# Chase Beisel

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 74 papers | 4,898 citations | 126907 33 h-index | 102487 66 g-index |
| 88 all docs | 88 docs citations | 88 times ranked | 5492 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Rapidly Characterizing CRISPR-Cas13 Nucleases Using Cell-Free Transcription-Translation Systems. Methods in Molecular Biology, 2022, 2404, 135-153. | 0.9 | 2 |
| 2 | Differentially Optimized Cell-Free Buffer Enables Robust Expression from Unprotected Linear DNA in Exonuclease-Deficient Extracts. ACS Synthetic Biology, 2022, 11, 732-746. | 3.8 | 16 |
| 3 | A TXTL-Based Assay to Rapidly Identify PAMs for CRISPR-Cas Systems with Multi-Protein Effector Complexes. Methods in Molecular Biology, 2022, 2433, 391-411. | 0.9 | 1 |
| 4 | Spacer prioritization in CRISPRâ€“Cas9 immunity is enabled by the leader RNA. Nature Microbiology, 2022, 7, 530-541. | 13.3 | 9 |
| 5 | Rapid cell-free characterization of multi-subunit CRISPR effectors and transposons. Molecular Cell, 2022, 82, 1210-1224.e6. | 9.7 | 10 |
| 6 | CRISPR memories in single cells. Molecular Systems Biology, 2022, 18, e11011. | 7.2 | 1 |
| 7 | Beneficial commensal bacteria promote Drosophila growth by downregulating the expression of peptidoglycan recognition proteins. IScience, 2022, 25, 104357. | 4.1 | 8 |
| 8 | Genome Editing with Cas9 in Lactobacilli. Methods in Molecular Biology, 2022, 2479, 245-261. | 0.9 | 3 |
| 9 | Anti-CRISPR prediction using deep learning reveals an inhibitor of Cas13b nucleases. Molecular Cell, 2022, 82, 2714-2726.e4. | 9.7 | 17 |
| 10 | A target expression threshold dictates invader defense and prevents autoimmunity by CRISPR-Cas13. Cell Host and Microbe, 2022, 30, 1151-1162.e6. | 11.0 | 9 |
| 11 | CRISPR technologies and the search for the PAM-free nuclease. Nature Communications, 2021, 12, 555. | 12.8 | 148 |
| 12 | Sequence-independent RNA sensing and DNA targeting by a split domain CRISPRâ€“Cas12a gRNA switch. Nucleic Acids Research, 2021, 49, 2985-2999. | 14.5 | 26 |
| 13 | Noncanonical crRNAs derived from host transcripts enable multiplexable RNA detection by Cas9. Science, 2021, 372, 941-948. | 12.6 | 83 |
| 14 | In Situ Biomanufacturing of Small Molecules in the Mammalian Gut by Probiotic Saccharomyces boulardii. ACS Synthetic Biology, 2021, 10, 1039-1052. | 3.8 | 32 |
| 15 | CRISPR transposons on the move. Cell Host and Microbe, 2021, 29, 675-677. | 11.0 | 2 |
| 16 | A genetically encoded anti-CRISPR protein constrains gene drive spread and prevents population suppression. Nature Communications, 2021, 12, 3977. | 12.8 | 34 |
| 17 | Coupling smartphone and <scp>CRISPRâ€“Cas12a</scp> for digital and multiplexed <scp>nucleic acid</scp> detection. AICHE Journal, 2021, 67, e17365. | 3.6 | 35 |
| 18 | The tracrRNA in CRISPR Biology and Technologies. Annual Review of Genetics, 2021, 55, 161-181. | 7.6 | 27 |

