
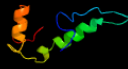
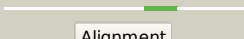

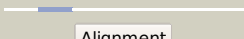


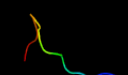

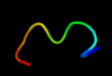





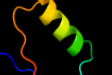






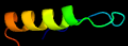

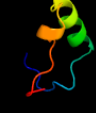








Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD0022c_(whiB5)_27023_27442
Date	Tue Jul 23 14:50:05 BST 2019
Unique Job ID	9ff7ded6047cfec

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5oayA_	 Alignment		98.0	35	PDB header: signaling protein Chain: A: PDB Molecule: transcriptional regulator whib1; PDBTitle: m. tuberculosis [4fe-4s] protein whib1 is a four-helix bundle that2 forms a no-sensitive complex with sigmaa and regulates the major3 virulence factor esx-1
2	c2k1oA_	 Alignment		50.8	64	PDB header: gene regulation Chain: A: PDB Molecule: putative; PDBTitle: nmr structure of helicobacter pylori jhp0511 (hp0564).
3	c2l6tA_	 Alignment		26.7	53	PDB header: antiviral protein Chain: A: PDB Molecule: vir-576; PDBTitle: efficacy of an hiv-1 entry inhibitor targeting the gp41 fusion peptide
4	c2l6sA_	 Alignment		26.7	53	PDB header: antiviral protein Chain: A: PDB Molecule: vir-576; PDBTitle: efficacy of an hiv-1 entry inhibitor targeting the gp41 fusion peptide
5	c2jsjA_	 Alignment		15.4	78	PDB header: hormone Chain: A: PDB Molecule: appetite-regulating hormone, obestatin; PDBTitle: obestatin in water solution
6	c5dmpA_	 Alignment		12.1	41	PDB header: hydrolase Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: structure of the archaeal nhej phosphoesterase from methanocella2 paludicola.
7	c1ei0A_	 Alignment		11.6	47	PDB header: cell cycle Chain: A: PDB Molecule: p8mtcp1; PDBTitle: nmr structure of the alpha-helical hairpin of p8mtcp1
8	d1aopa2	 Alignment		11.6	14	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
9	c6ba3A_	 Alignment		11.3	60	PDB header: toxin Chain: A: PDB Molecule: u21-hexatoxin-hi1a; PDBTitle: nmr structure of u21-hexatoxin-hi1a toxin from australian funnel-web2 spider hadronyche infensa
10	d1gpqa_	 Alignment		11.3	26	Fold: Inhibitor of vertebrate lysozyme, Ivy Superfamily: Inhibitor of vertebrate lysozyme, Ivy Family: Inhibitor of vertebrate lysozyme, Ivy
11	c2jshA_	 Alignment		10.6	78	PDB header: hormone Chain: A: PDB Molecule: appetite-regulating hormone, obestatin; PDBTitle: obestatin nmr structure in sds/dpc micellar solution

