

# Holger Stark

## List of Publications by Year in descending order

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Version: 2024-02-01

102  
papers

14,181  
citations

16451

64  
h-index

31849

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.  | 14.5 | 15        |
| 2  | Structural insights into how Prp5 proofreads the pre-mRNA branch site. <i>Nature</i> , 2021, 596, 296-300.  | 27.8 | 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.   | 9.7  | 26        |
| 4  | Atomic-resolution protein structure determination by cryo-EM. <i>Nature</i> , 2020, 587, 157-161.   | 27.8 | 454       |
| 5  | Mechanism of protein-guided folding of the active site U2/U6 RNA during spliceosome activation. <i>Science</i> , 2020, 370, .   | 12.6 | 50        |
| 6  | Molecular architecture of the human 17S U2 snRNP. <i>Nature</i> , 2020, 583, 310-313.   | 27.8 | 63        |
| 7  | Discovery of a Regulatory Subunit of the Yeast Fatty Acid Synthase. <i>Cell</i> , 2020, 180, 1130-1143.e20.   | 28.9 | 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.   | 3.3  | 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. | 7.1  | 22        |
| 10 | Structural Insights into Nuclear pre-mRNA Splicing in Higher Eukaryotes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a032417.   | 5.5  | 141       |
| 11 | Posing the APC/C E3 Ubiquitin Ligase to Orchestrate Cell Division. <i>Trends in Cell Biology</i> , 2019, 29, 117-134.   | 7.9  | 101       |
| 12 | Structure and Conformational Dynamics of the Human Spliceosomal Bact Complex. <i>Cell</i> , 2018, 172, 454-464.e11.   | 28.9 | 175       |
| 13 | Cryo-EM in drug discovery: achievements, limitations and prospects. <i>Nature Reviews Drug Discovery</i> , 2018, 17, 471-492.   | 46.4 | 304       |
| 14 | Cryo-EM structure of a human spliceosome activated for step 2 of splicing. <i>Nature</i> , 2017, 542, 318-323.  | 27.8 | 207       |
| 15 | Ribosome dynamics during decoding. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2017, 372, 20160182.   | 4.0  | 76        |
| 16 | Cryo-EM Structure of a Pre-catalytic Human Spliceosome Primed for Activation. <i>Cell</i> , 2017, 170, 701-713.e11.   | 28.9 | 217       |
| 17 | Topology and structure of an engineered human cohesin complex bound to Pds5B. <i>Nature Communications</i> , 2016, 7, 12523.  | 12.8 | 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.   | 7.1  | 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.                        | 7.1  | 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.   | 9.7  | 123       |
| 21 | Molecular architecture of the <i>Saccharomyces cerevisiae</i> activated spliceosome. Science, 2016, 353, 1399-1405.  | 12.6 | 165       |
| 22 | The pathway to GTPase activation of elongation factor SelB on the ribosome. Nature, 2016, 540, 80-85.  | 27.8 | 93        |
| 23 | Dual RING E3 Architectures Regulate Multiubiquitination and Ubiquitin Chain Elongation by APC/C. Cell, 2016, 165, 1440-1453.   | 28.9 | 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.                                 | 1.5  | 43        |
| 25 | Molecular architecture of the human U4/U6.U5 tri-snRNP. Science, 2016, 351, 1416-1420.   | 12.6 | 170       |
| 26 | Nanobodies: site-specific labeling for super-resolution imaging, rapid epitope-mapping and native protein complex isolation. ELife, 2015, 4, e11349.   | 6.0  | 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.  | 27.8 | 338       |
| 28 | ProteoPlex: stability optimization of macromolecular complexes by sparse-matrix screening of chemical space. Nature Methods, 2015, 12, 859-865.  | 19.0 | 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. | 7.1  | 80        |
| 30 | Molecular Basis of Transcription-Coupled Pre-mRNA Capping. Molecular Cell, 2015, 58, 1079-1089.  | 9.7  | 109       |
| 31 | Expression of enterovirus 71 virus-like particles in transgenic enoki ( <i>Flammulina velutipes</i> ). Applied Microbiology and Biotechnology, 2015, 99, 6765-6774.  | 3.6  | 4         |
| 32 | GraDeR: Membrane Protein Complex Preparation for Single-Particle Cryo-EM. Structure, 2015, 23, 1769-1775.  | 3.3  | 96        |
| 33 | Mechanism of Polyubiquitination by Human Anaphase-Promoting Complex: RING Repurposing for Ubiquitin Chain Assembly. Molecular Cell, 2014, 56, 246-260.   | 9.7  | 98        |
| 34 | Structural Basis of Assembly Chaperone-Mediated snRNP Formation. Molecular Cell, 2013, 49, 692-703.  | 9.7  | 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.   | 8.2  | 82        |
| 36 | Energy barriers and driving forces in tRNA translocation through the ribosome. Nature Structural and Molecular Biology, 2013, 20, 1390-1396.   | 8.2  | 150       |

