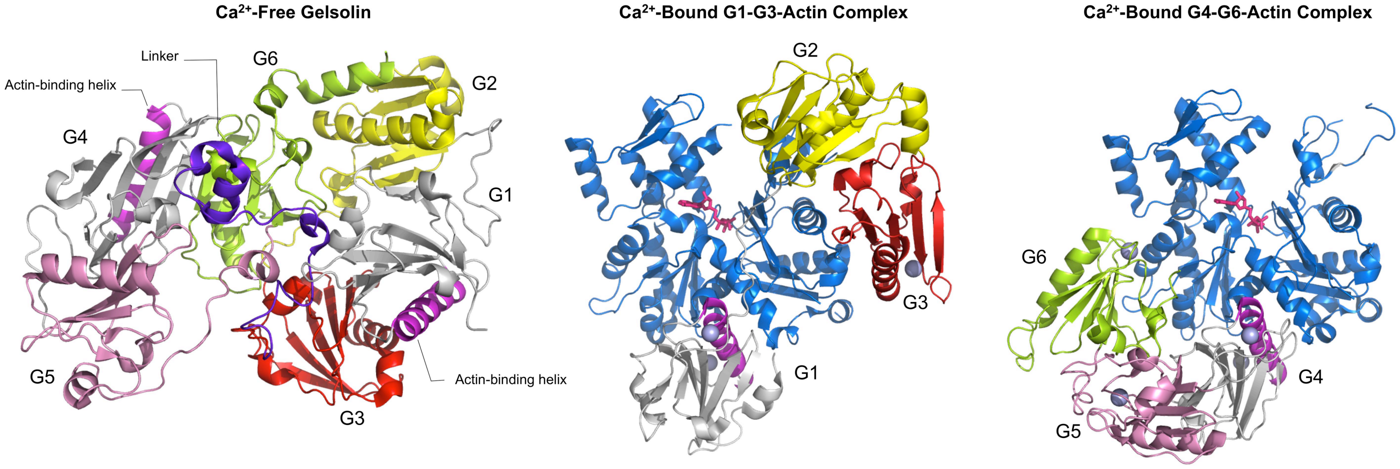
## Supplementary Figure 1

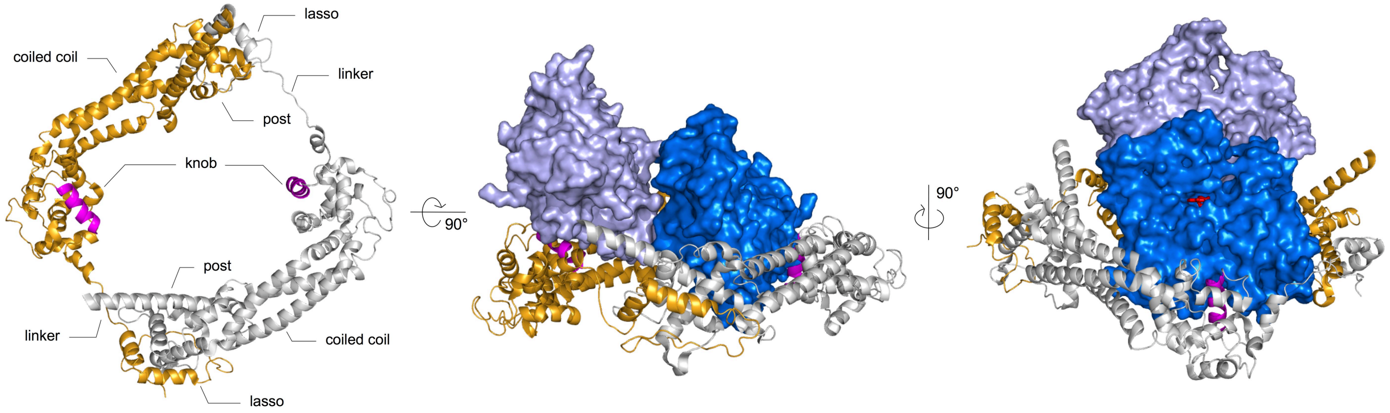

Ca²⁺-Free Gelsolin

Ca²⁺-Bound G1-G3-Actin Complex

Ca²⁺-Bound G4-G6-Actin Complex

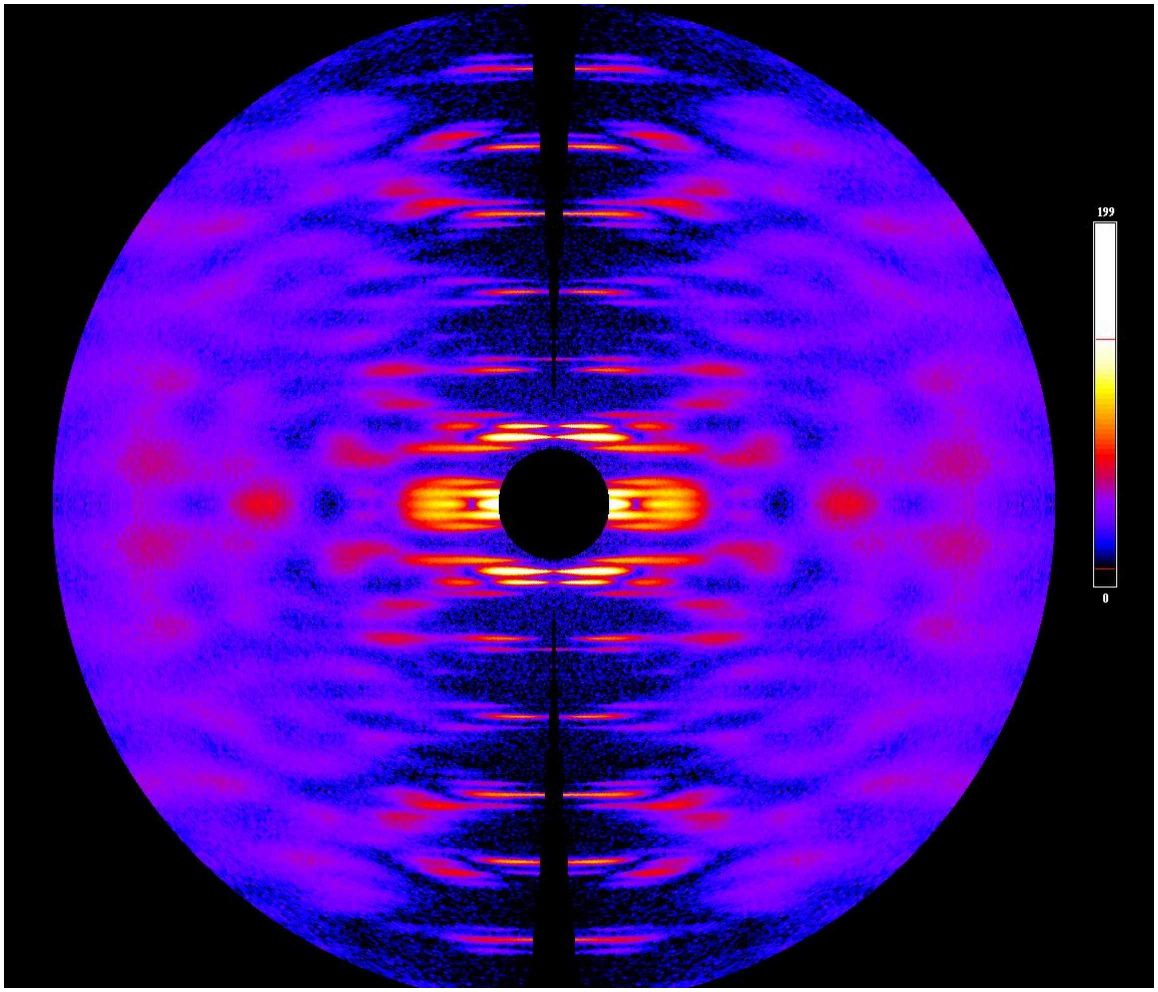
**Supplementary Figure 1.** Structures of gelsolin and gelsolin-actin complexes. The left diagram shows the structure of full-length $Ca^{2+}$-free gelsolin (PDB code 1D0N). Gelsolin consists of six homologous subdomains named G1 to G6. The structure shows the inactive, $Ca^{2+}$-free state of gelsolin, in which it adopts a compact conformation stabilized by intra-molecular interactions of its various domains. In this conformation, the actin-binding sites are masked. The diagrams in the middle and the right show complexes of actin with $Ca^{2+}$-bound gelsolin fragments G1-G3 (PDB code 1RGI) and G4-G6 (PDB code 1H1V), respectively. Domains G1 and G4 contain the two major actin binding sites. These domains bind similarly to actin, inserting a helix in the target-binding cleft of actin.