12	d1zj8a1	Alignment		10.5	23	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
13	c4ce0A	Alignment		10.3	25	PDB header: transferase Chain: A; PDB Molecule: o-methyltransferase; PDBTitle: crystal structure of sah-bound spinosyn rhamnosyl 4'-o-2 methyltransferase sphn from saccharopolyspora spinosa
14	c3b0nA	Alignment		9.8	34	PDB header: oxidoreductase Chain: A; PDB Molecule: nitrite reductase; PDBTitle: q448k mutant of assimilatory nitrite reductase (nii3) from tobacco2 leaf
15	c6c4vA	Alignment		9.3	29	PDB header: transport protein Chain: A; PDB Molecule: polyketide synthase pks13; PDBTitle: 1.9 angstrom resolution crystal structure of acyl carrier protein2 domain (residues 1350-1461) of polyketide synthase pks13 from3 mycobacterium tuberculosis
16	c3p4hA	Alignment		9.0	35	PDB header: hydrolase Chain: A; PDB Molecule: atp-dependent dna ligase, n-terminal domain protein; PDBTitle: structures of archaeal members of the ligd 3'-phosphoesterase dna2 repair enzyme superfamily
17	c5fwhA	Alignment		8.8	56	PDB header: structural protein Chain: A; PDB Molecule: essc; PDBTitle: n-terminal fha domain from essc a component of the2 bacterial type vii secretion apparatus
18	c2wk1A	Alignment		8.3	39	PDB header: transferase Chain: A; PDB Molecule: novp; PDBTitle: structure of the o-methyltransferase novp
19	c2n6rA	Alignment		8.0	50	PDB header: toxin Chain: A; PDB Molecule: u4-hexatoxin-hi1a; PDBTitle: nmr structure of spider toxin u4-hexatoxin-hi1a
20	d2pkqc1	Alignment		7.7	36	Fold: T-antigen specific domain-like Superfamily: T-antigen specific domain-like Family: T-antigen specific domain-like
21	c4ui9D	Alignment	not modelled	7.7	56	PDB header: cell cycle Chain: D; PDB Molecule: anaphase-promoting complex subunit 15; PDBTitle: atomic structure of the human anaphase-promoting complex
22	d2akja1	Alignment	not modelled	7.6	16	Fold: Ferredoxin-like Superfamily: Nitrite/Sulfite reductase N-terminal domain-like Family: Duplicated SiR/NiR-like domains 1 and 3
23	d1ytda2	Alignment	not modelled	7.5	20	Fold: alpha/beta-Hammerhead Superfamily: Nicotinate/Quinolinate PRTase N-terminal domain-like Family: NadC N-terminal domain-like
24	c2akjA	Alignment	not modelled	7.3	31	PDB header: oxidoreductase Chain: A; PDB Molecule: ferredoxin--nitrite reductase, chloroplast; PDBTitle: structure of spinach nitrite reductase
25	d1xp8a2	Alignment	not modelled	7.0	32	Fold: Anti-LPS factor/recA domain Superfamily: RecA protein, C-terminal domain Family: RecA protein, C-terminal domain
26	c4bgoA	Alignment	not modelled	6.8	18	PDB header: hydrolase Chain: A; PDB Molecule: efem m75 peptidase; PDBTitle: structural and functional role of the imelysin-like protein2 efem from pseudomonas syringae pv. syringae and3 implications in bacterial iron transport
27	c4pwuC	Alignment	not modelled	6.3	58	PDB header: signaling protein Chain: C; PDB Molecule: modulator protein mzra; PDBTitle: crystal structure of a modulator protein mzra (kpn_03524) from2 klebsiella pneumoniae subsp. pneumoniae mgh 78578 at 2.45 a3 resolution
28	c2l2rA	Alignment	not modelled	6.2	71	PDB header: antimicrobial protein Chain: A; PDB Molecule: antimicrobial peptide ecamp1; PDBTitle: helical hairpin structure of a novel antimicrobial peptide ecamp1 from2 seeds of barnyard grass (echinocloa crus-galli)

29	d2gboa1	Alignment	not modelled	6.2	22	Fold: Open three-helical up-and-down bundle Superfamily: EF2458-like Family: EF2458-like
30	c2gboB_	Alignment	not modelled	6.2	22	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: upf0358 protein ef2458; PDBTitle: protein of unknown function ef2458 from enterococcus faecalis
31	c1h7jA_	Alignment	not modelled	6.1	67	PDB header: acyltransferase Chain: A: PDB Molecule: aminolevulinic acid synthase 2, erythroid; PDBTitle: solution structure of the 26 aa presequence of 5-alias
32	d1f6fa_	Alignment	not modelled	6.0	18	Fold: 4-helical cytokines Superfamily: 4-helical cytokines Family: Long-chain cytokines
33	c2lgxA_	Alignment	not modelled	5.5	50	PDB header: cell adhesion Chain: A: PDB Molecule: fermitin family homolog 2; PDBTitle: nmr structure for kindle-2 n-terminus