

# 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	Conformational rearrangements upon start codon recognition in human 48S translation initiation complex. <i>Nucleic Acids Research</i> , 2022, 50, 5282-5298.	6.5	15
2	Structural insights into how Prp5 proofreads the pre-mRNA branch site. <i>Nature</i> , 2021, 596, 296-300.	13.7	28
3	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
4	Atomic-resolution protein structure determination by cryo-EM. <i>Nature</i> , 2020, 587, 157-161.	13.7	454
5	Mechanism of protein-guided folding of the active site U2/U6 RNA during spliceosome activation. <i>Science</i> , 2020, 370, .	6.0	50
6	Molecular architecture of the human 17S U2 snRNP. <i>Nature</i> , 2020, 583, 310-313.	13.7	63
7	Discovery of a Regulatory Subunit of the Yeast Fatty Acid Synthase. <i>Cell</i> , 2020, 180, 1130-1143.e20.	13.5	40
8	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
9	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
10	Structural Insights into Nuclear pre-mRNA Splicing in Higher Eukaryotes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032417.	2.3	141
11	Posing the APC/C E3 Ubiquitin Ligase to Orchestrate Cell Division. <i>Trends in Cell Biology</i> , 2019, 29, 117-134.	3.6	101
12	Structure and Conformational Dynamics of the Human Spliceosomal Bact Complex. <i>Cell</i> , 2018, 172, 454-464.e11.	13.5	175
13	Cryo-EM in drug discovery: achievements, limitations and prospects. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 471-492.	21.5	304
14	Cryo-EM structure of a human spliceosome activated for step 2 of splicing. <i>Nature</i> , 2017, 542, 318-323.	13.7	207
15	Ribosome dynamics during decoding. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160182.	1.8	76
16	Cryo-EM Structure of a Pre-catalytic Human Spliceosome Primed for Activation. <i>Cell</i> , 2017, 170, 701-713.e11.	13.5	217
17	Topology and structure of an engineered human cohesin complex bound to Pds5B. <i>Nature Communications</i> , 2016, 7, 12523.	5.8	42
18	Mechanism of APC/C <sup>CDC20</sup> 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

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19	biGBac enables rapid gene assembly for the expression of large multisubunit protein complexes. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E2564-9.	3.3	263
20	Cryo-EM of Mitotic Checkpoint Complex-Bound APC/C Reveals Reciprocal and Conformational Regulation of Ubiquitin Ligation. Molecular Cell, 2016, 63, 593-607.	4.5	123
21	Molecular architecture of the <i>Saccharomyces cerevisiae</i> activated spliceosome. Science, 2016, 353, 1399-1405.	6.0	165
22	The pathway to GTPase activation of elongation factor SelB on the ribosome. Nature, 2016, 540, 80-85.	13.7	93
23	Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. Cell, 2016, 165, 1440-1453.	13.5	126
24	Sample preparation of biological macromolecular assemblies for the determination of high-resolution structures by cryo-electron microscopy. Microscopy (Oxford, England), 2016, 65, 23-34.	0.7	43
25	Molecular architecture of the human U4/U6.U5 tri-snRNP. Science, 2016, 351, 1416-1420.	6.0	170
26	Nanobodies: site-specific labeling for super-resolution imaging, rapid epitope-mapping and native protein complex isolation. ELife, 2015, 4, e11349.	2.8	177
27	Structure of the E. coli ribosomeâ€EF-Tu complex at 3.3 Å resolution by Cs-corrected cryo-EM. Nature, 2015, 520, 567-570.	13.7	338
28	ProteoPlex: stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. Nature Methods, 2015, 12, 859-865.	9.0	87
29	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
30	Molecular Basis of Transcription-Coupled Pre-mRNA Capping. Molecular Cell, 2015, 58, 1079-1089.	4.5	109
31	Expression of enterovirus 71 virus-like particles in transgenic enoki ( <i>Flammulina velutipes</i> ). Applied Microbiology and Biotechnology, 2015, 99, 6765-6774.	1.7	4
32	GraDeR: Membrane Protein Complex Preparation for Single-Particle Cryo-EM. Structure, 2015, 23, 1769-1775.	1.6	96
33	Mechanism of Polyubiquitination by Human Anaphase-Promoting Complex: RING Repurposing for Ubiquitin Chain Assembly. Molecular Cell, 2014, 56, 246-260.	4.5	98
34	Structural Basis of Assembly Chaperone-Mediated snRNP Formation. Molecular Cell, 2013, 49, 692-703.	4.5	82
35	Electron microscopy structure of human APC/CCDH1â€EMI1 reveals multimodal mechanism of E3 ligase shutdown. Nature Structural and Molecular Biology, 2013, 20, 827-835.	3.6	82
36	Energy barriers and driving forces in tRNA translocation through the ribosome. Nature Structural and Molecular Biology, 2013, 20, 1390-1396.	3.6	150

