.9	47	Fold: Common fold of diphtheria toxin/transcription factors/cytochrome f Superfamily: Bacterial adhesins Family: Pilus subunits
67	c4z42A_	Alignment	not modelled	8.7	29	PDB header: hydrolase Chain: A: PDB Molecule: urease subunit gamma; PDBTitle: crystal structure of urease from yersinia enterocolitica
68	d4ubpa_	Alignment	not modelled	8.7	21	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
69	c2fvhB_	Alignment	not modelled	8.7	21	PDB header: hydrolase Chain: B: PDB Molecule: urease gamma subunit; PDBTitle: crystal structure of rv1848, a urease gamma subunit urea (urea2 amidohydrolase), from mycobacterium tuberculosis
70	d3elga1	Alignment	not modelled	8.6	9	Fold: BLIP-like Superfamily: BT0923-like Family: BT0923-like
71	c3metB_	Alignment	not modelled	8.5	26	PDB header: transcription Chain: B: PDB Molecule: saga-associated factor 29 homolog; PDBTitle: crystal structure of sgf29 in complex with h3k4me2
72	c3htyC_	Alignment	not modelled	8.3	22	PDB header: structural genomics, unknown function Chain: C: PDB Molecule: hypothetical protein bt_0869; PDBTitle: crystal structure of a lipocalin-like protein (bt_0869) from2 bacteroides thetaiotaomicron vpi-5482 at 1.95 a resolution
73	c2wv9A_	Alignment	not modelled	8.3	27	PDB header: hydrolase Chain: A: PDB Molecule: flavivirin protease ns2b regulatory subunit, flavivirin PDBTitle: crystal structure of the ns3 protease-helicase from murray2 valley encephalitis virus
74	d1e9ya2	Alignment	not modelled	8.2	21	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
75	c5c2mA_	Alignment	not modelled	8.1	24	PDB header: structural protein Chain: A: PDB Molecule: predicted protein; PDBTitle: the de novo evolutionary emergence of a symmetrical protein is shaped2 by folding constraints
76	c4chmB_	Alignment	not modelled	7.7	14	PDB header: cell cycle Chain: B: PDB Molecule: imc sub-compartment protein isp1; PDBTitle: structure of inner membrane complex (imc) sub-compartment protein 12 (isp1) from toxoplasma gondii
77	c5t49A_	Alignment	not modelled	7.6	30	PDB header: hydrolase Chain: A: PDB Molecule: bh0236 protein; PDBTitle: crystal structure of semet derivative bhgh81
78	d1olma2	Alignment	not modelled	7.6	15	Fold: Supernatant protein factor (SPF), C-terminal domain Superfamily: Supernatant protein factor (SPF), C-terminal domain Family: Supernatant protein factor (SPF), C-terminal domain
79	d1mkia_	Alignment	not modelled	7.6	25	Fold: beta-lactamase/transpeptidase-like Superfamily: beta-lactamase/transpeptidase-like Family: Glutaminase
80	d1ncbh1	Alignment	not modelled	7.3	26	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
81	d3bmva3	Alignment	not modelled	7.2	31	Fold: Glycosyl hydrolase domain Superfamily: Glycosyl hydrolase domain

						Family: alpha-Amylases, C-terminal beta-sheet domain
82	c2qqsB_	Alignment	not modelled	7.2	35	PDB header: oxidoreductase Chain: B: PDB Molecule: jmjc domain-containing histone demethylation PDBTitle: jmjd2a tandem tudor domains in complex with a trimethylated2 histone h4-k20 peptide
83	c3j20N_	Alignment	not modelled	7.1	16	PDB header: ribosome Chain: N: PDB Molecule: 30s ribosomal protein s12p; PDBTitle: promiscuous behavior of proteins in archaeal ribosomes revealed by2 cryo-em: implications for evolution of eukaryotic ribosomes (30s3 ribosomal subunit)
84	d1k3xa2	Alignment	not modelled	7.0	20	Fold: N-terminal domain of MutM-like DNA repair proteins Superfamily: N-terminal domain of MutM-like DNA repair proteins Family: N-terminal domain of MutM-like DNA repair proteins
85	c4rgiA_	Alignment	not modelled	6.9	25	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of ktsc domain protein ypo2434 from yersinia pestis
86	d1ejxa_	Alignment	not modelled	6.8	21	Fold: Urease, gamma-subunit Superfamily: Urease, gamma-subunit Family: Urease, gamma-subunit
87	d1ucbh1	Alignment	not modelled	6.8	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
88	c3jbhA_	Alignment	not modelled	6.8	10	PDB header: contractile protein Chain: A: PDB Molecule: myosin 2 heavy chain striated muscle; PDBTitle: two heavy meromyosin interacting-heads motifs flexible docked into2 tarantula thick filament 3d-map allows in depth study of intra- and3 intermolecular interactions
89	c5xcvE_	Alignment	not modelled	6.8	22	PDB header: immune system Chain: E: PDB Molecule: vl-sarah(s37c) chimera,vl-sarah(s37c) chimera; PDBTitle: crystal structure of nz-1 fv-clasp fragment with its antigen peptide
90	d1iqmh_	Alignment	not modelled	6.8	10	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
91	c3tu3A_	Alignment	not modelled	6.6	26	PDB header: toxin/toxin chaperone Chain: A: PDB Molecule: exou chaperone; PDBTitle: 1.92 angstrom resolution crystal structure of the full-length spcu in2 complex with full-length exou from the type iii secretion system of3 pseudomonas aeruginosa
92	c3ay2A_	Alignment	not modelled	6.6	10	PDB header: antitumor protein, antiviral protein Chain: A: PDB Molecule: lipid modified azurin protein; PDBTitle: crystal structure of neisserial azurin
93	c6dbdC_	Alignment	not modelled	6.6	21	PDB header: immune system Chain: C: PDB Molecule: nanobody vhh r326; PDBTitle: crystal structure of vhh r326
94	c2n5uA_	Alignment	not modelled	6.6	17	PDB header: photosynthesis Chain: A: PDB Molecule: tsr0524 protein; PDBTitle: solution structure of the cyanobacterial cytochrome b6f complex2 subunit petp
95	d1q1j1	Alignment	not modelled	6.6	19	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
96	c4i86A_	Alignment	not modelled	6.5	12	PDB header: transferase Chain: A: PDB Molecule: cellulose synthase 1; PDBTitle: crystal structure of pilz domain of cesa from cellulose synthesizing2 bacterium
97	d1wtla_	Alignment	not modelled	6.5	20	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)
98	d1xaua_	Alignment	not modelled	6.3	42	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: I set domains
99	d1f8th1	Alignment	not modelled	6.2	21	Fold: Immunoglobulin-like beta-sandwich Superfamily: Immunoglobulin Family: V set domains (antibody variable domain-like)