

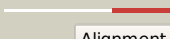

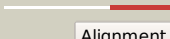

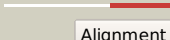

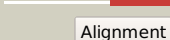

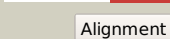

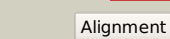

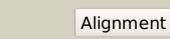







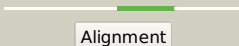




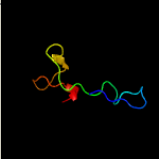
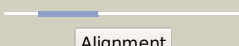
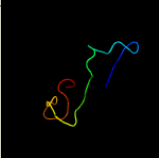
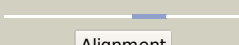
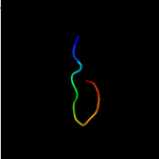
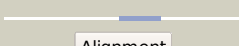
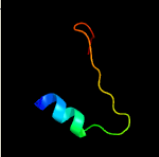

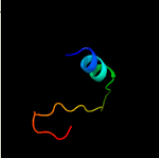




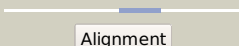


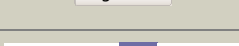
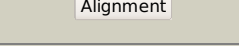
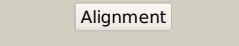
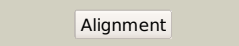




Phyre2

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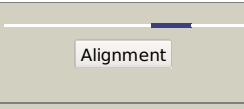
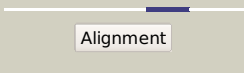
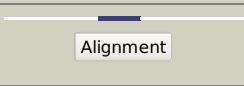
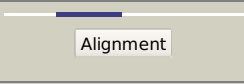
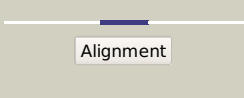
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2odkD_	 Alignment		99.1	23	PDB header: structural genomics, unknown function Chain: D: PDB Molecule: hypothetical protein; PDBTitle: putative prevent-host-death protein from nitrosomonas europaea
2	d2odka1	 Alignment		99.1	24	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
3	c3hryA_	 Alignment		98.7	23	PDB header: antitoxin Chain: A: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd in a trigonal space group and partially2 disordered
4	c3hs2H_	 Alignment		98.7	27	PDB header: antitoxin Chain: H: PDB Molecule: prevent host death protein; PDBTitle: crystal structure of phd truncated to residue 57 in an orthorhombic2 space group
5	d2a6qb1	 Alignment		98.2	26	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
6	c3g5oA_	 Alignment		98.1	22	PDB header: toxin/antitoxin Chain: A: PDB Molecule: uncharacterized protein rv2865; PDBTitle: the crystal structure of the toxin-antitoxin complex relbe2 (rv2865-2 2866) from mycobacterium tuberculosis
7	d2a6qa1	 Alignment		97.8	26	Fold: YefM-like Superfamily: YefM-like Family: YefM-like
8	c3d55A_	 Alignment		97.6	26	PDB header: toxin inhibitor Chain: A: PDB Molecule: uncharacterized protein rv3357/mt3465; PDBTitle: crystal structure of m. tuberculosis yefm antitoxin
9	c3oeiB_	 Alignment		97.6	26	PDB header: toxin, protein binding Chain: B: PDB Molecule: relj (antitoxin rv3357); PDBTitle: crystal structure of mycobacterium tuberculosis reljk (rv3357-rv3358-2 relbe3)
10	c3k6qB_	 Alignment		78.0	14	PDB header: ligand binding protein Chain: B: PDB Molecule: putative ligand binding protein; PDBTitle: crystal structure of an antitoxin part of a putative toxin/antitoxin2 system (swol_0700) from syntrophomonas wolfei subsp. wolfei at 1.80 a3 resolution
11	c1skoA_	 Alignment		68.3	22	PDB header: signaling protein Chain: A: PDB Molecule: mitogen-activated protein kinase kinase 1 PDBTitle: mp1-p14 complex

