Bei Yang

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A pan-coronavirus fusion inhibitor targeting the HR1 domain of human coronavirus spike. Science Advances, 2019, 5, eaav4580.	4.7	393
2	Base editing with a Cpf1–cytidine deaminase fusion. Nature Biotechnology, 2018, 36, 324-327.	9.4	333
3	Efficient base editing in methylated regions with a human APOBEC3A-Cas9 fusion. Nature Biotechnology, 2018, 36, 946-949.	9.4	190
4	Molecular mechanisms of "off-on switch―of activities of human IDH1 by tumor-associated mutation R132H. Cell Research, 2010, 20, 1188-1200.	5.7	103
5	Enhanced base editing by co-expression of free uracil DNA glycosylase inhibitor. Cell Research, 2017, 27, 1289-1292.	5.7	99
6	Vps4 disassembles an ESCRT-III filament by global unfolding and processive translocation. Nature Structural and Molecular Biology, 2015, 22, 492-498.	3.6	88
7	Discovery of SIAIS178 as an Effective BCR-ABL Degrader by Recruiting Von Hippel–Lindau (VHL) E3 Ubiquitin Ligase. Journal of Medicinal Chemistry, 2019, 62, 9281-9298.	2.9	79
8	Cas12a Base Editors Induce Efficient and Specific Editing with Low DNA Damage Response. Cell Reports, 2020, 31, 107723.	2.9	62
9	Structure of human tryptophanyl-tRNA synthetase in complex with tRNATrp reveals the molecular basis of tRNA recognition and specificity. Nucleic Acids Research, 2006, 34, 3246-3258.	6.5	60
10	Molecular Basis of the Acceleration of the GDP-GTP Exchange of Human Ras Homolog Enriched in Brain by Human Translationally Controlled Tumor Protein. Journal of Biological Chemistry, 2009, 284, 23754-23764.	1.6	60
11	APOBEC: From mutator to editor. Journal of Genetics and Genomics, 2017, 44, 423-437.	1.7	54
12	Highly efficient prime editing by introducing same-sense mutations in pegRNA or stabilizing its structure. Nature Communications, 2022, 13, 1669.	5.8	52
13	Eliminating base-editor-induced genome-wide and transcriptome-wide off-target mutations. Nature Cell Biology, 2021, 23, 552-563.	4.6	50
14	Selection of an ASIC1a-blocking combinatorial antibody that protects cells from ischemic death. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E7469-E7477.	3.3	48
15	Development and Application of Base Editors. CRISPR Journal, 2019, 2, 91-104.	1.4	46
16	APOBEC3 induces mutations during repair of CRISPR–Cas9-generated DNA breaks. Nature Structural and Molecular Biology, 2018, 25, 45-52.	3.6	42
17	Catalytic mechanism of the tryptophan activation reaction revealed by crystal structures of human tryptophanyl-tRNA synthetase in different enzymatic states. Nucleic Acids Research, 2008, 36, 1288-1299.	6.5	34
18	Crl activates transcription by stabilizing active conformation of the master stress transcription initiation factor. ELife, 2019, 8, .	2.8	26

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19	Comparison of cytosine base editors and development of the BEable-GPS database for targeting pathogenic SNVs. Genome Biology, 2019, 20, 218.	3.8	23
20	One Prime for All Editing. Cell, 2019, 179, 1448-1450.	13.5	23
21	Allosteric inhibition of CRISPR-Cas9 by bacteriophage-derived peptides. Genome Biology, 2020, 21, 51.	3.8	21
22	Crystal structure of the post-fusion core of the <i>Human coronavirus 229E</i> spike protein at 1.86â€Ã resolution. Acta Crystallographica Section D: Structural Biology, 2018, 74, 841-851.	1.1	18
23	Crystal structure of Pyrococcus horikoshii tryptophanyl-tRNA synthetase and structure-based phylogenetic analysis suggest an archaeal origin of tryptophanyl-tRNA synthetase. Nucleic Acids Research, 2010, 38, 1401-1412.	6.5	13
24	To BE or not to BE, that is the question. Nature Biotechnology, 2019, 37, 520-522.	9.4	11
25	Selection of a picomolar antibody that targets CXCR2-mediated neutrophil activation and alleviates EAE symptoms. Nature Communications, 2021, 12, 2547.	5.8	11
26	Inhibitory antibodies identify unique sites of therapeutic vulnerability in rhinovirus and other enteroviruses. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 13499-13508.	3.3	7
27	Making Sense of Vps4. Journal of Molecular Biology, 2014, 426, 503-506.	2.0	4