Phyre^2

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Description	Q9JMS0
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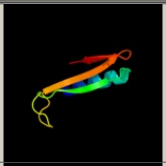
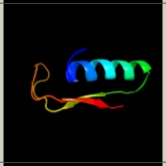
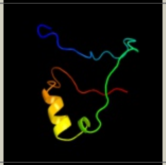
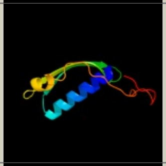
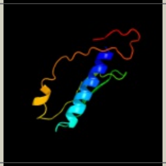
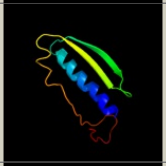
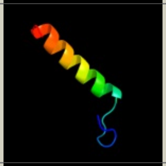
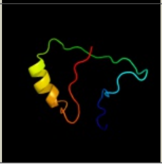
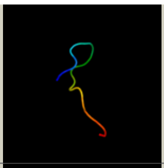
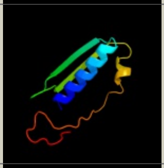
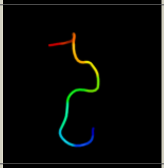
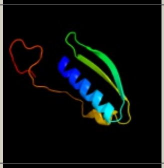
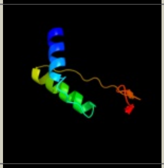
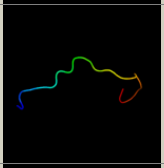
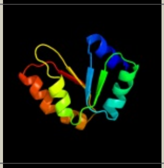
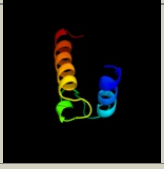
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	c3kd4A_	Alignment		79.8	19	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**putative protease; **PDBTitle:** crystal structure of a putative protease (bdi_1141) from2 parabacteroides distasonis atcc 8503 at 2.00 a resolution
2	d2f4ma1	Alignment		38.4	17	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
3	c3jubA_	Alignment		37.9	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**aig2-like domain-containing protein 1; **PDBTitle:** human gamma-glutamylamine cyclotransferase
4	d1rq0a_	Alignment		34.5	16	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
5	c1zbtA_	Alignment		29.2	19	**PDB header:**translation **Chain:** A: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** crystal structure of peptide chain release factor 1 (rf-1) (smu.1085)2 from streptococcus mutans at 2.34 a resolution
6	d1gqea_	Alignment		28.1	20	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
7	d2b3tb1	Alignment		26.2	17	**Fold:**Release factor **Superfamily:**Release factor **Family:**Release factor
8	c3u7jA_	Alignment		22.1	29	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-phosphate isomerase a from burkholderia2 thailandensis
9	c3nzlA_	Alignment		20.4	30	**PDB header:**transcription **Chain:** A: **PDB Molecule:**dna-binding protein satb1; **PDBTitle:** crystal structure of the n-terminal domain of dna-binding protein2 satb1 from homo sapiens, northeast structural genomics consortium3 target hr4435b
10	c3necD_	Alignment		19.8	29	**PDB header:**actin-binding protein **Chain:** D: **PDB Molecule:**inflammatory profilin; **PDBTitle:** crystal structure of toxoplasma gondii profilin
11	d1vkba_	Alignment		17.7	10	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like

12	c3h25A_	Alignment		17.5	38	**PDB header:**replication/dna **Chain:** A: **PDB Molecule:**replication protein b; **PDBTitle:** crystal structure of the catalytic domain of primase repb' in complex2 with initiator dna
13	c2ihr1_	Alignment		15.4	12	**PDB header:**translation **Chain:** 1: **PDB Molecule:**peptide chain release factor 2; **PDBTitle:** rf2 of thermus thermophilus
14	c3bg4D_	Alignment		13.7	40	**PDB header:**hydrolase/hydrolase inhibitor **Chain:** D: **PDB Molecule:**guamerin; **PDBTitle:** the crystal structure of guamerin in complex with2 chymotrypsin and the development of an elastase-specific3 inhibitor
15	c3d5cX_	Alignment		13.0	15	**PDB header:**ribosome **Chain:** X: **PDB Molecule:**peptide chain release factor 1; **PDBTitle:** structural basis for translation termination on the 70s ribosome. this2 file contains the 30s subunit, release factor 1 (rf1), two trna, and3 mrna molecules of the second 70s ribosome. the entire crystal4 structure contains two 70s ribosomes as described in remark 400.
