

# Stefan Raunser

## List of Publications by Year in descending order

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142  
papers

10,226  
citations

47006

47  
h-index

42399

92  
g-index

189  
all docs

189  
docs citations

189  
times ranked

12926  
citing authors

#	ARTICLE	IF	CITATIONS
1	A Virulence Locus of <i>Pseudomonas aeruginosa</i> Encodes a Protein Secretion Apparatus. <i>Science</i> , 2006, 312, 1526-1530.	12.6	984
2	SPHIRE-crYOLO is a fast and accurate fully automated particle picker for cryo-EM. <i>Communications Biology</i> , 2019, 2, 218.	4.4	860
3	STIM1 Clusters and Activates CRAC Channels via Direct Binding of a Cytosolic Domain to Orai1. <i>Cell</i> , 2009, 136, 876-890.	28.9	839
4	Structure of the F-actin-tropomyosin complex. <i>Nature</i> , 2015, 519, 114-117.	27.8	321
5	Structure of the Rigor Actin-Tropomyosin-Myosin Complex. <i>Cell</i> , 2012, 150, 327-338.	28.9	297
6	Architecture and conformational switch mechanism of the ryanodine receptor. <i>Nature</i> , 2015, 517, 39-43.	27.8	282
7	Death Domain Assembly Mechanism Revealed by Crystal Structure of the Oligomeric PIDDosome Core Complex. <i>Cell</i> , 2007, 128, 533-546.	28.9	244
8	The Fas-FADD death domain complex structure reveals the basis of DISC assembly and disease mutations. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1324-1329.	8.2	236
9	Molecular architecture of the multisubunit homotypic fusion and vacuole protein sorting (HOPS) tethering complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 1991-1996.	7.1	227
10	Cryo-EM structure of a human cytoplasmic actomyosin complex at near-atomic resolution. <i>Nature</i> , 2016, 534, 724-728.	27.8	212
11	Membrane Fusion Intermediates via Directional and Full Assembly of the SNARE Complex. <i>Science</i> , 2012, 336, 1581-1584.	12.6	210
12	An Interbacterial NAD(P) <sup>+</sup> Glycohydrolase Toxin Requires Elongation Factor Tu for Delivery to Target Cells. <i>Cell</i> , 2015, 163, 607-619.	28.9	203
13	Structural transitions of F-actin upon ATP hydrolysis at near-atomic resolution revealed by cryo-EM. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 528-537.	8.2	171
14	The Architecture of the Multisubunit TRAPP I Complex Suggests a Model for Vesicle Tethering. <i>Cell</i> , 2006, 127, 817-830.	28.9	166
15	Precipitation with polyethylene glycol followed by washing and pelleting by ultracentrifugation enriches extracellular vesicles from tissue culture supernatants in small and large scales. <i>Journal of Extracellular Vesicles</i> , 2018, 7, 1528109.	12.2	164
16	High-resolution Single Particle Analysis from Electron Cryo-microscopy Images Using SPHIRE. <i>Journal of Visualized Experiments</i> , 2017, . .	0.3	161
17	Mechanism of Tc toxin action revealed in molecular detail. <i>Nature</i> , 2014, 508, 61-65.	27.8	149
18	A syringe-like injection mechanism in <i>Photobacterium luminescens</i> toxins. <i>Nature</i> , 2013, 495, 520-523.	27.8	130