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|---|---|---|---|
| 19 | Illuminating the path to DNA repair. Cell, 2021, 184, 5503-5505. | 28.9 | 1 |
| 20 | An enhanced assay to characterize anti-CRISPR proteins using a cell-free transcription-translation system. Methods, 2020, 172, 42-50. | 3.8 | 21 |
| 21 | A positive, growth-based PAM screen identifies noncanonical motifs recognized by the S. pyogenes Cas9. Science Advances, 2020, 6, eabb4054. | 10.3 | 21 |
| 22 | Rapid Testing of CRISPR Nucleases and GuideÂRNAs in an E.Âcoli Cell-Free Transcription-Translation System. STAR Protocols, 2020, 1, 100003. | 1.2 | 5 |
| 23 | Your Base Editor Might Be Flirting with Single (Stranded) DNA: Faithful On-Target CRISPR Base Editing without Promiscuous Deamination. Molecular Cell, 2020, 79, 703-704. | 9.7 | 0 |
| 24 | Methods for characterizing, applying, and teaching CRISPR-Cas systems. Methods, 2020, 172, 1-2. | 3.8 | 0 |
| 25 | Competitive Exclusion Is a Major Bioprotective Mechanism of Lactobacilli against Fungal Spoilage in Fermented Milk Products. Applied and Environmental Microbiology, 2020, 86, . | 3.1 | 61 |
| 26 | Tunable self-cleaving ribozymes for modulating gene expression in eukaryotic systems. PLoS ONE, 2020, 15, e0232046. | 2.5 | 2 |
| 27 | Characterization of Cas12a nucleases reveals diverse PAM profiles between closely-related orthologs. Nucleic Acids Research, 2020, 48, 5624-5638. | 14.5 | 34 |
| 28 | An educational module to explore CRISPR technologies with a cell-free transcription-translation system. Synthetic Biology, 2019, 4, ysz005. | 2.2 | 34 |
| 29 | Modular one-pot assembly of CRISPR arrays enables library generation and reveals factors influencing crRNA biogenesis. Nature Communications, 2019, 10, 2948. | 12.8 | 75 |
| 30 | Barriers to genome editing with CRISPR in bacteria. Journal of Industrial Microbiology and Biotechnology, 2019, 46, 1327-1341. | 3.0 | 78 |
| 31 | The Acidaminococcus sp. Cas12a nuclease recognizes GTTV and GCTV as non-canonical PAMs. FEMS Microbiology Letters, 2019, 366, . | 1.8 | 17 |
| 32 | Characterization of the allâ€<scp>E. coli</scp> transcriptionâ€translation system myTXTL by mass spectrometry. Rapid Communications in Mass Spectrometry, 2019, 33, 1036-1048. | 1.5 | 38 |
| 33 | CRATES: A one-step assembly method for Class 2 CRISPR arrays. Methods in Enzymology, 2019, 629, 493-511. | 1.0 | 2 |
| 34 | Targeted transcriptional modulation with type I CRISPRâ€“Cas systems in human cells. Nature Biotechnology, 2019, 37, 1493-1501. | 17.5 | 73 |
| 35 | Genome Editing with CRISPRâ€Cas9 in Lactobacillus plantarum Revealed That Editing Outcomes Can Vary Across Strains and Between Methods. Biotechnology Journal, 2019, 14, 1700583. | 3.5 | 80 |
| 36 | Distinct timescales of RNA regulators enable the construction of a genetic pulse generator. Biotechnology and Bioengineering, 2019, 116, 1139-1151. | 3.3 | 40 |

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|---|---|---|---|
| 37 | The Francisella novicida Cas12a is sensitive to the structure downstream of the terminal repeat in CRISPR arrays. RNA Biology, 2019, 16, 404-412. | 3.1 | 17 |
| 38 | CRISPR-Cas Systems and the Paradox of Self-Targeting Spacers. Frontiers in Microbiology, 2019, 10, 3078. | 3.5 | 67 |
| 39 | CRISPR RNA-Dependent Binding and Cleavage of Endogenous RNAs by the Campylobacter jejuni Cas9. Molecular Cell, 2018, 69, 893-905.e7. | 9.7 | 122 |
| 40 | A detailed cell-free transcription-translation-based assay to decipher CRISPR protospacer-adjacent motifs. Methods, 2018, 143, 48-57. | 3.8 | 36 |
| 41 | Rapid and Scalable Characterization of CRISPR Technologies Using an E.Âcoli Cell-Free Transcription-Translation System. Molecular Cell, 2018, 69, 146-157.e3. | 9.7 | 165 |
| 42 | Mathematical Modeling of RNA-Based Architectures for Closed Loop Control of Gene Expression. ACS Synthetic Biology, 2018, 7, 1219-1228. | 3.8 | 42 |
| 43 | Synthetic Biology Approaches to Engineer Probiotics and Members of the Human Microbiota for Biomedical Applications. Annual Review of Biomedical Engineering, 2018, 20, 277-300. | 12.3 | 83 |
| 44 | CRISPR tool puts RNA on the record. Nature, 2018, 562, 347-349. | 27.8 | 1 |
| 45 | Advances in CRISPR Technologies for Microbial Strain Engineering. Biotechnology Journal, 2018, 13, e1800460. | 3.5 | 2 |
| 46 | Bacterial Adaptation to the Host's Diet Is a Key Evolutionary Force Shaping Drosophila-Lactobacillus Symbiosis. Cell Host and Microbe, 2018, 24, 109-119.e6. | 11.0 | 97 |
| 47 | Toward a genetic tool development pipeline for host-associated bacteria. Current Opinion in Microbiology, 2017, 38, 156-164. | 5.1 | 53 |
| 48 | Deciphering, Communicating, and Engineering the CRISPR PAM. Journal of Molecular Biology, 2017, 429, 177-191. | 4.2 | 147 |
| 49 | Advancing the design and delivery of CRISPR antimicrobials. Current Opinion in Biomedical Engineering, 2017, 4, 57-64. | 3.4 | 25 |
| 50 | Short DNA containing Ï‡ sites enhances DNA stability and gene expression in E. coli cellâ€free transcriptionâ€“translation systems. Biotechnology and Bioengineering, 2017, 114, 2137-2141. | 3.3 | 80 |
| 51 | Current and future prospects for CRISPRâ€based tools in bacteria. Biotechnology and Bioengineering, 2016, 113, 930-943. | 3.3 | 100 |
| 52 | Identifying and Visualizing Functional PAM Diversity across CRISPR-Cas Systems. Molecular Cell, 2016, 62, 137-147. | 9.7 | 290 |
| 53 | The CRISPR RNA-guided surveillance complex inEscherichia coliaccommodates extended RNA spacers. Nucleic Acids Research, 2016, 44, gkw421. | 14.5 | 42 |
| 54 | Rethinking the Hierarchy of Sugar Utilization in Bacteria. Journal of Bacteriology, 2016, 198, 374-376. | 2.2 | 26 |