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37	Structural Determinants and Mechanism of Mammalian CRM1 Allostery. <i>Structure</i> , 2013, 21, 1350-1360.	1.6	17
38	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
39	Structural basis for cooperativity of CRM1 export complex formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 960-965.	3.3	64
40	Novel insights into the architecture and protein interaction network of yeast eIF3. <i>Rna</i> , 2012, 18, 2306-2319.	1.6	13
41	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
42	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
43	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
44	Chromatin Affinity Purification and Quantitative Mass Spectrometry Defining the Interactome of Histone Modification Patterns. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.005371.	2.5	74
45	An Approach for De Novo Structure Determination of Dynamic Molecular Assemblies by Electron Cryomicroscopy. <i>Structure</i> , 2010, 18, 667-676.	1.6	22
46	Ribosome dynamics and tRNA movement by time-resolved electron cryomicroscopy. <i>Nature</i> , 2010, 466, 329-333.	13.7	400
47	Characterization of purified human B <sup>act</sup> spliceosomal complexes reveals compositional and morphological changes during spliceosome activation and first step catalysis. <i>Rna</i> , 2010, 16, 2384-2403.	1.6	142
48	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
49	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
50	GraFix: Stabilization of Fragile Macromolecular Complexes for Single Particle Cryo-EM. <i>Methods in Enzymology</i> , 2010, 481, 109-126.	0.4	187
51	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
52	Characterization of Tailor-Made Copolymers of Oligo(ethylene glycol) Methyl Ether Methacrylate and <i>N,N</i> -Dimethylaminoethyl Methacrylate as Nonviral Gene Transfer Agents: Influence of Macromolecular Structure on Gene Vector Particle Properties and Transfection Efficiency. <i>Biomacromolecules</i> , 2010, 11, 39-50.	2.6	61
53	Systematic Analysis of Human Protein Complexes Identifies Chromosome Segregation Proteins. <i>Science</i> , 2010, 328, 593-599.	6.0	465
54	Cryonegative Staining of Macromolecular Assemblies. <i>Methods in Enzymology</i> , 2010, 481, 127-145.	0.4	17

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55	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
56	Structural mapping of spliceosomes by electron microscopy. <i>Current Opinion in Structural Biology</i> , 2009, 19, 96-102.	2.6	38
57	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
58	Exon, intron and splice site locations in the spliceosomal B complex. <i>EMBO Journal</i> , 2009, 28, 2283-2292.	3.5	46
59	Snapshots of the RNA editing machine in trypanosomes captured at different assembly stages in vivo. <i>EMBO Journal</i> , 2009, 28, 766-778.	3.5	64
60	Self-assembly of a nanoscale DNA box with a controllable lid. <i>Nature</i> , 2009, 459, 73-76.	13.7	1,464
61	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
62	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
63	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
64	Structure of the Anaphase-Promoting Complex/Cyclosome Interacting with a Mitotic Checkpoint Complex. <i>Science</i> , 2009, 323, 1477-1481.	6.0	195
65	Localization of Prp8, Brr2, Snu114 and U4/U6 proteins in the yeast tri-snRNP by electron microscopy. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 1206-1212.	3.6	68
66	GraFix: sample preparation for single-particle electron cryomicroscopy. <i>Nature Methods</i> , 2008, 5, 53-55.	9.0	476
67	An Assembly Chaperone Collaborates with the SMN Complex to Generate Spliceosomal SnRNPs. <i>Cell</i> , 2008, 135, 497-509.	13.5	189
68	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
69	Towards understanding selenocysteine incorporation into bacterial proteins. <i>Biological Chemistry</i> , 2007, 388, 1061-1067.	1.2	16
70	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
71	Spontaneous reverse movement of mRNA-bound tRNA through the ribosome. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 318-324.	3.6	87
72	Structural insight into filament formation by mammalian septins. <i>Nature</i> , 2007, 449, 311-315.	13.7	406

