Jacob E Corn

List of Publications by Year
in descending order

44 papers	8,146 citations	136740 32 h-index	264894 42 g-index
56 all docs	56 docs citations	56 times ranked	14209 citing authors

#	Article	IF	Citations
1	Rosetta3. Methods in Enzymology, 2011, 487, 545-574.	0.4	1,620
2	Enhancing homology-directed genome editing by catalytically active and inactive CRISPR-Cas9 using asymmetric donor DNA. Nature Biotechnology, 2016, 34, 339-344.	9.4	935
3	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. ELife, 2016, 5, .	2.8	609
4	Nanoparticle delivery of Cas9 ribonucleoprotein and donor DNA in vivo induces homology-directed DNA repair. Nature Biomedical Engineering, 2017, 1, 889-901.	11.6	566
5	RosettaScripts: A Scripting Language Interface to the Rosetta Macromolecular Modeling Suite. PLoS ONE, 2011, 6, e20161.	1.1	506
6	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. Nature Genetics, 2017, 49, 1602-1612.	9.4	419
7	Disabling Cas9 by an anti-CRISPR DNA mimic. Science Advances, 2017, 3, e1701620.	4.7	289
8	Unbiased detection of CRISPR off-targets in vivo using DISCOVER-Seq. Science, 2019, 364, 286-289.	6.0	284
9	Advances in genome editing through control of DNA repair pathways. Nature Cell Biology, 2019, 21, 1468-1478.	4.6	271
10	USP30 and parkin homeostatically regulate atypical ubiquitin chains on mitochondria. Nature Cell Biology, 2015, 17, 160-169.	4.6	258
11	PnB Designer: a web application to design prime and base editor guide RNAs for animals and plants. BMC Bioinformatics, 2021, 22, 101.	1.2	254
12	CRISPR–Cas9 genome editing in human cells occurs via the Fanconi anemia pathway. Nature Genetics, 2018, 50, 1132-1139.	9.4	187
13	A Genome-wide ER-phagy Screen Highlights Key Roles of Mitochondrial Metabolism and ER-Resident UFMylation. Cell, 2020, 180, 1160-1177.e20.	13.5	163
14	A De Novo Protein Binding Pair By Computational Design and Directed Evolution. Molecular Cell, 2011, 42, 250-260.	4.5	159
15	Automated electron-density sampling reveals widespread conformational polymorphism in proteins. Protein Science, 2010, 19, 1420-1431.	3.1	155
16	Recognition of UbcH5c and the nucleosome by the Bmi1/Ring1b ubiquitin ligase complex. EMBO Journal, 2011, 30, 3285-3297.	3.5	130
17	Synthetically modified guide RNA and donor DNA are a versatile platform for CRISPR-Cas9 engineering. ELife, 2017, 6, .	2.8	121
18	CRISPR germline engineering—the community speaks. Nature Biotechnology, 2015, 33, 478-486.	9.4	110

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19	Atlastins remodel the endoplasmic reticulum for selective autophagy. Journal of Cell Biology, 2018, 217, 3354-3367.	2.3	110
20	Crosstalk between Primase Subunits Can Act to Regulate Primer Synthesis in trans. Molecular Cell, 2005, 20, 391-401.	4.5	100
21	Conformational stabilization of ubiquitin yields potent and selective inhibitors of USP7. Nature Chemical Biology, 2013, 9, 51-58.	3.9	90
22	Timed inhibition of CDC7 increases CRISPR-Cas9 mediated templated repair. Nature Communications, 2020, 11, 2109.	5.8	84
23	In vitroâ€"transcribed guide RNAs trigger an innate immune response via the RIG-I pathway. PLoS Biology, 2018, 16, e2005840.	2.6	81
24	Binding Mechanism of Metalâ‹…NTP Substrates and Stringent-Response Alarmones to Bacterial DnaG-Type Primases. Structure, 2012, 20, 1478-1489.	1.6	73
25	THAP proteins target specific DNA sites through bipartite recognition of adjacent major and minor grooves. Nature Structural and Molecular Biology, 2010, 17, 117-123.	3.6	67
26	Identification of a DNA primase template tracking site redefines the geometry of primer synthesis. Nature Structural and Molecular Biology, 2008, 15, 163-169.	3.6	55
27	Ubiquitin in inflammation: the right linkage makes all the difference. Nature Structural and Molecular Biology, 2014, 21, 297-300.	3.6	55
28	Controlled Cycling and Quiescence Enables Efficient HDR in Engraftment-Enriched Adult Hematopoietic Stem and Progenitor Cells. Cell Reports, 2020, 32, 108093.	2.9	54
29	CRISPR off-target detection with DISCOVER-seq. Nature Protocols, 2020, 15, 1775-1799.	5.5	45
30	BARD1 is necessary for ubiquitylation of nucleosomal histone H2A and for transcriptional regulation of estrogen metabolism genes. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1316-1321.	3.3	43
31	Suppression of unwanted CRISPR-Cas9 editing by co-administration of catalytically inactivating truncated guide RNAs. Nature Communications, 2020, 11, 2697.	5.8	42
32	Hotspot-Centric De Novo Design of Protein Binders. Journal of Molecular Biology, 2011, 413, 1047-1062.	2.0	41
33	Identification of novel HPFH-like mutations by CRISPR base editing that elevate the expression of fetal hemoglobin. ELife, 2022, 11, .	2.8	29
34	The Histone Chaperone FACT Induces Cas9 Multi-turnover Behavior and Modifies Genome Manipulation in Human Cells. Molecular Cell, 2020, 79, 221-233.e5.	4.5	28
35	Rosetta in CAPRI rounds 13â€"19. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3212-3218.	1.5	20
36	The CUL5 ubiquitin ligase complex mediates resistance to CDK9 and MCL1 inhibitors in lung cancer cells. ELife, 2019, 8, .	2.8	19

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37	FASTDXL: A Generalized Screen to Trap Disulfide-Stabilized Complexes for Use in Structural Studies. Structure, 2007, 15, 773-780.	1.6	13
38	Bioactive TGFâ€Î² can associate with lipoproteins and is enriched in those containing apolipoprotein E3. Journal of Neurochemistry, 2009, 110, 1254-1262.	2.1	10
39	Using Protein Motion to Read, Write, and Erase Ubiquitin Signals. Journal of Biological Chemistry, 2015, 290, 26437-26444.	1.6	5
40	Co-opting CRISPR to deliver functional RNAs. Nature Methods, 2015, 12, 613-614.	9.0	4
41	Sometimes youâ€™re the scooper, and sometimes you get scooped: How to turn both into something good. PLoS Biology, 2018, 16, e2006843.	2.6	3
42	The RosettaCon 2012 Special Collection: Code Writ on Water, Documentation Writ in Stone. PLoS ONE, 2013, 8, e73775.	1.1	1
43	Decoding a Chain Letter for Degradation. Structure, 2013, 21, 1068-1070.	1.6	0
44	E Pluribus Unum (â€œOut of Many, Oneâ€): CRISPR Modeling of Myeloid Expansion. Cell Stem Cell, 2017, 21, 415-416.	5.2	0