

Publication list - STEFAN RAUNSER

PUBLICATION LIST – STEFAN RAUNSER – October 2024

1. Boiero Sanders M, Oosterheert W, Hofnagel O, Bieling P, Raunser S (2024) Phalloidin and DNase I-bound F-actin pointed end structures reveal principles of filament stabilization and disassembly Nat Commun. 2024 Sep 11;15(1):7969. doi: 10.1038/s41467-024-52251-3. PMID: 39261469.
2. Oosterheert W, Boiero Sanders M, Funk J, Prumbaum D, Raunser S, Bieling P (2024) Molecular mechanism of actin filament elongation by formins. Science 2024 Apr 12;384(6692):eadn9560. doi: 10.1126/science.adn9560. Epub 2024 Apr 12. PMID: 38603491.
3. Redhardt M, Raunser S, Raisch T (2024) Cryo-EM structure of the Slo1 potassium channel with the auxiliary γ₁ subunit suggests a mechanism for depolarization-independent activation. FEBS Lett. 2024 Apr;598(8):875-888. doi: 10.1002/1873-3468.14863. Epub 2024 Mar 30. PMID: 38553946.
4. Polley S, Raisch T, Ghetti S, Körner M, Terbeck M, Gräter F, Raunser S, Aponte-Santamaria Camilo, Vetter IR, Musacchio A (2024) Structure of the human KMN complex and implications for regulation of its assembly. NSMB 2024 Mar 8. doi: 10.1038/s41594-024-01230-9. Online ahead of print. PMID: 38459128.
5. Sitsel O, Wang Z, Janning P, Kroczeck L, Wagner T, Raunser S. (2024) Yersinia entomophaga Tc toxin is released by T10SS-dependent lysis of specialized cell subpopulations, Nat Microbiol. 2024 Feb;9(2):390-404. doi: 10.1038/s41564-023-01571-z. Epub 2024 Jan 18.
6. Belyy A, Heilen P, Hagel P, Hofnagel O, Raunser S (2023) Structure and activation mechanism of the Makes caterpillars floppy 1 toxin. Nature Commun. 14(1):8226.
7. Tamborrini D, Wang Z, Wagner T, Tacke S, Stabrin M, Grange M, Kho AL, Rees M, Bennett P, Gautel M, Raunser S (2023) Structure of the native myosin filament in the relaxed cardiac sarcomere. Nature, 623(7988):863-871.
8. Raisch T and Raunser S (2023) The modes of action of ion-channel-targeting neurotoxic insecticides: lessons from structural biology. Nat Struct Mol Biol. 30(10):1411-1427.
9. Oosterheert W, Blanc FEC, Roy A, Belyy A, Sanders MB, Hofnagel O, Hummer G*, Bieling P*, Raunser S* (2023) Molecular mechanisms of inorganic-phosphate release from the core and barbed end of actin filaments. Nat Struct Mol Biol. 2023 Sep 25. doi: 10.1038/s41594-023-01101-9.
10. Quentin D, Schuhmacher JS, Klink BU, Lauer J, Shaikh TR, Huis In 't Veld PJ, Welp LM, Urlaub H, Zerial M*, Raunser S* (2023) Structural basis of mRNA binding by the human FERRY Rab5 effector complex. Mol Cell. 83(11):1856-1871.e9.
11. Rice G, Wagner T, Stabrin M, Sitsel O, Prumbaum D, Raunser S (2023) TomoTwin: generalized 3D localization of macromolecules in cryo-electron tomograms with structural data mining. Nat Methods 20, 871-880.
12. Wang Z, Raunser S (2023) Structural Biochemistry of Muscle Contraction. Ann Rev Biochem. doi: 10.1146/annurev-biochem-052521-042909.
13. Bürgi J, Lill P, Giannopoulou EA, Jeffries CM, Chojnowski G, Raunser S, Gatsogiannis C, Wilmanns M (2023) Asymmetric horseshoe-like assembly of peroxisomal yeast oxalyl-CoA synthetase. Biol Chem. 26;404(2-3):195-207.
14. Boltje DB, Hoogenboom JP, Jakobi AJ, Jensen GJ, Jonker CTH, Kaag MJ, Koster AJ, Last MGF, de Agrela Pinto C, Plitzko JM, Raunser S, Tacke S, Wang Z, van der Wee EB, Wepf R, den Hoedt S (2022) A cryogenic, coincident fluorescence, electron, and ion beam microscope. Elife. 11:e82891.
15. Oosterheert W, Klink BU, Belyy A, Pospich S, Raunser S (2022) Structural basis of actin filament assembly and aging. Nature. 611(7935):374-379.
16. Xu Y, Viswanatha R, Sitsel O, Roderer D, Zhao H, Ashwood C, Voelker C, Tian S, Raunser S*, Perrimon N*, Dong M* (2022) CRISPR screens in Drosophila cells identify Vsg as a Tc toxin receptor. Nature. 610(7931):349-355.
