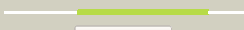


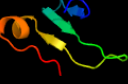
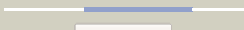
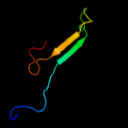

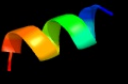



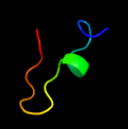

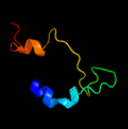










Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1580c_(-)_1783627_1783899
Date	Fri Aug 2 13:30:17 BST 2019
Unique Job ID	829278911ae716b2

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2js3B_	 Alignment		64.7	52	PDB header: structural genomics, unknown function Chain: B; PDB Molecule: uncharacterized protein; PDBTitle: nmr structure of protein q6n9a4_rhopa. northeast structural genomics2 consortium target rpt8
2	c2jr7A_	 Alignment		31.0	33	PDB header: metal binding protein Chain: A; PDB Molecule: dph3 homolog; PDBTitle: solution structure of human desr1
3	d2a1ka1	 Alignment		26.1	33	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Phage ssDNA-binding proteins
4	c6f0fB_	 Alignment		23.4	73	PDB header: chaperone Chain: B; PDB Molecule: ip2_s; PDBTitle: crystal structure asf1-ip2_s
5	c2hdeA_	 Alignment		22.0	35	PDB header: transcription Chain: A; PDB Molecule: histone deacetylase complex subunit sap18; PDBTitle: solution structure of human sap18
6	d1yfua1	 Alignment		21.2	32	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
7	c2i34B_	 Alignment		18.8	37	PDB header: hydrolase Chain: B; PDB Molecule: acid phosphatase; PDBTitle: the crystal structure of class c acid phosphatase from bacillus2 anthracis with tungstate bound
8	d1zvfa1	 Alignment		18.6	32	Fold: Double-stranded beta-helix Superfamily: RmlC-like cupins Family: 3-hydroxyanthranilic acid dioxygenase-like
9	d1libia1	 Alignment		12.2	75	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
10	c3et4A_	 Alignment		12.2	36	PDB header: hydrolase Chain: A; PDB Molecule: outer membrane protein p4, nadp phosphatase; PDBTitle: structure of recombinant haemophilus influenzae e(p4) acid phosphatase
11	c4s37F_	 Alignment		12.1	50	PDB header: metal binding protein Chain: F; PDB Molecule: phage baseplate protein; PDBTitle: crystal structure of r2 pyocin membrane-piercing spike

12	d1gpca_	Alignment		12.1	29	Fold: OB-fold Superfamily: Nucleic acid-binding proteins Family: Phage ssDNA-binding proteins
13	c3pctA_	Alignment		11.0	41	PDB header: hydrolase Chain: A: PDB Molecule: class c acid phosphatase; PDBTitle: structure of the class c acid phosphatase from pasteurella multocida
14	c2i5oA_	Alignment		10.9	56	PDB header: transferase Chain: A: PDB Molecule: dna polymerase eta; PDBTitle: solution structure of the ubiquitin-binding zinc finger2 (ubz) domain of the human dna y-polymerase eta
15	c5y0tD_	Alignment		10.6	34	PDB header: ligase Chain: D: PDB Molecule: thermotoga maritima tmcal; PDBTitle: crystal structure of thermotoga maritima tmcal bound with alpha-thio2 atp(form ii)
16	d1cta1	Alignment		9.3	75	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
17	d1kpta_	Alignment		8.3	19	Fold: Yeast killer toxins Superfamily: Yeast killer toxins Family: Virally encoded KP4 toxin
18	c4pl8H_	Alignment		8.2	70	PDB header: contractile protein/structural protein Chain: H: PDB Molecule: thymosin beta-4,protein cordon-bleu,thymosin beta-4; PDBTitle: structure of rabbit skeletal muscle actin in complex with a hybrid2 peptide comprising thymosin beta4 and the lysine-rich region of3 cordon-bleu
19	d2ciwa1	Alignment		8.1	42	Fold: EF Hand-like Superfamily: Cloroperoxidase Family: Cloroperoxidase
20	c2c9aA_	Alignment		8.0	23	PDB header: hydrolase Chain: A: PDB Molecule: receptor-type tyrosine-protein phosphatase mu; PDBTitle: crystal structure of the mam-ig module of receptor protein2 tyrosine phosphatase mu
21	c5y0nB_	Alignment	not modelled	7.4	45	PDB header: ligase Chain: B: PDB Molecule: upf0348 protein b4417_3650; PDBTitle: crystal structure of bacillus subtilis tmcal bound with atp (semet2 derivative)
22	c5i4rA_	Alignment	not modelled	7.3	35	PDB header: toxin/antitoxin Chain: A: PDB Molecule: contact-dependent inhibitor a; PDBTitle: contact-dependent inhibition system from escherichia coli nc101 -2 ternary cdia/cdii/ef-tu complex (trypsin-modified)
23	d1eyla_	Alignment	not modelled	6.9	27	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
24	c4ii0A_	Alignment	not modelled	6.7	28	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: cratabl; PDBTitle: crystal structure of cratabl, a trypsin inhibitor from crataeva tapia
25	c1r8oA_	Alignment	not modelled	6.5	31	PDB header: hydrolase inhibitor Chain: A: PDB Molecule: kunitz trypsin inhibitor; PDBTitle: crystal structure of an unusual kunitz-type trypsin inhibitor from2 copaifeira langsdorffii seeds
26	d1mhna_	Alignment	not modelled	6.4	19	Fold: SH3-like barrel Superfamily: Tudor/PWWP/MBT Family: Tudor domain
27	c3ts3D_	Alignment	not modelled	6.4	42	PDB header: viral protein Chain: D: PDB Molecule: capsid polyprotein; PDBTitle: crystal structure of the projection domain of the turkey astrovirus2 capsid protein at 1.5 angstrom resolution
28	d4fiva_	Alignment	not modelled	6.2	29	Fold: Acid proteases Superfamily: Acid proteases Family: Retroviral protease (retropepsin)
						Fold: Aromatic aminoacid monooxygenases, catalytic and