## Supplementary Figure 2



**Supplementary Figure 2.** Structure of the formin FH2 domain in complex with actin (PDB code 1Y64) (38). From left to right, the figure shows the crystallographic (related by a two-fold screw dyad axis) FH2 dimer, obtained after domain swapping the ‘lasso’ region from the lower subunit, and two orientations of the crystallographic FH2-actin dimer (actin subunits shown in blue and gray). Each FH2 domain is structurally subdivided into lasso, linker, knob, coiled coil, and post regions. A helix from the FH2 knob region inserts into the target-binding cleft of actin (magenta).

## Supplementary Figure 3



**Supplementary Figure 3.** An X-ray fiber diffraction pattern (false colors: blue low, red middle, white high intensity) from an orientated gel of F-actin, where the orientation has been improved by immersing it in an 18 Tesla magnetic field (ref 35 in main and 41 below). Note the very well orientated-layer lines.

# TABLE 1

## Structures of Actin and Arps listed in order of deposition and by species (August 31, 2010)

| Entry | Res. (Å) | Description | Reference |
|---|---|---|---|
| **α-skeletal actin** | | | |
| 1ATN | 2.80 | Complex with DNase I | (21) |
| 1EQY | 2.30 | Complex with Gelsolin G1 | (32) |
| 1ESV | 2.00 | Complex with Gelsolin G1 and Latrunculin A | (33) |
| 1H1V | 3.00 | Complex with Gelsolin G4-G6 | (10) |
| 1IJJ | 2.85 | Complex with Polylysine and Latrunculin A | (6) |
| 1J6Z | 1.54 | Uncomplexed TMR-actin in ADP state | (43) |
| 1KXP | 2.10 | Complex with vitamin D-binding protein (DBP) | (44) |
| 1LCU | 3.50 | Complex with Polylysine and Latrunculin A | (6) |
| 1LOT | 2.50 | Complex with Vitamin D-Binding Protein (DBP) | (16) |
| 1MA9 | 2.40 | Complex with Vitamin D-Binding Protein (DBP) | (54) |
| 1NWK | 1.85 | Uncomplexed TMR-actin with bound AMPPNP | (14) |
| 1P8Z | 2.60 | Complex with Gelsolin G1 and G1-G2 linker | (19) |
| 1QZ5 | 1.45 | Complex with marine macrolide Kabiramide C | (22) |
| 1QZ6 | 1.60 | Complex with marine macrolide Jaspisamide A | (22) |
| 1RDW | 2.30 | Complex with Latrunculin A | (47) |
| 1RFQ | 3.00 | Complex with Latrunculin A | (47) |
| 1RGI | 3.00 | Complex with Gelsolin G1-G3 | (7) |
| 1S22 | 1.60 | Complex with marine macrolide Ulapualide A | (2) |
| 1SQK | 2.50 | Complex with Ciboulot and Latrunculin A | (17) |
| 1T44 | 2.00 | Complex with hybrid protein Gelsolin(28-152)-Tβ4(153-171) | (20) |
| 1WUA | 1.45 | Complex with marine macrolide Aplyronine A | (18) |
| 1Y64 | 3.05 | Complex with Formin Homology 2 (FH2) domain | (42) |
| 1YXQ | 2.01 | Complex with marine macrolide Swinholide A | (23) |
| 2A3Z | 2.08 | Complex with DNase I and WH2 domain of WASP | (8) |
| 2A40 | 1.80 | Complex with DNase I and WH2 domain of WAVE | (8) |
| 2A41 | 2.60 | Complex with DNase I and WH2 domain of WIP | (8) |
| 2A42 | 1.85 | Complex with DNase I | (8) |
| 2A5X | 2.49 | Longitudinally cross-linked actin dimer | (25) |
| 2ASM | 1.60 | Complex with marine macrolide Reidispongiolide A | (3) |
| 2ASO | 1.70 | Complex with marine macrolide Sphinxolide B | (3) |
| 2ASP | 1.64 | Complex with marine macrolide Reidispongiolide A | (3) |
| 2D1K | 2.50 | Complex with DNase I and WH2 domain of MIM | (29) |
| 2FF3 | 2.00 | Complex with hybrid protein Gelsolin-WASP | (1) |
| 2FF6 | 2.05 | Complex with hybrid protein Gelsolin-Ciboulot | (1) |
| 2FXU | 1.35 | Complex with marine macrolide Bistramide A | (48) |
| 2GWJ | 1.90 | ADP-ribosylated at Arg177 by Salmonella SpvB protein | (30) |
| 2GWK | 2.00 | ADP-ribosylated at Arg177 by Salmonella SpvB protein | (30) |
| 2HMP | 1.90 | Cleaved between Gly42 and Val43 by ECP32 protease | (24) |
| 2PAV | 1.80 | Complex with Profilin and last Pro-rich motif of VASP | (13) |
| 2PBD | 1.50 | Complex with Profilin and Pro-rich-GAB domains of VASP | (13) |
| 2Q0R | 1.70 | Complex with marine macrolide Pectenotoxin-2 | (4) |
| 2Q0U | 1.45 | Complex with marine macrolide Pectenotoxin-2 and LatB | (4) |
| 2Q1N | 2.70 | Longitudinally cross-linked actin dimer | (51) |
| 2Q31 | 2.70 | Longitudinally cross-linked actin dimer | (51) |
| 2Q36 | 2.50 | Laterally cross-linked actin dimer complexed with Kabiramide C | (51) |
| 2Q97 | 2.50 | Complex with Toxofilin from *Toxoplasma gondii* | (28) |
| 2V51 | 2.35 | Complex with RPEL-1 from serum response factor coactivator MAL | (34) |

