

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
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189
all docs

189
docs citations

189
times ranked

12926
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of a bacterial Rhs effector exported by the type VI secretion system. <i>PLoS Pathogens</i> , 2022, 18, e1010182.	4.7	24
2	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
3	Structures from intact myofibrils reveal mechanism of thin filament regulation through nebulin. <i>Science</i> , 2022, 375, eabn1934.	12.6	69
4	Recent developments in automated single-particle selection. <i>Nature Reviews Methods Primers</i> , 2022, 2, .	21.2	2
5	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
6	Structure of the RZZ complex and molecular basis of Spindly-driven corona assembly at human kinetochores. <i>EMBO Journal</i> , 2022, 41, e110411.	7.8	20
7	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
8	Cryo-EM Resolves Molecular Recognition Of An Optojasp Photoswitch Bound To Actin Filaments In Both Switch States. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 8678-8682.	13.8	20
9	Cryo-EM Resolves Molecular Recognition Of An Optojasp Photoswitch Bound To Actin Filaments In Both Switch States. <i>Angewandte Chemie</i> , 2021, 133, 8760-8764.	2.0	4
10	The molecular basis for sarcomere organization in vertebrate skeletal muscle. <i>Cell</i> , 2021, 184, 2135-2150.e13.	28.9	99
11	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
12	Fluorescence-guided lamella fabrication with ENZEL, an integrated cryogenic CLEM solution for the cryo-electron tomography workflow. <i>Microscopy and Microanalysis</i> , 2021, 27, 3234-3235.	0.4	1
13	The molecular basis for sarcomere organization in vertebrate skeletal muscle. <i>Microscopy and Microanalysis</i> , 2021, 27, 2832-2835.	0.4	1
14	Structural basis of human separase regulation by securin and CDK1-cyclin B1. <i>Nature</i> , 2021, 596, 138-142.	27.8	51
15	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
16	Remodeling of the Fibrillation Pathway of Î±-Synuclein by Interaction with Antimicrobial Peptide LL-37. <i>Chemistry - A European Journal</i> , 2021, 27, 11845-11851.	3.3	12
17	New hardware for a streamlined cryo focused ion beam milling workflow. <i>Microscopy and Microanalysis</i> , 2021, 27, 2082-2086.	0.4	0
18	TSC1 binding to lysosomal PIPs is required for TSC complex translocation and mTORC1 regulation. <i>Molecular Cell</i> , 2021, 81, 2705-2721.e8.	9.7	25

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19	A streamlined workflow for automated cryo focused ion beam milling. <i>Journal of Structural Biology</i> , 2021, 213, 107743.	2.8	60
20	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
21	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
22	Mechanism of actin-dependent activation of nucleotidyl cyclase toxins from bacterial human pathogens. <i>Nature Communications</i> , 2021, 12, 6628.	12.8	13
23	Molecular architecture of black widow spider neurotoxins. <i>Nature Communications</i> , 2021, 12, 6956.	12.8	4
24	High-resolution structures of the actomyosin-V complex in three nucleotide states provide insights into the force generation mechanism. <i>ELife</i> , 2021, 10, .	6.0	27
25	Small molecule modulation of the <i>Drosophila</i> Slo channel elucidated by cryo-EM. <i>Nature Communications</i> , 2021, 12, 7164.	12.8	9
26	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
27	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
28	TranSPHIRE: automated and feedback-optimized on-the-fly processing for cryo-EM. <i>Nature Communications</i> , 2020, 11, 5716.	12.8	60
29	Glycan-dependent cell adhesion mechanism of Tc toxins. <i>Nature Communications</i> , 2020, 11, 2694.	12.8	24
30	Structural Effects and Functional Implications of Phalloidin and Jasplakinolide Binding to Actin Filaments. <i>Structure</i> , 2020, 28, 437-449.e5.	3.3	83
31	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
32	Two particle-picking procedures for filamentous proteins: <i>SPHIRE-crYOLO</i> filament mode and <i>SPHIRE-STRIPER</i> . <i>Acta Crystallographica Section D: Structural Biology</i> , 2020, 76, 613-620.	2.3	46
33	Structure of the Lifeact-F-actin complex. <i>PLoS Biology</i> , 2020, 18, e3000925.	5.6	40
34	Structure of the human BBSome core complex. <i>ELife</i> , 2020, 9, .	6.0	59
35	Structural basis of TRPC4 regulation by calmodulin and pharmacological agents. <i>ELife</i> , 2020, 9, .	6.0	38
36	Structural basis for effector transmembrane domain recognition by type VI secretion system chaperones. <i>ELife</i> , 2020, 9, .	6.0	26