12	d3cpta1	 Alignment		58.2	21	Fold: Profilin-like Superfamily: Roadblock/LC7 domain Family: Roadblock/LC7 domain
13	d1p2za2	 Alignment		37.0	35	Fold: Nucleoplasmin-like/VP (viral coat and capsid proteins) Superfamily: Group II dsDNA viruses VP Family: Adenovirus hexon
14	c2bviK_	 Alignment		26.4	35	PDB header: virus Chain: K: PDB Molecule: hexon protein; PDBTitle: the quasi-atomic model of human adenovirus type 52 capsid (part 2)
15	c3zifD_	 Alignment		26.2	35	PDB header: virus Chain: D: PDB Molecule: hexon protein; PDBTitle: cryo-em structures of two intermediates provide insight into 2 adenovirus assembly and disassembly
16	d2ns0a1	 Alignment		24.8	36	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: RHA1 ro06458-like
17	d1ogda_	 Alignment		24.3	30	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
18	c2wcvl_	 Alignment		22.0	19	PDB header: isomerase Chain: I: PDB Molecule: l-fucose mutarotase; PDBTitle: crystal structure of bacterial fucu
19	c4zdtB_	 Alignment		21.6	27	PDB header: hydrolase Chain: B: PDB Molecule: structure-specific endonuclease subunit slx4; PDBTitle: crystal structure of the ring finger domain of slx1 in complex with 2 the c-terminal domain of slx4
20	c3e7nB_	 Alignment		21.2	26	PDB header: transport protein Chain: B: PDB Molecule: d-ribose high-affinity transport system; PDBTitle: crystal structure of d-ribose high-affinity transport system from 2 salmonella typhimurium lt2
21	c3p13B_	 Alignment	not modelled	20.0	26	PDB header: isomerase Chain: B: PDB Molecule: d-ribose pyranase; PDBTitle: complex structure of d-ribose pyranase sa240 with d-ribose
22	c2wcuB_	 Alignment	not modelled	18.9	30	PDB header: isomerase Chain: B: PDB Molecule: protein fucu homolog; PDBTitle: crystal structure of mammalian fucu
23	c4a34L_	 Alignment	not modelled	18.1	23	PDB header: isomerase Chain: L: PDB Molecule: rbsd/fucu transport protein family protein; PDBTitle: crystal structure of the fucose mutarotase in complex with 2 l-fucose from streptococcus pneumoniae
24	c3mvaA_	 Alignment	not modelled	16.9	23	PDB header: isomerase Chain: A: PDB Molecule: protein fucu; PDBTitle: the crystal structure of fucu from bifidobacterium longum to 1.65a
25	c4v0bA_	 Alignment	not modelled	15.7	19	PDB header: hydrolase Chain: A: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: escherichia coli ftsh hexameric n-domain
26	d2ob5a1	 Alignment	not modelled	15.7	27	Fold: RbsD-like Superfamily: RbsD-like Family: RbsD-like
27	d2ve8a1	 Alignment	not modelled	14.6	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
28	c2muyA_	 Alignment	not modelled	14.4	15	PDB header: nucleotide binding protein Chain: A: PDB Molecule: atp-dependent zinc metalloprotease ftsh; PDBTitle: the solution structure of the ftsh periplasmic n-domain
		 Alignment				Fold: PUA domain-like

