

Holger Stark

List of Publications by Year in descending order

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102
papers

14,181
citations

16411

64
h-index

31759

101
g-index

107
all docs

107
docs citations

107
times ranked

14827
citing authors

#	ARTICLE	IF	CITATIONS
1	Self-assembly of a nanoscale DNA box with a controllable lid. <i>Nature</i> , 2009, 459, 73-76.	13.7	1,464
2	Single-particle electron cryo-microscopy: towards atomic resolution. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 307-369.	2.4	535
3	GraFix: sample preparation for single-particle electron cryomicroscopy. <i>Nature Methods</i> , 2008, 5, 53-55.	9.0	476
4	Systematic Analysis of Human Protein Complexes Identifies Chromosome Segregation Proteins. <i>Science</i> , 2010, 328, 593-599.	6.0	465
5	Atomic-resolution protein structure determination by cryo-EM. <i>Nature</i> , 2020, 587, 157-161.	13.7	454
6	Structural insight into filament formation by mammalian septins. <i>Nature</i> , 2007, 449, 311-315.	13.7	406
7	Ribosome dynamics and tRNA movement by time-resolved electron cryomicroscopy. <i>Nature</i> , 2010, 466, 329-333.	13.7	400
8	Structural Basis for the Function of the Ribosomal L7/12 Stalk in Factor Binding and GTPase Activation. <i>Cell</i> , 2005, 121, 991-1004.	13.5	354
9	Efficient encapsulation of antisense oligonucleotides in lipid vesicles using ionizable aminolipids: formation of novel small multilamellar vesicle structures. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2001, 1510, 152-166.	1.4	344
10	Visualization of elongation factor Tu on the Escherichia coli ribosome. <i>Nature</i> , 1997, 389, 403-406.	13.7	342
11	Structure of the E. coli ribosomeâ€EF-Tu complex at <3Å... resolution by Cs-corrected cryo-EM. <i>Nature</i> , 2015, 520, 567-570.	13.7	338
12	Cryo-EM in drug discovery: achievements, limitations and prospects. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 471-492.	21.5	304
13	Protein Composition and Electron Microscopy Structure of Affinity-Purified Human Spliceosomal B Complexes Isolated under Physiological Conditions. <i>Molecular and Cellular Biology</i> , 2006, 26, 5528-5543.	1.1	265
14	biGBac enables rapid gene assembly for the expression of large multisubunit protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2564-9.	3.3	263
15	The Evolutionarily Conserved Core Design of the Catalytic Activation Step of the Yeast Spliceosome. <i>Molecular Cell</i> , 2009, 36, 593-608.	4.5	255
16	Molecular Architecture of the Multiprotein Splicing Factor SF3b. <i>Science</i> , 2003, 300, 980-984.	6.0	246
17	The 70S Escherichia coli ribosome at 23 Å resolution: fitting the ribosomal RNA. <i>Structure</i> , 1995, 3, 815-821.	1.6	237
18	Cryo-EM Structure of a Pre-catalytic Human Spliceosome Primed for Activation. <i>Cell</i> , 2017, 170, 701-713.e11.	13.5	217

