Phyre^2

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Description	RVBD3912_(-)_4401047_4401811
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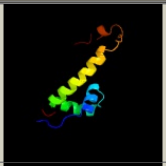
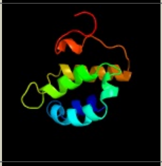
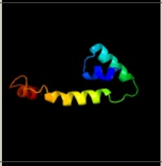
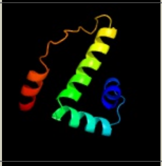
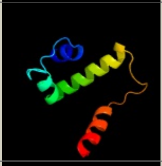
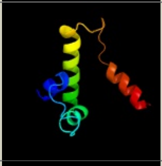
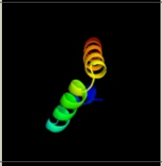
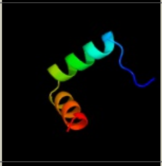
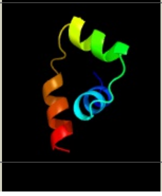
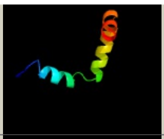
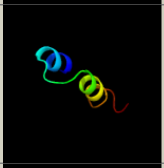
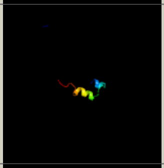
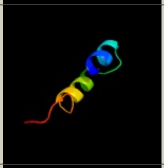
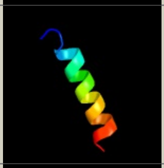
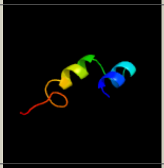
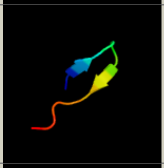
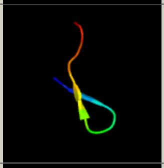
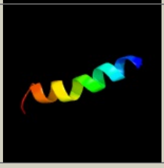
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c2z2sD_	Alignment		99.3	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**anti-sigma factor chrr, transcriptional activator chrr; **PDBTitle:** crystal structure of rhodobacter sphaeroides sige in complex with the2 anti-sigma chrr
2	c5wuqD_	Alignment		99.2	6	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**anti-sigma-w factor rsiw; **PDBTitle:** crystal structure of sigw in complex with its anti-sigma rsiw, a zinc2 binding form
3	c3hugJ_	Alignment		99.1	13	**PDB header:**transcription/membrane protein **Chain:** J: **PDB Molecule:**probable conserved membrane protein; **PDBTitle:** crystal structure of mycobacterium tuberculosis anti-sigma factor rsla2 in complex with -35 promoter binding domain of sigl
4	c5frhA_	Alignment		99.1	10	**PDB header:**transcription **Chain:** A: **PDB Molecule:**anti-sigma factor rsra; **PDBTitle:** solution structure of oxidised rsra
5	c3vdoB_	Alignment		98.9	29	**PDB header:**dna binding protein/protein binding **Chain:** B: **PDB Molecule:**anti-sigma-k factor rska; **PDBTitle:** structure of extra-cytoplasmic function(ecf) sigma factor sigk in2 complex with its negative regulator rska from mycobacterium3 tuberculosis
6	c6in7A_	Alignment		98.1	12	**PDB header:**transcription **Chain:** A: **PDB Molecule:**sigma factor algu negative regulatory protein; **PDBTitle:** crystal structure of algu in complex with muca(cyto)
7	c1or7C_	Alignment		95.9	16	**PDB header:**transcription **Chain:** C: **PDB Molecule:**sigma-e factor negative regulatory protein; **PDBTitle:** crystal structure of escherichia coli sigmae with the cytoplasmic2 domain of its anti-sigma rsea
8	d1or7c_	Alignment		95.9	16	**Fold:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Superfamily:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA **Family:**N-terminal, cytoplasmic domain of anti-sigmaE factor RseA
9	c5camC_	Alignment		95.8	15	**PDB header:**transcription **Chain:** C: **PDB Molecule:**pupr protein; **PDBTitle:** crystal structure of the cytoplasmic domain of the pseudomonas putida2 anti-sigma factor pupr (semet)
10	c4ynhA_	Alignment		74.9	26	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**spindle assembly abnormal protein 5; **PDBTitle:** structure of the c. elegans sas-5 implico dimerization domain
11	c5m45I_	Alignment		28.5	20	**PDB header:**ligase **Chain:** I: **PDB Molecule:**acetone carboxylase gamma subunit; **PDBTitle:** structure of acetone carboxylase purified from xanthobacter2 autotrophicus