29	d1x6va1	Alignment	not modelled	14.0	15	Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
30	d2j5pa1	Alignment	not modelled	13.0	16	Fold: DNA/RNA-binding 3-helical bundle Superfamily: "Winged helix" DNA-binding domain Family: FtsK C-terminal domain-like
31	c5ax7A	Alignment	not modelled	12.8	27	PDB header: transferase Chain: A: PDB Molecule: pyruvyl transferase 1; PDBTitle: yeast pyruvyltransferase pvg1p
32	c2inyA	Alignment	not modelled	12.3	33	PDB header: viral protein Chain: A: PDB Molecule: hexon protein; PDBTitle: nanoporous crystals of chicken embryo lethal orphan (celo) adenovirus2 major coat protein, hexon
33	d1p94a	Alignment	not modelled	12.2	27	Fold: Ribbon-helix-helix Superfamily: Ribbon-helix-helix Family: CopG-like
34	c1gk7A	Alignment	not modelled	11.0	24	PDB header: vimentin Chain: A: PDB Molecule: vimentin; PDBTitle: human vimentin coil 1a fragment (1a)
35	c3tuoA	Alignment	not modelled	10.8	25	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein satb1; PDBTitle: crystal structure of n-terminal domain of dna-binding protein satb1
36	c4heoA	Alignment	not modelled	10.8	50	PDB header: viral protein Chain: A: PDB Molecule: phosphoprotein; PDBTitle: hendra virus phosphoprotein c terminal domain
37	c4jj0B	Alignment	not modelled	10.7	10	PDB header: electron transport Chain: B: PDB Molecule: mamp; PDBTitle: crystal structure of mamp
38	d2hq7a1	Alignment	not modelled	10.6	9	Fold: Split barrel-like Superfamily: FMN-binding split barrel Family: PNP-oxidase like
39	c6f9gE	Alignment	not modelled	10.4	16	PDB header: signaling protein Chain: E: PDB Molecule: methyl-accepting chemotaxis protein mcpu; PDBTitle: ligand binding domain of p. putida kt2440 polyamine chemoreceptors2 mcpu in complex putrescine.
40	c2vm2C	Alignment	not modelled	9.7	10	PDB header: oxidoreductase Chain: C: PDB Molecule: thioredoxin h isoform 1.; PDBTitle: crystal structure of barley thioredoxin h isoform 1 crystallized using2 peg as precipitant
41	c5flvA	Alignment	not modelled	9.1	22	PDB header: transcription Chain: A: PDB Molecule: homeobox protein nkx-2.5, t-box transcription factor tbx5; PDBTitle: crystal structure of nkx2-5 and tbx5 bound to the nppa2 promoter region
42	c5lddA	Alignment	not modelled	8.7	30	PDB header: protein transport Chain: A: PDB Molecule: mon1; PDBTitle: crystal structure of the heterodimeric gef mon1-ccc1 in complex with2 ypt7
43	d1y8xb1	Alignment	not modelled	8.5	25	Fold: Activating enzymes of the ubiquitin-like proteins Superfamily: Activating enzymes of the ubiquitin-like proteins Family: Ubiquitin activating enzymes (UBA)
44	c5yadA	Alignment	not modelled	8.4	25	PDB header: rna binding protein Chain: A: PDB Molecule: meiosis regulator and mrna stability factor 1; PDBTitle: crystal structure of marf1 lotus domain from mus musculus
45	d1f8fa2	Alignment	not modelled	8.3	11	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
46	c5zf2A	Alignment	not modelled	8.1	14	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin (h-type,trx-h); PDBTitle: crystal structure of trxp from edwardsiella tarda eib202
47	c3v62C	Alignment	not modelled	8.0	50	PDB header: protein binding/dna binding protein Chain: C: PDB Molecule: atp-dependent dna helicase srs2; PDBTitle: structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
48	c3v62F	Alignment	not modelled	8.0	50	PDB header: protein binding/dna binding protein Chain: F: PDB Molecule: atp-dependent dna helicase srs2; PDBTitle: structure of the s. cerevisiae srs2 c-terminal domain in complex with2 pcna conjugated to sumo on lysine 164
49	c5u1sA	Alignment	not modelled	8.0	22	PDB header: hydrolase Chain: A: PDB Molecule: separin; PDBTitle: crystal structure of the saccharomyces cerevisiae separase-securin2 complex at 3.0 angstrom resolution
50	c4cgbE	Alignment	not modelled	7.9	37	PDB header: cell cycle Chain: E: PDB Molecule: echinoderm microtubule-associated protein-like 2; PDBTitle: crystal structure of the trimerization domain of eml2
51	c3s4rB	Alignment	not modelled	7.7	24	PDB header: structural protein Chain: B: PDB Molecule: vimentin; PDBTitle: crystal structure of vimentin coil1a/1b fragment with a stabilizing2 mutation
52	c1u2zC	Alignment	not modelled	7.5	18	PDB header: transferase Chain: C: PDB Molecule: histone-lysine n-methyltransferase, h3 lysine-79 PDBTitle: crystal structure of histone k79 methyltransferase dot1p2 from yeast
53	d1u2za	Alignment	not modelled	7.3	15	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: Catalytic, N-terminal domain of histone methyltransferase Dot1l
54	c3ssmB	Alignment	not modelled	7.0	25	PDB header: transferase Chain: B: PDB Molecule: methyltransferase; PDBTitle: myce methyltransferase from the mycinamycin