17. Belyy A, Lindemann F, Roderer D, Funk J, Bardiaux B, Protze J, Bieling P, Oschkinat H*, Raunser S* (2022) Mechanism of threonine ADP-ribosylation of F-actin by a Tc toxin. Nat Commun. 13(1):4202.
18. Schönfeld F, Stabrin M, Shaikh TR, Wagner T, Raunser S (2022). Accelerated 2D Classification With ISAC Using GPUs. Front Mol Biosci. 9:919994.

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19. Pesenti ME, Raisch T, Conti D, Walstein K, Hoffmann I, Vogt D, Prumbaum D, Vetter IR*, Raunser S*, Musacchio A* (2022) Structure of the human inner kinetochore CCAN complex and its significance for human centromere organization. *Mol Cell.* 82(11):2113-2131.e8.
20. Raisch T, Ciossani G, d'Amico E, Cmentowski V, Carmignani S, Maffini S, Merino F, Wohlgemuth S, Vetter IR*, Raunser S*, Musacchio A* (2022) Structure of the RZZ complex and molecular basis of Spindly-driven corona assembly at human kinetochores. *EMBO J.* 41(9):e110411.
21. Urlaub D, Wolfsdorff N, Hoffmann JE, Dorok S, Hoffmann M, Anft M, Pieris N, Günther P, Schaaf B, Cassens U, Bröde P, Claus M, Picard LK, Wingert S, Backes S, Durak D, Babel N, Pöhlmann S, Renken F, Raunser S, Watzl C. (2022) Neutralizing antibody responses 300 days after SARS-CoV-2 infection and induction of high antibody titers after vaccination. *Eur J Immunol.* doi: 10.1002/eji.202149758.
22. Wang Z, Grange M, Pospich S, Wagner T, Kho AL, Gautel M, Raunser S (2022) Structure of the thin filament in native skeletal muscles reveals its interaction with nebulin and two distinct conformations of myosin. *Science.* 375(6582):eabn1934.
23. Klink B, Herrmann E, Antoni C, Langemeyer L, Kiontke S, Gatsogiannis C, Ungermaann C, Raunser S*, Kümmel D* (2022) Structure of the Mon1-Ccz1 complex reveals molecular basis of membrane binding for Rab7 activation. *Proc Natl Acad Sci U S A.* 119(6):e2121494119.
24. Günther P, Quentin D, Ahmad S, Sachar K, Gatsogiannis C, Whitney JC*, Raunser S* (2022) Structure of a bacterial Rhs effector exported by the type VI secretion system. *PLoS Pathog.* 18(1):e1010182.
25. Raisch T, Brockmann A, Ebbinghaus-Kintscher U, Freigang J, Gutbrod O, Kubicek J, Maertens B, Hofnagel O, Raunser S (2021) Small molecule modulation of the Drosophila Slo channel elucidated by cryo-EM. *Nat Commun.* 12(1):7164.
26. Chen M, Blum D, Engelhard L, Raunser S, Wagner R, Gatsogiannis C (2021) Molecular architecture of black widow spider neurotoxins. *Nat Commun.* 12(1):6956.
27. Pospich S, Sweeney HL, Houdusse A, Raunser S (2021) High-resolution structures of the actomyosin-V complex in three nucleotide states provide insights into the force generation mechanism. *Elife* 10, e73724.
28. Belyy A, Merino F, Mechold U, Raunser S (2021) Mechanism of actin-dependent activation of nucleotidyl cyclase toxins from bacterial human pathogens. *Nat Commun.* 12(1):6628.
29. Schoppe J, Schubert E, Apelbaum A, Yavavli E, Birkholz O, Stephanowitz H, Han Y, Perz A, Hofnagel O, Liu F, Piehler J, Raunser S*, Ungermaann C* (2021) Flexible open conformation of the AP-3 complex explains its role in cargo recruitment at the Golgi. *J Biol Chem.* 297(5):101334.
30. Funk J, Merino F, Schaks M, Rottner K, Raunser S*, Bieling P* (2021) A barbed end interference mechanism reveals how capping protein promotes nucleation in branched actin networks. *Nat Commun.* 12(1):5329.
31. Yu J, Raia P, Ghent CM, Raisch T, Sadian Y, Cavadini S, Sabale PM, Barford D, Raunser S, Morgan DO, Boland A (2021) Structural basis of human separase regulation by securin and CDK1-cyclin B1. *Nature.* 596(7870):138-142.
32. Oliva R, Mukherjee SK, Ostermeier L, Pasurek LA, Kriegler S, Bader V, Prumbaum D, Raunser S, Winklhofer KF, Tatzelt J, Winter R (2021) Remodeling of the Fibrillation Pathway of α-Synuclein by Interaction with Antimicrobial Peptide LL-III. *Chemistry.* 27(46):11845-11851.
