

# Brad Gulko

## List of Publications by Year in Descending Order

**Source:** <https://exaly.com/author-pdf/1612945/brad-gulko-publications-by-year.pdf>

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

9  
papers

912  
citations

7  
h-index

10  
g-index

10  
ext. papers

1,202  
ext. citations

31.8  
avg, IF

4.45  
L-index

#	Paper	IF	Citations
9	An inferred fitness consequence map of the rice genome. <i>Nature Plants</i> , <b>2020</b> , 6, 119-130	11.5	14
8	An evolutionary framework for measuring epigenomic information and estimating cell-type-specific fitness consequences. <i>Nature Genetics</i> , <b>2019</b> , 51, 335-342	36.3	16
7	Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data. <i>Nature Genetics</i> , <b>2017</b> , 49, 618-624	36.3	178
6	Is a super-enhancer greater than the sum of its parts?. <i>Nature Genetics</i> , <b>2016</b> , 49, 2-3	36.3	44
5	A method for calculating probabilities of fitness consequences for point mutations across the human genome. <i>Nature Genetics</i> , <b>2015</b> , 47, 276-83	36.3	175
4	Genome-wide inference of natural selection on human transcription factor binding sites. <i>Nature Genetics</i> , <b>2013</b> , 45, 723-9	36.3	95
3	Bayesian inference of ancient human demography from individual genome sequences. <i>Nature Genetics</i> , <b>2011</b> , 43, 1031-4	36.3	387
2	How Much Information is Provided by Human Epigenomic Data? An Evolutionary View		1
1	Fast, scalable prediction of deleterious noncoding variants from functional and population genomic data		2