Phyre^2

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Description	P0ADK6
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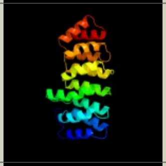
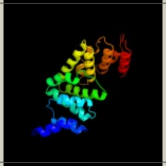
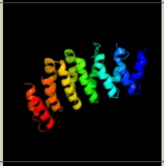
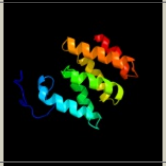
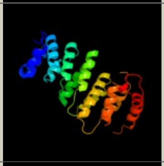
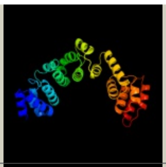
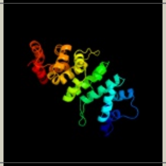
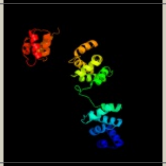
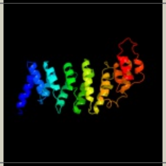
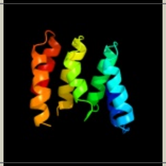
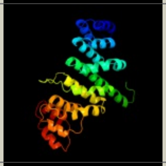
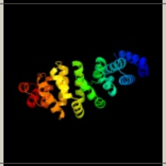
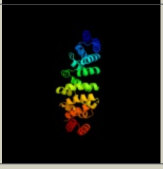
Detailed template information

#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1oyza_	Alignment		100.0	99	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**PBS lyase HEAT-like repeat
2	c3ltjA_	Alignment		99.9	24	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**alpharep-4; **PDBTitle:** structure of a new family of artificial alpha helicoidal repeat2 proteins (alpha-rep) based on thermostable heat-like repeats
3	c2db0B_	Alignment		99.7	17	**PDB header:**protein binding **Chain:** B: **PDB Molecule:**253aa long hypothetical protein; **PDBTitle:** crystal structure of ph0542
4	d1gw5b_	Alignment		99.7	13	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Clathrin adaptor core protein
5	c3c5wA_	Alignment		99.6	17	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**pp2a a subunit; **PDBTitle:** complex between pp2a-specific methylesterase pme-1 and pp2a core2 enzyme
6	c3l6yA_	Alignment		99.5	11	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**catenin delta-1; **PDBTitle:** crystal structure of p120 catenin in complex with e-cadherin
7	d1te4a_	Alignment		99.5	17	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**PBS lyase HEAT-like repeat
8	c3b2aA_	Alignment		99.5	11	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the archaeal heat-like repeats protein ton_19372 from thermococcus onnurineus na1
9	c3l9tA_	Alignment		99.5	16	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**putative uncharacterized protein smu.31; **PDBTitle:** the crystal structure of smu.31 from streptococcus mutans ua159
10	c1w63A_	Alignment		99.4	13	**PDB header:**endocytosis **Chain:** A: **PDB Molecule:**adapter-related protein complex 1 gamma 1 **PDBTitle:** ap1 clathrin adaptor core
11	d1lrva_	Alignment		99.4	25	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Leucine-rich repeat variant

12	c2jkrL_	Alignment		99.2	10	**PDB header:**endocytosis **Chain:** L: **PDB Molecule:**ap-2 complex subunit alpha-2; **PDBTitle:** ap2 clathrin adaptor core with dileucine peptide rm(2 phosphos)qikrllse
13	c3nmwA_	Alignment		99.1	13	**PDB header:**cell adhesion/cell cycle **Chain:** A: **PDB Molecule:**apc variant protein; **PDBTitle:** crytal structure of armadillo repeats domain of apc
14	d1v18a1	Alignment		99.1	12	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
15	d1xm9a1	Alignment		99.1	10	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Plakophilin 1 helical region
16	d1u6gc_	Alignment		99.0	14	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**HEAT repeat
17	d1b3ua_	Alignment		99.0	14	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**HEAT repeat
18	c1m5nS_	Alignment		99.0	10	**PDB header:**protein transport **Chain:** S: **PDB Molecule:**importin beta-1 subunit; **PDBTitle:** crystal structure of heat repeats (1-11) of importin b2 bound to the non-classical nls(67-94) of pthrp
19	c3ifqB_	Alignment		98.9	14	**PDB header:**cell adhesion **Chain:** B: **PDB Molecule:**plakoglobin; **PDBTitle:** interction of plakoglobin and beta-catenin with desmosomal2 cadherins
20	d1jdha_	Alignment		98.9	14	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
21	c3nowA_	Alignment	not modelled	98.9	17	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**unc-45 protein, sd10334p; **PDBTitle:** unc-45 from drosophila melanogaster
22	c2z6hA_	Alignment	not modelled	98.9	15	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**catenin beta-1; **PDBTitle:** crystal structure of beta-catenin armadillo repeat region2 and its c-terminal domain
23	c4a0cB_	Alignment	not modelled	98.8	16	**PDB header:**cell cycle **Chain:** B: **PDB Molecule:**cullin-associated nedd8-dissociated protein 1; **PDBTitle:** structure of the cand1-cul4b-rbx1 complex
24	d1lsha1	Alignment	not modelled	98.7	11	**Fold:**alpha-alpha superhelix **Superfamily:**Lipovitellin-phosvitin complex, superhelical domain **Family:**Lipovitellin-phosvitin complex, superhelical domain
25	c2z6gA_	Alignment	not modelled	98.7	13	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**b-catenin; **PDBTitle:** crystal structure of a full-length zebrafish beta-catenin
