Phyre2

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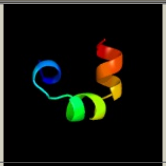
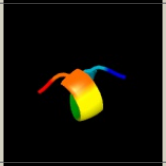
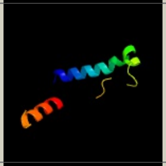
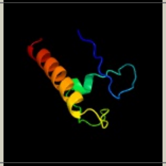
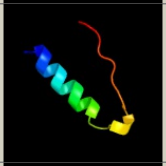
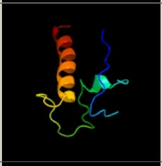
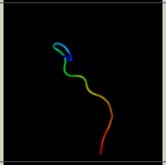
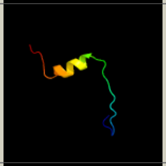
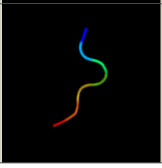
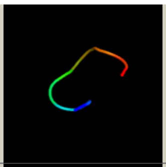
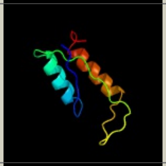
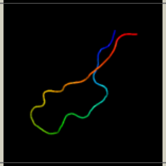
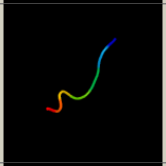
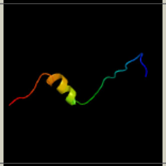
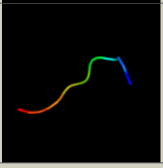
Description	RVBD2023A_(RVBD2023A)_2268276_2268734
Date	Mon Aug 5 13:25:13 BST 2019
Unique Job ID	d9fc328d0ac78edd

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c5zkeA_	Alignment		28.7	45	**PDB header:**ligase **Chain:** A: **PDB Molecule:**aminoacyl trna synthetase complex-interacting **PDBTitle:** crystal structure of n-terminal domain of plasmodium vivax p43 in2 space group p212121
2	c5tdyA_	Alignment		21.4	100	**PDB header:**motor protein **Chain:** A: **PDB Molecule:**flagellar m-ring protein; **PDBTitle:** structure of cofolded flifc:flign complex from thermotoga maritima
3	c5o1mA_	Alignment		19.0	22	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**rubber oxygenase; **PDBTitle:** structure of latex clearing protein lcp in the closed state
4	c5tdyC_	Alignment		18.4	60	**PDB header:**motor protein **Chain:** C: **PDB Molecule:**flagellar m-ring protein; **PDBTitle:** structure of cofolded flifc:flign complex from thermotoga maritima
5	c2ogsA_	Alignment		12.5	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**thermostable carboxylesterase est50; **PDBTitle:** crystal structure of the geobacillus stearothermophilus2 carboxylesterase est55 at ph 6.2
6	c2cpmA_	Alignment		11.6	25	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**sperm-associated antigen 7; **PDBTitle:** solution structure of the r3h domain of human sperm-2 associated antigen 7
7	c4hxhC_	Alignment		9.4	60	**PDB header:**rna/rna binding protein/hydrolase **Chain:** C: **PDB Molecule:**histone rna hairpin-binding protein; **PDBTitle:** structure of mrna stem-loop, human stem-loop binding protein and2 3'hexo ternary complex
8	c2fj0A_	Alignment		9.4	20	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**carboxylic ester hydrolase; **PDBTitle:** crystal structure of juvenile hormone esterase from manduca sexta,2 with otfp covalently attached
9	c4i3rG_	Alignment		9.2	38	**PDB header:**viral protein/immune system **Chain:** G: **PDB Molecule:**outer domain of hiv-1 gp120 (ker2018 od4.2.2); **PDBTitle:** crystal structure of the outer domain of hiv-1 gp120 in complex with2 vrc-pg04 space group p3221
10	c3dnoC_	Alignment		9.1	30	**PDB header:**viral protein **Chain:** C: **PDB Molecule:**hiv-1 envelope glycoprotein gp120; **PDBTitle:** molecular structure for the hiv-1 gp120 trimer in the cd4-bound state
11	c5yl1A_	Alignment		9.1	100	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** t=1 subviral particle of penaeus vannamei nodavirus capsid protein2 deletion mutant (delta 1-37 & 251-368)

