Phyre2

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Description	P77598
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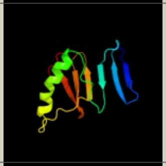
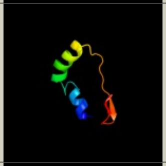
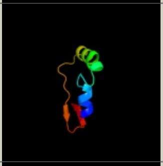
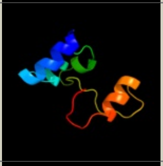
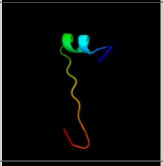
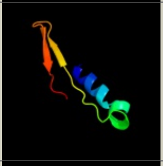
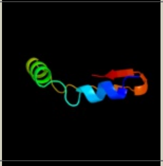
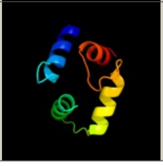
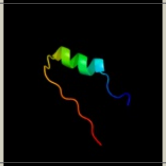
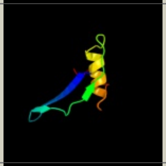
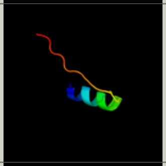
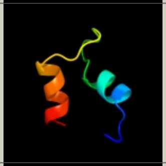
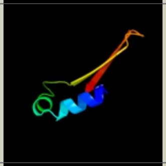
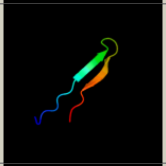
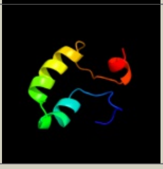
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d2hh8a1	Alignment		100.0	80	**Fold:**YdfO-like **Superfamily:**YdfO-like **Family:**YdfO-like
2	d3elga1	Alignment		81.9	11	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
3	c2qlxA_	Alignment		41.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**l-rhamnose mutarotase; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum in complex with l-rhamnose
4	c2qlwA_	Alignment		41.0	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**rhau; **PDBTitle:** crystal structure of rhamnose mutarotase rhau of rhizobium2 leguminosarum
5	d3duea1	Alignment		39.4	4	**Fold:**BLIP-like **Superfamily:**BT0923-like **Family:**BT0923-like
6	c1f8aB_	Alignment		26.7	10	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**peptidyl-prolyl cis-trans isomerase nima- **PDBTitle:** structural basis for the phosphoserine-proline recognition2 by group iv ww domains
7	c2ph7B_	Alignment		26.6	38	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein af_2093; **PDBTitle:** crystal structure of af2093 from archaeoglobus fulgidus
8	c1irjG_	Alignment		25.8	15	**PDB header:**metal binding protein **Chain:** G: **PDB Molecule:**migration inhibitory factor-related protein 14; **PDBTitle:** crystal structure of the mrp14 complexed with chaps
9	c2w3nA_	Alignment		25.2	24	**PDB header:**lyase **Chain:** A: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** structure and inhibition of the co2-sensing carbonic2 anhydrase can2 from the pathogenic fungus cryptococcus3 neoformans
10	d1x8da1	Alignment		24.3	14	**Fold:**Ferredoxin-like **Superfamily:**Dimeric alpha+beta barrel **Family:**YiiL-like
11	d1avsa_	Alignment		23.4	17	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like

12	c2k7bA_	Alignment		23.2	14	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** nmr structure of mg2+-bound cabp1 n-domain
13	c3l23A_	Alignment		21.6	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of sugar phosphate isomerase/epimerase2 (yp_001303399.1) from parabacteroides distasonis atcc 8503 at 1.70 a3 resolution
14	c3ec8A_	Alignment		18.7	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**putative uncharacterized protein flj10324; **PDBTitle:** the crystal structure of the ra domain of flj10324 (radil)
15	c3obeB_	Alignment		17.9	11	**PDB header:**isomerase **Chain:** B: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_3400)2 from parabacteroides distasonis atcc 8503 at 1.70 a resolution
16	d1xk4a1	Alignment		17.4	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
17	d1ekja_	Alignment		16.6	10	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
18	d1m39a_	Alignment		16.4	20	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
19	d1g5ca_	Alignment		15.8	13	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
20	c2i18A_	Alignment		15.7	9	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calcium-binding protein; **PDBTitle:** the refined structure of c-terminal domain of an ef-hand2 calcium binding protein from entamoeba histolytica
21	c3ot2B_	Alignment	not modelled	14.2	15	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
22	c3ot2A_	Alignment	not modelled	14.2	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** crystal structure of a putative nuclease belonging to duf8202 (ava_3926) from anabaena variabilis atcc 29413 at 1.96 a resolution
23	d1k8ua_	Alignment	not modelled	14.0	31	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
24	d1g33a_	Alignment	not modelled	13.2	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