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19	Modular Assembly of RWD Domains on the Mis12 Complex Underlies Outer Kinetochores Organization. <i>Molecular Cell</i> , 2014, 53, 591-605.	9.7	116
20	Haptoglobin. <i>Antioxidants and Redox Signaling</i> , 2017, 26, 814-831.	5.4	113
21	The pseudo GTPase CENP-M drives human kinetochores assembly. <i>ELife</i> , 2014, 3, e02978.	6.0	107
22	Structural Insight into Pre-B Cell Receptor Function. <i>Science</i> , 2007, 316, 291-294.	12.6	101
23	The molecular basis for sarcomere organization in vertebrate skeletal muscle. <i>Cell</i> , 2021, 184, 2135-2150.e13.	28.9	99
24	Structural Characterization of Polyglutamine Fibrils by Solid-State NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2011, 412, 121-136.	4.2	88
25	Determinants of amyloid fibril degradation by the PDZ protease HTRA1. <i>Nature Chemical Biology</i> , 2015, 11, 862-869.	8.0	88
26	Membrane insertion of a Tc toxin in near-atomic detail. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 884-890.	8.2	88
27	Mechanism of loading and translocation of type VI secretion system effector Tse6. <i>Nature Microbiology</i> , 2018, 3, 1142-1152.	13.3	88
28	Electron cryo-microscopy structure of the canonical TRPC4 ion channel. <i>ELife</i> , 2018, 7, .	6.0	83
29	Structural Effects and Functional Implications of Phalloidin and Jasplakinolide Binding to Actin Filaments. <i>Structure</i> , 2020, 28, 437-449.e5.	3.3	83
30	Profilin and formin constitute a pacemaker system for robust actin filament growth. <i>ELife</i> , 2019, 8, .	6.0	80
31	FHOD1 is a combined actin filament capping and bundling factor that selectively associates with actin arcs and stress fibers. <i>Journal of Cell Science</i> , 2013, 126, 1891-901.	2.0	74
32	pH-Regulated Selectivity in Supramolecular Polymerizations: Switching between Co- and Homopolymers. <i>Chemistry - A European Journal</i> , 2015, 21, 3304-3309.	3.3	69
33	A recombinant BBSome core complex and how it interacts with ciliary cargo. <i>ELife</i> , 2017, 6, .	6.0	69
34	Structures from intact myofibrils reveal mechanism of thin filament regulation through nebulin. <i>Science</i> , 2022, 375, eabn1934.	12.6	69
35	Reconstitution of a 26-Subunit Human Kinetochores Reveals Cooperative Microtubule Binding by CENP-OPQUR and NDC80. <i>Molecular Cell</i> , 2018, 71, 923-939.e10.	9.7	68
36	Cryo-EM structure of the ClpXP protein degradation machinery. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 946-954.	8.2	68

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37	Electron Crystallography as a Technique to Study the Structure on Membrane Proteins in a Lipidic Environment. <i>Annual Review of Biophysics</i> , 2009, 38, 89-105.	10.0	66
38	Structure of the RZZ complex and molecular basis of its interaction with Spindly. <i>Journal of Cell Biology</i> , 2017, 216, 961-981.	5.2	65
39	Reconstitution of recombinant human CCR4-NOT reveals molecular insights into regulated deadenylation. <i>Nature Communications</i> , 2019, 10, 3173.	12.8	65
40	The role of Cdc42 and Gic1 in the regulation of septin filament formation and dissociation. <i>ELife</i> , 2013, 2, e01085.	6.0	65
41	Near-atomic structure of jasplakinolide-stabilized malaria parasite F-actin reveals the structural basis of filament instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 10636-10641.	7.1	64
42	Towards a structural understanding of the remodeling of the actin cytoskeleton. <i>Seminars in Cell and Developmental Biology</i> , 2020, 102, 51-64.	5.0	63
43	TranSPHIRE: automated and feedback-optimized on-the-fly processing for cryo-EM. <i>Nature Communications</i> , 2020, 11, 5716.	12.8	60
44	A streamlined workflow for automated cryo focused ion beam milling. <i>Journal of Structural Biology</i> , 2021, 213, 107743.	2.8	60
45	Architecture and mechanism of the late endosomal Rab7-like Ypt7 guanine nucleotide exchange factor complex Mon1â€“Ccz1. <i>Nature Communications</i> , 2017, 8, 14034.	12.8	59
46	Lipid Nanodiscs as a Tool for High-Resolution Structure Determination of Membrane Proteins by Single-Particle Cryo-EM. <i>Methods in Enzymology</i> , 2017, 594, 1-30.	1.0	59
47	Micellar Brønsted Acid Mediated Synthesis of DNA-Tagged Heterocycles. <i>Journal of the American Chemical Society</i> , 2019, 141, 10546-10555.	13.7	59
48	Structure of the human BBSome core complex. <i>ELife</i> , 2020, 9, .	6.0	59
49	Structure of GlnK1 with bound effectors indicates regulatory mechanism for ammonia uptake. <i>EMBO Journal</i> , 2007, 26, 589-599.	7.8	57
50	A barbed end interference mechanism reveals how capping protein promotes nucleation in branched actin networks. <i>Nature Communications</i> , 2021, 12, 5329.	12.8	57
51	Multivalent Rab interactions determine tether-mediated membrane fusion. <i>Molecular Biology of the Cell</i> , 2017, 28, 322-332.	2.1	54
52	Gestalt-Binding of tropomyosin on actin during thin filament activation. <i>Journal of Muscle Research and Cell Motility</i> , 2013, 34, 155-163.	2.0	53
53	Functional characterization of the human Î±-cardiac actin mutations Y166C and M305L involved in hypertrophic cardiomyopathy. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 3457-3479.	5.4	52
54	Functional Characterization of Human Myosin-18A and Its Interaction with F-actin and GOLPH3. <i>Journal of Biological Chemistry</i> , 2013, 288, 30029-30041.	3.4	52

