Phyre^2

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Description	Q02885
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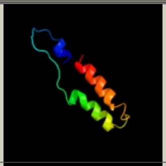
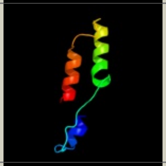
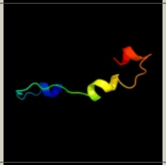
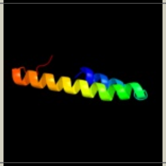
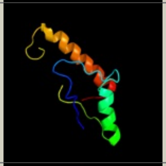
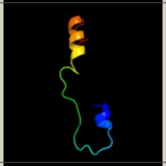
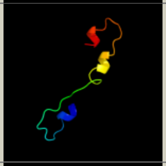
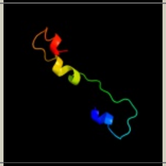
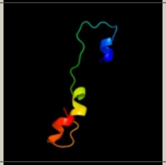
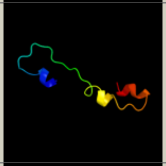
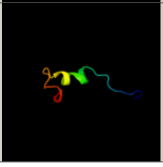
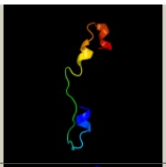
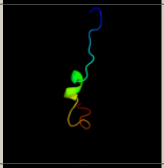
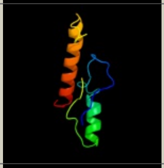
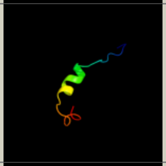
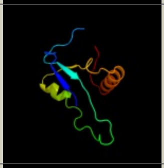
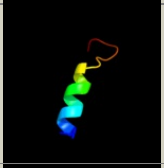
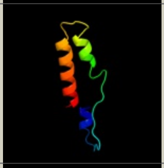
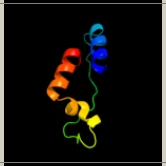
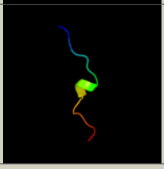
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3mbfA_	Alignment		79.9	31	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose bisphosphate aldolase from2 encephalitozoon cuniculi, bound to fructose 1,6-bisphosphate
2	c3kx6C_	Alignment		58.1	27	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose-1,6-bisphosphate aldolase from babesia2 bovis at 2.1a resolution
3	d1zaia1	Alignment		47.2	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
4	d2itba1	Alignment		43.3	21	**Fold:**Ferritin-like **Superfamily:**Ferritin-like **Family:**MiaE-like
5	d1tz9a_	Alignment		39.6	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Xylose isomerase-like **Family:**UxuA-like
6	d1qo5b_	Alignment		39.1	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
7	d1fdja_	Alignment		38.6	23	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
8	d1f2ja_	Alignment		31.8	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
9	c2qapC_	Alignment		30.5	20	**PDB header:**lyase **Chain:** C: **PDB Molecule:**fructose-1,6-bisphosphate aldolase; **PDBTitle:** fructose-1,6-bisphosphate aldolase from leishmania mexicana
10	d2qapa1	Alignment		30.2	20	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
11	c3mmtC_	Alignment		27.3	34	**PDB header:**hydrolase **Chain:** C: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose bisphosphate aldolase from bartonella2 henselae, bound to fructose bisphosphate

12	d1xfba1	Alignment		24.2	26	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
13	c2pc4B_	Alignment		22.8	38	**PDB header:**lyase **Chain:** B: **PDB Molecule:**fructose-bisphosphate aldolase; **PDBTitle:** crystal structure of fructose-bisphosphate aldolase from plasmodium2 falciparum in complex with trap-tail determined at 2.4 angstrom3 resolution
14	c3bdkB_	Alignment		22.2	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**d-mannonate dehydratase; **PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue
15	d1a5ca_	Alignment		21.8	38	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
16	d1ro5a_	Alignment		21.3	19	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Autoinducer synthetase
17	c2dt7A_	Alignment		17.7	21	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**splicing factor 3a subunit 3; **PDBTitle:** solution structure of the second surp domain of human2 splicing factor sf3a120 in complex with a fragment of3 human splicing factor sf3a60
18	d1fbaa_	Alignment		16.3	22	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**Class I aldolase
19	c2ekcA_	Alignment		14.7	22	**PDB header:**lyase **Chain:** A: **PDB Molecule:**tryptophan synthase alpha chain; **PDBTitle:** structural study of project id aq_1548 from aquifex aeolicus vf5
20	c2iqtA_	Alignment		13.8	29	**PDB header:**lyase **Chain:** A: **PDB Molecule:**fructose-bisphosphate aldolase class 1; **PDBTitle:** crystal structure of fructose-bisphosphate aldolase, class i from2 porphyromonas gingivalis
21	c3q4nA_	Alignment	not modelled	13.5	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein mj0754; **PDBTitle:** crystal structure of hypothetical protein mj0754 from methanococcus2 jannaschii dsm 2661
22	c2kp7A_	Alignment	not modelled	12.6	28	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**crossover junction endonuclease mus81; **PDBTitle:** solution nmr structure of the mus81 n-terminal hhh.2 northeast structural genomics consortium target mmt1a
23	c3p2fA_	Alignment	not modelled	12.2	17	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**ahl synthase; **PDBTitle:** crystal structure of tofi in an apo form
24	d1ofcx1	Alignment	not modelled	12.1	37	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Homeodomain-like **Family:**Myb/SANT domain
25	c3lo3E_	Alignment	not modelled	10.6	25	**PDB header:**structure genomics, unknown function **Chain:** E: **PDB Molecule:**uncharacterized conserved protein; **PDBTitle:** the crystal structure of a conserved functionally unknown2 protein from colwellia psychrerythraea 34h.
26	d1kzfa_	Alignment	not modelled	10.4	20	**Fold:**Acyl-CoA N-acyltransferases (Nat) **Superfamily:**Acyl-CoA N-acyltransferases (Nat) **Family:**Autoinducer synthetase
27	c2ktaA_	Alignment	not modelled	8.6	22	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative helicase; **PDBTitle:** solution nmr structure of a domain of protein a6ky75 from bacteroides2 vulgatus, northeast structural genomics target bvr106a
28	d1udxa3	Alignment	not modelled	8.1	13	**Fold:**Obg GTP-binding protein C-terminal domain **Superfamily:**Obg GTP-binding protein C-terminal domain **Family:**Obg GTP-binding protein C-terminal domain