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|----|--|------|-----------|
| 37 | Structural Determinants and Mechanism of Mammalian CRM1 Allostery. <i>Structure</i> , 2013, 21, 1350-1360.   | 3.3  | 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.  | 2.8  | 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.  | 7.1  | 64        |
| 40 | Novel insights into the architecture and protein interaction network of yeast eIF3. <i>Rna</i> , 2012, 18, 2306-2319.  | 3.5  | 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.   | 8.2  | 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.  | 8.2  | 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.  | 3.4  | 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.  | 3.8  | 74        |
| 45 | An Approach for De Novo Structure Determination of Dynamic Molecular Assemblies by Electron Cryomicroscopy. <i>Structure</i> , 2010, 18, 667-676.  | 3.3  | 22        |
| 46 | Ribosome dynamics and tRNA movement by time-resolved electron cryomicroscopy. <i>Nature</i> , 2010, 466, 329-333.  | 27.8 | 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.   | 3.5  | 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.   | 3.8  | 10        |
| 49 | The MIS12 complex is a protein interaction hub for outer kinetochore assembly. <i>Journal of Cell Biology</i> , 2010, 190, 835-852.  | 5.2  | 196       |
| 50 | GraFix: Stabilization of Fragile Macromolecular Complexes for Single Particle Cryo-EM. <i>Methods in Enzymology</i> , 2010, 481, 109-126.  | 1.0  | 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.  | 9.7  | 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. | 5.4  | 61        |
| 53 | Systematic Analysis of Human Protein Complexes Identifies Chromosome Segregation Proteins. <i>Science</i> , 2010, 328, 593-599.  | 12.6 | 465       |
| 54 | Cryonegative Staining of Macromolecular Assemblies. <i>Methods in Enzymology</i> , 2010, 481, 127-145.   | 1.0  | 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.                                 | 14.5 | 9         |
| 56 | Structural mapping of spliceosomes by electron microscopy. <i>Current Opinion in Structural Biology</i> , 2009, 19, 96-102.   | 5.7  | 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.  | 7.8  | 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.  | 7.8  | 64        |
| 60 | Self-assembly of a nanoscale DNA box with a controllable lid. <i>Nature</i> , 2009, 459, 73-76.   | 27.8 | 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.             | 8.2  | 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. | 5.4  | 42        |
| 63 | The Evolutionarily Conserved Core Design of the Catalytic Activation Step of the Yeast Spliceosome. <i>Molecular Cell</i> , 2009, 36, 593-608.  | 9.7  | 255       |
| 64 | Structure of the Anaphase-Promoting Complex/Cyclosome Interacting with a Mitotic Checkpoint Complex. <i>Science</i> , 2009, 323, 1477-1481.   | 12.6 | 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.                        | 8.2  | 68        |
| 66 | GraFix: sample preparation for single-particle electron cryomicroscopy. <i>Nature Methods</i> , 2008, 5, 53-55.   | 19.0 | 476       |
| 67 | An Assembly Chaperone Collaborates with the SMN Complex to Generate Spliceosomal SnRNPs. <i>Cell</i> , 2008, 135, 497-509.  | 28.9 | 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.   | 3.5  | 25        |
| 69 | Towards understanding selenocysteine incorporation into bacterial proteins. <i>Biological Chemistry</i> , 2007, 388, 1061-1067.   | 2.5  | 16        |
| 70 | Composition and three-dimensional EM structure of double affinity-purified, human prespliceosomal A complexes. <i>EMBO Journal</i> , 2007, 26, 1737-1748.   | 7.8  | 178       |
