

Publication

Actin's propensity for dynamic filament patterning

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ID 1421838 Author(s) Schoenenberger, Cora-Ann; Bischler, Nicolas; Fahrenkrog, Birthe; Aebi, Ueli Author(s) at UniBasel Schönenberger, Cora-Ann; Fahrenkrog, Birthe; Year 2002 Title Actin's propensity for dynamic filament patterning Journal FEBS letters Volume 529 Number 1 Pages / Article-Number 27-33 Keywords actin, branching, bundling, dimer, nucleus

Actin, through its various forms of assembly, provides the basic framework for cell motility, cell shape and intracellular organization in all eukaryotic cells. Many other cellular processes, for example endocytosis and cytokinesis, are also associated with dynamic changes of the actin cytoskeleton. Important prerequisites for actin's functional diversity are its intrinsic ability to rapidly assemble and disassemble filaments and its spatially and temporally well-controlled supramolecular organization. A large number of proteins that interact with actin, collectively referred to as actin-binding proteins (ABPs), carefully orchestrate different scenarios. Since its isolation in 1994 [Machesky, L.M. et al. (1994) J. Cell Biol. 127, 107-115], the Arp2/3 complex containing the actin-related proteins Arp2 and Arp3 has evolved to be one of the main players in the assembly and maintenance of many actin-based structures in the cell (for review see [Borths, E.L. and Welch, M.D. (2002) Structure 10, 131-135; May, R.C. (2001) Cell Mol. Life Sci. 58, 1607-1626; Pollard, T.D. et al. (2000) Rev. Biophys. Biomol. Struct. 29, 545-576; Welch, M.D. (1999) Trends Cell Biol. 11, 423-427]). In particular, when it comes to the assembly of the intricate branched actin network at the leading edge of lamellipodia, the Arp2/3 complex seems to have received all the attention in recent years. In parallel, but not so much in the spotlight, several reports showed that actin on its own can assume different conformations [Bubb, M.R. et al. (2002) J. Biol. Chem. 277, 20999-21006; Schoenenberger, C.-A. et al. (1999) Microsc. Res. Tech. 47, 38-50; Steinmetz, M.O. et al. (1998) J. Mol. Biol. 278, 793-811; Steinmetz, M.O. et al. (1997) J. Cell Biol. 138, 559-574; Millonig, R., Salvo, H. and Aebi, U. (1988) J. Cell Biol. 106, 785-796] through which it drives its supramolecular patterning, and which ultimately generate its functional diversity.

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