

# Bratati Kahali

## List of Publications by Year in Descending Order

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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.

24  
papers

5,089  
citations

15  
h-index

27  
g-index

27  
ext. papers

6,422  
ext. citations

15.3  
avg, IF

3.28  
L-index

#	Paper	IF	Citations
24	Concurrent outcomes from multiple approaches of epistasis analysis for human body mass index associated loci provide insights into obesity biology.. <i>Scientific Reports</i> , <b>2022</b> , 12, 7306	4.9	0
23	Allele-specific variation at APOE increases nonalcoholic fatty liver disease and obesity but decreases risk of Alzheimers disease and myocardial infarction. <i>Human Molecular Genetics</i> , <b>2021</b> , 30, 1443-1456	5.6	5
22	A Noncoding Variant Near PPP1R3B Promotes Liver Glycogen Storage and MetS, but Protects Against Myocardial Infarction. <i>Journal of Clinical Endocrinology and Metabolism</i> , <b>2021</b> , 106, 372-387	5.6	3
21	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , <b>2019</b> , 51, 452-469	36.3	44
20	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , <b>2018</b> , 50, 26-41	36.3	186
19	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , <b>2017</b> , 542, 186-190	50.4	412
18	Association Between Telomere Length and Risk of Cancer and Non-Neoplastic Diseases: A Mendelian Randomization Study. <i>JAMA Oncology</i> , <b>2017</b> , 3, 636-651	13.4	236
17	TM6SF2: catch-22 in the fight against nonalcoholic fatty liver disease and cardiovascular disease?. <i>Gastroenterology</i> , <b>2015</b> , 148, 679-84	13.3	58
16	Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 6849-60	5.6	44
15	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , <b>2015</b> , 47, 1357-62	36.3	186
14	Mendelian Randomization Study of Body Mass Index and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2015</b> , 24, 1024-31	4	54
13	Insights from Genome-Wide Association Analyses of Nonalcoholic Fatty Liver Disease. <i>Seminars in Liver Disease</i> , <b>2015</b> , 35, 375-91	7.3	37
12	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , <b>2015</b> , 518, 187-196	50.4	920
11	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , <b>2015</b> , 518, 197-206	50.4	2687
10	Characterization of European ancestry nonalcoholic fatty liver disease-associated variants in individuals of African and Hispanic descent. <i>Hepatology</i> , <b>2013</b> , 58, 966-75	11.2	91
9	Disorderness in Escherichia coli proteome: perception of folding fidelity and protein-protein interactions. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2013</b> , 31, 472-6	3.6	15
8	Insights into Eukaryotic Interacting Protein Evolution <b>2011</b> , 51-70		2

7	Selective constraints in yeast genes with differential expressivity: codon pair usage and mRNA stability perspectives. <i>Gene</i> , <b>2011</b> , 481, 76-82	3.8	4
6	Protein complex forming ability is favored over the features of interacting partners in determining the evolutionary rates of proteins in the yeast protein-protein interaction networks. <i>BMC Systems Biology</i> , <b>2010</b> , 4, 155	3.5	10
5	Exploring the evolutionary rate differences of party hub and date hub proteins in <i>Saccharomyces cerevisiae</i> protein-protein interaction network. <i>Gene</i> , <b>2009</b> , 429, 18-22	3.8	18
4	Evolutionary constraints on hub and non-hub proteins in human protein interaction network: insight from protein connectivity and intrinsic disorder. <i>Gene</i> , <b>2009</b> , 434, 50-5	3.8	25
3	Delving deeper into the unexpected correlation between gene expressivity and codon usage bias of <i>Escherichia coli</i> genome. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2008</b> , 25, 655-61	3.6	8
2	Reinvestigating the codon and amino acid usage of <i>S. cerevisiae</i> genome: a new insight from protein secondary structure analysis. <i>Biochemical and Biophysical Research Communications</i> , <b>2007</b> , 354, 693-9	3.4	35
1	Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution		1