# Martin Jinek

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6032938/publications.pdf

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| 82 | 26,619 | 57631 | 79541 |
|---|---|---|---|
| papers | citations | 44 h-index | 73 g-index |

| 106 | 106 | 106 | 26259 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | A Programmable Dual-RNAâ€“Guided DNA Endonuclease in Adaptive Bacterial Immunity. Science, 2012, 337, 816-821. | 6.0 | 12,811 |
| 2 | RNA-programmed genome editing in human cells. ELife, 2013, 2, e00471. | 2.8 | 1,830 |
| 3 | DNA interrogation by the CRISPR RNA-guided endonuclease Cas9. Nature, 2014, 507, 62-67. | 13.7 | 1,573 |
| 4 | Structural basis of PAM-dependent target DNA recognition by the Cas9 endonuclease. Nature, 2014, 513, 569-573. | 13.7 | 1,075 |
| 5 | Structures of Cas9 Endonucleases Reveal RNA-Mediated Conformational Activation. Science, 2014, 343, 1247997. | 6.0 | 938 |
| 6 | A three-dimensional view of the molecular machinery of RNA interference. Nature, 2009, 457, 405-412. | 13.7 | 651 |
| 7 | Sequence- and Structure-Specific RNA Processing by a CRISPR Endonuclease. Science, 2010, 329, 1355-1358. | 6.0 | 599 |
| 8 | A prudent path forward for genomic engineering and germline gene modification. Science, 2015, 348, 36-38. | 6.0 | 541 |
| 9 | Structural Biology of Nucleocytoplasmic Transport. Annual Review of Biochemistry, 2007, 76, 647-671. | 5.0 | 458 |
| 10 | Structural Basis for Guide RNA Processing and Seed-Dependent DNA Targeting by CRISPR-Cas12a. Molecular Cell, 2017, 66, 221-233.e4. | 4.5 | 408 |
| 11 | Structural insights into the molecular mechanism of the m6A writer complex. ELife, 2016, 5, . | 2.8 | 386 |
| 12 | Type III CRISPRâ€“Cas systems produce cyclic oligoadenylate second messengers. Nature, 2017, 548, 543-548. | 13.7 | 377 |
| 13 | Mammalian miRNA RISC Recruits CAF1 and PABP to Affect PABP-Dependent Deadenylation. Molecular Cell, 2009, 35, 868-880. | 4.5 | 331 |
| 14 | Mechanistic Insights into the cis- and trans-Acting DNase Activities of Cas12a. Molecular Cell, 2019, 73, 589-600.e4. | 4.5 | 298 |
| 15 | The superhelical TPR-repeat domain of O-linked GlcNAc transferase exhibits structural similarities to importin Î±. Nature Structural and Molecular Biology, 2004, 11, 1001-1007. | 3.6 | 263 |
| 16 | Maximizing mutagenesis with solubilized CRISPR-Cas9 ribonucleoprotein complexes.. Development (Cambridge), 2016, 143, 2025-37. | 1.2 | 244 |
| 17 | Structural Basis for DNase Activity of a Conserved Protein Implicated in CRISPR-Mediated Genome Defense. Structure, 2009, 17, 904-912. | 1.6 | 228 |
| 18 | In vivo adenine base editing of PCSK9 in macaques reduces LDL cholesterol levels. Nature Biotechnology, 2021, 39, 949-957. | 9.4 | 196 |