33. Klika Škopić M, Gramse C, Oliva R, Pospich S, Neukirch L, Manisegaran M, Raunser S, Winter R, Weberskirch R, Brunschweiger A (2021) Towards DNA-Encoded Micellar Chemistry: DNA-Micelle Association and Environment Sensitivity of Catalysis. *Chemistry.* 27(39):10048-10057.
34. Fitzian K, Brückner A, Brohé L, Zech R, Antoni C, Kiontke S, Gasper R, Linard Matos AL, Beel S, Wilhelm S, Gerke V, Ungermaann C, Nellist M, Raunser S, Demetriades C, Oeckinghaus A, Kümmel D (2021) TSC1 binding to lysosomal PIPs is required for TSC complex translocation and mTORC1 regulation. *Mol Cell.* 81(13):2705-2721.
35. Tacke S, Erdmann P, Wang Z, Klumpe S, Grange M, Plitzko JM*, Raunser S* (2021) A streamlined workflow for automated cryo focused ion beam milling. *J. Struct Biol.* 213(3):107743.
36. Wang Z, Grange M, Wagner T, Kho AL, Gautel M, Raunser S (2021) The molecular basis for sarcomere organization in vertebrate skeletal muscle. *Cell.* 184(8):2135-2150.
37. Pospich S, Küllmer F, Nasufovic V, Funk J, Belyy A, Bieling P, Arndt HD*, Raunser S* (2021) Cryo-EM resolves molecular recognition of an optojasp photoswitch bound to actin filaments in both switch states. *Angew Chem Int Ed Engl.* 60(16):8678-8682.

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38. Ahmad S, Tsang KK, Sachar K, Quentin D, Tashin TM, Bullen NP, Raunser S, McArthur AG, Prehna G, Whitney JC (2020) Structural basis for effector transmembrane domain recognition by type VI secretion system chaperones. *eLife*. 9:e62816.
39. Vinayagam D, Quentin D, Yu-Strzelczyk J, Sitsel O, Merino F, Stabrin M, Hofnagel O, Yu M, Ledeboer MW, Nagel G, Malojcic G, Raunser S (2020) Structural basis of TRPC4 regulation by calmodulin and pharmacological agents. *eLife*. 9:e60603.
40. Belyy A, Merino F, Sitsel O, Raunser S (2020) Structure of the Lifeact-F-actin complex. *PLoS Biol*. 18(11):e3000925.
41. Stabrin M, Schoenfeld F, Wagner T, Pospich S, Gatsogiannis C, Raunser S (2020) TranSPHIRE: automated and feedback-optimized on-the-fly processing for cryo-EM. *Nat Commun*. 11(1):5716.
42. Antoni C, Quentin D, Lang AE, Aktories K, Gatsogiannis C, Raunser S (2020) Cryo-EM structure of the fully-loaded asymmetric anthrax lethal toxin in its heptameric pre-pore state. *PLoS Pathog*. 16(8):e1008530.
43. Wagner T, Lusnig L, Pospich S, Stabrin M, Schönfeld F, Raunser S (2020) Two particle-picking procedures for filamentous proteins: SPHIRE-crYOLO filament mode and SPHIRE-STRIPER. *Acta Crystallogr D Struct Biol*. 76(Pt 7):613-620.
44. Roderer D, Bröcker F, Sitsel O, Kaplonek P, Leidreiter F, Seeberger PH, Raunser S (2020) Glycan-dependent cell adhesion mechanism of Tc toxins. *Nat Commun*. 11(1):2694.
45. Pospich S, Merino F, Raunser S (2020) Structural Effects and Functional Implications of Phalloidin and Jasplakinolide Binding to Actin Filaments. *Structure*. 28(4):437-449.
46. Wagner T, Raunser S (2020) The evolution of SPHIRE-crYOLO particle picking and its application in automated cryo-EM processing workflows. *Commun Biol*. 3(1):61.
47. Klink BU, Gatsogiannis C, Hofnagel O, Wittinghofer A, Raunser S (2020) Structure of the human BBSome core complex. *eLife*. 9:e53910.
48. Merino F, Pospich S, Raunser S (2019) Towards a structural understanding of the remodeling of the actin cytoskeleton. *Semin Cell Dev Biol*. 102:51-64, review.
49. Roderer D, Schubert E, Sitsel O, Raunser S (2019) Towards the application of Tc toxins as a universal protein translocation system. *Nat Commun*. 10(1):5263.
50. Roderer D, Hofnagel O, Benz R, Raunser S (2019) Structure of a Tc holotoxin pore provides insights into the translocation mechanism. *Proc Natl Acad Sci U S A*. 116(46):23083-23090.
