

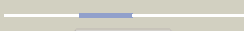


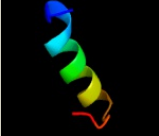

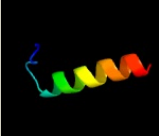







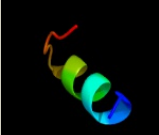





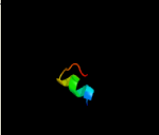


Phyre2

Email	mdejesus@rockefeller.edu
Description	RVBD1810_(-)_2052940_2053296
Date	Fri Aug 2 13:30:42 BST 2019
Unique Job ID	d45005dc3aada256

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c6c3rB_	 Alignment		63.7	24	PDB header: viral protein Chain: B: PDB Molecule: cricket paralysis virus 1a protein; PDBTitle: cricket paralysis virus rna1 suppressor protein crpv-1a
2	d2csua3	 Alignment		22.4	25	Fold: Flavodoxin-like Superfamily: Succinyl-CoA synthetase domains Family: Succinyl-CoA synthetase domains
3	c1vjqB_	 Alignment		16.9	30	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of f2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal3 predicted stability.
4	d1mkea1	 Alignment		16.6	22	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
5	c2mp6A_	 Alignment		13.4	67	PDB header: signaling protein Chain: A: PDB Molecule: suppressor of cytokine signaling 5; PDBTitle: structure and function of the jak interaction region in the2 intrinsically disordered n-terminus of socs5
6	c4inaA_	 Alignment		12.6	33	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q7mss8_wolsu protein from wolinella2 succinogenes. northeast structural genomics consortium target wsr35
7	c4rl6A_	 Alignment		12.5	24	PDB header: oxidoreductase Chain: A: PDB Molecule: saccharopine dehydrogenase; PDBTitle: crystal structure of the q04i03_strp2 protein from streptococcus2 pneumoniae. northeast structural genomics consortium target spr105
8	c5uqdA_	 Alignment		11.9	44	PDB header: oxidoreductase Chain: A: PDB Molecule: dumpy; shorter than wild-type; PDBTitle: dpy-21 in complex with fe(ii) and alpha-ketoglutarate
9	c5l78A_	 Alignment		11.7	32	PDB header: oxidoreductase Chain: A: PDB Molecule: alpha-aminoadipic semialdehyde synthase, mitochondrial; PDBTitle: crystal structure of human aminoadipate semialdehyde synthase,2 saccharopine dehydrogenase domain (in nad+ bound form)
10	c5k9xA_	 Alignment		11.2	24	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase alpha chain from legionella2 pneumophila subsp. pneumophila
11	c2lweA_	 Alignment		10.3	13	PDB header: signaling protein Chain: A: PDB Molecule: probable atp-dependent rna helicase ddx58; PDBTitle: solution structure of mutant (t170e) second card of human rig-i