25	d1j55a_	Alignment	not modelled	12.9	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
26	c3ucoB_	Alignment	not modelled	12.6	15	**PDB header:**lyase/lyase inhibitor **Chain:** B: **PDB Molecule:**carbonic anhydrase; **PDBTitle:** coccomyxa beta-carbonic anhydrase in complex with iodide
27	c2kaxA_	Alignment	not modelled	12.3	23	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein s100-a5; **PDBTitle:** solution structure and dynamics of s100a5 in the apo and2 ca2+ -bound states
28	d1e8aa_	Alignment	not modelled	12.2	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins

29	c2rqsA_	Alignment	not modelled	12.2	15	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**parvulin-like peptidyl-prolyl isomerase; **PDBTitle:** 3d structure of pin from the psychrophilic archeon cenarcheaum2 symbiosum (cspin)
30	d1pvaa_	Alignment	not modelled	11.7	12	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
31	d4icba_	Alignment	not modelled	11.6	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calbindin D9K
32	d1wxaa1	Alignment	not modelled	11.5	6	**Fold:**beta-Grasp (ubiquitin-like) **Superfamily:**Ubiquitin-like **Family:**Ras-binding domain, RBD
33	d1i6pa_	Alignment	not modelled	11.2	14	**Fold:**Resolvase-like **Superfamily:**beta-carbonic anhydrase, cab **Family:**beta-carbonic anhydrase, cab
34	c2rgiA_	Alignment	not modelled	11.1	27	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**protein s100-a2; **PDBTitle:** crystal structure of ca2+-free s100a2 at 1.6 a resolution
35	c2hklB_	Alignment	not modelled	11.1	9	**PDB header:**transferase **Chain:** B: **PDB Molecule:**l,d-transpeptidase; **PDBTitle:** crystal structure of enterococcus faecium l,d-2 transpeptidase c442s mutant
36	c2z4hB_	Alignment	not modelled	11.1	12	**PDB header:**signaling protein activator **Chain:** B: **PDB Molecule:**copper homeostasis protein cutf; **PDBTitle:** crystal structure of the cpx pathway activator nlpe from2 escherichia coli
37	c2ggmA_	Alignment	not modelled	11.0	14	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**centrin-2; **PDBTitle:** human centrin 2 xeroderma pigmentosum group c protein2 complex
38	d1xk4c1	Alignment	not modelled	10.8	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
39	c2a4jA_	Alignment	not modelled	10.6	13	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**centrin 2; **PDBTitle:** solution structure of the c-terminal domain (t94-y172) of2 the human centrin 2 in complex with a 17 residues peptide3 (p1-xpc) from xeroderma pigmentosum group c protein
40	c2k2aA_	Alignment	not modelled	10.4	23	**PDB header:**contractile protein **Chain:** A: **PDB Molecule:**troponin c; **PDBTitle:** solution structure of the apo c terminal domain of lethocerus troponin2 c isoform f1
41	c2b1uA_	Alignment	not modelled	10.3	11	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calmodulin-like protein 5; **PDBTitle:** solution structure of calmodulin-like skin protein c2 terminal domain
42	c2pmyB_	Alignment	not modelled	10.2	24	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**ras and ef-hand domain-containing protein; **PDBTitle:** ef-hand domain of human rasef
43	c2a5vB_	Alignment	not modelled	10.1	11	**PDB header:**lyase **Chain:** B: **PDB Molecule:**carbonic anhydrase (carbonate dehydratase) (carbonic **PDBTitle:** crystal structure of m. tuberculosis beta carbonic anhydrase, rv3588c,2 tetrameric form
44	d1eq3a_	Alignment	not modelled	9.9	5	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
45	c2a8cE_	Alignment	not modelled	9.9	11	**PDB header:**lyase **Chain:** E: **PDB Molecule:**carbonic anhydrase 2; **PDBTitle:** haemophilus influenzae beta-carbonic anhydrase
46	c1ponB_	Alignment	not modelled	9.7	20	**PDB header:**calcium-binding protein **Chain:** B: **PDB Molecule:**troponin c; **PDBTitle:** site iii-site iv troponin c heterodimer, nmr
47	d1c7va_	Alignment	not modelled	9.6	9	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
48	c3p6lA_	Alignment	not modelled	9.5	4	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**sugar phosphate isomerase/epimerase; **PDBTitle:** crystal structure of a sugar phosphate isomerase/epimerase (bdi_1903)2 from parabacteroides distasonis atcc 8503 at 1.85 a resolution
