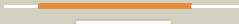

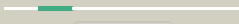


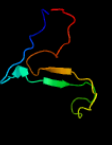



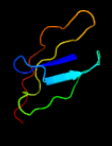

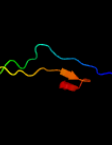












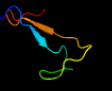
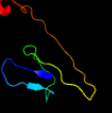
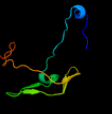
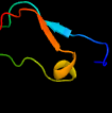

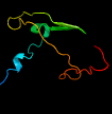
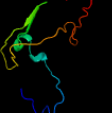


Phyre2

Email	mgiovine@unige.it
Description	University
Date	Wed Jun 17 16:51:04 BST 2020
Unique Job ID	7fa6611bbc4ced80

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3ilaG_	 Alignment		86.0	18	PDB header: signaling protein Chain: G; PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of rabbit ryanodine receptor 1 n-terminal domain (9-2 205)
2	d2cqea1	 Alignment		49.4	36	Fold: CCCH zinc finger Superfamily: CCCH zinc finger Family: CCCH zinc finger
3	c1xzza_	 Alignment		31.2	29	PDB header: membrane protein Chain: A; PDB Molecule: inositol 1,4,5-trisphosphate receptor type 1; PDBTitle: crystal structure of the ligand binding suppressor domain of type 12 inositol 1,4,5-trisphosphate receptor
4	c3qr5B_	 Alignment		29.4	22	PDB header: signaling protein Chain: B; PDB Molecule: cardiac ca2+ release channel; PDBTitle: structure of the first domain of a cardiac ryanodine receptor mutant2 with exon 3 deleted
5	d2cspa1	 Alignment		27.1	28	Fold: Immunoglobulin-like beta-sandwich Superfamily: Fibronectin type III Family: Fibronectin type III
6	c4qslC_	 Alignment		19.9	37	PDB header: ligase Chain: C; PDB Molecule: pyruvate carboxylase; PDBTitle: crystal structure of listeria monocytogenes pyruvate carboxylase
7	c4b4rA_	 Alignment		18.2	88	PDB header: cell adhesion Chain: A; PDB Molecule: f18 fimbrial adhesin ac; PDBTitle: crystal structure of the lectin domain of f18 fimbrial2 adhesin fedf in complex with blood group b type 13 hexasaccharide
8	c4n7vB_	 Alignment		17.9	43	PDB header: cell cycle Chain: B; PDB Molecule: serine/threonine-protein kinase plk4; PDBTitle: crystal structure of human plk4 cryptic polo box (cpb) in complex with2 a cep152 n-terminal fragment
9	c4nhyC_	 Alignment		17.7	24	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)
10	c3pe0B_	 Alignment		17.2	17	PDB header: structural protein Chain: B; PDB Molecule: plectin; PDBTitle: structure of the central region of the plakin domain of plectin
11	d1rutx3	 Alignment		16.7	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain

12	c2l0zA_	Alignment		16.7	32	PDB header: viral protein Chain: A: PDB Molecule: glycoprotein g2; PDBTitle: solution structure of a zinc-binding domain from the junin virus2 envelope glycoprotein
13	c5y9vA_	Alignment		14.9	20	PDB header: transport protein Chain: A: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of diamondback moth ryanodine receptor n-terminal2 domain
14	c2xoaA_	Alignment		13.9	23	PDB header: metal transport Chain: A: PDB Molecule: ryanodine receptor 1; PDBTitle: crystal structure of the n-terminal three domains of the2 skeletal muscle ryanodine receptor (ryr1)
15	c6juqA_	Alignment		11.5	27	PDB header: oxidoreductase Chain: A: PDB Molecule: prolyl 4-hydroxylase; PDBTitle: crystal structure and expression patterns of prolyl 4-hydroxylases2 from phytophthora capsici
16	d1q9ha_	Alignment		11.3	33	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
17	c4ojpC_	Alignment		11.2	38	PDB header: viral protein Chain: C: PDB Molecule: tailspike protein; PDBTitle: crystal structure of putative tailspike protein (tsp1, orf210) from2 escherichia coli o157:h7 bacteriohage cba120 in complex with maltose
18	c2b68A_	Alignment		11.0	100	PDB header: antimicrobial protein Chain: A: PDB Molecule: defensin; PDBTitle: solution structure of the recombinant crassostrea gigas2 defensin
19	c2rfyB_	Alignment		11.0	22	PDB header: hydrolase Chain: B: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: crystal structure of cellobiohydrolase from melanocarpus albomyces2 complexed with cellobiose
20	c4zpzB_	Alignment		11.0	25	PDB header: hydrolase Chain: B: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: dictyostelium purpureum cellobiohydrolase cel7a apo structure
21	d2icya2	Alignment	not modelled	10.8	32	Fold: Nucleotide-diphospho-sugar transferases Superfamily: Nucleotide-diphospho-sugar transferases Family: UDP-glucose pyrophosphorylase
22	c4l4iA_	Alignment	not modelled	9.6	23	PDB header: metal transport Chain: A: PDB Molecule: ryanodine receptor 2; PDBTitle: crystal structure of mouse ryanodine receptor isoform 2 (ryr2) 1-5472 disease mutant r420q
23	c5j3tC_	Alignment	not modelled	9.6	67	PDB header: hydrolase Chain: C: PDB Molecule: edc1; PDBTitle: crystal structure of s. pombe dcp2:dcp1:edc1 mrna decapping complex
24	c5o60K_	Alignment	not modelled	9.4	30	PDB header: ribosome Chain: K: PDB Molecule: 50s ribosomal protein l13; PDBTitle: structure of the 50s large ribosomal subunit from mycobacterium2 smegmatis
25	c5n2vC_	Alignment	not modelled	9.0	67	PDB header: rna binding protein Chain: C: PDB Molecule: edc1; PDBTitle: changes in conformational equilibria regulate the activity of the dcp22 decapping enzyme
26	c5n2vF_	Alignment	not modelled	9.0	67	PDB header: rna binding protein Chain: F: PDB Molecule: edc1; PDBTitle: changes in conformational equilibria regulate the activity of the dcp22 decapping enzyme
27	c2dhkA_	Alignment	not modelled	8.9	32	PDB header: immune system Chain: A: PDB Molecule: tbc1 domain family member 2; PDBTitle: solution structure of the ph domain of tbc1 domain family2 member 2 protein from human
28	c5jp4B_	Alignment	not modelled	8.9	67	PDB header: peptide binding protein Chain: B: PDB Molecule: uncharacterized protein c18g6.09c; PDBTitle: crystal structure of s. pombe dcp1 in complex with the decapping2 enhancer edc
						PDB header: transferase