16	c2z8tX_	Alignment		12.8	14	**PDB header:**hydrolase **Chain:** X: **PDB Molecule:**protein-glutaminase; **PDBTitle:** crystal structure of protein-glutaminase of c.proteolyticum2 strain 9670
17	c3d9wA_	Alignment		12.2	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**putative acetyltransferase; **PDBTitle:** crystal structure analysis of nocardia farcinica arylamine2 n-acetyltransferase
18	c3imkA_	Alignment		12.1	35	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**putative molybdenum carrier protein; **PDBTitle:** crystal structure of putative molybdenum carrier protein (yp_461806.1)2 from syntrophus aciditrophicus sb at 1.45 a resolution
19	d1ozha2	Alignment		11.9	15	**Fold:**Thiamin diphosphate-binding fold (THDP-binding) **Superfamily:**Thiamin diphosphate-binding fold (THDP-binding) **Family:**Pyruvate oxidase and decarboxylase Pyr module
20	c2kp7A_	Alignment		11.2	19	**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
21	d1f2ka_	Alignment	not modelled	10.7	26	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
22	d1x3za1	Alignment	not modelled	10.5	20	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Transglutaminase core
23	d2r4qa1	Alignment	not modelled	10.1	21	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
24	d1hn6a_	Alignment	not modelled	9.7	54	**Fold:**Apical membrane antigen 1 **Superfamily:**Apical membrane antigen 1 **Family:**Apical membrane antigen 1
25	d1pnea_	Alignment	not modelled	9.3	9	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
26	d1bx7a_	Alignment	not modelled	9.0	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Huristasin-like
27	c3rq4A_	Alignment	not modelled	8.8	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**histone-lysine n-methyltransferase suv420h2; **PDBTitle:** crystal structure of suppressor of variegation 4-20 homolog 2
28	d2hlya1	Alignment	not modelled	8.4	20	**Fold:**Cysteine proteinases **Superfamily:**Cysteine proteinases **Family:**Atu2299-like
						Fold: Profilin-like

29	d1acfa_	Alignment	not modelled	8.2	26	**Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
30	c3pifD_	Alignment	not modelled	8.1	14	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**5'->3' exoribonuclease (xrn1); **PDBTitle:** crystal structure of the 5'->3' exoribonuclease xrn1, e178q mutant in2 complex with manganese
31	d3nula_	Alignment	not modelled	8.0	32	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
32	d1cqaa_	Alignment	not modelled	8.0	27	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
33	d1brza_	Alignment	not modelled	8.0	19	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Scorpion toxin-like **Family:**Plant defensins
34	d1g71a_	Alignment	not modelled	7.8	22	**Fold:**Prim-pol domain **Superfamily:**Prim-pol domain **Family:**PriA-like
35	d2pbdp1	Alignment	not modelled	7.7	9	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
36	d2c1ha1	Alignment	not modelled	7.3	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
37	d1g5ua_	Alignment	not modelled	7.3	27	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
38	d2r48a1	Alignment	not modelled	7.3	26	**Fold:**Phosphotyrosine protein phosphatases I-like **Superfamily:**PTS system IIB component-like **Family:**PTS system, Fructose specific IIB subunit-like
39	c3davA_	Alignment	not modelled	7.2	26	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**profilin; **PDBTitle:** schizosaccharomyces pombe profilin crystallized from sodium2 formate