						biosynthetic pathway in2 complex with mg and sah, crystal form 1 PDB header: cell cycle Chain: A: PDB Molecule: echinoderm microtubule-associated protein-like 2; PDBTitle: crystal structure of the trimerization domain of eml2
55	c4cgbA_	Alignment	not modelled	6.8	37	PDB header: receptor Chain: A: PDB Molecule: nr1 m2; PDBTitle: transmembrane segment 2 of nmda receptor nr1, nmr, 102 structures
56	c2nr1A_	Alignment	not modelled	6.8	33	PDB header: viral protein Chain: E: PDB Molecule: protein delta; PDBTitle: crystal structure of the orsay virus delta protein n-terminal fragment2 (aa 1~66)
57	c5jieE_	Alignment	not modelled	6.7	18	PDB header: hydrolase Chain: B: PDB Molecule: formyltetrahydrofolate deformylase; PDBTitle: crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution
58	c3louB_	Alignment	not modelled	6.7	17	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: uncharacterized protein; PDBTitle: crystal structure of thioredoxin-like protein bce_0499 from bacillus2 cereus atcc 10987
59	c4euyA_	Alignment	not modelled	6.5	28	PDB header: signaling protein Chain: C: PDB Molecule: protein (phosducin); PDBTitle: structural analysis of phosducin and its phosphorylation-2 regulated interaction with transducin
60	c1b9xC_	Alignment	not modelled	6.4	16	PDB header: transferase Chain: A: PDB Molecule: dna polymerase mu; PDBTitle: the solution structure of the brct domain from human2 polymerase reveals homology with the tdt brct domain
61	c2htfA_	Alignment	not modelled	6.4	33	Fold: PUA domain-like Superfamily: PUA domain-like Family: ATP sulfurylase N-terminal domain
62	d1g8fa1	Alignment	not modelled	6.3	19	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: putative hydrogenase expression/formation protein hupg; PDBTitle: crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodospseudomonas palustris cga009
63	c2qsiB_	Alignment	not modelled	6.3	3	PDB header: metal binding protein Chain: B: PDB Molecule: orf131 protein; PDBTitle: crystal structure of apo-form czce from c. metallidurans ch34
64	c2wtoB_	Alignment	not modelled	6.2	17	Fold: PurM C-terminal domain-like Superfamily: PurM C-terminal domain-like Family: PurM C-terminal domain-like
65	d1t3ta7	Alignment	not modelled	6.1	25	PDB header: splicing Chain: A: PDB Molecule: far upstream element-binding protein 2; PDBTitle: solution nmr structure of the second and third kh domains2 of ksrp
66	c2jvzA_	Alignment	not modelled	6.1	15	PDB header: transport protein Chain: D: PDB Molecule: hypothetical 12.0 kda protein in ade3-ser2 intergenic PDBTitle: structure of the yeast escrt-i heterotetramer core
67	c2p22D_	Alignment	not modelled	6.0	10	PDB header: ligase Chain: B: PDB Molecule: 4-substituted benzoates-glutamate ligase gh3.12; PDBTitle: crystal structure of gh3.12 in complex with ampcpp
68	c4ewvB_	Alignment	not modelled	6.0	22	PDB header: hydrolase Chain: C: PDB Molecule: domain of unknown function duf1849; PDBTitle: crystal structure of beta-barrel-like, putative atp binding protein of2 domain of unknown function duf1849 from brucella abortus
69	c5uc2C_	Alignment	not modelled	5.9	24	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin-2; PDBTitle: crystal structure of thioredoxin-2
70	c2pptA_	Alignment	not modelled	5.9	17	Fold: DNA/RNA-binding 3-helical bundle Superfamily: C-terminal effector domain of the bipartite response regulators Family: PhoB-like
71	d2ff4a1	Alignment	not modelled	5.8	18	Fold: Pyruvate kinase C-terminal domain-like Superfamily: PK C-terminal domain-like Family: Pyruvate kinase, C-terminal domain
72	d2g50a3	Alignment	not modelled	5.8	13	PDB header: protein binding Chain: H: PDB Molecule: hepatocyte growth factor-regulated tyrosine kinase PDBTitle: human escrt-0 core complex
73	c3f1iH_	Alignment	not modelled	5.6	17	Fold: PK beta-barrel domain-like Superfamily: PK beta-barrel domain-like Family: Pyruvate kinase beta-barrel domain
74	d1pkma1	Alignment	not modelled	5.6	10	PDB header: dna binding protein Chain: A: PDB Molecule: dna-binding protein satb1; PDBTitle: a novel structure-based mechanism for dna-binding of satb1
75	c4q2jA_	Alignment	not modelled	5.5	28	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
76	d1umka1	Alignment	not modelled	5.4	17	PDB header: transferase Chain: B: PDB Molecule: pyruvate kinase isozymes m1/m2; PDBTitle: structure of m2 pyruvate kinase in complex with phenylalanine
77	c4fxjB_	Alignment	not modelled	5.4	13	Fold: Reductase/isomerase/elongation factor common domain Superfamily: Riboflavin synthase domain-like Family: Ferredoxin reductase FAD-binding domain-like
78	d1qx4a1	Alignment	not modelled	5.3	12	Fold: NAD(P)-binding Rossmann-fold domains Superfamily: NAD(P)-binding Rossmann-fold domains Family: Alcohol dehydrogenase-like, C-terminal domain
79	d2jhfa2	Alignment	not modelled	5.3	9	