12	c2ekcA_	Alignment		9.4	21	PDB header: lyase Chain: A: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: structural study of project id aq_1548 from aquifex aeolicus vf5
13	c3ss4C_	Alignment		9.4	38	PDB header: hydrolase Chain: C: PDB Molecule: glutaminase c; PDBTitle: crystal structure of mouse glutaminase c, phosphate-bound form
14	d1p9sa_	Alignment		9.2	57	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
15	d2duca1	Alignment		9.1	57	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
16	c3d23A_	Alignment		8.7	57	PDB header: hydrolase/hydrolase inhibitor Chain: A: PDB Molecule: 3c-like proteinase; PDBTitle: main protease of hcov-hku1
17	d1lvoa_	Alignment		8.1	43	Fold: Trypsin-like serine proteases Superfamily: Trypsin-like serine proteases Family: Viral cysteine protease of trypsin fold
18	c4gicB_	Alignment		8.1	50	PDB header: oxidoreductase Chain: B: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of a putative histidinol dehydrogenase (target psi-2 014034) from methylococcus capsulatus
19	c2q6fB_	Alignment		8.1	57	PDB header: hydrolase Chain: B: PDB Molecule: infectious bronchitis virus (ibv) main protease; PDBTitle: crystal structure of infectious bronchitis virus (ibv) main protease2 in complex with a michael acceptor inhibitor n3
20	c4xfqB_	Alignment		7.8	43	PDB header: hydrolase Chain: B: PDB Molecule: pedv main protease; PDBTitle: crystal structure basis for pedv 3c like protease
21	c2ynbA_	Alignment	not modelled	7.7	43	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like proteinase; PDBTitle: crystal structure of the main protease of coronavirus hku4 in complex2 with a michael acceptor sg85
22	c2ifsA_	Alignment	not modelled	7.7	22	PDB header: signaling protein Chain: A: PDB Molecule: wiskott-aldrich syndrome protien interacting protein and PDBTitle: structure of the n-wasp evh1 domain in complex with an extended wip2 peptide
23	c4v19S_	Alignment	not modelled	7.6	18	PDB header: ribosome Chain: S: PDB Molecule: mitoribosomal protein ul18m, mrpl18; PDBTitle: structure of the large subunit of the mammalian mitoribosome, part 12 of 2
24	c3tloA_	Alignment	not modelled	7.4	43	PDB header: hydrolase Chain: A: PDB Molecule: 3c-like proteinase; PDBTitle: crystal structure of hcov-nl63 3c-like protease
25	c2kktA_	Alignment	not modelled	7.0	38	PDB header: transcription Chain: A: PDB Molecule: ataxin-7-like protein 3; PDBTitle: solution structure of the sca7 domain of human ataxin-7-13 protein
26	c5us3A_	Alignment	not modelled	6.6	100	PDB header: de novo protein Chain: A: PDB Molecule: heterogeneous-backbone variant of the sp1-3 zinc finger: n- PDBTitle: heterogeneous-backbone foldamer mimic of the sp1-3 zinc finger
27	d1xoda1	Alignment	not modelled	6.4	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Enabled/VASP homology 1 domain (EVH1 domain)
28	c1zi7C_	Alignment	not modelled	6.4	40	PDB header: lipid binding protein Chain: C: PDB Molecule: kes1 protein; PDBTitle: structure of truncated yeast oxysterol binding protein