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37	Structure of the Lifeact-F-actin complex. , 2020, 18, e3000925.		0
38	Structure of the Lifeact-F-actin complex. , 2020, 18, e3000925.		0
39	Structure of the Lifeact-F-actin complex. , 2020, 18, e3000925.		0
40	Structure of the Lifeact-F-actin complex. , 2020, 18, e3000925.		0
41	Structure of the Lifeact-F-actin complex. , 2020, 18, e3000925.		0
42	Structure of the Lifeact-F-actin complex. , 2020, 18, e3000925.		0
43	Title is missing!. , 2020, 16, e1008530.		0
44	Title is missing!. , 2020, 16, e1008530.		0
45	Title is missing!. , 2020, 16, e1008530.		0
46	Title is missing!. , 2020, 16, e1008530.		0
47	Reconstitution of recombinant human CCR4-NOT reveals molecular insights into regulated deadenylation. <i>Nature Communications</i> , 2019, 10, 3173.	12.8	65
48	Common architecture of Tc toxins from human and insect pathogenic bacteria. <i>Science Advances</i> , 2019, 5, eaax6497.	10.3	29
49	Structure of a Tc holotoxin pore provides insights into the translocation mechanism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 23083-23090.	7.1	32
50	Cryo-EM structure of the ClpXP protein degradation machinery. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 946-954.	8.2	68
51	Big insights from tiny crystals. <i>Nature Chemistry</i> , 2019, 11, 106-108.	13.6	5
52	SPHIRE-crYOLO is a fast and accurate fully automated particle picker for cryo-EM. <i>Communications Biology</i> , 2019, 2, 218.	4.4	860
53	Micellar Brønsted Acid Mediated Synthesis of DNA-Tagged Heterocycles. <i>Journal of the American Chemical Society</i> , 2019, 141, 10546-10555.	13.7	59
54	Tc Toxin Complexes: Assembly, Membrane Permeation, and Protein Translocation. <i>Annual Review of Microbiology</i> , 2019, 73, 247-265.	7.3	36

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55	Towards the application of Tc toxins as a universal protein translocation system. <i>Nature Communications</i> , 2019, 10, 5263.	12.8	27
56	Cryo-EM reveals the asymmetric assembly of squid hemocyanin. <i>IUCr</i> , 2019, 6, 426-437.	2.2	7
57	Profilin and formin constitute a pacemaker system for robust actin filament growth. <i>ELife</i> , 2019, 8, .	6.0	80
58	Arrest of trans-SNARE zippering uncovers loosely and tightly docked intermediates in membrane fusion. <i>Journal of Biological Chemistry</i> , 2018, 293, 8645-8655.	3.4	26
59	The complex simplicity of the bacterial cytoskeleton. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 3205-3206.	7.1	0
60	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
61	Tc toxin activation requires unfolding and refolding of a \hat{I}^2 -propeller. <i>Nature</i> , 2018, 563, 209-213.	27.8	45
62	Modulation of septin higher-order structure by the Cdc28 protein kinase. <i>Biologia (Poland)</i> , 2018, 73, 1025-1033.	1.5	4
63	Mechanism of loading and translocation of type VI secretion system effector Tse6. <i>Nature Microbiology</i> , 2018, 3, 1142-1152.	13.3	88
64	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
65	Electron cryo-microscopy structure of the canonical TRPC4 ion channel. <i>ELife</i> , 2018, 7, .	6.0	83
66	Single particle cryo-EM "an optimal tool to study cytoskeletal proteins. <i>Current Opinion in Structural Biology</i> , 2018, 52, 16-24.	5.7	11
67	Electron cryomicroscopy as a powerful tool in biomedical research. <i>Journal of Molecular Medicine</i> , 2018, 96, 483-493.	3.9	11
68	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
69	Membrane insertion of \hat{I}^2 -xenorhabdolyisin in near-atomic detail. <i>ELife</i> , 2018, 7, .	6.0	27
70	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
71	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
72	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