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|---|---|---|---|
| 19 | An RNA-induced conformational change required for CRISPR RNA cleavage by the endoribonuclease Cse3. Nature Structural and Molecular Biology, 2011, 18, 680-687. | 3.6 | 166 |
| 20 | Cas9 versus Cas12a/Cpf1: Structureâ€"function comparisons and implications for genome editing. Wiley Interdisciplinary Reviews RNA, 2018, 9, e1481. | 3.2 | 164 |
| 21 | Structural Plasticity of PAM Recognition by Engineered Variants of the RNA-Guided Endonuclease Cas9. Molecular Cell, 2016, 61, 895-902. | 4.5 | 161 |
| 22 | Coupled 5â€² Nucleotide Recognition and Processivity in Xrn1-Mediated mRNA Decay. Molecular Cell, 2011, 41, 600-608. | 4.5 | 155 |
| 23 | CrispRVariants charts the mutation spectrum of genome engineering experiments. Nature Biotechnology, 2016, 34, 701-702. | 9.4 | 149 |
| 24 | CRISPR-Cas9 conformational activation as elucidated from enhanced molecular simulations. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 7260-7265. | 3.3 | 133 |
| 25 | Structural basis for the endoribonuclease activity of the type III-A CRISPR-associated protein Csm6. Rna, 2016, 22, 318-329. | 1.6 | 128 |
| 26 | Covalent linkage of the DNA repair template to the CRISPR-Cas9 nuclease enhances homology-directed repair. ELife, 2018, 7, . | 2.8 | 127 |
| 27 | DNA-guided DNA cleavage at moderate temperatures by Clostridium butyricum Argonaute. Nucleic Acids Research, 2019, 47, 5809-5821. | 6.5 | 115 |
| 28 | Structures of the tRNA export factor in the nuclear and cytosolic states. Nature, 2009, 461, 60-65. | 13.7 | 108 |
| 29 | Protospacer Adjacent Motif-Induced Allostery Activates CRISPR-Cas9. Journal of the American Chemical Society, 2017, 139, 16028-16031. | 6.6 | 104 |
| 30 | Striking Plasticity of CRISPR-Cas9 and Key Role of Non-target DNA, as Revealed by Molecular Simulations. ACS Central Science, 2016, 2, 756-763. | 5.3 | 103 |
| 31 | Deciphering Off-Target Effects in CRISPR-Cas9 through Accelerated Molecular Dynamics. ACS Central Science, 2019, 5, 651-662. | 5.3 | 99 |
| 32 | In Vitro Enzymology of Cas9. Methods in Enzymology, 2014, 546, 1-20. | 0.4 | 97 |
| 33 | Structural basis of AAUAAA polyadenylation signal recognition by the human CPSF complex. Nature Structural and Molecular Biology, 2018, 25, 135-138. | 3.6 | 96 |
| 34 | Structural insights into the human GW182-PABC interaction in microRNA-mediated deadenylation. Nature Structural and Molecular Biology, 2010, 17, 238-240. | 3.6 | 92 |
| 35 | An internal promoter underlies the difference in disease severity between N- and C-terminal truncation mutations of Titin in zebrafish. ELife, 2015, 4, e09406. | 2.8 | 83 |
| 36 | Mechanistic insights into mRNA 3â€²-end processing. Current Opinion in Structural Biology, 2019, 59, 143-150. | 2.6 | 83 |