						osh4
29	c5vldC_	Alignment	not modelled	6.2	60	PDB header: oxidoreductase Chain: C: PDB Molecule: histidinol dehydrogenase, chloroplastic; PDBTitle: crystal structure of medicago truncatula l-histidinol dehydrogenase in2 complex with l-histidine and nad+
30	c2v75A_	Alignment	not modelled	6.2	25	PDB header: nuclear protein Chain: A: PDB Molecule: nuclear polyadenylated rna-binding protein nab2; PDBTitle: n-terminal domain of nab2
31	c3uo9B_	Alignment	not modelled	6.2	38	PDB header: hydrolase/hydrolase inhibitor Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: crystal structure of human gac in complex with glutamate and bptes
32	d1k75a_	Alignment	not modelled	6.1	60	Fold: ALDH-like Superfamily: ALDH-like Family: L-histidinol dehydrogenase HisD
33	c2djca_	Alignment	not modelled	6.1	60	PDB header: cytokine Chain: A: PDB Molecule: growth-blocking peptide; PDBTitle: solution structure of growth-blocking peptide of the2 tobacco cutworm, spodoptera litura
34	c1b5nA_	Alignment	not modelled	5.9	60	PDB header: signaling protein Chain: A: PDB Molecule: protein (plasmatocyte-spreading peptide); PDBTitle: nmr structure of psp1, plasmatocyte-spreading peptide from2 pseudoplusia includens
35	c1b1vA_	Alignment	not modelled	5.9	60	PDB header: cytokine Chain: A: PDB Molecule: protein (plasmatocyte-spreading peptide); PDBTitle: nmr structure of psp1, plasmatocyte-spreading peptide from2 pseudoplusia includens
36	c5uqeB_	Alignment	not modelled	5.9	38	PDB header: hydrolase Chain: B: PDB Molecule: glutaminase kidney isoform, mitochondrial; PDBTitle: multidomain structure of human kidney-type glutaminase(kga/gls)
37	c1irra_	Alignment	not modelled	5.9	60	PDB header: cytokine Chain: A: PDB Molecule: paralytic peptide; PDBTitle: solution structure of paralytic peptide of the silkworm,2 bombyx mori
38	c1bonB_	Alignment	not modelled	5.8	50	PDB header: hormone Chain: B: PDB Molecule: bombyxin-ii,bombyxin a-6; PDBTitle: three-dimensional structure of bombyxin-ii, an insulin-2 related brain-secretory peptide of the silkworm bombyx3 mori: comparison with insulin and relaxin
39	c2mula_	Alignment	not modelled	5.7	67	PDB header: protein binding Chain: A: PDB Molecule: e3 ubiquitin-protein ligase huwe1; PDBTitle: solution structure of the ubm1 domain of human huwe1/arf-bp1
40	d1zhxa1	Alignment	not modelled	5.7	40	Fold: Oxysterol-binding protein-like Superfamily: Oxysterol-binding protein-like Family: Oxysterol-binding protein
41	c1bomB_	Alignment	not modelled	5.6	50	PDB header: insulin-like brain-secretory peptide Chain: B: PDB Molecule: bombyxin-ii,bombyxin a-6; PDBTitle: three-dimensional structure of bombyxin-ii, an insulin-2 related brain-secretory peptide of the silkworm bombyx3 mori: comparison with insulin and relaxin
42	c6dria_	Alignment	not modelled	5.6	67	PDB header: immune system Chain: A: PDB Molecule: acan1; PDBTitle: nmr solution structure of acan1 from the ancylostoma caninum hookworm
43	c4g07A_	Alignment	not modelled	5.6	40	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: the crystal structure of the c366s mutant of hdh from brucella suis
44	c3pvsA_	Alignment	not modelled	5.6	17	PDB header: recombination Chain: A: PDB Molecule: replication-associated recombination protein a; PDBTitle: structure and biochemical activities of escherichia coli mgsa
45	c5tchG_	Alignment	not modelled	5.4	26	PDB header: lyase Chain: G: PDB Molecule: tryptophan synthase alpha chain; PDBTitle: crystal structure of tryptophan synthase from m. tuberculosis -2 ligand-free form, trpa-g66v mutant
46	c2ffwA_	Alignment	not modelled	5.3	50	PDB header: ligase Chain: A: PDB Molecule: midline-1; PDBTitle: solution structure of the rbcc/trim b-box1 domain of human2 mid1: b-box with a ring
47	c2dj9A_	Alignment	not modelled	5.3	60	PDB header: cytokine Chain: A: PDB Molecule: growth-blocking peptide; PDBTitle: solution structure of growth-blocking peptide of the2 cabbage armyworm, mamestra brassicae
48	c1hrlA_	Alignment	not modelled	5.2	60	PDB header: toxin Chain: A: PDB Molecule: paralytic peptide i; PDBTitle: structure of a paralytic peptide from an insect, manduca sexta
49	d2j9ga2	Alignment	not modelled	5.2	11	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
50	c6hv6A_	Alignment	not modelled	5.2	17	PDB header: toxin Chain: A: PDB Molecule: toxin pau_02230; PDBTitle: crystal structure of patoxp, a cysteine protease-like domain of2 photorhabdus asymbiotica toxin patox
51	d1ulza2	Alignment	not modelled	5.2	22	Fold: PreATP-grasp domain Superfamily: PreATP-grasp domain Family: BC N-terminal domain-like
52	c6an0A_	Alignment	not modelled	5.2	60	PDB header: oxidoreductase Chain: A: PDB Molecule: histidinol dehydrogenase; PDBTitle: crystal structure of histidinol dehydrogenase from elizabethkingia2 anophelis