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73	Architecture and mechanism of the late endosomal Rab7-like Ypt7 guanine nucleotide exchange factor complex Mon1â€Ccz1. Nature Communications, 2017, 8, 14034.	12.8	59
74	The molecular basis of Alzheimer's plaques. Science, 2017, 358, 45-46.	12.6	24
75	Lipid Nanodiscs as a Tool for High-Resolution Structure Determination of Membrane Proteins by Single-Particle Cryo-EM. Methods in Enzymology, 2017, 594, 1-30.	1.0	59
76	Near-atomic structure of jasplakinolide-stabilized malaria parasite F-actin reveals the structural basis of filament instability. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 10636-10641.	7.1	64
77	High-resolution Single Particle Analysis from Electron Cryo-microscopy Images Using SPHIRE. Journal of Visualized Experiments, 2017, , .	0.3	161
78	Cryoâ€EM Revolutionizes the Structure Determination of Biomolecules. Angewandte Chemie - International Edition, 2017, 56, 16450-16452.	13.8	14
79	Eine coole Technik: Kryoelektronenmikroskopie. Nachrichten Aus Der Chemie, 2017, 65, 1086-1088.	0.0	0
80	Structural basis for tRNA-dependent cysteine biosynthesis. Nature Communications, 2017, 8, 1521.	12.8	6
81	Electron Cryoâ€microscopy as a Tool for Structureâ€Based Drug Development. Angewandte Chemie - International Edition, 2017, 56, 2846-2860.	13.8	36
82	Kryoâ€Elektronenmikroskopie als Methode fÃ¼r die strukturbasierte Wirkstoffentwicklung. Angewandte Chemie, 2017, 129, 2890-2905.	2.0	10
83	Haptoglobin. Antioxidants and Redox Signaling, 2017, 26, 814-831.	5.4	113
84	Multivalent Rab interactions determine tether-mediated membrane fusion. Molecular Biology of the Cell, 2017, 28, 322-332.	2.1	54
85	Kryoâ€Elektronenmikroskopie revolutioniert die Strukturbestimmung von BiomolekÃ¼len. Angewandte Chemie, 2017, 129, 16670-16672.	2.0	2
86	A recombinant BBSome core complex and how it interacts with ciliary cargo. ELife, 2017, 6, .	6.0	69
87	Molecular requirements for the inter-subunit interaction and kinetochore recruitment of SKAP and Astrin. Nature Communications, 2016, 7, 11407.	12.8	31
88	Membrane insertion of a Tc toxin in near-atomic detail. Nature Structural and Molecular Biology, 2016, 23, 884-890.	8.2	88
89	Cryo-EM structure of a human cytoplasmic actomyosin complex at near-atomic resolution. Nature, 2016, 534, 724-728.	27.8	212
90	Insights from the reconstitution of the divergent outer kinetochore of <i>Drosophila melanogaster</i> . Open Biology, 2016, 6, 150236.	3.6	41

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91	The mother of all actins?. <i>ELife</i> , 2016, 5, .	6.0	3
92	Condensation Agents Determine the Temperature-Pressure Stability of Actin Bundles. <i>Angewandte Chemie - International Edition</i> , 2015, 54, 11088-11092.	13.8	8
93	Deciphering the Tubulin Code. <i>Cell</i> , 2015, 161, 960-961.	28.9	10
94	pH-Regulated Selectivity in Supramolecular Polymerizations: Switching between Coiled and Homopolymers. <i>Chemistry - A European Journal</i> , 2015, 21, 3304-3309.	3.3	69
95	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
96	Functional homologies in vesicle tethering. <i>FEBS Letters</i> , 2015, 589, 2487-2497.	2.8	27
97	The role of Bni5 in the regulation of septin higher-order structure formation. <i>Biological Chemistry</i> , 2015, 396, 1325-1337.	2.5	19
98	An Interbacterial NAD(P) ⁺ Glycohydrolase Toxin Requires Elongation Factor Tu for Delivery to Target Cells. <i>Cell</i> , 2015, 163, 607-619.	28.9	203
99	Determinants of amyloid fibril degradation by the PDZ protease HTRA1. <i>Nature Chemical Biology</i> , 2015, 11, 862-869.	8.0	88
100	Structure of the F-actin-tropomyosin complex. <i>Nature</i> , 2015, 519, 114-117.	27.8	321
101	Structure of Mega-Hemocyanin Reveals Protein Origami in Snails. <i>Structure</i> , 2015, 23, 93-103.	3.3	27
102	Architecture and conformational switch mechanism of the ryanodine receptor. <i>Nature</i> , 2015, 517, 39-43.	27.8	282
103	Exploring the Stability Limits of Actin and Its Suprastructures. <i>Biophysical Journal</i> , 2014, 107, 2982-2992.	0.5	23
104	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
105	A Facile Method for Preparation of Tailored Scaffolds for DNA Origami. <i>Small</i> , 2014, 10, 73-77.	10.0	44
106	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
107	Mechanism of Tc toxin action revealed in molecular detail. <i>Nature</i> , 2014, 508, 61-65.	27.8	149
108	Prebiotic Cell Membranes that Survive Extreme Environmental Pressure Conditions. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 8397-8401.	13.8	18