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55	Structural basis of human separase regulation by securin and CDK1-cyclin B1. <i>Nature</i> , 2021, 596, 138-142.	27.8	51
56	The evolution of SPHIRE-crYOLO particle picking and its application in automated cryo-EM processing workflows. <i>Communications Biology</i> , 2020, 3, 61.	4.4	49
57	Revival of electron crystallography. <i>Current Opinion in Structural Biology</i> , 2007, 17, 389-395.	5.7	48
58	Two particle-picking procedures for filamentous proteins: SPHIRE-crYOLO filament mode and SPHIRE-STRIPER. <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 613-620.	2.3	46
59	Role of centrosomal adaptor proteins of the TACC family in the regulation of microtubule dynamics during mitotic cell division. <i>Biological Chemistry</i> , 2013, 394, 1411-1423.	2.5	45
60	Tc toxin activation requires unfolding and refolding of a $\beta^2$ -propeller. <i>Nature</i> , 2018, 563, 209-213.	27.8	45
61	A Facile Method for Preparation of Tailored Scaffolds for DNA Origami. <i>Small</i> , 2014, 10, 73-77.	10.0	44
62	Ras GTPase activating (RasGAP) activity of the dual specificity GAP protein Rasal requires colocalization and C2 domain binding to lipid membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 111-116.	7.1	41
63	Insights from the reconstitution of the divergent outer kinetochore of <i>Drosophila melanogaster</i> . <i>Open Biology</i> , 2016, 6, 150236.	3.6	41
64	Structure of the Lifeact-F-actin complex. <i>PLoS Biology</i> , 2020, 18, e3000925.	5.6	40
65	The Centrosomal Adaptor TACC3 and the Microtubule Polymerase chTOG Interact via Defined C-terminal Subdomains in an Aurora-A Kinase-independent Manner. <i>Journal of Biological Chemistry</i> , 2014, 289, 74-88.	3.4	39
66	Structural basis of TRPC4 regulation by calmodulin and pharmacological agents. <i>ELife</i> , 2020, 9, .	6.0	38
67	Structure of the human inner kinetochore CCAN complex and its significance for human centromere organization. <i>Molecular Cell</i> , 2022, 82, 2113-2131.e8.	9.7	37
68	Electron Cryo-microscopy as a Tool for Structure-Based Drug Development. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 2846-2860.	13.8	36
69	Tc Toxin Complexes: Assembly, Membrane Permeation, and Protein Translocation. <i>Annual Review of Microbiology</i> , 2019, 73, 247-265.	7.3	36
70	Structure and Function of Prokaryotic Glutamate Transporters from <i>Escherichia coli</i> and <i>Pyrococcus horikoshii</i> . <i>Biochemistry</i> , 2006, 45, 12796-12805.	2.5	35
71	The Habc Domain of the SNARE Vam3 Interacts with the HOPS Tethering Complex to Facilitate Vacuole Fusion. <i>Journal of Biological Chemistry</i> , 2015, 290, 5405-5413.	3.4	35
72	Retromer-driven membrane tubulation separates endosomal recycling from Rab7/Ypt7-dependent fusion. <i>Molecular Biology of the Cell</i> , 2017, 28, 783-791.	2.1	32

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73	Structure of a Tc holotoxin pore provides insights into the translocation mechanism. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 23083-23090.	7.1	32
74	Real-space processing of helical filaments in SPARX. Journal of Structural Biology, 2012, 177, 302-313.	2.8	31
75	Molecular requirements for the inter-subunit interaction and kinetochore recruitment of SKAP and Astrin. Nature Communications, 2016, 7, 11407.	12.8	31
76	Oligomeric Structure of the Carnitine Transporter CaiT from Escherichia coli. Journal of Biological Chemistry, 2006, 281, 4795-4801.	3.4	30
77	Molecular architecture of the human protein deacetylase Sirt1 and its regulation by AROS and resveratrol. Bioscience Reports, 2013, 33, .	2.4	30
78	Common architecture of Tc toxins from human and insect pathogenic bacteria. Science Advances, 2019, 5, eaax6497.	10.3	29
79	Rubisco in complex with Rubisco large subunit methyltransferase. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 3160-3165.	7.1	27
80	Functional homologies in vesicle tethering. FEBS Letters, 2015, 589, 2487-2497.	2.8	27
81	Structure of Mega-Hemocyanin Reveals Protein Origami in Snails. Structure, 2015, 23, 93-103.	3.3	27
82	Towards the application of Tc toxins as a universal protein translocation system. Nature Communications, 2019, 10, 5263.	12.8	27
83	Membrane insertion of Î±-xenorhabdolyisin in near-atomic detail. ELife, 2018, 7, .	6.0	27
84	High-resolution structures of the actomyosin-V complex in three nucleotide states provide insights into the force generation mechanism. ELife, 2021, 10, .	6.0	27
85	Assembly of the Major Light-harvesting Chlorophyll-a/b Complex. Journal of Biological Chemistry, 2006, 281, 25156-25166.	3.4	26
86	Arrest of trans-SNARE zippering uncovers loosely and tightly docked intermediates in membrane fusion. Journal of Biological Chemistry, 2018, 293, 8645-8655.	3.4	26
87	Structural basis for effector transmembrane domain recognition by type VI secretion system chaperones. ELife, 2020, 9, .	6.0	26
88	High-yield Expression, Reconstitution and Structure of the Recombinant, Fully Functional Glutamate Transporter GLT-1 from Rattus norvegicus. Journal of Molecular Biology, 2005, 351, 598-613.	4.2	25
89	TSC1 binding to lysosomal PIPs is required for TSC complex translocation and mTORC1 regulation. Molecular Cell, 2021, 81, 2705-2721.e8.	9.7	25
90	The molecular basis of Alzheimer's plaques. Science, 2017, 358, 45-46.	12.6	24