|  |  |  |  |
|---|---|---|---|
| 2V52 | 1.45 | Complex with RPEL-2 from serum response factor coactivator MAL | (34) |
| 2VCP | 3.20 | Complex with N-WASP WH2 Domain | TBP |
| 2VYP | 2.35 | Complex with macrolide rhizopodin from Myxobacteria | (15) |
| 3BUZ | 2.81 | Complex with *Clostridium perfringens* ADP-ribosylating iota-toxin | (53) |
| 3CJB | 3.21 | Glu270-Lys50 RTX toxin cross-linked complex with Gelsolin G1 | (26) |
| 3CJC | 3.90 | RTX toxin cross-linked complex with Gelsolin G1 and DNase I | (26) |
| 3DAW | 2.55 | Complex with Twinfilin(167-322) C-terminal ADF-homology domain | (45) |
| 3FFK | 3.00 | Complex with $Ca^{2+}$-bound Gelsolin G1-G3 | (35) |
| 3HBT | 2.70 | Monomeric actin crystallized alone in the presence of Hsp27 | (56) |
| 3MN5 | 1.50 | Complex with WH2 domain of Spire | (12) |
| 3M1F | 2.89 | Complex with cross-linked WH2 domain from VopL | (46) |
| 3M3N | 7.00 | Longitudinal Actin Dimer Assembled by Tandem W Domains | (46) |
| 1MDU | 2.20 | Cross-linked trimer of chicken α-skeletal actin complexed with G1 | (11) |
| **β-actin** |  |  |  |
| 2BTF | 2.55 | Complex with Profilin (original structure) | (52) |
| 1HLU | 2.65 | Complex with Profilin (open state obtained by crystal manipulation) | (9) |
| 2OAN | 2.61 | Oxidized, Cys374-Cys374 cross-linked, antiparallel dimer | (27) |
| ***Dictyostelium* actin** |  |  |  |
| 1C0F | 2.40 | Complex with Gelsolin G1 | (31) |
| 1C0G | 2.00 | *Dictyostelium* actin mutant in complex with Gelsolin G1 | (31) |
| 1DEJ | 2.40 | *Dictyostelium* actin mutant in complex with Gelsolin G1 | (31) |
| 1NLV | 1.80 | Complex with Gelsolin G1 ($Ca^{2+}$-ATP) | (55) |
| 1NM1 | 1.80 | Complex with Gelsolin G1 ($Mg^{2+}$-ATP) | (55) |
| 1NMD | 1.90 | Complex with Gelsolin G1 (Lithium ATP) | (55) |
| 3CHW | 2.30 | Complex with Profilin and Last Pro-rich motif of VASP | (5) |
| 3CI5 | 1.70 | Tyr53 phosphorylated in complex with Gelsolin G1 | (5) |
| 3CIP | 1.60 | Complex with Gelsolin G1 | (5) |
| **Yeast actin** |  |  |  |
| 1YAG | 1.90 | Complex with Gelsolin G1 | (55) |
| 1YVN | 2.10 | Val159Asn mutant complexed with Gelsolin G1 | TBP |
| ***Drosophila melanogaster* (Fruit fly)** |  |  |  |