12	c2kjmA_	Alignment		8.7	60	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**histone rna hairpin-binding protein; **PDBTitle:** solution structure of slbp rna binding domain fragment
13	d1dzfa1	Alignment		8.6	60	**Fold:**Restriction endonuclease-like **Superfamily:**Eukaryotic RPB5 N-terminal domain **Family:**Eukaryotic RPB5 N-terminal domain
14	c4r33A_	Alignment		8.4	12	**PDB header:**lyase **Chain:** A: **PDB Molecule:**nosl; **PDBTitle:** x-ray structure of the tryptophan lyase nosl with tryptophan and s-2 adenosyl-l-homocysteine bound
15	c6ab6A_	Alignment		8.4	100	**PDB header:**virus like particle **Chain:** A: **PDB Molecule:**capsid protein; **PDBTitle:** cryo-em structure of t=3 penaeus vannamei nodavirus
16	c4zelA_	Alignment		7.6	20	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dopamine beta-hydroxylase; **PDBTitle:** human dopamine beta-hydroxylase
17	c6ab6C_	Alignment		7.6	100	**PDB header:**virus like particle **Chain:** C: **PDB Molecule:**capsid protein; **PDBTitle:** cryo-em structure of t=3 penaeus vannamei nodavirus
18	c3lkxA_	Alignment		7.4	70	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**transcription factor btf3; **PDBTitle:** human nac dimerization domain
19	c3ngbI_	Alignment		7.4	37	**PDB header:**viral protein/immune system **Chain:** I: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** crystal structure of broadly and potently neutralizing antibody vrc012 in complex with hiv-1 gp120
20	d2qqra1	Alignment		7.2	44	**Fold:**SH3-like barrel **Superfamily:**Tudor/PWWP/MBT **Family:**Tudor domain
21	c6h2bC_	Alignment	not modelled	7.1	71	**PDB header:**virus like particle **Chain:** C: **PDB Molecule:**capsid protein; **PDBTitle:** structure of the macrobrachium rosenbergii nodavirus
22	c6gq9A_	Alignment	not modelled	7.0	50	**PDB header:**allergen **Chain:** A: **PDB Molecule:**major allergen cor a 1.0401; **PDBTitle:** solution structure of the hazel allergen cor a 1.0401
23	c5x6cE_	Alignment	not modelled	6.8	38	**PDB header:**rna binding protein **Chain:** E: **PDB Molecule:**uncharacterized protein mj1481; **PDBTitle:** crystal structure of seprs-sepcyse from methanocaldococcus jannaschii
24	c5x6cF_	Alignment	not modelled	6.8	38	**PDB header:**rna binding protein **Chain:** F: **PDB Molecule:**uncharacterized protein mj1481; **PDBTitle:** crystal structure of seprs-sepcyse from methanocaldococcus jannaschii
25	c3rwsA_	Alignment	not modelled	6.8	42	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**mtn13 protein; **PDBTitle:** crystal structure of medicago truncatula nodulin 13 (mtn13) in complex2 with trans-zeatin
26	c4tvpG_	Alignment	not modelled	6.5	33	**PDB header:**viral protein/immune system **Chain:** G: **PDB Molecule:**envelope glycoprotein gp160; **PDBTitle:** crystal structure of the hiv-1 bg505 sosip.664 env trimer ectodomain,2 comprising atomic-level definition of pre-fusion gp120 and gp41, in3 complex with human antibodies pgt122 and 35o22
27	c2yukA_	Alignment	not modelled	6.4	42	**PDB header:**transferase **Chain:** A: **PDB Molecule:**myeloid/lymphoid or mixed-lineage leukemia **PDBTitle:** solution structure of the hmg box of human myeloid/lymphoid2 or mixed-lineage leukemia protein 3 homolog
28	d1ukca_	Alignment	not modelled	6.4	10	**Fold:**alpha/beta-Hydrolases **Superfamily:**alpha/beta-Hydrolases **Family:**Fungal lipases

29	c3j5ml_	Alignment	not modelled	6.2	33	**PDB header:**viral protein/immune system **Chain:** I: **PDB Molecule:**bg505 sosip gp120; **PDBTitle:** cryo-em structure of the bg505 sosip.664 hiv-1 env trimer with 3 pgv042 fabs
30	c2ww9B_	Alignment	not modelled	6.1	35	**PDB header:**ribosome **Chain:** B: **PDB Molecule:**protein transport protein sss1; **PDBTitle:** cryo-em structure of the active yeast ssh1 complex bound to the yeast2 80s ribosome
31	d2bk0a1	Alignment	not modelled	6.1	25	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
32	c6h3vA_	Alignment	not modelled	6.0	23	**PDB header:**viral protein **Chain:** A: **PDB Molecule:**envelopment polyprotein; **PDBTitle:** bunyamwera virus glycoprotein gc head domain
33	d1txca1	Alignment	not modelled	5.7	25	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
34	c5csjC_	Alignment	not modelled	5.7	53	**PDB header:**transferase **Chain:** C: **PDB Molecule:**ribosomal protein s6 kinase alpha-1; **PDBTitle:** s100b-rsk1 crystal structure b
35	d1qmra_	Alignment	not modelled	5.6	33	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
36	d1fm4a_	Alignment	not modelled	5.5	25	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
37	d2gy9p1	Alignment	not modelled	5.4	15	**Fold:**Ribosomal protein S16 **Superfamily:**Ribosomal protein S16 **Family:**Ribosomal protein S16
38	c5j12A_	Alignment	not modelled	5.4	38	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**thymic stromal lymphopoietin; **PDBTitle:** structure of human tslp:tslpr in complex with mouse il-7ralpha
39	c1bcrA_	Alignment	not modelled	5.3	50	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** A: **PDB Molecule:**serine carboxypeptidase ii; **PDBTitle:** complex of the wheat serine carboxypeptidase, cpdw-ii, with the2 microbial peptide aldehyde inhibitor, antipain, and arginine at room3 temperature
40	d1e09a_	Alignment	not modelled	5.3	50	**Fold:**TBP-like **Superfamily:**Bet v1-like **Family:**Pathogenesis-related protein 10 (PR10)-like
41	c3ie5A_	Alignment	not modelled	5.3	25	**PDB header:**plant protein, biosynthetic protein **Chain:** A: **PDB Molecule:**phenolic oxidative coupling protein hyp-1; **PDBTitle:** crystal structure of hyp-1 protein from hypericum perforatum (st2 john's wort) involved in hypericin biosynthesis
42	d1eo0a_	Alignment	not modelled	5.2	14	**Fold:**N-cbl like **Superfamily:**Conserved domain common to transcription factors TFIIS, elongin A, CRSP70 **Family:**Conserved domain common to transcription factors TFIIS, elongin A, CRSP70
43	d2b7oa1	Alignment	not modelled	5.2	34	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class-II DAHP synthetase