51. Leidreiter F, Roderer D, Meusch D, Gatsogiannis C, Benz R, Raunser S (2019) Common architecture of Tc toxins from human and insect pathogenic bacteria. *Sci Adv*. 5(10):6497.
52. Funk J, Merino F, Venkova L, Heydenreich L, Kierfeld J, Vargas P, Raunser S, Piel M, Bieling P (2019) Profilin and formin constitute a pacemaker system for robust actin filament growth. *eLife*. 8:e50963.
53. Gatsogiannis C, Balogh D, Merino F, Sieber SA*, Raunser S* (2019) Cryo-EM structure of the ClpXP protein degradation machinery. *Nat Struct Mol Biol*. 26(10):946-954.
54. Raisch T, Chang CT, Levandansky Y, Muthukumar S, Raunser S, Valkov E (2019) Reconstitution of recombinant human CCR4-NOT reveals molecular insights into regulated deadenylation. *Nat Commun*. 10(1):3173.
55. Škopić MK, Götte K, Gramse C, Dieter M, Pospich S, Raunser S, Weberskirch R, Brunschweiger A (2019) Micellar Brønsted Acid Mediated Synthesis of DNA-Tagged Heterocycles. *J Am Chem Soc*. 141(26):10546-10555.
56. Wagner T, Merino F, Stabrin M, Moriya T, Antoni C, Apelbaum A, Hagel P, Sitsel O, Raisch T, Prumbaum D, Quentin D, Roderer D, Tacke S, Siebolds B, Schubert E, Shaikh TR, Lill P, Gatsogiannis C, Raunser S (2019) SPHIRE-crYOLO is a fast and accurate fully automated particle picker for cryo-EM. *Commun Biol*. 2:218.
57. Roderer D, Raunser S (2019) Tc Toxin Complexes: Assembly, Membrane Permeation, and Protein Translocation. *Annu Rev Microbiol*. 73:247-265.
58. Tanaka Y, Kato S, Stabrin M, Raunser S, Matsui T, Gatsogiannis C (2019) Cryo-EM reveals the asymmetric assembly of squid hemocyanin. *IUCrJ*. 6(Pt 3):426-437.
59. Sitsel O, Raunser S (2019) Big insights from tiny crystals. *Nat Chem*. 11(2):106-108.
60. Ludwig AK, De Miroschedji K, Doeppner TR, Börger V, Ruesing J, Rebmann V, Durst S, Jansen S, Bremer M, Behrmann E, Singer BB, Jastrow H, Kuhlmann JD, El Magraoui F, Meyer HE, Hermann DM, Opalka B, Raunser S, Epple M, Horn PA, Giebel B (2018) Precipitation with polyethylene glycol followed by washing and pelleting

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- by ultracentrifugation enriches extracellular vesicles from tissue culture supernatants in small and large scales. *J Extracell Vesicles*. 7(1):1528109.
61. Gatsogiannis C, Merino F, Roderer D, Balchin D, Schubert E, Kuhlee A, Hayer-Hartl M, Raunser S (2018) Tc toxin activation requires unfolding and refolding of a β -propeller. *Nature*. 563(7730):209-213.
 62. Quentin D, Ahmad S, Shanthamoorthy P, Mougous JD, Whitney JC*, Raunser S* (2018) Mechanism of loading and translocation of type VI secretion system effector Tse6. *Nat Microbiol*. 3(10):1142-1152.
 63. Pesenti ME, Prumbaum D, Auckland P, Smith CM, Faesen AC, Petrovic A, Erent M, Maffini S, Pentakota S, Weir JR, Lin YC, Raunser S, McAinsh AD, Musacchio A (2018) Reconstitution of a 26-Subunit Human Kinetochore Reveals Cooperative Microtubule Binding by CENP-OPQUR and NDC80. *Mol Cell*. 71(6):923-939.
 64. Pospich S, Raunser S (2018) Single particle cryo-EM-an optimal tool to study cytoskeletal proteins. *Curr Opin Struct Biol*. 52:16-24, review.
 65. Schubert E, Vetter IR, Prumbaum D, Penczek PA, Raunser S (2018) Membrane insertion of α -xenorhabdolysin in near-atomic detail. *eLife*. 7:e38017.
 66. Merino F, Pospich S, Funk J, Wagner T, Kullmer F, Arndt HD, Bieling P, Raunser S (2018) Structural transitions of F-actin upon ATP hydrolysis at near-atomic resolution revealed by cryo-EM. *Nat Struct Mol Biol*. 25(6):528-537.
 67. Quentin D, Raunser S (2018) Electron cryomicroscopy as a powerful tool in biomedical research. *J Mol Med (Berl)*. 96(6):483-493, review.
 68. Vinayagam D, Mager T, Apelbaum A, Bothe A, Merino F, Hofnagel O, Gatsogiannis C, Raunser S (2018) Electron cryo-microscopy structure of the canonical TRPC4 ion channel. *eLife*. 7:e36615.