| 71 | Spontaneous reverse movement of mRNA-bound tRNA through the ribosome. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 318-324.   | 8.2  | 87        |
| 72 | Structural insight into filament formation by mammalian septins. <i>Nature</i> , 2007, 449, 311-315.  | 27.8 | 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.     | 2.3  | 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.                        | 9.7  | 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.  | 7.1  | 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.  | 3.3  | 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.   | 3.4  | 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.   | 8.2  | 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.                          | 9.7  | 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.  | 9.7  | 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.                                 | 2.8  | 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.  | 28.9 | 354       |
| 84 | Three-dimensional structure of a pre-catalytic human spliceosomal complex B. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 463-468.  | 8.2  | 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.   | 4.2  | 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. | 4.2  | 24        |
| 87 | Molecular Architecture of the Multiprotein Splicing Factor SF3b. <i>Science</i> , 2003, 300, 980-984.   | 12.6 | 246       |
| 88 | Experience with liquid helium cooling in electron cryomicroscopy. <i>Microscopy and Microanalysis</i> , 2003, 9, 397-397.   | 0.4  | 0         |
| 89 | Three-Dimensional Electron Cryomicroscopy of Ribosomes. <i>Current Protein and Peptide Science</i> , 2002, 3, 79-91.  | 1.4  | 22        |
| 90 | Three-Dimensional Structure of the Anaphase-Promoting Complex. <i>Molecular Cell</i> , 2001, 7, 907-913.  | 9.7  | 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.  | 2.6  | 344       |
| 92  | Arrangement of RNA and proteins in the spliceosomal U1 small nuclear ribonucleoprotein particle. <i>Nature</i> , 2001, 409, 539-542.  | 27.8 | 210       |
| 93  | Single-particle electron cryo-microscopy: towards atomic resolution. <i>Quarterly Reviews of Biophysics</i> , 2000, 33, 307-369.  | 5.7  | 535       |
| 94  | Structure of a molluscan hemocyanin dodecamer (HtH1 from <i>Haliotis tuberculata</i> ) at 12 Å... resolution by cryoelectron microscopy. <i>Journal of Molecular Biology</i> , 2000, 298, 21-34.  | 4.2  | 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.   | 3.3  | 41        |
| 96  | Structure of influenza haemagglutinin at neutral and at fusogenic pH by electron cryo-microscopy. <i>FEBS Letters</i> , 1999, 463, 255-259.   | 2.8  | 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.                                       | 4.2  | 62        |
| 98  | 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). Edited by D. E. Draper. <i>Journal of Molecular Biology</i> , 1997, 271, 566-587. | 4.2  | 76        |
| 99  | Visualization of elongation factor Tu on the Escherichia coli ribosome. <i>Nature</i> , 1997, 389, 403-406.   | 27.8 | 342       |
| 100 | Stacked bilayer helices: a new structural organization of amphiphilic molecules. <i>Ultramicroscopy</i> , 1996, 62, 133-139.  | 1.9  | 43        |
| 101 | Electron radiation damage to protein crystals of bacteriorhodopsin at different temperatures. <i>Ultramicroscopy</i> , 1996, 63, 75-79.   | 1.9  | 81        |
| 102 | The 70S Escherichia coli ribosome at 23 Å resolution: fitting the ribosomal RNA. <i>Structure</i> , 1995, 3, 815-821.   | 3.3  | 237       |