26	d1ibrb_	Alignment	not modelled	98.6	11	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
27	d1ee4a_	Alignment	not modelled	98.6	17	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
28	c3gq2B_	Alignment	not modelled	98.5	14	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**general vesicular transport factor p115; **PDBTitle:** crystal structure of the dimer of the p115 tether globular head domain
						Fold:alpha-alpha superhelix

29	d1q1sc_	Alignment	not modelled	98.5	16	**Superfamily:**ARM repeat **Family:**Armadillo repeat
30	c2w3cA_	Alignment	not modelled	98.5	9	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**general vesicular transport factor p115; **PDBTitle:** globular head region of the human general vesicular2 transport factor p115
31	c1pjmB_	Alignment	not modelled	98.4	16	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**importin alpha-2 subunit; **PDBTitle:** mouse importin alpha-bipartite nls from human2 retinoblastoma protein complex
32	c3bctA_	Alignment	not modelled	98.3	11	**PDB header:**armadillo repeat **Chain:** A: **PDB Molecule:**beta-catenin; **PDBTitle:** the armadillo repeat region from murine beta-catenin
33	c3t7uA_	Alignment	not modelled	98.2	14	**PDB header:**cell adhesion **Chain:** A: **PDB Molecule:**adenomatous polyposis coli protein; **PDBTitle:** a new crytal structure of apc-arm
34	c2qnaA_	Alignment	not modelled	98.2	11	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**importin subunit beta-1; **PDBTitle:** crystal structure of human importin-beta (127-876) in complex with the2 ibb-domain of snurportin1 (1-65)
35	c2c1tA_	Alignment	not modelled	98.2	17	**PDB header:**protein transport/membrane protein **Chain:** A: **PDB Molecule:**importin alpha subunit; **PDBTitle:** structure of the kap60p:nup2 complex
36	c2ot8B_	Alignment	not modelled	98.2	15	**PDB header:**transport protein **Chain:** B: **PDB Molecule:**transportin-1; **PDBTitle:** karyopherin beta2/transportin-hnrnpm nls complex
37	c1xqrA_	Alignment	not modelled	98.1	13	**PDB header:**chaperone **Chain:** A: **PDB Molecule:**hspbp1 protein; **PDBTitle:** crystal structure of the hspbp1 core domain
38	c2jdqB_	Alignment	not modelled	98.1	15	**PDB header:**protein transport **Chain:** B: **PDB Molecule:**importin alpha-1 subunit; **PDBTitle:** c-terminal domain of influenza a virus polymerase pb22 subunit in complex with human importin alpha5
39	c1lshA_	Alignment	not modelled	98.1	10	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**lipovitellin (lv-1n, lv-1c); **PDBTitle:** lipid-protein interactions in lipovitellin
40	d1xqra1	Alignment	not modelled	98.1	13	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**HspBP1 domain
41	c3nmzB_	Alignment	not modelled	98.0	10	**PDB header:**cell adhesion/cell cycle **Chain:** B: **PDB Molecule:**apc variant protein; **PDBTitle:** crytal structure of apc complexed with asef
42	c2of3A_	Alignment	not modelled	98.0	13	**PDB header:**structural protein, cell cycle **Chain:** A: **PDB Molecule:**zyg-9; **PDBTitle:** tog domain structure from c.elegans zyg9
43	c2qk2A_	Alignment	not modelled	98.0	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**lp04448p; **PDBTitle:** structural basis of microtubule plus end tracking by xmap215, clip-1702 and eb1
44	c2qk1A_	Alignment	not modelled	97.8	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**protein stu2; **PDBTitle:** structural basis of microtubule plus end tracking by2 xmap215, clip-170 and eb1
45	c1wa5B_	Alignment	not modelled	97.5	14	**PDB header:**nuclear transport **Chain:** B: **PDB Molecule:**importin alpha subunit; **PDBTitle:** crystal structure of the exportin cse1p complexed with its2 cargo (kap60p) and rangtp
46	d1wa5b_	Alignment	not modelled	97.5	14	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
47	d1qbkb_	Alignment	not modelled	97.3	12	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
48	c3oqsA_	Alignment	not modelled	97.2	12	**PDB header:**protein transport **Chain:** A: **PDB Molecule:**importin subunit alpha-2; **PDBTitle:** crystal structure of importin-alpha bound to a clic4 nls peptide
49	c3oc3B_	Alignment	not modelled	97.0	12	**PDB header:**hydrolase/transcription **Chain:** B: **PDB Molecule:**helicase mot1; **PDBTitle:** crystal structure of the mot1 n-terminal domain in complex with tbp
50	d1qgra_	Alignment	not modelled	94.3	11	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
51	d2bpta1	Alignment	not modelled	94.2	11	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
52	d2i9ca1	Alignment	not modelled	91.5	16	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**RPA1889-like
53	c2wxoA_	Alignment	not modelled	90.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** the crystal structure of the murine class ia pi 3-kinase2 p110delta in complex with as5.