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91	Glycan-dependent cell adhesion mechanism of Tc toxins. <i>Nature Communications</i> , 2020, 11, 2694.	12.8	24
92	Structure of a bacterial Rhs effector exported by the type VI secretion system. <i>PLoS Pathogens</i> , 2022, 18, e1010182.	4.7	24
93	Exploring the Stability Limits of Actin and Its Suprastructures. <i>Biophysical Journal</i> , 2014, 107, 2982-2992.	0.5	23
94	Oligomeric Structure and Functional Characterization of the Urea Transporter from <i>Actinobacillus pleuropneumoniae</i> . <i>Journal of Molecular Biology</i> , 2009, 387, 619-627.	4.2	22
95	Sensory Rhodopsin I and Sensory Rhodopsin II Form Trimers of Dimers in Complex with their Cognate Transducers. <i>Photochemistry and Photobiology</i> , 2017, 93, 796-804.	2.5	20
96	Cryo-EM Resolves Molecular Recognition Of An Opto-jasp Photoswitch Bound To Actin Filaments In Both Switch States. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 8678-8682.	13.8	20
97	Structure of the RZZ complex and molecular basis of Spindle-driven corona assembly at human kinetochores. <i>EMBO Journal</i> , 2022, 41, e110411.	7.8	20
98	The role of Bni5 in the regulation of septin higher-order structure formation. <i>Biological Chemistry</i> , 2015, 396, 1325-1337.	2.5	19
99	Prebiotic Cell Membranes that Survive Extreme Environmental Pressure Conditions. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 8397-8401.	13.8	18
100	Cryo-EM structure of the fully-loaded asymmetric anthrax lethal toxin in its heptameric pre-pore state. <i>PLoS Pathogens</i> , 2020, 16, e1008530.	4.7	17
101	Heterologously Expressed GLT-1 Associates in $\sim$ 200-nm Protein-Lipid Islands. <i>Biophysical Journal</i> , 2006, 91, 3718-3726.	0.5	15
102	Cryo-EM Revolutionizes the Structure Determination of Biomolecules. <i>Angewandte Chemie - International Edition</i> , 2017, 56, 16450-16452.	13.8	14
103	Structural Identification of the Vps18 $\hat{I}^2$ -Propeller Reveals a Critical Role in the HOPS Complex Stability and Function. <i>Journal of Biological Chemistry</i> , 2014, 289, 33503-33512.	3.4	13
104	Mechanism of actin-dependent activation of nucleotidyl cyclase toxins from bacterial human pathogens. <i>Nature Communications</i> , 2021, 12, 6628.	12.8	13
105	Remodeling of the Fibrillation Pathway of $\hat{I}^{\pm}$ Synuclein by Interaction with Antimicrobial Peptide LL-37. <i>Chemistry - A European Journal</i> , 2021, 27, 11845-11851.	3.3	12
106	Structure of the Mon1-Ccz1 complex reveals molecular basis of membrane binding for Rab7 activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	7.1	12
107	Single particle cryo-EM is an optimal tool to study cytoskeletal proteins. <i>Current Opinion in Structural Biology</i> , 2018, 52, 16-24.	5.7	11
108	Electron cryomicroscopy as a powerful tool in biomedical research. <i>Journal of Molecular Medicine</i> , 2018, 96, 483-493.	3.9	11

