Phyre^2

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Description	Q2M7M3
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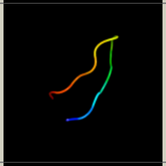
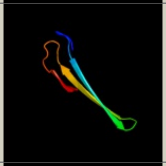
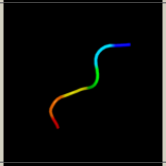
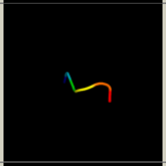
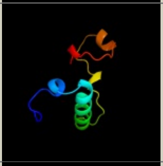
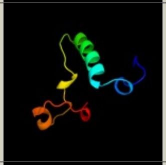
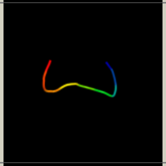
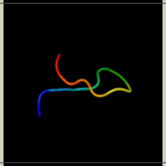
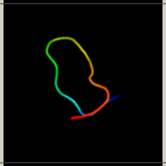
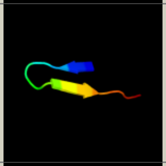
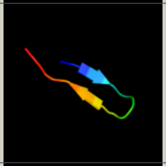
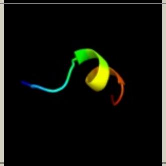
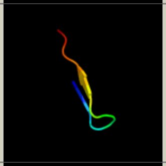
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1gr0a1	Alignment		24.0	35	**Fold:**NAD(P)-binding Rossmann-fold domains **Superfamily:**NAD(P)-binding Rossmann-fold domains **Family:**Glyceraldehyde-3-phosphate dehydrogenase-like, N-terminal domain
2	c1fmeA_	Alignment		22.3	53	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**fsd-ey peptide; **PDBTitle:** solution structure of fsd-ey, a novel peptide assuming a2 beta-beta-alpha fold
3	d2o62a1	Alignment		19.9	11	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**All1756-like
4	c2ixsB_	Alignment		16.4	19	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**sdai restriction endonuclease; **PDBTitle:** structure of sdai restriction endonuclease
5	c2e72A_	Alignment		15.2	33	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**pogo transposable element with znf domain; **PDBTitle:** solution structure of the zinc finger domain of human2 kiaa0461
6	d1tf3a1	Alignment		14.2	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
7	d1tf6a1	Alignment		10.7	50	**Fold:**beta-beta-alpha zinc fingers **Superfamily:**beta-beta-alpha zinc fingers **Family:**Classic zinc finger, C2H2
8	d1uf2a_	Alignment		10.1	27	**Fold:**Reovirus inner layer core protein p3 **Superfamily:**Reovirus inner layer core protein p3 **Family:**Phytoreovirus core
9	c1uf2A_	Alignment		10.1	27	**PDB header:**virus **Chain:** A: **PDB Molecule:**core protein p3; **PDBTitle:** the atomic structure of rice dwarf virus (rdv)
10	c2k6rA_	Alignment		10.1	56	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**full sequence design 1 synthetic superstable; **PDBTitle:** protein folding on a highly rugged landscape: experimental2 observation of glassy dynamics and structural frustration
11	d1q5qh_	Alignment		10.0	10	**Fold:**Ntn hydrolase-like **Superfamily:**N-terminal nucleophile aminohydrolases (Ntn hydrolases) **Family:**Proteasome subunits

12	c2h6jI_	Alignment		9.3	10	**PDB header:**hydrolase **Chain:** I: **PDB Molecule:**proteasome beta-type subunit 1; **PDBTitle:** crystal structure of the beta f145a rhodococcus proteasome (casp2 target)
13	c1fsvA_	Alignment		9.0	43	**PDB header:**beta beta alpha motif **Chain:** A: **PDB Molecule:**full sequence design 1 of beta beta alpha motif; **PDBTitle:** full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, minimized average structure
14	c1fsdA_	Alignment		9.0	43	**PDB header:**novel sequence **Chain:** A: **PDB Molecule:**full sequence design 1 of beta beta alpha motif; **PDBTitle:** full sequence design 1 (fsd-1) of beta beta alpha motif,2 nmr, 41 structures
15	d1fnga2	Alignment		8.5	31	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
16	d1jk8a2	Alignment		8.1	21	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
17	c1mk2B_	Alignment		8.0	46	**PDB header:**transcription **Chain:** B: **PDB Molecule:**madh-interacting protein; **PDBTitle:** smad3 sbd complex
18	d1uvqa2	Alignment		7.7	15	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
19	d1s9va2	Alignment		7.6	21	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
20	c3gqiB_	Alignment		7.6	22	**PDB header:**transferase/transferase inhibitor **Chain:** B: **PDB Molecule:**phospholipase c-gamma-1; **PDBTitle:** crystal structure of activated receptor tyrosine kinase in2 complex with substrates
21	d1es0a2	Alignment	not modelled	7.4	23	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
22	c1vd8A_	Alignment	not modelled	7.3	55	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fibroin-modulator-binding-protein-1; **PDBTitle:** solution structure of fmbp-1 tandem repeat 2
23	c1wnmA_	Alignment	not modelled	7.2	55	**PDB header:**transcription **Chain:** A: **PDB Molecule:**fibroin-modulator binding-protein-1; **PDBTitle:** nmr structure of fmbp-1 tandem repeat 2 in 30%(v/v) tfe2 solution
24	d1xa6a2	Alignment	not modelled	6.8	14	**Fold:**SH2-like **Superfamily:**SH2 domain **Family:**SH2 domain
25	d2o0qa1	Alignment	not modelled	6.6	73	**Fold:**ADP-ribosylation **Superfamily:**ADP-ribosylation **Family:**CC0527-like
26	c2pidB_	Alignment	not modelled	6.3	30	**PDB header:**ligase **Chain:** B: **PDB Molecule:**tyrosyl-trna synthetase; **PDBTitle:** crystal structure of human mitochondrial tyrosyl-trna synthetase in2 complex with an adenylate analog
27	d2gtlm1	Alignment	not modelled	6.2	54	**Fold:**Streptavidin-like **Superfamily:**Extracellular hemoglobin linker subunit, receptor domain **Family:**Extracellular hemoglobin linker subunit, receptor domain
28	d1muja2	Alignment	not modelled	6.1	15	**Fold:**MHC antigen-recognition domain **Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
						Fold:MHC antigen-recognition domain

29	d2p24a2	Alignment	not modelled	5.5	15	**Superfamily:**MHC antigen-recognition domain **Family:**MHC antigen-recognition domain
30	d2gtlo1	 Alignment	not modelled	5.4	33	**Fold:**Streptavidin-like **Superfamily:**Extracellular hemoglobin linker subunit, receptor domain **Family:**Extracellular hemoglobin linker subunit, receptor domain