54	c3opbA_	Alignment	not modelled	87.6	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**swi5-dependent ho expression protein 4; **PDBTitle:** crystal structure of she4p
55	c2y3aA_	Alignment	not modelled	85.8	14	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** crystal structure of p110beta in complex with icsh2 of

						p85beta and2 the drug gdc-0941
56	c2rd0A_	Alignment	not modelled	84.9	12	**PDB header:**transferase/oncoprotein **Chain:** A: **PDB Molecule:**phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic **PDBTitle:** structure of a human p110alpha/p85alpha complex
57	d1ho8a_	Alignment	not modelled	83.3	7	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Regulatory subunit H of the V-type ATPase
58	d1e7ua1	Alignment	not modelled	82.8	17	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Phoshoinositide 3-kinase (PI3K) helical domain
59	c1e8zA_	Alignment	not modelled	80.9	18	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase catalytic subunit; **PDBTitle:** structure determinants of phosphoinositide 3-kinase2 inhibition by wortmannin, ly294002, quercetin, myricetin3 and staurosporine
60	c2l1lB_	Alignment	not modelled	80.6	14	**PDB header:**nuclear protein **Chain:** B: **PDB Molecule:**exportin-1; **PDBTitle:** nmr solution structure of the phi0 pki nes peptide in complex with2 crm1-rangtp
61	c3o2qD_	Alignment	not modelled	76.8	12	**PDB header:**hydrolase **Chain:** D: **PDB Molecule:**symplekin; **PDBTitle:** crystal structure of the human symplekin-ssu72-ctd phosphopeptide2 complex
62	c3odsA_	Alignment	not modelled	75.9	14	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**symplekin; **PDBTitle:** crystal structure of the k185a mutant of the n-terminal domain of2 human symplekin
63	c3o2tA_	Alignment	not modelled	75.4	12	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**symplekin; **PDBTitle:** crystal structure of the n-terminal domain of human symplekin
64	c3odrA_	Alignment	not modelled	62.3	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**symplekin; **PDBTitle:** crystal structure of the n-terminal domain of human symplekin
65	d2b6ca1	Alignment	not modelled	59.0	12	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**BC3264-like
66	d1wa5c_	Alignment	not modelled	51.7	12	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Armadillo repeat
67	c2iw3B_	Alignment	not modelled	47.6	10	**PDB header:**translation **Chain:** B: **PDB Molecule:**elongation factor 3a; **PDBTitle:** elongation factor 3 in complex with adp
68	c1vsy5_	Alignment	not modelled	44.9	17	**PDB header:**hydrolase **Chain:** 5: **PDB Molecule:**proteasome activator blm10; **PDBTitle:** proteasome activator complex
69	d1z3xa1	Alignment	not modelled	38.3	18	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**GUN4-associated domain
70	c3gs3A_	Alignment	not modelled	34.8	15	**PDB header:**transcription, protein binding **Chain:** A: **PDB Molecule:**symplekin; **PDBTitle:** structure of the n-terminal heat domain of symplekin from d.2 melanogaster
71	d1t06a_	Alignment	not modelled	33.4	9	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**BC3264-like
72	c2x6kB_	Alignment	not modelled	33.3	10	**PDB header:**transferase **Chain:** B: **PDB Molecule:**phosphotidylinositol 3 kinase 59f; **PDBTitle:** the crystal structure of the drosophila class iii pi3-kinase2 vps34 in complex with pi-103
73	d1l5ja1	Alignment	not modelled	28.1	24	**Fold:**alpha-alpha superhelix **Superfamily:**Aconitase B, N-terminal domain **Family:**Aconitase B, N-terminal domain
74	c3ls8A_	Alignment	not modelled	24.2	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**phosphatidylinositol 3-kinase catalytic subunit **PDBTitle:** crystal structure of human pik3c3 in complex with 3-[4-(4-2 morpholinyl)thieno[3,2-d]pyrimidin-2-yl]-phenol