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109	Modular Assembly of RWD Domains on the Mis12 Complex Underlies Outer Kinetochores Organization. <i>Molecular Cell</i> , 2014, 53, 591-605.	9.7	116
110	The pseudo GTPase CENP-M drives human kinetochores assembly. <i>ELife</i> , 2014, 3, e02978.	6.0	107
111	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
112	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
113	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
114	A syringe-like injection mechanism in <i>Photobacterium luminescens</i> toxins. <i>Nature</i> , 2013, 495, 520-523.	27.8	130
115	Molecular architecture of the human protein deacetylase Sirt1 and its regulation by AROS and resveratrol. <i>Bioscience Reports</i> , 2013, 33, .	2.4	30
116	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
117	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
118	The role of Cdc42 and Gic1 in the regulation of septin filament formation and dissociation. <i>ELife</i> , 2013, 2, e01085.	6.0	65
119	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
120	Real-space processing of helical filaments in SPARX. <i>Journal of Structural Biology</i> , 2012, 177, 302-313.	2.8	31
121	Structure of the Rigor Actin-Tropomyosin-Myosin Complex. <i>Cell</i> , 2012, 150, 327-338.	28.9	297
122	Membrane Fusion Intermediates via Directional and Full Assembly of the SNARE Complex. <i>Science</i> , 2012, 336, 1581-1584.	12.6	210
123	Tropomyosin Movement on F-actin Analyzed by Energy Landscape Determination. <i>Biophysical Journal</i> , 2012, 102, 17a.	0.5	1
124	Functional characterization of the human β -cardiac actin mutations Y166C and M305L involved in hypertrophic cardiomyopathy. <i>Cellular and Molecular Life Sciences</i> , 2012, 69, 3457-3479.	5.4	52
125	Structural Characterization of Polyglutamine Fibrils by Solid-State NMR Spectroscopy. <i>Journal of Molecular Biology</i> , 2011, 412, 121-136.	4.2	88
126	The Fasâ€œFADD 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

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127	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
128	STIM1 Clusters and Activates CRAC Channels via Direct Binding of a Cytosolic Domain to Orai1. Cell, 2009, 136, 876-890.	28.9	839
129	Oligomeric Structure and Functional Characterization of the Urea Transporter from Actinobacillus pleuropneumoniae. Journal of Molecular Biology, 2009, 387, 619-627.	4.2	22
130	Electron Crystallography as a Technique to Study the Structure on Membrane Proteins in a Lipidic Environment. Annual Review of Biophysics, 2009, 38, 89-105.	10.0	66
131	Death Domain Assembly Mechanism Revealed by Crystal Structure of the Oligomeric PIDDosome Core Complex. Cell, 2007, 128, 533-546.	28.9	244
132	Structure of GlnK1 with bound effectors indicates regulatory mechanism for ammonia uptake. EMBO Journal, 2007, 26, 589-599.	7.8	57
133	Revival of electron crystallography. Current Opinion in Structural Biology, 2007, 17, 389-395.	5.7	48
134	Structural Insight into Pre-B Cell Receptor Function. Science, 2007, 316, 291-294.	12.6	101
135	A Virulence Locus of Pseudomonas aeruginosa Encodes a Protein Secretion Apparatus. Science, 2006, 312, 1526-1530.	12.6	984
136	Heterologously Expressed GLT-1 Associates in ~200-nm Protein-Lipid Islands. Biophysical Journal, 2006, 91, 3718-3726.	0.5	15
137	Structure and Function of Prokaryotic Glutamate Transporters from Escherichia coli and Pyrococcus horikoshii. Biochemistry, 2006, 45, 12796-12805.	2.5	35
138	The Architecture of the Multisubunit TRAPP I Complex Suggests a Model for Vesicle Tethering. Cell, 2006, 127, 817-830.	28.9	166
139	Assembly of the Major Light-harvesting Chlorophyll-a/b Complex. Journal of Biological Chemistry, 2006, 281, 25156-25166.	3.4	26
140	Oligomeric Structure of the Carnitine Transporter CaiT from Escherichia coli. Journal of Biological Chemistry, 2006, 281, 4795-4801.	3.4	30
141	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
142	Accelerated 2D Classification With ISAC Using GPUs. Frontiers in Molecular Biosciences, 0, 9, .	3.5	4