 69. Yavuz H, Kattan I, Hernandez JM, Hofnagel O, Witkowska A, Raunser S, Walla PJ, Jahn R (2018) Arrest of trans-SNARE zippering uncovers loosely and tightly docked intermediates in membrane fusion. *J Biol Chem*. 293(22):8645-8655.
 70. Merino F, Raunser S (2018) The complex simplicity of the bacterial cytoskeleton. *Proc Natl Acad Sci USA*. 115(13):3205-3206.
 71. Raunser S (2017) Cryo-EM Revolutionizes the Structure Determination of Biomolecules. *Angew Chem Int Ed Engl*. 56(52):16450-16452.
 72. Klink BU, Zent E, Juneja P, Kuhlee A, Raunser S*, Wittinghofer A* (2017) A recombinant BBSome core complex and how it interacts with ciliary cargo. *eLife*. 6:e27434.
 73. Chen M, Kato K, Kubo Y, Tanaka Y, Liu Y, Long F, Whitman WB, Lill P, Gatsogiannis C, Raunser S, Shimizu N, Shinoda A, Nakamura A, Tanaka I, Yao M (2017) Structural basis for tRNA-dependent cysteine biosynthesis. *Nat Commun*. 8(1):1521.
 74. Pospich S, Raunser S (2017) The molecular basis of Alzheimer's plaques. *Science*. 358(6359):45-46.
 75. Pospich S, Kumpula EP, von der Ecken J, Vahokoski J, Kursula I, Raunser S (2017) Near-atomic structure of jasplakinolide-stabilized malaria parasite F-actin reveals the structural basis of filament instability. *Proc Natl Acad Sci USA*. 114(40):10636-10641.
 76. Efremov RG, Gatsogiannis C, Raunser S (2017) Lipid Nanodiscs as a Tool for High-Resolution Structure Determination of Membrane Proteins by Single-Particle Cryo-EM. *Methods Enzymol*. 594:1-30.
 77. Moriya T, Saur M, Stabrin M, Merino F, Voicu H, Huang Z, Penczek PA, Raunser S*, Gatsogiannis C* (2017) High-resolution Single Particle Analysis from Electron Cryo-microscopy Images Using SPHIRE. *J Vis Exp*. 123:55448.
 78. Orekhov P, Bothe A, Steinhoff HJ, Shaitan KV, Raunser S, Fotiadis D, Schlesinger R, Klare JP, Engelhard M (2017) Sensory Rhodopsin I and Sensory Rhodopsin II Form Trimers of Dimers in Complex with their Cognate Transducers. *Photochem Photobiol*. 93(3):796-804.
 79. Mosalaganti S, Keller J, Altenfeld A, Winzker M, Rombaut P, Saur M, Petrovic A, Wehenkel A, Wohlgemuth S, Müller F, Maffini S, Bange T, Herzog F, Waldmann H, Raunser S*, Musacchio A* (2017) Structure of the RZZ complex and molecular basis of its interaction with Spindly. *J Cell Biol*. 216(4):961-981.
 80. Purushothaman LK, Arlt H, Kuhlee A, Raunser S, Ungermann C (2017) Retromer-driven membrane tubulation separates endosomal recycling from Rab7/Ypt7-dependent fusion. *Mol Biol Cell*. 28(6):783-791.

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81. Kiontke S, Langemeyer L, Kuhlee A, Schuback S, Raunser S, Ungermann C, Kümmel D (2017) Architecture and mechanism of the late endosomal Rab7-like Ypt7 guanine nucleotide exchange factor complex Mon1-Ccz1. *Nat Commun.* 8:14034.
82. Merino F, Raunser S (2016) The mother of all actins? *eLife.* 5:e23354.
83. Merino F, Raunser S (2017) Electron Cryo-microscopy as a Tool for Structure-Based Drug Development. *Angew Chem Int Ed Engl.* 56(11):2846-2860.
84. Lürick A, Gao J, Kuhlee A, Yavavli E, Langemeyer L, Perz A, Raunser S, Ungermann C (2017) Multivalent Rab interactions determine tether-mediated membrane fusion. *Mol Biol Cell.* 28(2):322-332.
85. Andersen CB, Stødkilde K, Sæderup KL, Kuhlee A, Raunser S, Graversen JH, Moestrup SK (2017) Haptoglobin. *Antioxid Redox Signal.* 26(14):814-831.
86. Gatsogiannis C, Merino F, Prumbaum D, Roderer D, Leidreiter F, Meusch D, Raunser S (2016) Membrane insertion of a Tc toxin in near-atomic detail. *Nat Struct Mol Biol.* 23(10):884-890.