29	c2luIA_	Alignment	not modelled	8.7	14	Chain: A: PDB Molecule: tyrosine-protein kinase tec; PDBTitle: solution nmr structure of ph domain of tyrosine-protein kinase tec2 from homo sapiens, northeast structural genomics consortium (nesg)3 target hr3504c
30	c1pxqA_	Alignment	not modelled	8.3	83	PDB header: antimicrobial protein Chain: A: PDB Molecule: subtilisin a; PDBTitle: structure of subtilisin a
31	c5ergB_	Alignment	not modelled	8.3	15	PDB header: transferase Chain: B: PDB Molecule: trna (adenine(58)-n(1))-methyltransferase catalytic subunit PDBTitle: crystal structure of the two-subunit trna m1a58 methyltransferase2 trm6-trm61 in complex with sam
32	c2jopA_	Alignment	not modelled	8.2	46	PDB header: immune system Chain: A: PDB Molecule: t-cell surface glycoprotein cd5; PDBTitle: solution structure of the n-terminal extracellular domain of the t lymphocyte receptor cd5 (cd5 domain 1)
33	c3maIA_	Alignment	not modelled	8.1	33	PDB header: plant protein Chain: A: PDB Molecule: stromal cell-derived factor 2-like protein; PDBTitle: crystal structure of the sdf2-like protein from arabidopsis thaliana
34	d1x1fa1	Alignment	not modelled	8.1	18	Fold: PH domain-like barrel Superfamily: PH domain-like Family: Pleckstrin-homology domain (PH domain)
35	c6qyyD_	Alignment	not modelled	8.0	50	PDB header: virus Chain: D: PDB Molecule: capsid fiber protein; PDBTitle: the crystal structure of head fiber gp8.5 n base in bacteriophage2 phi29
36	c6bj5F_	Alignment	not modelled	7.3	71	PDB header: immunosuppressant Chain: F: PDB Molecule: serine proteinase inhibitor 1; PDBTitle: structure of the clinically used myxomaviral serine protease inhibitor2 1 (serp-1)
37	c4m6tA_	Alignment	not modelled	7.2	31	PDB header: transcription regulator Chain: A: PDB Molecule: rna polymerase ii-associated factor 1 homolog, linker, rna PDBTitle: structure of human paf1 and leo1 complex
38	c2jnvA_	Alignment	not modelled	7.0	40	PDB header: metal transport Chain: A: PDB Molecule: nifu-like protein 1, chloroplast; PDBTitle: solution structure of c-terminal domain of nifu-like2 protein from oryza sativa
39	c2qsdB_	Alignment	not modelled	6.4	45	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized conserved protein; PDBTitle: crystal structure of a protein il1583 from idiomarina loihiensis
40	c4mnoA_	Alignment	not modelled	6.0	23	PDB header: translation Chain: A: PDB Molecule: translation initiation factor 1a; PDBTitle: crystal structure of aif1a from pyrococcus abyssi
41	c1t2yA_	Alignment	not modelled	5.9	58	PDB header: metal binding protein Chain: A: PDB Molecule: metallothionein; PDBTitle: nmr solution structure of the protein part of cu6-2 neurospora crassa mt
42	c2lg1A_	Alignment	not modelled	5.8	19	PDB header: metal binding protein Chain: A: PDB Molecule: ca-kinase anchor protein 13; PDBTitle: solution structure of the human akap13 ph domain and stabilizing dh2 helix
43	d1xkia_	Alignment	not modelled	5.8	8	Fold: Lipocalins Superfamily: Lipocalins Family: Retinol binding protein-like
44	d1xhja_	Alignment	not modelled	5.8	27	Fold: Alpha-lytic protease prodomain-like Superfamily: Fe-S cluster assembly (FSCA) domain-like Family: NifU C-terminal domain-like
45	c2q4jB_	Alignment	not modelled	5.7	40	PDB header: transferase Chain: B: PDB Molecule: probable utp-glucose-1-phosphate uridylyltransferase 2; PDBTitle: ensemble refinement of the protein crystal structure of gene product2 from arabidopsis thaliana at3g03250, a putative udp-glucose3 pyrophosphorylase
46	d1knxa1	Alignment	not modelled	5.7	10	Fold: MurF and HprK N-domain-like Superfamily: HprK N-terminal domain-like Family: HPr kinase/phosphatase HprK N-terminal domain
47	d1k78a2	Alignment	not modelled	5.6	41	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Paired domain
48	d1efna_	Alignment	not modelled	5.5	14	Fold: SH3-like barrel Superfamily: SH3-domain Family: SH3-domain
49	c2v6zM_	Alignment	not modelled	5.5	20	PDB header: transferase Chain: M: PDB Molecule: dna polymerase epsilon subunit 2; PDBTitle: solution structure of amino-terminal domain of human dna polymerase2 epsilon subunit b
50	d1gpia_	Alignment	not modelled	5.4	38	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
51	c4afzC_	Alignment	not modelled	5.4	11	PDB header: hydrolase/de novo protein Chain: C: PDB Molecule: fynomer; PDBTitle: human chymase - fynomer complex
52	d1nxza1	Alignment	not modelled	5.4	19	Fold: PUA domain-like Superfamily: PUA domain-like Family: YggJ N-terminal domain-like
53	c2zkrj_	Alignment	not modelled	5.4	15	PDB header: ribosomal protein/rna Chain: J: PDB Molecule: rna expansion segment es15 part ii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an 80s complex2 obtained by docking homology models of the rna and proteins into an3 8.7 a cryo-em map
54	d6paxa2	Alignment	not modelled	5.3	41	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like

						Family: Paired domain
55	c2yg1A_	Alignment	not modelled	5.2	30	PDB header: hydrolase Chain: A: PDB Molecule: cellulose 1,4-beta-cellobiosidase; PDBTitle: apo structure of cellobiohydrolase 1 (cel7a) from heterobasidion2 annosum
56	d1o98a1	Alignment	not modelled	5.2	21	Fold: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Superfamily: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain Family: 2,3-Bisphosphoglycerate-independent phosphoglycerate mutase, substrate-binding domain
57	c2k06A_	Alignment	not modelled	5.2	26	PDB header: transcription Chain: A: PDB Molecule: transcription antitermination protein nusg; PDBTitle: solution structure of the aminoterminal domain of e. coli nusg
58	d1oja_	Alignment	not modelled	5.2	21	Fold: Concanavalin A-like lectins/glucanases Superfamily: Concanavalin A-like lectins/glucanases Family: Glycosyl hydrolase family 7 catalytic core
59	d1h8ac1	Alignment	not modelled	5.1	33	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Myb/SANT domain