29	d1j8ua_	Alignment	not modelled	5.9	40	oligomerization domains Superfamily: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
30	d1mlwa_	Alignment	not modelled	5.9	40	Fold: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
31	d1d4va1	Alignment	not modelled	5.8	27	Fold: TNF receptor-like Superfamily: TNF receptor-like Family: TNF receptor-like
32	d1phza2	Alignment	not modelled	5.8	40	Fold: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains Superfamily: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains Family: Aromatic aminoacid monoxygenases, catalytic and oligomerization domains
33	c1ee8A_	Alignment	not modelled	5.7	32	PDB header: dna binding protein Chain: A: PDB Molecule: mutm (fpg) protein; PDBTitle: crystal structure of mutm (fpg) protein from thermophilus hb8
34	c2m6oA_	Alignment	not modelled	5.6	67	PDB header: transcription Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: the actinobacterial transcription factor rbpa binds to the principal2 sigma subunit of rna polymerase
35	d1tiea_	Alignment	not modelled	5.4	30	Fold: beta-Trefoil Superfamily: STI-like Family: Kunitz (STI) inhibitors
36	c3e2tA_	Alignment	not modelled	5.4	45	PDB header: oxidoreductase Chain: A: PDB Molecule: tryptophan 5-hydroxylase 1; PDBTitle: the catalytic domain of chicken tryptophan hydroxylase 12 with bound tryptophan
37	c3gycB_	Alignment	not modelled	5.3	56	PDB header: hydrolase Chain: B: PDB Molecule: putative glycoside hydrolase; PDBTitle: crystal structure of putative glycoside hydrolase (yp_001304622.1)2 from parabacteroides distazonis atcc 8503 at 1.85 a resolution
38	c1hvwa_	Alignment	not modelled	5.3	67	PDB header: toxin Chain: A: PDB Molecule: omega-atracotoxin-hv1a; PDBTitle: hairpinless mutant of omega-atracotoxin-hv1a
39	d1hvwa_	Alignment	not modelled	5.3	67	Fold: Knottins (small inhibitors, toxins, lectins) Superfamily: omega toxin-like Family: Spider toxins
40	c2go2A_	Alignment	not modelled	5.3	25	PDB header: protein binding Chain: A: PDB Molecule: kunitz-type serine protease inhibitor bbki; PDBTitle: crystal structure of bbki, a kunitz-type kallikrein inhibitor
41	c5w1sM_	Alignment	not modelled	5.3	24	PDB header: transferase Chain: M: PDB Molecule: protein trar; PDBTitle: x-ray crystal structure of escherichia coli rna polymerase and trar2 complex
42	c2qn4B_	Alignment	not modelled	5.1	31	PDB header: hydrolase inhibitor Chain: B: PDB Molecule: alpha-amylase/subtilisin inhibitor; PDBTitle: structure and function study of rice bifunctional alpha-2 amylase/subtilisin inhibitor from oryza sativa