87. von der Ecken J, Heissler SM, Pathan-Chhatbar S, Manstein DJ, Raunser S (2016) Cryo-EM structure of a human cytoplasmic actomyosin complex at near-atomic resolution. *Nature.* 534(7609):724-8.
88. Friese A, Faesen AC, Huis in 't Veld PJ, Fischböck J, Prumbaum D, Petrovic A, Raunser S, Herzog F, Musacchio A (2016) Molecular requirements for the inter-subunit interaction and kinetochore recruitment of SKAP and Astrin. *Nat Commun.* 7:11407.
89. Liu Y, Petrovic A, Rombaut P, Mosalaganti S, Keller J, Raunser S, Herzog F, Musacchio A (2016) Insights from the reconstitution of the divergent outer kinetochore of *Drosophila melanogaster*. *Open Biol.* 6(2):150236.
90. Whitney JC, Quentin D, Sawai S, LeRoux M, Harding BN, Ledvina HE, Tran BQ, Robinson H, Goo YA, Goodlett DR, Raunser S*, Mougous JD* (2015) An interbacterial NAD(P)(+) glycohydrolase toxin requires elongation factor Tu for delivery to target cells. *Cell.* 163(3):607-19.
91. Poepsel S, Sprengel A, Sacca B, Kaschani F, Kaiser M, Gatsogiannis C, Raunser S, Clausen T, Ehrmann M (2015) Determinants of amyloid fibril degradation by the PDZ protease HTRA1. *Nat Chem Biol.* 11(11):862-9.
92. Patasi C, Godočíková J, Michlíková S, Nie Y, Káceríková R, Kválová K, Raunser S, Farkašovský M (2015) The role of Bni5 in the regulation of septin higher-order structure formation. *Biol Chem.* 396(12):1325-37.
93. Gao M, Berghaus M, von der Ecken J, Raunser S, Winter R (2015) Condensation agents determine the temperature-pressure stability of F-actin bundles. *Angew Chem Int Ed Engl.* 54(38):11088-92.
94. Kuhlee A, Raunser S*, Ungermann C* (2015) Functional homologies in vesicle tethering. *FEBS Lett.* 589(19 Pt A):2487-97, review.
95. Raunser S, Gatsogiannis C (2015) Deciphering the tubulin code. *Cell.* 161(5):960-961.
96. Frisch H, Nie Y, Raunser S, Besenius P (2015) pH-regulated selectivity in supramolecular polymerizations: switching between Co- and homopolymers. *Chemistry.* 21(8):3304-9.
97. Lürick A, Kuhlee A, Bröcker C, Kümmel D, Raunser S, Ungermann C (2015) The Habc domain of the SNARE Vam3 interacts with the HOPS tethering complex to facilitate vacuole fusion. *J Biol Chem.* 290(9):5405-13.
98. Rosin C, Erlkamp M, von der Ecken J, Raunser S, Winter R (2014) Exploring the stability limits of actin and its suprastructures, *Biophys J.* 107(12):2982-92.
99. Gatsogiannis C, Hofnagel O, Markl J, Raunser S (2015) Structure of mega-hemocyanin reveals protein origami in snails. *Structure.* 23(1):93-103.
100. von der Ecken J, Müller M, Lehman W, Manstein DJ, Penczek PA, Raunser S (2015) Structure of the F-actin-tropomyosin complex. *Nature.* 519(7541):114-7.
101. Efremov RG, Leitner A, Aebersold R, Raunser S (2015) Architecture and conformational switch mechanism of the ryanodine receptor. *Nature.* 517(7532):39-43.
102. Behrmann H, Lürick A, Kuhlee A, Balderhaar HK, Bröcker C, Kümmel D, Engelbrecht-Vandré S, Gohlke U, Raunser S, Heinemann U, Ungermann C (2014) Structural identification of the Vps18 β-propeller reveals a critical role in the HOPS complex stability and function. *J Biol Chem.* 289(48):33503-12.
103. Basilico F, Maffini S, Weir JR, Prumbaum D, Rojas AM, Zimniak T, De Antoni A, Jeganathan S, Voss B, van Gerwen S, Krenn V, Massamiliano L, Valencia A, Vetter IR, Herzog F, Raunser S, Pasqualato S, Musacchio A (2014) The pseudo GTPase CENP-M drives human kinetochore assembly. *eLife.* 3:e02978.

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104. Kapoor S, Berghaus M, Suladze S, Prumbaum D, Grobelny S, Degen P, Raunser S, Winter R (2014) Prebiotic cell membranes that survive extreme environmental pressure conditions. *Angew Chem Int Ed Engl.* 53(32):8397-401.
105. Meusch D, Gatsogiannis C, Efremov RG, Lang AE, Hofnagel O, Vetter IR, Aktories K, Raunser S (2014) Mechanism of Tc toxin action revealed in molecular detail. *Nature.* 508(7494):61-5.