75	c3m1iC_	Alignment	not modelled	22.2	15	**PDB header:**protein transport **Chain:** C: **PDB Molecule:**exportin-1; **PDBTitle:** crystal structure of yeast crm1 (xpo1p) in complex with yeast ranbp12 (yrb1p) and yeast rangtp (gsp1pgtp)
76	d2p7vb1	Alignment	not modelled	16.7	15	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain
77	c1dvpA_	Alignment	not modelled	16.2	10	**PDB header:**transferase **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine **PDBTitle:** crystal structure of the vhs and fyve tandem domains of hrs,2 a protein involved in membrane trafficking and signal3 transduction
78	c2l7kA_	Alignment	not modelled	12.9	14	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution nmr structure of protein cd1104.2 from clostridium difficile,2 northeast structural genomics consortium target cfr130
79	c3zyqA_	Alignment	not modelled	12.8	13	**PDB header:**signaling **Chain:** A: **PDB Molecule:**hepatocyte growth factor-regulated tyrosine kinase **PDBTitle:** crystal structure of the tandem vhs and fyve domains of hepatocyte2 growth factor-regulated tyrosine kinase substrate (hgs-hrs) at 1.483 a resolution

80	c3ibvB_	Alignment	not modelled	10.6	12	**PDB header:**rna binding protein **Chain:** B: **PDB Molecule:**exportin-t; **PDBTitle:** karyopherin cytosolic state
81	d1upka_	Alignment	not modelled	10.5	19	**Fold:**alpha-alpha superhelix **Superfamily:**ARM repeat **Family:**Mo25 protein
82	c3gjxD_	Alignment	not modelled	9.9	21	**PDB header:**protein transport **Chain:** D: **PDB Molecule:**exportin-1; **PDBTitle:** crystal structure of the nuclear export complex crm1-2 snurportin1-rangtp
83	d1x3zb1	Alignment	not modelled	9.9	12	**Fold:**XPC-binding domain **Superfamily:**XPC-binding domain **Family:**XPC-binding domain
84	c1x4qA_	Alignment	not modelled	7.3	11	**PDB header:**rna binding protein **Chain:** A: **PDB Molecule:**u4/u6 small nuclear ribonucleoprotein prp3; **PDBTitle:** solution structure of pwi domain in u4/u6 small nuclear2 ribonucleoprotein prp3(hprp3)
85	c2qsgX_	Alignment	not modelled	6.6	12	**PDB header:**dna binding protein/dna **Chain:** X: **PDB Molecule:**uv excision repair protein rad23; **PDBTitle:** crystal structure of rad4-rad23 bound to a uv-damaged dna
86	c2x19B_	Alignment	not modelled	6.5	11	**PDB header:**nuclear transport **Chain:** B: **PDB Molecule:**importin-13; **PDBTitle:** crystal structure of importin13 - rangtp complex
87	c1l5jB_	Alignment	not modelled	6.1	23	**PDB header:**lyase **Chain:** B: **PDB Molecule:**aconitate hydratase 2; **PDBTitle:** crystal structure of e. coli aconitase b.
88	c3bvsA_	Alignment	not modelled	5.9	12	**PDB header:**hydrolase **Chain:** A: **PDB Molecule:**alkylpurine dna glycosylase alkd; **PDBTitle:** crystal structure of bacillus cereus alkylpurine dna glycosylase alkd
89	c1x5bA_	Alignment	not modelled	5.9	13	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**signal transducing adaptor molecule 2; **PDBTitle:** the solution structure of the vhs domain of human signal2 transducing adaptor molecule 2
90	d1dvpa1	Alignment	not modelled	5.5	10	**Fold:**alpha-alpha superhelix **Superfamily:**ENTH/VHS domain **Family:**VHS domain
91	d1bvsa1	Alignment	not modelled	5.4	23	**Fold:**RuvA C-terminal domain-like **Superfamily:**DNA helicase RuvA subunit, C-terminal domain **Family:**DNA helicase RuvA subunit, C-terminal domain
92	d1ttya_	Alignment	not modelled	5.1	8	**Fold:**DNA/RNA-binding 3-helical bundle **Superfamily:**Sigma3 and sigma4 domains of RNA polymerase sigma factors **Family:**Sigma4 domain