Phyre2

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Description	RVBD2963_(-)_3315246_3316466
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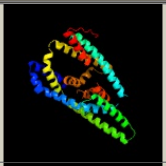
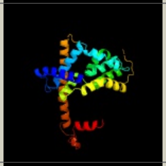
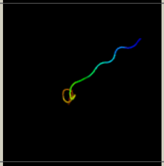
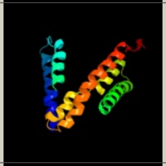
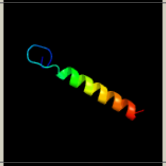
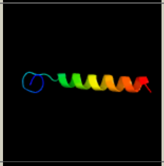
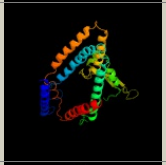
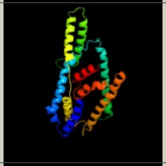
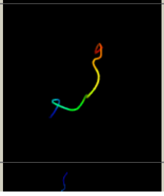
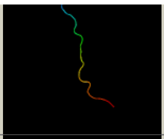
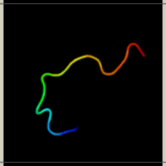
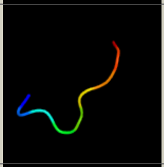
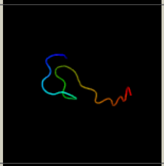
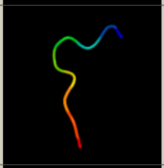
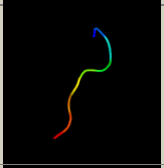
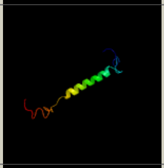
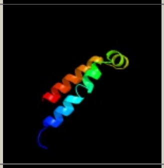
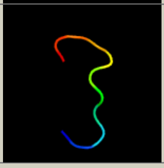
Unique Job ID	91ead3e914fafd84

Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c4ky0B_	Alignment		87.0	13	**PDB header:**transport protein, membrane protein **Chain:** B: **PDB Molecule:**proton/glutamate symporter, sdf family; **PDBTitle:** crystal structure of a substrate-free glutamate transporter homologue2 from thermococcus kodakarensis
2	c5l2bC_	Alignment		75.1	14	**PDB header:**transport protein **Chain:** C: **PDB Molecule:**nucleoside permease; **PDBTitle:** structure of cntnw n149s, e332a in an outward-facing state
3	c3tijA_	Alignment		68.4	16	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**nupc family protein; **PDBTitle:** crystal structure of a concentrative nucleoside transporter from2 vibrio cholerae
4	c3vu1A_	Alignment		60.1	50	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein ph0242; **PDBTitle:** crystal structure of the c-terminal globular domain of2 oligosaccharyltransferase (phaglb-l, o74088_pyrho) from pyrococcus3 horikoshii
5	c4n7wA_	Alignment		58.4	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**transporter, sodium/bile acid symporter family; **PDBTitle:** crystal structure of the sodium bile acid symporter from yersinia2 frederiksenii
6	c6b2zf_	Alignment		42.7	29	**PDB header:**membrane protein **Chain:** F: **PDB Molecule:**atp synthase subunit c, mitochondrial; **PDBTitle:** cryo-em structure of the dimeric fo region of yeast mitochondrial atp2 synthase
7	c2xq2A_	Alignment		42.6	13	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sodium/glucose cotransporter; **PDBTitle:** structure of the k294a mutant of vsglt
8	c6b8ht_	Alignment		40.7	29	**PDB header:**membrane protein **Chain:** T: **PDB Molecule:**atp synthase subunit 9, mitochondrial; **PDBTitle:** mosaic model of yeast mitochondrial atp synthase monomer
9	c6gctA_	Alignment		39.4	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**neutral amino acid transporter b(0); **PDBTitle:** cryo-em structure of the human neutral amino acid transporter asct2
10	d2nwwa1	Alignment		33.5	16	**Fold:**Proton glutamate symport protein **Superfamily:**Proton glutamate symport protein **Family:**Proton glutamate symport protein
11	c5xbcB_	Alignment		32.0	36	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**nsp1 protein; **PDBTitle:** crystal structure basis for pedv nsp1
						