40	d1v30a_	Alignment	not modelled	6.9	6	**Fold:**Gamma-glutamyl cyclotransferase-like **Superfamily:**Gamma-glutamyl cyclotransferase-like **Family:**Gamma-glutamyl cyclotransferase-like
41	c3enpA_	Alignment	not modelled	6.8	24	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**tp53rk-binding protein; **PDBTitle:** crystal structure of human cgi121
42	d1ejab_	Alignment	not modelled	6.8	40	**Fold:**Knottins (small inhibitors, toxins, lectins) **Superfamily:**Leech antihemostatic proteins **Family:**Huristasin-like
43	d1s7ja_	Alignment	not modelled	6.7	12	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
44	d1ypra_	Alignment	not modelled	6.6	26	**Fold:**Profilin-like **Superfamily:**Profilin (actin-binding protein) **Family:**Profilin (actin-binding protein)
45	d1l6sa_	Alignment	not modelled	6.0	21	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
46	d1umga_	Alignment	not modelled	5.9	31	**Fold:**Sulfolobus fructose-1,6-bisphosphatase-like **Superfamily:**Sulfolobus fructose-1,6-bisphosphatase-like **Family:**Sulfolobus fructose-1,6-bisphosphatase-like
47	d1o8bb1	Alignment	not modelled	5.6	25	**Fold:**NagB/RpiA/CoA transferase-like **Superfamily:**NagB/RpiA/CoA transferase-like **Family:**D-ribose-5-phosphate isomerase (RpiA), catalytic domain
48	d2zgwa2	Alignment	not modelled	5.6	14	**Fold:**Class II aaRS and biotin synthetases **Superfamily:**Class II aaRS and biotin synthetases **Family:**Biotin holoenzyme synthetase
49	d1gzga_	Alignment	not modelled	5.6	25	**Fold:**TIM beta/alpha-barrel **Superfamily:**Aldolase **Family:**5-aminolaevulinate dehydratase, ALAD (porphobilinogen synthase)
50	c2kl8A_	Alignment	not modelled	5.5	50	**PDB header:**de novo protein **Chain:** A: **PDB Molecule:**or15; **PDBTitle:** solution nmr structure of de novo designed ferredoxin-like2 fold protein, northeast structural genomics consortium3 target or15
51	d1l0nk_	Alignment	not modelled	5.5	50	**Fold:**Single transmembrane helix **Superfamily:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase) **Family:**Subunit XI (6.4 kDa protein) of cytochrome bc1 complex (Ubiquinol-cytochrome c reductase)
52	c3kewA_	Alignment	not modelled	5.5	27	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dhha1 domain protein; **PDBTitle:** crystal structure of probable alanyl-trna-synthase from clostridium2 perfringens
53	d2e1ba1	Alignment	not modelled	5.4	47	**Fold:**Reductase/isomerase/elongation factor common domain **Superfamily:**Translation proteins **Family:**AlaX-M N-terminal domain-like
54	d1qy9a1	Alignment	not modelled	5.3	14	**Fold:**Diaminopimelate epimerase-like **Superfamily:**Diaminopimelate epimerase-like **Family:**PhzC/PhzF-like
55	c3kwmC_	Alignment	not modelled	5.2	24	**PDB header:**isomerase **Chain:** C: **PDB Molecule:**ribose-5-phosphate isomerase a; **PDBTitle:** crystal structure of ribose-5-isomerase a

56	c2kyrA_	Alignment	not modelled	5.2	19	**PDB header:**transferase **Chain:** A: **PDB Molecule:**fructose-like phosphotransferase enzyme iib component 1; **PDBTitle:** solution structure of enzyme iib subunit of pts system from2 escherichia coli k12. northeast structural genomics consortium target3 er315/ontario center for structural proteomics target ec0544
57	d2ifaa1	Alignment	not modelled	5.1	10	**Fold:**FMN-dependent nitroreductase-like **Superfamily:**FMN-dependent nitroreductase-like **Family:**NADH oxidase/flavin reductase
58	c3mp2A_	Alignment	not modelled	5.0	13	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**non-structural protein 3; **PDBTitle:** crystal structure of transmissible gastroenteritis virus papain-like2 protease 1