49	c2kz2A_	Alignment	not modelled	9.4	0	**PDB header:**metal binding protein **Chain:** A: **PDB Molecule:**calmodulin; **PDBTitle:** calmodulin, c-terminal domain, f92e mutant
50	d1oqpa_	Alignment	not modelled	9.4	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
51	d1zmba1	Alignment	not modelled	9.4	12	**Fold:**Flavodoxin-like **Superfamily:**SGNH hydrolase **Family:**Putative acetylxylan esterase-like
52	d1a4pa_	Alignment	not modelled	9.3	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
53	d1dj0a_	Alignment	not modelled	9.3	12	**Fold:**Pseudouridine synthase **Superfamily:**Pseudouridine synthase **Family:**Pseudouridine synthase I TruA
54	d1urra_	Alignment	not modelled	9.3	21	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like

55	c2l0vB_	Alignment	not modelled	9.2	15	**PDB header:**metal binding protein **Chain:** B: **PDB Molecule:**protein s100-a16; **PDBTitle:** solution structure of calcium(ii) bound s100a16
56	d1apsa_	Alignment	not modelled	8.9	7	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
57	d2p5zx2	Alignment	not modelled	8.8	12	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
58	c1q88B_	Alignment	not modelled	8.8	11	**PDB header:**dna binding protein **Chain:** B: **PDB Molecule:**39 kda initiator binding protein; **PDBTitle:** crystal structure of the c-domain of the t.vaginalis inr2 binding protein, ibp39 (monoclinic form)
59	d1ksoa_	Alignment	not modelled	8.6	27	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
60	c3h4sE_	Alignment	not modelled	8.6	3	**PDB header:**motor protein/calcium binding protein **Chain:** E: **PDB Molecule:**kcbp interacting ca2+-binding protein; **PDBTitle:** structure of the complex of a mitotic kinesin with its2 calcium binding regulator
61	d2gaxa1	Alignment	not modelled	8.6	19	**Fold:**Peptidyl-tRNA hydrolase II **Superfamily:**Peptidyl-tRNA hydrolase II **Family:**Peptidyl-tRNA hydrolase II
62	d1yuta1	Alignment	not modelled	8.2	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
63	d2pv2a1	Alignment	not modelled	8.2	17	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
64	d1j6ya_	Alignment	not modelled	8.1	9	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
65	c3ddcB_	Alignment	not modelled	8.1	13	**PDB header:**hydrolase/apoptosis **Chain:** B: **PDB Molecule:**ras association domain-containing family protein 5; **PDBTitle:** crystal structure of nore1a in complex with ras
66	d3d37a1	Alignment	not modelled	8.1	17	**Fold:**Phage tail proteins **Superfamily:**Phage tail proteins **Family:**Baseplate protein-like
67	d2pq3a1	Alignment	not modelled	8.1	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
68	d1m45a_	Alignment	not modelled	8.0	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
69	c2p5zX_	Alignment	not modelled	8.0	12	**PDB header:**structural genomics, unknown function **Chain:** X: **PDB Molecule:**type vi secretion system component; **PDBTitle:** the e. coli c3393 protein is a component of the type vi secretion2 system and exhibits structural similarity to t4 bacteriophage tail3 proteins gp27 and gp5
70	d1cb1a_	Alignment	not modelled	8.0	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calbindin D9K
71	d1qlka_	Alignment	not modelled	7.9	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
72	c1bomB_	Alignment	not modelled	7.8	17	**PDB header:**insulin-like brain-secretory peptide **Chain:** B: **PDB Molecule:**bombyxin-ii,bombyxin a-6; **PDBTitle:** three-dimensional structure of bombyxin-ii, an insulin-2 related brain-secretory peptide of the silkmoth bombyx3 mori: comparison with insulin and relaxin
73	d1wrka1	Alignment	not modelled	7.7	10	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
74	d3cr5x1	Alignment	not modelled	7.7	19	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
75	c3ox6C_	Alignment	not modelled	7.6	15	**PDB header:**calcium binding protein **Chain:** C: **PDB Molecule:**calcium-binding protein 1; **PDBTitle:** crystal structure of the calcium sensor calcium-binding protein 12 (cabp1)
76	d1j3ea_	Alignment	not modelled	7.6	24	**Fold:**Replication modulator SeqA, C-terminal DNA-binding domain **Superfamily:**Replication modulator SeqA, C-terminal DNA-binding domain **Family:**Replication modulator SeqA, C-terminal DNA-binding domain
77	d1psra_	Alignment	not modelled	7.5	17	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**S100 proteins