12	c1kn7A_	Alignment		25.4	38	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**voltage-gated potassium channel protein kv1.4; **PDBTitle:** solution structure of the tandem inactivation domain2 (residues 1-75) of potassium channel rck4 (kv1.4)
13	c2jmrA_	Alignment		23.6	29	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**fimf; **PDBTitle:** nmr structure of the e. coli type 1 pilus subunit fimf
14	c3nk3C_	Alignment		21.7	36	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**zona pellucida 3; **PDBTitle:** crystal structure of full-length sperm receptor zp3 at 2.6 a2 resolution
15	c2k2bA_	Alignment		21.2	29	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**degenerin mec-4; **PDBTitle:** sparse-constraint solution nmr structure of micelle-2 solublized cytosolic amino terminal domain of c. elegans3 mechanosensory ion channel subunit mec-4. new york4 consortium on membrane protein structure (nycomps) (casp5 target)
16	c3nk4C_	Alignment		21.0	38	**PDB header:**cell adhesion **Chain:** C: **PDB Molecule:**zona pellucida 3; **PDBTitle:** crystal structure of full-length sperm receptor zp3 at 2.0 a2 resolution
17	c2iifA_	Alignment		19.1	33	**PDB header:**recombination/dna **Chain:** A: **PDB Molecule:**integration host factor; **PDBTitle:** single chain integration host factor mutant protein (scihf2-k45ae) in2 complex with dna
18	c2k74A_	Alignment		17.2	21	**PDB header:**membrane protein, oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond formation protein b; **PDBTitle:** solution nmr structure of dsbb-ubiquinone complex
19	d2r6gf1	Alignment		14.8	14	**Fold:**MalF N-terminal region-like **Superfamily:**MalF N-terminal region-like **Family:**MalF N-terminal region-like
20	c2gj0A_	Alignment		13.5	27	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**cycloviolacin o14; **PDBTitle:** cycloviolacin o14
21	c6dhrA_	Alignment	not modelled	13.5	29	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**rivi3; **PDBTitle:** nmr solution structure of rivi3
22	c2wpnB_	Alignment	not modelled	13.4	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**periplasmic [nifese] hydrogenase, large subunit, **PDBTitle:** structure of the oxidised, as-isolated nifese hydrogenase from d.2 vulgaris hildenborough
23	c1orxA_	Alignment	not modelled	13.2	14	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** solution structure of the acyclic permutant des-(24-28)-2 kalata b1.
24	c2bbjB_	Alignment	not modelled	12.3	14	**PDB header:**metal transport/membrane protein **Chain:** B: **PDB Molecule:**divalent cation transport-related protein; **PDBTitle:** crystal structure of the cora mg2+ transporter
25	c2k7gA_	Alignment	not modelled	12.3	29	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**varv peptide f; **PDBTitle:** solution structure of varv f
26	c3e4hA_	Alignment	not modelled	12.2	29	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**varv peptide f; **PDBTitle:** crystal structure of the cyclotide varv f
27	c3wdoA_	Alignment	not modelled	11.8	15	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**mfs transporter; **PDBTitle:** structure of e. coli yajr transporter
28	c2lamA_	Alignment	not modelled	11.3	29	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**cyclotide cter m; **PDBTitle:** three-dimensional structure of the cyclotide cter m
29	c5y50A_	Alignment	not modelled	11.1	11	**PDB header:**membrane protein **Chain:** A: **PDB Molecule:**protein detoxification 14;