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19	Arrangement of RNA and proteins in the spliceosomal U1 small nuclear ribonucleoprotein particle. <i>Nature</i> , 2001, 409, 539-542.	13.7	210
20	Cryo-EM structure of a human spliceosome activated for step 2 of splicing. <i>Nature</i> , 2017, 542, 318-323.	13.7	207
21	The MIS12 complex is a protein interaction hub for outer kinetochore assembly. <i>Journal of Cell Biology</i> , 2010, 190, 835-852.	2.3	196
22	Structure of the Anaphase-Promoting Complex/Cyclosome Interacting with a Mitotic Checkpoint Complex. <i>Science</i> , 2009, 323, 1477-1481.	6.0	195
23	An Assembly Chaperone Collaborates with the SMN Complex to Generate Spliceosomal SnRNPs. <i>Cell</i> , 2008, 135, 497-509.	13.5	189
24	GraFix: Stabilization of Fragile Macromolecular Complexes for Single Particle Cryo-EM. <i>Methods in Enzymology</i> , 2010, 481, 109-126.	0.4	187
25	Composition and three-dimensional EM structure of double affinity-purified, human prespliceosomal A complexes. <i>EMBO Journal</i> , 2007, 26, 1737-1748.	3.5	178
26	Nanobodies: site-specific labeling for super-resolution imaging, rapid epitope-mapping and native protein complex isolation. <i>ELife</i> , 2015, 4, e11349.	2.8	177
27	Structure and Conformational Dynamics of the Human Spliceosomal Bact Complex. <i>Cell</i> , 2018, 172, 454-464.e11.	13.5	175
28	Molecular architecture of the human U4/U6.U5 tri-snRNP. <i>Science</i> , 2016, 351, 1416-1420.	6.0	170
29	Molecular architecture of the <i>Saccharomyces cerevisiae</i> activated spliceosome. <i>Science</i> , 2016, 353, 1399-1405.	6.0	165
30	Structure of the Hepatitis C Virus IRES Bound to the Human 80S Ribosome: Remodeling of the HCV IRES. <i>Structure</i> , 2005, 13, 1695-1706.	1.6	163
31	Architecture of the Human Ndc80-Hec1 Complex, a Critical Constituent of the Outer Kinetochore. <i>Journal of Biological Chemistry</i> , 2005, 280, 29088-29095.	1.6	157
32	Reconstitution of both steps of <i>Saccharomyces cerevisiae</i> splicing with purified spliceosomal components. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 1237-1243.	3.6	150
33	Energy barriers and driving forces in tRNA translocation through the ribosome. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1390-1396.	3.6	150
34	Characterization of purified human B ^{act} spliceosomal complexes reveals compositional and morphological changes during spliceosome activation and first step catalysis. <i>Rna</i> , 2010, 16, 2384-2403.	1.6	142
35	Structural Insights into Nuclear pre-mRNA Splicing in Higher Eukaryotes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032417.	2.3	141
36	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. <i>Cell</i> , 2016, 165, 1440-1453.	13.5	126

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37	Cryo-EM of Mitotic Checkpoint Complex-Bound APC/C Reveals Reciprocal and Conformational Regulation of Ubiquitin Ligation. <i>Molecular Cell</i> , 2016, 63, 593-607.	4.5	123
38	APC15 mediates CDC20 autoubiquitylation by APC/CMCC and disassembly of the mitotic checkpoint complex. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1116-1123.	3.6	118
39	The Three-dimensional Structure of an Ionotropic Glutamate Receptor Reveals a Dimer-of-dimers Assembly. <i>Journal of Molecular Biology</i> , 2004, 344, 435-442.	2.0	113
40	Mechanism of APC/C ^{CDC20} activation by mitotic phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E2570-8.	3.3	112
41	Molecular Basis of Transcription-Coupled Pre-mRNA Capping. <i>Molecular Cell</i> , 2015, 58, 1079-1089.	4.5	109
42	Posing the APC/C E3 Ubiquitin Ligase to Orchestrate Cell Division. <i>Trends in Cell Biology</i> , 2019, 29, 117-134.	3.6	101
43	Mechanism of Polyubiquitination by Human Anaphase-Promoting Complex: RING Repurposing for Ubiquitin Chain Assembly. <i>Molecular Cell</i> , 2014, 56, 246-260.	4.5	98
44	GraDeR: Membrane Protein Complex Preparation for Single-Particle Cryo-EM. <i>Structure</i> , 2015, 23, 1769-1775.	1.6	96
45	The pathway to GTPase activation of elongation factor SelB on the ribosome. <i>Nature</i> , 2016, 540, 80-85.	13.7	93
46	Structure of influenza haemagglutinin at neutral and at fusogenic pH by electron cryo-microscopy. <i>FEBS Letters</i> , 1999, 463, 255-259.	1.3	90
47	Substrate binding on the APC/C occurs between the coactivator Cdh1 and the processivity factor Doc1. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 6-13.	3.6	89
48	Spontaneous reverse movement of mRNA-bound tRNA through the ribosome. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 318-324.	3.6	87
49	ProteoPlex: stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. <i>Nature Methods</i> , 2015, 12, 859-865.	9.0	87
50	Localization of the Coactivator Cdh1 and the Cullin Subunit Apc2 in a Cryo-Electron Microscopy Model of Vertebrate APC/C. <i>Molecular Cell</i> , 2005, 20, 867-879.	4.5	85
51	CRYO-ELECTRON MICROSCOPY OF SPLICEOSOMAL COMPONENTS. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006, 35, 435-457.	18.3	82
52	Structural Basis of Assembly Chaperone- Mediated snRNP Formation. <i>Molecular Cell</i> , 2013, 49, 692-703.	4.5	82
53	Electron microscopy structure of human APC/CCDH1&EEM11 reveals multimodal mechanism of E3 ligase shutdown. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 827-835.	3.6	82
54	Electron radiation damage to protein crystals of bacteriorhodopsin at different temperatures. <i>Ultramicroscopy</i> , 1996, 63, 75-79.	0.8	81