29	d2cpya1	Alignment	not modelled	8.0	27	**Fold:**Ferredoxin-like **Superfamily:**RNA-binding domain, RBD **Family:**Canonical RBD
30	c3cz8A_	Alignment	not modelled	7.9	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative sporulation-specific glycosylase ydhd; **PDBTitle:** crystal structure of putative sporulation-specific glycosylase ydhd2 from bacillus subtilis
31	d1wapa_	Alignment	not modelled	7.7	64	**Fold:**Double-stranded beta-helix **Superfamily:**TRAP-like **Family:**Trp RNA-binding attenuation protein (TRAP)
32	d1gtfa_	Alignment	not modelled	7.5	64	**Fold:**Double-stranded beta-helix **Superfamily:**TRAP-like **Family:**Trp RNA-binding attenuation protein (TRAP)
33	d1e0ba_	Alignment	not modelled	7.5	45	**Fold:**SH3-like barrel **Superfamily:**Chromo domain-like **Family:**Chromo domain
34	d1iapa_	Alignment	not modelled	6.9	21	**Fold:**Regulator of G-protein signaling, RGS **Superfamily:**Regulator of G-protein signaling, RGS **Family:**Regulator of G-protein signaling, RGS
35	c3qpiA_	Alignment	not modelled	6.7	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**chlorite dismutase; **PDBTitle:** crystal structure of dimeric chlorite dismutases from nitrobacter2 winogradskyi
36	d1q4ra_	Alignment	not modelled	6.7	26	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**Plant stress-induced protein
37	c1y7xA_	Alignment	not modelled	6.5	57	**PDB header:**structural protein, protein binding **Chain:** A: **PDB Molecule:**major vault protein; **PDBTitle:** solution structure of a two-repeat fragment of major vault2 protein
38	d1usta_	Alignment	not modelled	6.3	29	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**"Winged helix" DNA-binding domain **Family:**Linker histone H1/H5
39	c2rh0B_	Alignment	not modelled	6.3	24	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**nudc domain-containing protein 2; **PDBTitle:** crystal structure of nudc domain-containing protein 22 (13542905) from mus musculus at 1.95 a resolution
40	c3cxnB_	Alignment	not modelled	5.9	21	**PDB header:**chaperone **Chain:** B: **PDB Molecule:**urease accessory protein uref; **PDBTitle:** structure of the urease accessory protein uref from helicobacter2 pylori
41	d2nt0a2	Alignment	not modelled	5.9	29	**Fold:**TIM beta/alpha-barrel **Superfamily:**(Trans)glycosidases **Family:**beta-glycanases
42	c2rqpA_	Alignment	not modelled	5.5	23	**PDB header:**gene regulation **Chain:** A: **PDB Molecule:**heterochromatin protein 1-binding protein 3; **PDBTitle:** the solution structure of heterochromatin protein 1-binding2 protein 74 histone h1 like domain
43	c1u6tA_	Alignment	not modelled	5.4	14	**PDB header:**protein binding, signaling protein **Chain:** A: **PDB Molecule:**sh3 domain-binding glutamic acid-rich-like **PDBTitle:** crystal structure of the human sh3 binding glutamic-rich2 protein like
44	c2qr4B_	Alignment	not modelled	5.3	14	**PDB header:**hydrolase **Chain:** B: **PDB Molecule:**peptidase m3b, oligoendopeptidase f; **PDBTitle:** crystal structure of oligoendopeptidase-f from enterococcus faecium