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|---|---|---|---|
| 37 | Key role of the REC lobe during CRISPRâ€“Cas9 activation by â€˜sensingâ€™, â€˜regulatingâ€™, and â€˜lockingâ€™ the catalytic HNH domain. Quarterly Reviews of Biophysics, 2018, 51, . | 2.4 | 79 |
| 38 | Hakai is required for stabilization of core components of the m6A mRNA methylation machinery. Nature Communications, 2021, 12, 3778. | 5.8 | 77 |
| 39 | Structural insights into the assembly and polyA signal recognition mechanism of the human CPSF complex. ELife, 2017, 6, . | 2.8 | 71 |
| 40 | Evolution of CRISPR RNA recognition and processing by Cas6 endonucleases. Nucleic Acids Research, 2014, 42, 1341-1353. | 6.5 | 68 |
| 41 | Activation and self-inactivation mechanisms of the cyclic oligoadenylate-dependent CRISPR ribonuclease Csm6. Nature Communications, 2020, 11, 1596. | 5.8 | 67 |
| 42 | Molecular architectures and mechanisms of Class 2 CRISPR-associated nucleases. Current Opinion in Structural Biology, 2017, 47, 157-166. | 2.6 | 65 |
| 43 | Catalytic Mechanism of Non-Target DNA Cleavage in CRISPR-Cas9 Revealed by Ab Initio Molecular Dynamics. ACS Catalysis, 2020, 10, 13596-13605. | 5.5 | 63 |
| 44 | Bacteriophage DNA glucosylation impairs target DNA binding by type I and II but not by type V CRISPRâ€“Cas effector complexes. Nucleic Acids Research, 2018, 46, 873-885. | 6.5 | 57 |
| 45 | Molecular architecture of <scp>LSM</scp> 14 interactions involved in the assembly of <scp>mRNA</scp> silencing complexes. EMBO Journal, 2018, 37, . | 3.5 | 51 |
| 46 | Molecular basis for cytoplasmic <scp>RNA</scp> surveillance by uridylationâ€triggered decay in Drosophila. EMBO Journal, 2016, 35, 2417-2434. | 3.5 | 50 |
| 47 | Molecular Dynamics Reveals a DNA-Induced Dynamic Switch Triggering Activation of CRISPR-Cas12a. Journal of Chemical Information and Modeling, 2020, 60, 6427-6437. | 2.5 | 43 |
| 48 | Data-collection strategy for challenging native SAD phasing. Acta Crystallographica Section D: Structural Biology, 2016, 72, 421-429. | 1.1 | 42 |
| 49 | Target site selection and remodelling by type V CRISPR-transposon systems. Nature, 2021, 599, 497-502. | 13.7 | 42 |
| 50 | Structural insights into the Notch-modifying glycosyltransferase Fringe. Nature Structural and Molecular Biology, 2006, 13, 945-946. | 3.6 | 35 |
| 51 | Molecular mechanism of the RNA helicase DHX37 and its activation by UTP14A in ribosome biogenesis. Rna, 2019, 25, 685-701. | 1.6 | 33 |
| 52 | Structural and Biochemical Studies of a Fluoroacetyl-CoA-Specific Thioesterase Reveal a Molecular Basis for Fluorine Selectivity. Biochemistry, 2010, 49, 9269-9279. | 1.2 | 31 |
| 53 | The C-terminal region of Ge-1 presents conserved structural features required for P-body localization. Rna, 2008, 14, 1991-1998. | 1.6 | 30 |
| 54 | Structural mimicry in transcription regulation of human RNA polymerase II by the DNA helicase RECQL5. Nature Structural and Molecular Biology, 2013, 20, 892-899. | 3.6 | 27 |