78	c3fs7D_	Alignment	not modelled	7.4	15	**PDB header:**metal binding protein **Chain:** D: **PDB Molecule:**parvalbumin, thymic; **PDBTitle:** crystal structure of gallus gallus beta-parvalbumin (avian2 thymic hormone)
79	c3cnyA_	Alignment	not modelled	7.4	17	**PDB header:**biosynthetic protein **Chain:** A: **PDB Molecule:**inositol catabolism protein iole; **PDBTitle:** crystal structure of a putative inositol catabolism protein iole2 (iole, lp_3607) from lactobacillus plantarum wcfs1 at 1.85 a3 resolution
80	d1qx2a_	Alignment	not modelled	7.4	13	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calbindin D9K

81	c2amiA_	Alignment	not modelled	7.2	16	**PDB header:**cell cycle **Chain:** A: **PDB Molecule:**caltractin; **PDBTitle:** solution structure of the calcium-loaded n-terminal sensor2 domain of centrin
82	c2ktgA_	Alignment	not modelled	7.2	17	**PDB header:**ca-binding protein **Chain:** A: **PDB Molecule:**calmodulin, putative; **PDBTitle:** calmodulin like protein from entamoeba histolytica: solution structure2 and calcium binding properties of a partially folded protein
83	d2obha1	Alignment	not modelled	7.2	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
84	d1zaca_	Alignment	not modelled	7.1	16	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Calmodulin-like
85	c3lmzA_	Alignment	not modelled	7.0	9	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative sugar isomerase; **PDBTitle:** crystal structure of putative sugar isomerase. (yp_001305105.1) from2 parabacteroides distasonis atcc 8503 at 1.44 a resolution
86	d1q88a_	Alignment	not modelled	6.9	13	**Fold:**39 kda initiator binding protein, IBP39, C-terminal domains **Superfamily:**39 kda initiator binding protein, IBP39, C-terminal domains **Family:**39 kda initiator binding protein, IBP39, C-terminal domains
87	d1ftpa_	Alignment	not modelled	6.9	7	**Fold:**Lipocalins **Superfamily:**Lipocalins **Family:**Fatty acid binding protein-like
88	c2vtgA_	Alignment	not modelled	6.9	7	**PDB header:**metal-binding protein **Chain:** A: **PDB Molecule:**ionized calcium-binding adapter molecule 2; **PDBTitle:** crystal structure of human iba2, trigonal crystal form
89	d2acya_	Alignment	not modelled	6.8	10	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
90	d1m5ya3	Alignment	not modelled	6.8	9	**Fold:**FKBP-like **Superfamily:**FKBP-like **Family:**FKBP immunophilin/proline isomerase
91	c3br8A_	Alignment	not modelled	6.8	10	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**probable acylphosphatase; **PDBTitle:** crystal structure of acylphosphatase from bacillus subtilis
92	c3ngfA_	Alignment	not modelled	6.7	18	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ap endonuclease, family 2; **PDBTitle:** crystal structure of ap endonuclease, family 2 from brucella2 melitensis
93	c2kdhA_	Alignment	not modelled	6.6	11	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** the solution structure of human cardiac troponin c in2 complex with the green tea polyphenol; (-)-3 epigallocatechin-3-gallate
94	d1w2ia_	Alignment	not modelled	6.6	21	**Fold:**Ferredoxin-like **Superfamily:**Acylphosphatase/BLUF domain-like **Family:**Acylphosphatase-like
95	d5pala_	Alignment	not modelled	6.5	15	**Fold:**EF Hand-like **Superfamily:**EF-hand **Family:**Parvalbumin
96	c1yw5A_	Alignment	not modelled	6.5	8	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**peptidyl prolyl cis/trans isomerase; **PDBTitle:** peptidyl-prolyl isomerase ess1 from candida albicans
97	c2dk6A_	Alignment	not modelled	6.5	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**parp11 protein; **PDBTitle:** solution structure of wwe domain in poly (adp-ribose)2 polymerase family, member 11 (parp 11)
98	c3cu2A_	Alignment	not modelled	6.4	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**ribulose-5-phosphate 3-epimerase; **PDBTitle:** crystal structure of ribulose-5-phosphate 3-epimerase (yp_718263.1)2 from haemophilus somnus 129pt at 1.91 a resolution
99	c1ozsA_	Alignment	not modelled	6.4	9	**PDB header:**structural protein **Chain:** A: **PDB Molecule:**troponin c, slow skeletal and cardiac muscles; **PDBTitle:** c-domain of human cardiac troponin c in complex with the2 inhibitory region of human cardiac troponin i