

# Jacob E Corn

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/6127375/jacob-e-corn-publications-by-year.pdf>

**Version:** 2024-04-20

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

48  
papers

5,385  
citations

27  
h-index

56  
g-index

56  
ext. papers

7,048  
ext. citations

15.3  
avg, IF

5.63  
L-index

#	Paper	IF	Citations
48	Identification of novel HPFH-like mutations by CRISPR base editing that elevate the expression of fetal hemoglobin.. <i>ELife</i> , <b>2022</b> , 11,	8.9	3
47	PnB Designer: a web application to design prime and base editor guide RNAs for animals and plants. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 101	3.6	15
46	Suppression of unwanted CRISPR-Cas9 editing by co-administration of catalytically inactivating truncated guide RNAs. <i>Nature Communications</i> , <b>2020</b> , 11, 2697	17.4	19
45	A Genome-wide ER-phagy Screen Highlights Key Roles of Mitochondrial Metabolism and ER-Resident UFMylation. <i>Cell</i> , <b>2020</b> , 180, 1160-1177.e20	56.2	58
44	The Histone Chaperone FACT Induces Cas9 Multi-turnover Behavior and Modifies Genome Manipulation in Human Cells. <i>Molecular Cell</i> , <b>2020</b> , 79, 221-233.e5	17.6	12
43	Timed inhibition of CDC7 increases CRISPR-Cas9 mediated templated repair. <i>Nature Communications</i> , <b>2020</b> , 11, 2109	17.4	34
42	Controlled Cycling and Quiescence Enables Efficient HDR in Engraftment-Enriched Adult Hematopoietic Stem and Progenitor Cells. <i>Cell Reports</i> , <b>2020</b> , 32, 108093	10.6	22
41	CRISPR off-target detection with DISCOVER-seq. <i>Nature Protocols</i> , <b>2020</b> , 15, 1775-1799	18.8	26
40	Unbiased detection of CRISPR off-targets in vivo using DISCOVER-Seq. <i>Science</i> , <b>2019</b> , 364, 286-289	33.3	180
39	The CUL5 ubiquitin ligase complex mediates resistance to CDK9 and MCL1 inhibitors in lung cancer cells. <i>ELife</i> , <b>2019</b> , 8,	8.9	11
38	Advances in genome editing through control of DNA repair pathways. <i>Nature Cell Biology</i> , <b>2019</b> , 21, 1468-1478	34	146
37	BARD1 is necessary for ubiquitylation of nucleosomal histone H2A and for transcriptional regulation of estrogen metabolism genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 1316-1321	11.5	27
36	CRISPR-Cas9 genome editing in human cells occurs via the Fanconi anemia pathway. <i>Nature Genetics</i> , <b>2018</b> , 50, 1132-1139	36.3	126
35	In vitro-transcribed guide RNAs trigger an innate immune response via the RIG-I pathway. <i>PLoS Biology</i> , <b>2018</b> , 16, e2005840	9.7	50
34	Sometimes you're the scooper, and sometimes you get scooped: How to turn both into something good. <i>PLoS Biology</i> , <b>2018</b> , 16, e2006843	9.7	3
33	Atlastins remodel the endoplasmic reticulum for selective autophagy. <i>Journal of Cell Biology</i> , <b>2018</b> , 217, 3354-3367	7.3	65
32	Nanoparticle delivery of Cas9 ribonucleoprotein and donor DNA induces homology-directed DNA repair. <i>Nature Biomedical Engineering</i> , <b>2017</b> , 1, 889-901	19	404