80	c1vjgB_	 Alignment	not modelled	5.3	41	PDB header: structural genomics, de novo protein Chain: B: PDB Molecule: designed protein; PDBTitle: designed protein based on backbone conformation of 2 procarboxypeptidase-a (1aye) with sidechains chosen for maximal predicted stability.
81	c1v98A_	 Alignment	not modelled	5.2	24	PDB header: oxidoreductase Chain: A: PDB Molecule: thioredoxin; PDBTitle: crystal structure analysis of thioredoxin from thermophilus
82	c5vf0B_	 Alignment	not modelled	5.1	24	PDB header: transferase Chain: B: PDB Molecule: e3 ubiquitin-protein ligase rad18; PDBTitle: solution nmr structure of human rad18 (198-240) in complex with 2 ubiquitin
83	c5w82E_	 Alignment	not modelled	5.0	19	PDB header: viral protein Chain: E: PDB Molecule: protein delta; PDBTitle: crystal structure of orsay virus delta protein n-terminal fragment (aa2 1-101)
84	c3o6uB_	 Alignment	not modelled	5.0	13	PDB header: structural genomics, unknown function Chain: B: PDB Molecule: uncharacterized protein cpe2226; PDBTitle: crystal structure of cpe2226 protein from clostridium perfringens.2 northeast structural genomics consortium target cpr195