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73	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
74	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. <i>Molecular Cell</i> , 2006, 24, 267-278.	4.5	70
75	CRYO-ELECTRON MICROSCOPY OF SPLICEOSOMAL COMPONENTS. <i>Annual Review of Biophysics and Biomolecular Structure</i> , 2006, 35, 435-457.	18.3	82
76	Crystal structure of a core spliceosomal protein interface. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 1266-1271.	3.3	70
77	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
78	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
79	Aerosolized nanogram quantities of plasmid DNA mediate highly efficient gene delivery to mouse airway epithelium. <i>Molecular Therapy</i> , 2005, 12, 493-501.	3.7	64
80	Major Conformational Change in the Complex SF3b upon Integration into the Spliceosomal U11/U12 di-snRNP as Revealed by Electron Cryomicroscopy. <i>Molecular Cell</i> , 2005, 17, 869-883.	4.5	70
81	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
82	Advantages of CCD detectors for de novo three-dimensional structure determination in single-particle electron microscopy. <i>Journal of Structural Biology</i> , 2005, 151, 92-105.	1.3	59
83	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
84	Three-dimensional structure of a pre-catalytic human spliceosomal complex B. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 463-468.	3.6	66
85	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
86	Quaternary Structure of the European Spiny Lobster ( <i>Palinurus elephas</i> ) 1 $\text{\AA}$ -6-mer Hemocyanin from cryoEM and Amino Acid Sequence Data. <i>Journal of Molecular Biology</i> , 2003, 325, 99-109.	2.0	24
87	Molecular Architecture of the Multiprotein Splicing Factor SF3b. <i>Science</i> , 2003, 300, 980-984.	6.0	246
88	Experience with liquid helium cooling in electron cryomicroscopy. <i>Microscopy and Microanalysis</i> , 2003, 9, 397-397.	0.2	0
89	Three-Dimensional Electron Cryomicroscopy of Ribosomes. <i>Current Protein and Peptide Science</i> , 2002, 3, 79-91.	0.7	22
90	Three-Dimensional Structure of the Anaphase-Promoting Complex. <i>Molecular Cell</i> , 2001, 7, 907-913.	4.5	69

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91	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
92	Arrangement of RNA and proteins in the spliceosomal U1 small nuclear ribonucleoprotein particle. <i>Nature</i> , 2001, 409, 539-542.	13.7	210
93	Single-particle electron cryo-microscopy: towards atomic resolution. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 307-369.	2.4	535
94	Structure of a molluscan hemocyanin didecamer (HtH1 from <i>Haliotis tuberculata</i> ) at 12 Å... resolution by cryoelectron microscopy. <i>Journal of Molecular Biology</i> , 2000, 298, 21-34.	2.0	55
95	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
96	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
97	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. <i>Journal of Molecular Biology</i> , 1998, 279, 403-421.	2.0	62
98	A new model for the three-dimensional folding of <i>Escherichia coli</i> 16 s ribosomal RNA. III. The topography of the functional centre 1. Paper II in this series is an accompanying paper, Mueller & Brimacombe (1997b). Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1997, 271, 566-587.	2.0	76
99	Visualization of elongation factor Tu on the <i>Escherichia coli</i> ribosome. <i>Nature</i> , 1997, 389, 403-406.	13.7	342
100	Stacked bilayer helices: a new structural organization of amphiphilic molecules. <i>Ultramicroscopy</i> , 1996, 62, 133-139.	0.8	43
101	Electron radiation damage to protein crystals of bacteriorhodopsin at different temperatures. <i>Ultramicroscopy</i> , 1996, 63, 75-79.	0.8	81
102	The 70S <i>Escherichia coli</i> ribosome at 23 Å resolution: fitting the ribosomal RNA. <i>Structure</i> , 1995, 3, 815-821.	1.6	237