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55	RING E3 mechanism for ubiquitin ligation to a disordered substrate visualized for human anaphase-promoting complex. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5272-5279.	3.3	80
56	A new model for the three-dimensional folding of Escherichia coli 16 s ribosomal RNA. III . The topography of the functional centre 1 . Paper II in this series is an accompanying paper, Mueller & Brimacombe (1997b). 1 Edited by D. E. Draper. Journal of Molecular Biology, 1997, 271, 566-587.	2.0	76
57	Ribosome dynamics during decoding. Philosophical Transactions of the Royal Society B: Biological Sciences, 2017, 372, 20160182.	1.8	76
58	Chromatin Affinity Purification and Quantitative Mass Spectrometry Defining the Interactome of Histone Modification Patterns. Molecular and Cellular Proteomics, 2011, 10, M110.005371.	2.5	74
59	Major Conformational Change in the Complex SF3b upon Integration into the Spliceosomal U11/U12 di-snRNP as Revealed by Electron Cryomicroscopy. Molecular Cell, 2005, 17, 869-883.	4.5	70
60	Organization of Core Spliceosomal Components U5 snRNA Loop I and U4/U6 Di-snRNP within U4/U6.U5 Tri-snRNP as Revealed by Electron Cryomicroscopy. Molecular Cell, 2006, 24, 267-278.	4.5	70
61	Crystal structure of a core spliceosomal protein interface. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 1266-1271.	3.3	70
62	Three-Dimensional Structure of the Anaphase-Promoting Complex. Molecular Cell, 2001, 7, 907-913.	4.5	69
63	Localization of Prp8, Brr2, Snu114 and U4/U6 proteins in the yeast tri-snRNP by electron microscopy. Nature Structural and Molecular Biology, 2008, 15, 1206-1212.	3.6	68
64	Three-dimensional structure of a pre-catalytic human spliceosomal complex B. Nature Structural and Molecular Biology, 2004, 11, 463-468.	3.6	66
65	Aerosolized nanogram quantities of plasmid DNA mediate highly efficient gene delivery to mouse airway epithelium. Molecular Therapy, 2005, 12, 493-501.	3.7	64
66	Snapshots of the RNA editing machine in trypanosomes captured at different assembly stages in vivo. EMBO Journal, 2009, 28, 766-778.	3.5	64
67	Structural basis for cooperativity of CRM1 export complex formation. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 960-965.	3.3	64
68	Molecular architecture of the human 17S U2 snRNP. Nature, 2020, 583, 310-313.	13.7	63
69	Correlation of the expansion segments in mammalian rRNA with the fine structure of the 80 s ribosome; a cryoelectron microscopic reconstruction of the rabbit reticulocyte ribosome at 21 Å resolution. Journal of Molecular Biology, 1998, 279, 403-421.	2.0	62
70	Characterization of Tailor-Made Copolymers of Oligo(ethylene glycol) Methyl Ether Methacrylate and N-Dimethylaminoethyl Methacrylate as Nonviral Gene Transfer Agents: Influence of Macromolecular Structure on Gene Vector Particle Properties and Transfection Efficiency. Biomacromolecules, 2010, 11, 39-50.	2.6	61
71	Advantages of CCD detectors for de novo three-dimensional structure determination in single-particle electron microscopy. Journal of Structural Biology, 2005, 151, 92-105.	1.3	59
72	Structure of a molluscan hemocyanin didecamer (HtH1 from Haliotis tuberculata) at 12 Å resolution by cryoelectron microscopy. Journal of Molecular Biology, 2000, 298, 21-34.	2.0	55