12	c3kb4D_	Alignment		18.5	20	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**alr8543 protein; **PDBTitle:** crystal structure of the alr8543 protein in complex with2 geranylgeranyl monophosphate and magnesium ion from nostoc sp. pcc3 7120, northeast structural genomics consortium target nsr141
13	c5oynB_	Alignment		18.3	22	**PDB header:**lyase **Chain:** B: **PDB Molecule:**dehydratase, ilvd/edd family; **PDBTitle:** crystal structure of d-xylonate dehydratase in holo-form
14	c5ze4A_	Alignment		16.7	19	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxy-acid dehydratase, chloroplastic; **PDBTitle:** the structure of holo- structure of dhad complex with [2fe-2s] cluster
15	c6ovtD_	Alignment		12.0	22	**PDB header:**lyase **Chain:** D: **PDB Molecule:**dihydroxy-acid dehydratase; **PDBTitle:** crystal structure of ilvd from mycobacterium tuberculosis
16	d2f8aa1	Alignment		11.6	10	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
17	c5j84A_	Alignment		11.4	11	**PDB header:**lyase **Chain:** A: **PDB Molecule:**dihydroxy-acid dehydratase; **PDBTitle:** crystal structure of l-arabinonate dehydratase in holo-form
18	d1igqa_	Alignment		11.0	38	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
19	d1igub_	Alignment		9.9	38	**Fold:**SH3-like barrel **Superfamily:**C-terminal domain of transcriptional repressors **Family:**Transcriptional repressor protein KorB
20	c2qsiB_	Alignment		9.8	15	**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 rhodopseudomonas palustris cga009
21	d1v58a1	Alignment	not modelled	9.7	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
22	c5lbmD_	Alignment	not modelled	9.3	17	**PDB header:**transcription **Chain:** D: **PDB Molecule:**transcriptional repressor frmr; **PDBTitle:** the asymmetric tetrameric structure of the formaldehyde sensing2 transcriptional repressor frmr from escherichia coli
23	c3gv1A_	Alignment	not modelled	9.2	7	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**disulfide interchange protein; **PDBTitle:** crystal structure of disulfide interchange protein from neisseria2 gonorrhoeae
24	d2cwla1	Alignment	not modelled	9.1	21	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**Manganese catalase (T-catalase)
25	d2nrka1	Alignment	not modelled	8.4	19	**Fold:**Nucleotidyltransferase **Superfamily:**Nucleotidyltransferase **Family:**GrpB-like
26	d1j08a1	Alignment	not modelled	8.2	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
27	d1z6ma1	Alignment	not modelled	8.1	9	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
28	c2mjlA_	Alignment	not modelled	7.3	15	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**peptidyl-trna hydrolase; **PDBTitle:** solution structure of peptidyl-trna hyrolase from vibrio cholerae
29	d1z6na1	Alignment	not modelled	7.0	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase

30	d1t3ba1	Alignment	not modelled	6.7	6	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
31	c4rs7R_	Alignment	not modelled	6.7	21	**PDB header:**dna binding protein **Chain:** R: **PDB Molecule:**parb-c; **PDBTitle:** structure of pnob8 parb-c
32	c2qv8B_	Alignment	not modelled	6.5	4	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general secretion pathway protein h; **PDBTitle:** structure of the minor pseudopilin epsh from the type 2 secretion2 system of vibrio cholerae
33	c2odkD_	Alignment	not modelled	6.5	17	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**hypothetical protein; **PDBTitle:** putative prevent-host-death protein from nitrosomonas europaea
34	d1ftra1	Alignment	not modelled	6.4	39	**Fold:**Ferredoxin-like **Superfamily:**Formylmethanofuran:tetrahydromethanopterin formyltransferase **Family:**Formylmethanofuran:tetrahydromethanopterin formyltransferase
35	c5lcyD_	Alignment	not modelled	6.0	16	**PDB header:**transcription **Chain:** D: **PDB Molecule:**frmr; **PDBTitle:** formaldehyde-responsive regulator frmr e64h variant from salmonella2 enterica serovar typhimurium
36	c1wx4B_	Alignment	not modelled	5.8	8	**PDB header:**oxidoreductase/metal transport **Chain:** B: **PDB Molecule:**melc; **PDBTitle:** crystal structure of the oxy-form of the copper-bound streptomyces2 castaneoglobisporus tyrosinase complexed with a caddie protein3 prepared by the addition of dithiothreitol
37	c2hh7A_	Alignment	not modelled	5.5	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**hypothetical protein csor; **PDBTitle:** crystal structure of cu(i) bound csor from mycobacterium tuberculosis.
38	c3tsaA_	Alignment	not modelled	5.2	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**ndp-rhamnosyltransferase; **PDBTitle:** spinosyn rhamnosyltransferase spng