						PDBTitle: crystal structure of eukaryotic mate transporter atdtx14
30	c2yvxD_	Alignment	not modelled	11.0	16	**PDB header:**transport protein **Chain:** D: **PDB Molecule:**mg2+ transporter mgte; **PDBTitle:** crystal structure of magnesium transporter mgte
31	c2voyB_	Alignment	not modelled	10.8	15	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sarcoplasmic/endoplasmic reticulum calcium atpase 1; **PDBTitle:** cryoem model of copa, the copper transporting atpase from2 archaeoglobus fulgidus
32	c1k48A_	Alignment	not modelled	10.4	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** refined structure and disulfide pairing of the kalata b12 peptide
33	c1jjzA_	Alignment	not modelled	10.3	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** refined structure and disulfide pairing of the kalata b12 peptide
34	c1n1uA_	Alignment	not modelled	10.3	0	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** nmr structure of [ala1,15]kalata b1
35	d1n1ua_	Alignment	not modelled	10.3	0	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
36	d1pt4a_	Alignment	not modelled	10.3	29	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
37	c4ttnA_	Alignment	not modelled	10.0	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** quasi-racemic structure of [g6a]kalata b1
38	c4ttoA_	Alignment	not modelled	10.0	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** quasi-racemic structure of [v25a] kalata b1
39	c4ttmA_	Alignment	not modelled	9.8	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** racemic structure of kalata b1 (kb1)
40	c2khbA_	Alignment	not modelled	9.8	14	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of linear kalata b1 (loop 6)
41	c2f2iA_	Alignment	not modelled	9.8	14	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of [p20d,v21k]-kalata b1
42	c6re80_	Alignment	not modelled	9.8	35	**PDB header:**proton transport **Chain:** 0: **PDB Molecule:**asa-10: polytomella f-atp synthase associated subunit 10; **PDBTitle:** cryo-em structure of polytomella f-atp synthase, rotary substate 2d,2 composite map
43	c2f2jA_	Alignment	not modelled	9.5	14	**PDB header:**antimicrobial protein **Chain:** A: **PDB Molecule:**kalata-b1; **PDBTitle:** solution structure of [w19k, p20n, v21k]-kalata b1
44	d1nb1a_	Alignment	not modelled	9.5	14	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Cyclotides **Family:**Kalata B1
45	c1nb1A_	Alignment	not modelled	9.5	14	**PDB header:**antibiotic **Chain:** A: **PDB Molecule:**kalata b1; **PDBTitle:** high resolution solution structure of kalata b1
46	c6k1hE_	Alignment	not modelled	9.2	15	**PDB header:**protein transport **Chain:** E: **PDB Molecule:**pts mannose/fructose/sorbose transporter subunit iic; **PDBTitle:** structure of membrane protein
47	c2mn1A_	Alignment	not modelled	9.1	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**kalata b1[w23ww]; **PDBTitle:** solution structure of kalata b1[w23ww]
48	c4b4aA_	Alignment	not modelled	9.1	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sec-independent protein translocase protein tatc; **PDBTitle:** structure of the tatc core of the twin arginine protein2 translocation system
49	c2l69A_	Alignment	not modelled	9.1	32	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**rossmann 2x3 fold protein; **PDBTitle:** solution nmr structure of de novo designed protein, p-loop ntpase2 fold, northeast structural genomics consortium target or28
50	d1o9ga_	Alignment	not modelled	9.0	14	**Fold:**S-adenosyl-L-methionine-dependent methyltransferases **Superfamily:**S-adenosyl-L-methionine-dependent methyltransferases **Family:**rRNA methyltransferase AviRa
51	c2mfrA_	Alignment	not modelled	7.9	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**insulin receptor; **PDBTitle:** solution structure of the transmembrane domain of the insulin receptor2 in micelles
52	c6d79A_	Alignment	not modelled	7.8	12	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**sulfate transporter cysz; **PDBTitle:** structure of cysz, a sulfate permease from pseudomonas fragi
53	c2fqaA_	Alignment	not modelled	7.4	29	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**violacin 1; **PDBTitle:** violacin a
54	c3v8vB_	Alignment	not modelled	7.4	19	**PDB header:**transferase **Chain:** B: **PDB Molecule:**ribosomal rna large subunit methyltransferase l; **PDBTitle:** crystal structure of bifunctional methyltransferase ycby (rlmlk) from2 escherichia coli, sam binding
						PDB header:dna binding protein

55	c1g5hA_	Alignment	not modelled	7.3	33	**Chain:** A: **PDB Molecule:**mitochondrial dna polymerase accessory subunit; **PDBTitle:** crystal structure of the accessory subunit of murine mitochondrial2 polymerase gamma
56	c2m9oA_	Alignment	not modelled	7.3	14	**PDB header:**plant protein **Chain:** A: **PDB Molecule:**kalata-b7; **PDBTitle:** solution structure of kalata b7
57	c4eq7B_	Alignment	not modelled	7.1	38	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**abc transporter, substrate binding protein (polyamine); **PDBTitle:** structure of atu4243-gaba receptor
58	c2kukA_	Alignment	not modelled	6.5	9	**PDB header:**antiviral protein **Chain:** A: **PDB Molecule:**leaf cyclotide 2; **PDBTitle:** solution structure of vhl-2
59	d1wuil1	Alignment	not modelled	6.4	0	**Fold:**HydB/Nqo4-like **Superfamily:**HydB/Nqo4-like **Family:**Nickel-iron hydrogenase, large subunit
60	c2n2uA_	Alignment	not modelled	6.2	47	**PDB header:**unknown function, structural genomics **Chain:** A: **PDB Molecule:**or358; **PDBTitle:** solution nmr structure of de novo designed ferredoxin fold protein2 sfr3, northeast structural genomics consortium (nesg) target or358
61	c2fqcA_	Alignment	not modelled	5.5	21	**PDB header:**toxin **Chain:** A: **PDB Molecule:**conotoxin pl14a; **PDBTitle:** solution structure of conotoxin pl14a
62	c3ianA_	Alignment	not modelled	5.3	33	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**chitinase; **PDBTitle:** crystal structure of a chitinase from lactococcus lactis subsp. lactis
63	c2kvoA_	Alignment	not modelled	5.1	23	**PDB header:**photosynthesis **Chain:** A: **PDB Molecule:**photosystem ii reaction center psb28 protein; **PDBTitle:** solution nmr structure of photosystem ii reaction center psb28 protein2 from synechocystis sp.(strain pcc 6803), northeast structural3 genomics consortium target sgr171
64	c3ldgA_	Alignment	not modelled	5.0	5	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.472; **PDBTitle:** crystal structure of smu.472, a putative methyltransferase complexed2 with sah