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List of Publications by Year
in descending order

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29 papers	1,814 citations	471509 17 h-index	501196 28 g-index
37 all docs	37 docs citations	37 times ranked	2700 citing authors

#	Article	IF	Citations
1	A BAFF ligand-based CAR-T cell targeting three receptors and multiple B cell cancers. Nature Communications, 2022, 13, 217.	12.8	27
2	CRISPR-Cas9 cytidine and adenosine base editing of splice-sites mediates highly-efficient disruption of proteins in primary and immortalized cells. Nature Communications, 2021, 12, 2437.	12.8	50
3	Comparative international incidence of Ewing sarcoma 1988 to 2012. International Journal of Cancer, 2021, 149, 1054-1066.	5.1	16
4	Engineering T cells to enhance 3D migration through structurally and mechanically complex tumor microenvironments. Nature Communications, 2021, 12, 2815.	12.8	73
5	An irradiated marrow niche reveals a small non-collagenous protein mediator of homing, dermatopontin. Blood Advances, 2021, 5, 3609-3622.	5.2	2
6	MultiEditR: The first tool for the detection and quantification of RNA editing from Sanger sequencing demonstrates comparable fidelity to RNA-seq. Molecular Therapy - Nucleic Acids, 2021, 25, 515-523.	5.1	11
7	Base Editor Correction of COL7A1 in RecessiveÂDystrophic Epidermolysis Bullosa Patient-Derived Fibroblasts and iPSCs. Journal of Investigative Dermatology, 2020, 140, 338-347.e5.	0.7	69
8	A Genetically Engineered Primary Human Natural Killer Cell Platform for Cancer Immunotherapy. Molecular Therapy, 2020, 28, 52-63.	8.2	120
9	Genome Engineering of Primary Human B Cells Using CRISPR/Cas9. Journal of Visualized Experiments, 2020, , .	0.3	4
10	Efficient targeted integration directed by short homology in zebrafish and mammalian cells. ELife, 2020, 9, .	6.0	93
11	Highly efficient multiplex human T cell engineering without double-strand breaks using Cas9 base editors. Nature Communications, 2019, 10, 5222.	12.8	135
12	CRISPR/Cas9-Based Cellular Engineering for Targeted Gene Overexpression. International Journal of Molecular Sciences, 2018, 19, 946.	4.1	19
13	Engineering of Primary Human B cells with CRISPR/Cas9 Targeted Nuclease. Scientific Reports, 2018, 8, 12144.	3.3	55
14	EditR: A Method to Quantify Base Editing from Sanger Sequencing. CRISPR Journal, 2018, 1, 239-250.	2.9	304
15	Multiplex Human T Cell Engineering without Double-Strand Break Induction Using the Cas9 Base Editor System. Blood, 2018, 132, 3495-3495.	1.4	2
16	Aryl hydrocarbon receptor inhibition promotes hematolymphoid development from human pluripotent stem cells. Blood, 2017, 129, 3428-3439.	1.4	56
17	Rapid generation of Col7a1â^'/â^' mouse model of recessive dystrophic epidermolysis bullosa and partial rescue via immunosuppressive dermal mesenchymal stem cells. Laboratory Investigation, 2017, 97, 1218-1224.	3.7	29
18	Dermatopontin in Bone Marrow Extracellular Matrix Regulates Adherence but Is Dispensable for Murine Hematopoietic Cell Maintenance. Stem Cell Reports, 2017, 9, 770-778.	4.8	7

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19	Angiotensin receptor blockade mediated amelioration of mucopolysaccharidosis type I cardiac and craniofacial pathology. Journal of Inherited Metabolic Disease, 2017, 40, 281-289.	3.6	12
20	CRISPR/Cas9-Mediated Correction of the FANCD1 Gene in Primary Patient Cells. International Journal of Molecular Sciences, 2017, 18, 1269.	4.1	23
21	CRISPR/Cas9-based genetic correction for recessive dystrophic epidermolysis bullosa. Npj Regenerative Medicine, 2016, 1, .	5.2	74
22	CRISPR/Cas9 Targeted Gene Editing and Cellular Engineering in Fanconi Anemia. Stem Cells and Development, 2016, 25, 1591-1603.	2.1	24
23	Evaluation of TCR Gene Editing Achieved by TALENs, CRISPR/Cas9, and megaTAL Nucleases. Molecular Therapy, 2016, 24, 570-581.	8.2	168
24	Fanconi Anemia Gene Editing by the CRISPR/Cas9 System. Human Gene Therapy, 2015, 26, 114-126.	2.7	94
25	From Marrow to Matrix: Novel Gene and Cell Therapies for Epidermolysis Bullosa. Molecular Therapy, 2015, 23, 987-992.	8.2	11
26	TALEN-based Gene Correction for Epidermolysis Bullosa. Molecular Therapy, 2013, 21, 1151-1159.	8.2	232
27	Hematopoietic differentiation of induced pluripotent stem cells from patients with mucopolysaccharidosis type I (Hurler syndrome). Blood, 2011, 117, 839-847.	1.4	82
28	DNA Methylation Profile of Runx1 Regulatory Regions Is Correlated with Transition From Primitive to Definitive Hematopoietic Potential In Vitro and In Vivo. Blood, 2011, 118, 389-389.	1.4	0
29	Myosin Heavy Chain Converter Domain Mutations Drive Early-Stage Changes in Extracellular Matrix Dynamics in Hypertrophic Cardiomyopathy. Frontiers in Cell and Developmental Biology, 0, 10, .	3.7	8