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109	Deciphering the Tubulin Code. <i>Cell</i> , 2015, 161, 960-961.	28.9	10
110	Kryo-Elektronenmikroskopie als Methode für die strukturbasierte Wirkstoffentwicklung. <i>Angewandte Chemie</i> , 2017, 129, 2890-2905.	2.0	10
111	Neutralizing antibody responses 300 days after SARS-CoV-2 infection and induction of high antibody titers after vaccination. <i>European Journal of Immunology</i> , 2022, 52, 810-815.	2.9	9
112	Small molecule modulation of the <i>Drosophila</i> Slo channel elucidated by cryo-EM. <i>Nature Communications</i> , 2021, 12, 7164.	12.8	9
113	Condensation Agents Determine the Temperature-Pressure Stability of Actin Bundles. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 11088-11092.	13.8	8
114	Towards DNA-Encoded Micellar Chemistry: DNA-Micelle Association and Environment Sensitivity of Catalysis. <i>Chemistry - A European Journal</i> , 2021, 27, 10048-10057.	3.3	8
115	Flexible open conformation of the AP-3 complex explains its role in cargo recruitment at the Golgi. <i>Journal of Biological Chemistry</i> , 2021, 297, 101334.	3.4	8
116	Cryo-EM reveals the asymmetric assembly of squid hemocyanin. <i>IUCr</i> , 2019, 6, 426-437.	2.2	7
117	Structural basis for tRNA-dependent cysteine biosynthesis. <i>Nature Communications</i> , 2017, 8, 1521.	12.8	6
118	Big insights from tiny crystals. <i>Nature Chemistry</i> , 2019, 11, 106-108.	13.6	5
119	Modulation of septin higher-order structure by the Cdc28 protein kinase. <i>Biologia (Poland)</i> , 2018, 73, 1025-1033.	1.5	4
120	Cryo-EM Resolves Molecular Recognition Of An Opto-Photoswitch Bound To Actin Filaments In Both Switch States. <i>Angewandte Chemie</i> , 2021, 133, 8760-8764.	2.0	4
121	Molecular architecture of black widow spider neurotoxins. <i>Nature Communications</i> , 2021, 12, 6956.	12.8	4
122	Accelerated 2D Classification With ISAC Using GPUs. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	3.5	4
123	The mother of all actins?. <i>ELife</i> , 2016, 5, .	6.0	3
124	Kryo-Elektronenmikroskopie revolutioniert die Strukturbestimmung von Biomolekülen. <i>Angewandte Chemie</i> , 2017, 129, 16670-16672.	2.0	2
125	ENZEL - A cryogenic, retrofittable, coincident fluorescence, electron, and ion beam solution for the cryo-electron tomography workflow.. <i>Microscopy and Microanalysis</i> , 2021, 27, 3228-3229.	0.4	2
126	Recent developments in automated single-particle selection. <i>Nature Reviews Methods Primers</i> , 2022, 2, .	21.2	2



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127	Tropomyosin Movement on F-actin Analyzed by Energy Landscape Determination. Biophysical Journal, 2012, 102, 17a.	0.5	1
128	Fluorescence-guided lamella fabrication with ENZEL, an integrated cryogenic CLEM solution for the cryo-electron tomography workflow. Microscopy and Microanalysis, 2021, 27, 3234-3235.	0.4	1
129	The molecular basis for sarcomere organization in vertebrate skeletal muscle. Microscopy and Microanalysis, 2021, 27, 2832-2835.	0.4	1
130	Eine coole Technik: Kryoelektronenmikroskopie. Nachrichten Aus Der Chemie, 2017, 65, 1086-1088.	0.0	0
131	The complex simplicity of the bacterial cytoskeleton. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3205-3206.	7.1	0
132	New hardware for a streamlined cryo focused ion beam milling workflow. Microscopy and Microanalysis, 2021, 27, 2082-2086.	0.4	0
133	Structure of the Lifeactâ€F-actin complex. , 2020, 18, e3000925.		0
134	Structure of the Lifeactâ€F-actin complex. , 2020, 18, e3000925.		0
135	Structure of the Lifeactâ€F-actin complex. , 2020, 18, e3000925.		0
136	Structure of the Lifeactâ€F-actin complex. , 2020, 18, e3000925.		0
137	Structure of the Lifeactâ€F-actin complex. , 2020, 18, e3000925.		0
138	Structure of the Lifeactâ€F-actin complex. , 2020, 18, e3000925.		0
139	Title is missing!. , 2020, 16, e1008530.		0
140	Title is missing!. , 2020, 16, e1008530.		0
141	Title is missing!. , 2020, 16, e1008530.		0
142	Title is missing!. , 2020, 16, e1008530.		0