31	E Pluribus Unum ("Out of Many, One"): CRISPR Modeling of Myeloid Expansion. <i>Cell Stem Cell</i> , <b>2017</b> , 21, 415-416	18	
30	Enhancer connectome in primary human cells identifies target genes of disease-associated DNA elements. <i>Nature Genetics</i> , <b>2017</b> , 49, 1602-1612	36.3	253
29	Synthetically modified guide RNA and donor DNA are a versatile platform for CRISPR-Cas9 engineering. <i>ELife</i> , <b>2017</b> , 6,	8.9	93
28	Disabling Cas9 by an anti-CRISPR DNA mimic. <i>Science Advances</i> , <b>2017</b> , 3, e1701620	14.3	216
27	Enhancing homology-directed genome editing by catalytically active and inactive CRISPR-Cas9 using asymmetric donor DNA. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 339-44	44.5	658
26	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. <i>ELife</i> , <b>2016</b> , 5,	8.9	343
25	Co-opting CRISPR to deliver functional RNAs. <i>Nature Methods</i> , <b>2015</b> , 12, 613-4	21.6	4
24	CRISPR germline engineering--the community speaks. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 478-86	44.5	91
23	Using protein motion to read, write, and erase ubiquitin signals. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 26437-44	5.4	4
22	USP30 and parkin homeostatically regulate atypical ubiquitin chains on mitochondria. <i>Nature Cell Biology</i> , <b>2015</b> , 17, 160-9	23.4	186
21	Ubiquitin in inflammation: the right linkage makes all the difference. <i>Nature Structural and Molecular Biology</i> , <b>2014</b> , 21, 297-300	17.6	43
20	Decoding a chain letter for degradation. <i>Structure</i> , <b>2013</b> , 21, 1068-70	5.2	
19	Conformational stabilization of ubiquitin yields potent and selective inhibitors of USP7. <i>Nature Chemical Biology</i> , <b>2013</b> , 9, 51-8	11.7	72
18	The RosettaCon 2012 Special Collection: Code Writ on Water, Documentation Writ in Stone. <i>PLoS ONE</i> , <b>2013</b> , 8, e73775	3.7	1
17	Binding mechanism of metal?NTP substrates and stringent-response alarmones to bacterial DnaG-type primases. <i>Structure</i> , <b>2012</b> , 20, 1478-89	5.2	58
16	ROSETTA3: an object-oriented software suite for the simulation and design of macromolecules. <i>Methods in Enzymology</i> , <b>2011</b> , 487, 545-74	1.7	1216
15	A de novo protein binding pair by computational design and directed evolution. <i>Molecular Cell</i> , <b>2011</b> , 42, 250-60	17.6	141
14	Hotspot-centric de novo design of protein binders. <i>Journal of Molecular Biology</i> , <b>2011</b> , 413, 1047-62	6.5	32

13	RosettaScripts: a scripting language interface to the Rosetta macromolecular modeling suite. <i>PLoS ONE</i> , <b>2011</b> , 6, e20161	3.7	311
12	Recognition of UbcH5c and the nucleosome by the Bmi1/Ring1b ubiquitin ligase complex. <i>EMBO Journal</i> , <b>2011</b> , 30, 3285-97	13	105
11	THAP proteins target specific DNA sites through bipartite recognition of adjacent major and minor grooves. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 117-23	17.6	54
10	Automated electron-density sampling reveals widespread conformational polymorphism in proteins. <i>Protein Science</i> , <b>2010</b> , 19, 1420-31	6.3	112
9	Rosetta in CAPRI rounds 13-19. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2010</b> , 78, 3212-8	4.2	17
8	Bioactive TGF-beta can associate with lipoproteins and is enriched in those containing apolipoprotein E3. <i>Journal of Neurochemistry</i> , <b>2009</b> , 110, 1254-62	6	9
7	Identification of a DNA primase template tracking site redefines the geometry of primer synthesis. <i>Nature Structural and Molecular Biology</i> , <b>2008</b> , 15, 163-9	17.6	43
6	FASTDXL: a generalized screen to trap disulfide-stabilized complexes for use in structural studies. <i>Structure</i> , <b>2007</b> , 15, 773-80	5.2	13
5	Crosstalk between primase subunits can act to regulate primer synthesis in trans. <i>Molecular Cell</i> , <b>2005</b> , 20, 391-401	17.6	85
4	Disabling Cas9 by an anti-CRISPR DNA mimic		6
3	CRISPR-Cas9 genome editing in human cells works via the Fanconi Anemia pathway		14
2	ATF4 mediates fetal globin upregulation in response to reduced $\beta$ globin		1
1	Timed inhibition of CDC7 increases CRISPR-Cas9 mediated templated repair		2