

Bei Yang

List of Publications by Year in descending order

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Version: 2024-02-01

27
papers

1,953
citations

393982

19
h-index

525886

27
g-index

30
all docs

30
docs citations

30
times ranked

3062
citing authors

#	ARTICLE	IF	CITATIONS
1	Highly efficient prime editing by introducing same-sense mutations in pegRNA or stabilizing its structure. <i>Nature Communications</i> , 2022, 13, 1669.	5.8	52
2	Selection of a picomolar antibody that targets CXCR2-mediated neutrophil activation and alleviates EAE symptoms. <i>Nature Communications</i> , 2021, 12, 2547.	5.8	11
3	Eliminating base-editor-induced genome-wide and transcriptome-wide off-target mutations. <i>Nature Cell Biology</i> , 2021, 23, 552-563.	4.6	50
4	Cas12a Base Editors Induce Efficient and Specific Editing with Low DNA Damage Response. <i>Cell Reports</i> , 2020, 31, 107723.	2.9	62
5	Inhibitory antibodies identify unique sites of therapeutic vulnerability in rhinovirus and other enteroviruses. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13499-13508.	3.3	7
6	Allosteric inhibition of CRISPR-Cas9 by bacteriophage-derived peptides. <i>Genome Biology</i> , 2020, 21, 51.	3.8	21
7	Comparison of cytosine base editors and development of the BEable-GPS database for targeting pathogenic SNVs. <i>Genome Biology</i> , 2019, 20, 218.	3.8	23
8	Discovery of SIAIS178 as an Effective BCR-ABL Degradator by Recruiting Von Hippel-Lindau (VHL) E3 Ubiquitin Ligase. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 9281-9298.	2.9	79
9	To BE or not to BE, that is the question. <i>Nature Biotechnology</i> , 2019, 37, 520-522.	9.4	11
10	Development and Application of Base Editors. <i>CRISPR Journal</i> , 2019, 2, 91-104.	1.4	46
11	A pan-coronavirus fusion inhibitor targeting the HR1 domain of human coronavirus spike. <i>Science Advances</i> , 2019, 5, eaav4580.	4.7	393
12	One Prime for All Editing. <i>Cell</i> , 2019, 179, 1448-1450.	13.5	23
13	Crl activates transcription by stabilizing active conformation of the master stress transcription initiation factor. <i>ELife</i> , 2019, 8, .	2.8	26
14	Base editing with a Cpf1-cytidine deaminase fusion. <i>Nature Biotechnology</i> , 2018, 36, 324-327.	9.4	333
15	APOBEC3 induces mutations during repair of CRISPR-Cas9-generated DNA breaks. <i>Nature Structural and Molecular Biology</i> , 2018, 25, 45-52.	3.6	42
16	Crystal structure of the post-fusion core of the Human coronavirus 229E spike protein at 1.86 Å resolution. <i>Acta Crystallographica Section D: Structural Biology</i> , 2018, 74, 841-851.	1.1	18
17	Selection of an ASIC1a-blocking combinatorial antibody that protects cells from ischemic death. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E7469-E7477.	3.3	48
18	Efficient base editing in methylated regions with a human APOBEC3A-Cas9 fusion. <i>Nature Biotechnology</i> , 2018, 36, 946-949.	9.4	190

#	ARTICLE	IF	CITATIONS
19	Enhanced base editing by co-expression of free uracil DNA glycosylase inhibitor. <i>Cell Research</i> , 2017, 27, 1289-1292.	5.7	99
20	APOBEC: From mutator to editor. <i>Journal of Genetics and Genomics</i> , 2017, 44, 423-437.	1.7	54
21	Vps4 disassembles an ESCRT-III filament by global unfolding and processive translocation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 492-498.	3.6	88
22	Making Sense of Vps4. <i>Journal of Molecular Biology</i> , 2014, 426, 503-506.	2.0	4
23	Molecular mechanisms of "off-on switch" of activities of human IDH1 by tumor-associated mutation R132H. <i>Cell Research</i> , 2010, 20, 1188-1200.	5.7	103
24	Crystal structure of <i>Pyrococcus horikoshii</i> tryptophanyl-tRNA synthetase and structure-based phylogenetic analysis suggest an archaeal origin of tryptophanyl-tRNA synthetase. <i>Nucleic Acids Research</i> , 2010, 38, 1401-1412.	6.5	13
25	Molecular Basis of the Acceleration of the GDP-GTP Exchange of Human Ras Homolog Enriched in Brain by Human Translationally Controlled Tumor Protein. <i>Journal of Biological Chemistry</i> , 2009, 284, 23754-23764.	1.6	60
26	Catalytic mechanism of the tryptophan activation reaction revealed by crystal structures of human tryptophanyl-tRNA synthetase in different enzymatic states. <i>Nucleic Acids Research</i> , 2008, 36, 1288-1299.	6.5	34
27	Structure of human tryptophanyl-tRNA synthetase in complex with tRNA ^{Trp} reveals the molecular basis of tRNA recognition and specificity. <i>Nucleic Acids Research</i> , 2006, 34, 3246-3258.	6.5	60