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|---|---|---|---|
| 55 | Selfâ€Assembled DNA Nanoclews for the Efficient Delivery of CRISPRâ€“Cas9 for Genome Editing. Angewandte Chemie - International Edition, 2015, 54, 12029-12033. | 13.8 | 517 |
| 56 | Impact of Residual Inducer on Titratable Expression Systems. PLoS ONE, 2015, 10, e0137421. | 2.5 | 0 |
| 57 | Trade-offs in Engineering Sugar Utilization Pathways for Titratable Control. ACS Synthetic Biology, 2015, 4, 141-149. | 3.8 | 12 |
| 58 | Repurposing endogenous type I CRISPR-Cas systems for programmable gene repression. Nucleic Acids Research, 2015, 43, 674-681. | 14.5 | 202 |
| 59 | A CRISPR design for next-generation antimicrobials. Genome Biology, 2014, 15, 516. | 8.8 | 57 |
| 60 | Programmable Removal of Bacterial Strains by Use of Genome-Targeting CRISPR-Cas Systems. MBio, 2014, 5, e00928-13. | 4.1 | 315 |
| 61 | Guide RNA Functional Modules Direct Cas9 Activity and Orthogonality. Molecular Cell, 2014, 56, 333-339. | 9.7 | 214 |
| 62 | Bacterial sugar utilization gives rise to distinct singleâ€cell behaviours. Molecular Microbiology, 2014, 93, 1093-1103. | 2.5 | 51 |
| 63 | Construction of Ligand-Responsive MicroRNAs that Operate Through Inhibition of Drosha Processing. Methods in Molecular Biology, 2014, 1111, 259-267. | 0.9 | 6 |
| 64 | Understanding and exploiting feedback in synthetic biology. Chemical Engineering Science, 2013, 103, 79-90. | 3.8 | 25 |
| 65 | Multiple factors dictate target selection by Hfq-binding small RNAs. EMBO Journal, 2012, 31, 1961-1974. | 7.8 | 99 |
| 66 | The Base-Pairing RNA Spot 42 Participates in a Multioutput Feedforward Loop to Help Enact Catabolite Repression in Escherichia coli. Molecular Cell, 2011, 41, 286-297. | 9.7 | 197 |
| 67 | Discriminating tastes. RNA Biology, 2011, 8, 766-770. | 3.1 | 23 |
| 68 | Design of small molecule-responsive microRNAs based on structural requirements for Drosha processing. Nucleic Acids Research, 2011, 39, 2981-2994. | 14.5 | 130 |
| 69 | Base pairing small RNAs and their roles in global regulatory networks. FEMS Microbiology Reviews, 2010, 34, 866-882. | 8.6 | 256 |
| 70 | Design Principles for Riboswitch Function. PLoS Computational Biology, 2009, 5, e1000363. | 3.2 | 115 |
| 71 | Synthetic control of a fitness tradeoff in yeast nitrogen metabolism. Journal of Biological Engineering, 2009, 3, 1. | 4.7 | 59 |
| 72 | Modelâ€guided design of ligandâ€regulated RNAi for programmable control of gene expression. Molecular Systems Biology, 2008, 4, 224. | 7.2 | 104 |

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|---|---|---|---|
| 73 | Conformational analysis of gossypol and its derivatives by molecular mechanics. Computational and Theoretical Chemistry, 2005, 730, 51-58. | 1.5 | 3 |
| 74 | Cochlear whole mount in situ hybridization: identification of longitudinal and radial gradients. Brain Research Protocols, 2002, 9, 65-76. | 1.6 | 42 |