106. Petrovic A, Mosalaganti S, Keller J, Mattiuzzo M, Overlack K, Krenn V, De Antoni A, Wohlgemuth S, Cecatiello V, Pasqualato S, Raunser S, Musacchio A (2014) Modular assembly of RWD domains on the Mis12 complex underlies outer kinetochore organization. *Mol Cell.* 53(4):591-605.
107. Sadian Y, Gatsogiannis C, Patasi C, Hofnagel O, Goody RS, Farkasovsky M, Raunser S (2013) The Role of Cdc42 and Gic1 in the regulation of septin filament formation and dissociation. *eLife.* 2:e01085.
108. Thakur HC, Singh M, Nagel-Steger L, Kremer J, Prumbaum D, Fansa EK, Ezzahoui H, Nouri K, Gremer L, Abts A, Schmitt L, Raunser S, Ahmadian MR, Piekorz RP (2014) The centrosomal adaptor TACC3 and the microtubule polymerase chTOG interact via defined C-terminal subdomains in an Aurora-A kinase-independent manner. *J Biol Chem.* 289(1):74-88.
109. Taft MH, Behrmann E, Munske-Weidemann LC, Thiel C, Raunser S, Manstein DJ (2013) Functional characterization of human myosin-18A and its interaction with F-actin and GOLPH3. *J Biol Chem.* 288(42):30029-41.
110. Erkelenz M, Bauer DM, Meyer R, Gatsogiannis C, Raunser S, Saccà B, Niemeyer CM (2014) A facile method for preparation of tailored scaffolds for DNA-origami. *Small.* 10(1):73-7.
111. Thakur HC, Singh M, Nagel-Steger L, Prumbaum D, Fansa EK, Gremer L, Ezzahoui H, Abts A, Schmitt L, Raunser S, Ahmadian MR, Piekorz RP (2013) Role of centrosomal adaptor proteins of the TACC family in the regulation of microtubule dynamics during mitotic cell division. *Biol Chem.* 394(11):1411-23, review.
112. Lehman W, Orzechowski M, Li XE, Fischer S, Raunser S (2013) Gestalt-binding of tropomyosin on actin during thin filament activation. *J Muscle Res Cell Motil.* 34(3-4):155-63, review.
113. Lakshminarasimhan M, Curth U, Mosalaganti S, Raunser S, Steegborn C (2013) Molecular architecture of the human protein deacetylase Sirt1 and its regulation by AROS and resveratrol. *Biosci Rep.* 33(3).
114. Gatsogiannis C, Lang AE, Meusch D, Pfaumann V, Hofnagel O, Benz R, Aktories K*, Raunser S* (2013) A syringe-like injection mechanism in *Photorhabdus luminescens* toxins. *Nature.* 495(7442):520-3.
115. Schönichen A, Mannherz HG, Behrmann E, Mazur AJ, Kühn S, Silván U, Schoenenberger CA, Fackler OT, Raunser S, Dehmelt L, Geyer M (2013) FHOD1 is a combined actin filament capping and bundling factor that selectively associates with actin arcs and stress fibers. *J Cell Sci.* 126(Pt 8):1891-901.
116. Sot B, Behrmann E, Raunser S, Wittinghofer A (2013) Ras GTPase activating (RasGAP) activity of the dual specificity GAP protein Rasal requires colocalization and C2 domain binding to lipid membranes. *Proc Natl Acad Sci USA.* 110(1):111-6.
117. Behrmann E, Müller M, Penczek PA, Mannherz HG, Manstein DJ*, Raunser S* (2012) Structure of the rigor actin-tropomyosin-myosin complex. *Cell.* 150(2):327-38.
118. Hernandez JM, Stein A, Behrmann E, Riedel D, Cypionka A, Farsi Z, Walla PJ, Raunser S, Jahn R (2012) Membrane fusion intermediates via directional and full assembly of the SNARE complex. *Science.* 336(6088):1581-4.
119. Müller M, Mazur AJ, Behrmann E, Diensthuber RP, Radke MB, Qu Z, Littwitz C, Raunser S, Schöninenberger C, Manstein DJ, Mannherz HG (2012) Functional characterization of the human α-cardiac actin mutations Y166C and M305L involved in hypertrophic cardiomyopathy. *Cell Mol Life Sci.* 69(20):3457-79.
120. Bröcker C, Kuhlee A, Gatsogiannis C, kleine Balderhaar H, Hönscher C, Engelbrecht-Vandré S, Ungermaann C*, Raunser S* (2012) Molecular architecture of the multisubunit homotypic fusion and vacuole protein sorting (HOPS) tethering complex. *Proc Natl Acad Sci USA.* 109(6):1991-6.
121. Behrmann E, Tao G, Stokes DL, Egelman EH, Raunser S*, Penczek PA* (2012) Real-space processing of helical filaments in SPARX. *J Struct Biol.* 177(2):302-13.