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73	Mechanism of protein-guided folding of the active site U2/U6 RNA during spliceosome activation. <i>Science</i> , 2020, 370, .	6.0	50
74	Structure of the Lassa Virus Nucleoprotein Revealed by X-ray Crystallography, Small-angle X-ray Scattering, and Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2011, 286, 38748-38756.	1.6	47
75	Exon, intron and splice site locations in the spliceosomal B complex. <i>EMBO Journal</i> , 2009, 28, 2283-2292.	3.5	46
76	Stacked bilayer helices: a new structural organization of amphiphilic molecules. <i>Ultramicroscopy</i> , 1996, 62, 133-139.	0.8	43
77	3D Cryo-EM Structure of an Active Step I Spliceosome and Localization of Its Catalytic Core. <i>Molecular Cell</i> , 2010, 40, 927-938.	4.5	43
78	Sample preparation of biological macromolecular assemblies for the determination of high-resolution structures by cryo-electron microscopy. <i>Microscopy (Oxford, England)</i> , 2016, 65, 23-34.	0.7	43
79	Self-Assembly of Ternary Insulin~Polyethylenimine (PEI)~DNA Nanoparticles for Enhanced Gene Delivery and Expression in Alveolar Epithelial Cells. <i>Biomacromolecules</i> , 2009, 10, 2912-2920.	2.6	42
80	Topology and structure of an engineered human cohesin complex bound to Pds5B. <i>Nature Communications</i> , 2016, 7, 12523.	5.8	42
81	Elucidating the medium-resolution structure of ribosomal particles: an interplay between electron cryo-microscopy and X-ray crystallography. <i>Structure</i> , 1999, 7, 931-941.	1.6	41
82	Discovery of a Regulatory Subunit of the Yeast Fatty Acid Synthase. <i>Cell</i> , 2020, 180, 1130-1143.e20.	13.5	40
83	Structural mapping of spliceosomes by electron microscopy. <i>Current Opinion in Structural Biology</i> , 2009, 19, 96-102.	2.6	38
84	Structural insights into how Prp5 proofreads the pre-mRNA branch site. <i>Nature</i> , 2021, 596, 296-300.	13.7	28
85	Structural Insights into the Roles of Metazoan-Specific Splicing Factors in the Human Step 1 Spliceosome. <i>Molecular Cell</i> , 2020, 80, 127-139.e6.	4.5	26
86	Structure of yeast U6 snRNPs: Arrangement of Prp24p and the LSM complex as revealed by electron microscopy. <i>Rna</i> , 2008, 14, 2528-2537.	1.6	25
87	Quaternary Structure of the European Spiny Lobster (<i>Palinurus elephas</i>) 1Å—6-mer Hemocyanin from cryoEM and Amino Acid Sequence Data. <i>Journal of Molecular Biology</i> , 2003, 325, 99-109.	2.0	24
88	Parallel, distributed and GPU computing technologies in single-particle electron microscopy. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 659-671.	2.5	24
89	Structural and Functional Analyses of the Human PDH Complex Suggest a "Division-of-Labor" Mechanism by Local E1 and E3 Clusters. <i>Structure</i> , 2019, 27, 1124-1136.e4.	1.6	23
90	An Approach for De Novo Structure Determination of Dynamic Molecular Assemblies by Electron Cryomicroscopy. <i>Structure</i> , 2010, 18, 667-676.	1.6	22

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91	Protein engineering of a ubiquitin-variant inhibitor of APC/C identifies a cryptic K48 ubiquitin chain binding site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 17280-17289.	3.3	22
92	Three-Dimensional Electron Cryomicroscopy of Ribosomes. <i>Current Protein and Peptide Science</i> , 2002, 3, 79-91.	0.7	22
93	Cryonegative Staining of Macromolecular Assemblies. <i>Methods in Enzymology</i> , 2010, 481, 127-145.	0.4	17
94	Structural Determinants and Mechanism of Mammalian CRM1 Allostery. <i>Structure</i> , 2013, 21, 1350-1360.	1.6	17
95	Towards understanding selenocysteine incorporation into bacterial proteins. <i>Biological Chemistry</i> , 2007, 388, 1061-1067.	1.2	16
96	Conformational rearrangements upon start codon recognition in human 48S translation initiation complex. <i>Nucleic Acids Research</i> , 2022, 50, 5282-5298.	6.5	15
97	Novel insights into the architecture and protein interaction network of yeast eIF3. <i>Rna</i> , 2012, 18, 2306-2319.	1.6	13
98	Merging Molecular Electron Microscopy and Mass Spectrometry by Carbon Film-assisted Endoproteinase Digestion. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1729-1741.	2.5	10
99	DNA translocation activity of the multifunctional replication protein ORF904 from the archaeal plasmid pRN1. <i>Nucleic Acids Research</i> , 2009, 37, 6831-6848.	6.5	9
100	Automated correlation of single particle tilt pairs for Random Conical Tilt and Orthogonal Tilt Reconstructions. <i>Journal of Structural Biology</i> , 2013, 181, 149-154.	1.3	5
101	Expression of enterovirus 71 virus-like particles in transgenic enoki (<i>Flammulina velutipes</i>). <i>Applied Microbiology and Biotechnology</i> , 2015, 99, 6765-6774.	1.7	4
102	Experience with liquid helium cooling in electron cryomicroscopy. <i>Microscopy and Microanalysis</i> , 2003, 9, 397-397.	0.2	0