| 2HF3 | 1.80 | Subdomain 4 double-mutant (Ala204Glu Pro243Lys) in ADP state | (50) |
| 2HF4 | 1.80 | Subdomain 4 double-mutant (Ala204Glu Pro243Lys) in ATP state | (50) |
| 3EKS | 1.80 | Ala204Glu, Pro243Lys mutant complex cytochalasin D | (36) |
| 3EKU | 2.50 | Ala204Glu, Pro243Lys mutant with cytochalasin D (soaked) | (36) |
| 3EL2 | 2.50 | Ala204Glu, Pro243Lys mutant with cytochalasin D | (36) |
| 3MMV | 2.80 | Ala204Glu, Pro243Lys mutant complex with WH2 domain of Spire | (12) |
| 3MN6 | 2.00 | Ala204Glu, Pro243Lys mutant complex with WH2 domain of Spire | (12) |
| 3MN7 | 2.00 | Ala204Glu, Pro243Lys mutant complex with WH2 domain of Spire | (12) |
| 3MN9 | 2.00 | Ala204Glu, Pro243Lys mutant complex with WH2 domain of Spire | (12) |
| ***Caenorhabditis elegans* actin** |  |  |  |
| 1D4X | 1.75 | Complex with Gelsolin G1 | (55) |
| **Arps** |  |  |  |
| 1K8K | 2.00 | Arp2/3 complex (nucleotide free Arps) | (49) |
| 1TYQ | 2.55 | Arp2/3 complex ($Ca^{2+}$-ATP Arps) | (37) |
| 1U2V | 2.55 | Arp2/3 complex ($Ca^{2+}$-ADP Arps) | (37) |
| 2P9I | 2.46 | Arp2/3 complex ($Ca^{2+}$-ADP Arps, gluteraldehyde crosslinked) | (38) |
| 2P9K | 2.59 | Arp2/3 complex ($Ca^{2+}$-ATP Arps, gluteraldehyde crosslinked) | (38) |
| 2P9L | 2.65 | Arp2/3 complex (nucleotide free Arps) | (38) |
| 2P9N | 2.85 | Arp2/3 complex ($Ca^{2+}$-ADP Arps) | (38) |

| | | | |
|---|---|---|---|
| 2P9P | 2.90 | Arp2/3 complex (Ca$^{2+}$-ADP Arps) | (38) |
| 2P9S | 2.68 | Arp2/3 complex (Mg$^{2+}$-ATP Arps) | (38) |
| 2P9U | 2.75 | Arp2/3 complex (Mg$^{2+}$-ANP Arps) | (38) |
| 3DXK | 2.70 | Arp2/3 Complex with bound inhibitor CK0944636 | (40) |
| 3DXM | 2.85 | Arp2/3 Complex with bound inhibitor CK0993548 | (40) |
| 3DWL | 3.78 | Yeast Arp2/3 complex lacking subunit Arp2 | (39) |

TBP – To be published

Different background colors indicate complexes with different protein domains or macrolides. A white background indicates structures that do not fall into any of these categories.

DNase I
Gelsolin
Profilin
Iota toxin
WH2/Tβ4 domain
RPEL-1 domain
ADF-homology domain
Vitamin D-binding protein (DBP)
Toxofilin
Formin Homology 2 (FH2) domain
Marine macrolides

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