122. Schneider R, Schumacher MC, Mueller H, Nand D, Klaukien V, Heise H, Riedel D, Wolf G, Behrmann E, Raunser S, Seidel R, Engelhard M, Baldus M (2011) Structural characterization of polyglutamine fibrils by solid-state NMR spectroscopy. *J Mol Biol.* 412(1):121-36.
123. Wang L, Yang JK, Kabaleeswaran V, Rice AJ, Cruz AC, Park AY, Yin Q, Damko E, Jang SB, Raunser S, Robinson

Publication list - STEFAN RAUNSER

- CV, Siegel RM, Walz T, Wu H (2010) The Fas-FADD death domain complex structure reveals the basis of DISC assembly and disease mutations. *Nat Struct Mol Biol.* 17(11):1324-9.
124. Raunser S, Walz T (2009) Electron crystallography as a technique to study the structure on membrane proteins in a lipidic environment. *Annu Rev Biophys.* 38:89-105, review.
125. Raunser S, Mathai JC, Abeyrathne PD, Rice AJ, Zeidel ML, Walz T (2009) Oligomeric structure and functional characterization of the urea transporter from *Actinobacillus pleuropneumoniae*. *J Mol Biol.* 387(3):619-27.
126. Park CY, Hoover PJ, Mullins FM, Bachhawat P, Covington ED, Raunser S, Walz T, Garcia KC, Dolmetsch RE, Lewis RS (2009) STIM1 clusters and activates CRAC channels via direct binding of a cytosolic domain to Orai1. *Cell.* 136(5):876-90.
127. Raunser S, Magnani R, Huang Z, Houtz RL, Trievle RC, Penczek PA, Walz T. (2009) Rubisco in complex with Rubisco large subunit methyltransferase. *Proc Natl Acad Sci USA.* 106(9):3160-5.
128. Hite RK, Raunser S, Walz T (2007) Revival of electron crystallography. *Curr Opin Struct Biol.* 17(4): 389-95, review.
129. Bankovich AJ, Raunser S, Juo ZS, Walz T, Davis MM, Garcia KC (2007) Structural insight into pre-B cell receptor function. *Science.* 316(5822):291-4.
130. Park HH, Logette E, Raunser S, Cuenin S, Walz T, Tschoopp J, Wu H (2007) Death domain assembly mechanism revealed by crystal structure of the oligomeric PIDDosome core complex. *Cell.* 128(3):533-46.
131. Yildiz O, Kalthoff C, Raunser S, Kühlbrandt W (2007) Structure of GlnK1 with bound effectors indicates regulatory mechanism for ammonia uptake. *EMBO J.* 26(2):589-99.
132. Kim YG, Raunser S, Munger C, Wagner J, Song YL, Cygler M, Walz T, Oh BH, Sacher M (2006) The architecture of the multisubunit TRAPP I complex suggests a model for vesicle tethering. *Cell.* 127(4):817-30.
133. Raunser S, Appel M, Ganea C, Geldmacher-Kaufer U, Fendler K, Kühlbrandt W (2006) Structure and function of prokaryotic glutamate transporters from *Escherichia coli* and *Pyrococcus horikoshii*. *Biochemistry.* 45(42):12796-805.
134. Raunser S, Haase W, Franke C, Eckert GP, Müller WE, Kühlbrandt W (2006) Heterologously expressed GLT-1 associates in approximately 200-nm protein-lipid islands. *Biophys J.* 91(10):3718-26.
135. Hobe S, Trostmann I, Raunser S, Paulsen H (2006) Assembly of the major light-harvesting chlorophyll-a/b complex: Thermodynamics and kinetics of neoxanthin binding. *J Biol Chem.* 281(35):25156-66.
136. Mougous JD, Cuff ME, Raunser S, Shen A, Zhou M, Gifford CA, Goodman AL, Joachimiak G, Ordoñez CL, Lory S, Walz T, Joachimiak A, Mekalanos JJ (2006) A virulence locus of *Pseudomonas aeruginosa* encodes a protein secretion apparatus. *Science.* 312(5779):1526-30.
137. Vinothkumar KR, Raunser S, Jung H, Kühlbrandt W (2006) Oligomeric structure of the carnitine transporter CaiT from *Escherichia coli*. *J Biol Chem.* 281(8):4795-801.
138. Raunser S, Haase W, Bostina M, Parcej DN, Kühlbrandt W (2005) High-yield expression, reconstitution and structure of the recombinant, fully functional glutamate transporter GLT-1 from *Rattus norvegicus*. *J Mol Biol.* 351(3):598-613.
139. Raunser S (2005) „Biochemische Kristallisation von Membranproteinen und die Kunst“ in Begegnungen von Kunst und Technik. Wachholtz Verlag Neumünster.