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|---|---|---|---|
| 55 | Conformational control of Cas9 by CRISPR hybrid RNA-DNA guides mitigates off-target activity in TÂcells. Molecular Cell, 2021, 81, 3637-3649.e5. | 4.5 | 27 |
| 56 | In Vitro Reconstitution and Crystallization of Cas9 Endonuclease Bound to a Guide RNA and a DNA Target. Methods in Enzymology, 2015, 558, 515-537. | 0.4 | 23 |
| 57 | ANGEL2 is a member of the CCR4 family of deadenylases with 2â€²,3â€²-cyclic phosphatase activity. Science, 2020, 369, 524-530. | 6.0 | 23 |
| 58 | Human MARF1 is an endoribonuclease that interacts with the DCP1:2 decapping complex and degrades target mRNAs. Nucleic Acids Research, 2018, 46, 12008-12021. | 6.5 | 22 |
| 59 | Molecular architecture of the human tRNA ligase complex. ELife, 2021, 10, . | 2.8 | 22 |
| 60 | The oxidoreductase PYROXD1 uses NAD(P)+ as an antioxidant to sustain tRNA ligase activity in pre-tRNA splicing and unfolded protein response. Molecular Cell, 2021, 81, 2520-2532.e16. | 4.5 | 21 |
| 61 | Heterologous Expression and Purification of the CRISPR-Cas12a/Cpf1 Protein. Bio-protocol, 2018, 8, e2842. | 0.2 | 21 |
| 62 | Introducing gene deletions by mouse zygote electroporation of Cas12a/Cpf1. Transgenic Research, 2019, 28, 525-535. | 1.3 | 20 |
| 63 | Preparation and electroporation of Cas12a/Cpf1-guide RNA complexes for introducing large gene deletions in mouse embryonic stem cells. Methods in Enzymology, 2019, 616, 241-263. | 0.4 | 16 |
| 64 | Crystal structure of the C-terminal 2â€²,5â€²-phosphodiesterase domain of group a rotavirus protein VP3. Proteins: Structure, Function and Bioinformatics, 2015, 83, 997-1002. | 1.5 | 14 |
| 65 | Structural basis for acceptor RNA substrate selectivity of the 3â€² terminal uridylyl transferase Tailor. Nucleic Acids Research, 2019, 47, 1030-1042. | 6.5 | 13 |
| 66 | In vitro Generation of CRISPR-Cas9 Complexes with Covalently Bound Repair Templates for Genome Editing in Mammalian Cells. Bio-protocol, 2019, 9, . | 0.2 | 13 |
| 67 | Use of RNA Tertiary Interaction Modules for the Crystallisation of the Spliceosomal snRNP Core Domain. Journal of Molecular Biology, 2010, 402, 154-164. | 2.0 | 11 |
| 68 | CRISPR-Directed Therapeutic Correction at the NCF1 Locus Is Challenged by Frequent Incidence of Chromosomal Deletions. Molecular Therapy - Methods and Clinical Development, 2020, 17, 936-943. | 1.8 | 8 |
| 69 | Multiplexed Single-Molecule Experiments Reveal Nucleosome Invasion Dynamics of the Cas9 Genome Editor. Journal of the American Chemical Society, 2021, 143, 16313-16319. | 6.6 | 6 |
| 70 | Specialized Weaponry: How a Type III-A CRISPR-Cas System Excels at Combating Phages. Cell Host and Microbe, 2017, 22, 258-259. | 5.1 | 5 |
| 71 | Two-Metal Ion Mechanism of DNA Cleavage in CRISPR-Cas9. Biophysical Journal, 2020, 118, 64a. | 0.2 | 2 |
| 72 | The CRISPR-RNA World: An Interview with Martin JÃnek. CRISPR Journal, 2020, 3, 68-72. | 1.4 | 2 |

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| 73 | The Oxidoreductase PYROXD1 Utilizes NAD(P)+ As an Antioxidant to Sustain tRNA Ligase Activity in Pre-tRNA Splicing and Unfolded Protein Response. SSRN Electronic Journal, 0, , . | 0.4 | 1 |
| 74 | Eukaryotic expression, purification, crystallization and preliminary X-ray analysis of murine Manic Fringe. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 774-777. | 0.7 | 0 |
| 75 | CRISPR-Cas9: Computational Insights Toward Improved Genome Editing. Biophysical Journal, 2017, 112, 72a. | 0.2 | 0 |
| 76 | Cover Image, Volume 9, Issue 5. Wiley Interdisciplinary Reviews RNA, 2018, 9, e1505. | 3.2 | 0 |
| 77 | A PAM-Induced Signalling Activates the Communication between HNH and RUVC in CRISPR-Cas9. Biophysical Journal, 2018, 114, 250a. | 0.2 | 0 |
| 78 | Editorial overview: Proteinâ€“nucleic acid interactions â€“ cryo-EM, what else?. Current Opinion in Structural Biology, 2019, 59, vi-viii. | 2.6 | 0 |
| 79 | Uncut but Primed for Change. CRISPR Journal, 2019, 2, 352-354. | 1.4 | 0 |
| 80 | Critical Role of Conserved Histidine Residues in Genome Editing and Recombination. Biophysical Journal, 2021, 120, 137a-138a. | 0.2 | 0 |
| 81 | Cooperative Dynamics of REC-Nuc Lobes Prime Cas12a for DNA Processing. Biophysical Journal, 2021, 120, 16a-17a. | 0.2 | 0 |
| 82 | Multi-microsecond molecular dynamics unveils the mechanism of DNA traversal within CRISPR-Cas12a. Biophysical Journal, 2022, 121, 322a. | 0.2 | 0 |