# Kousik Kundu

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/2883446/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 22 papers | 2,897 citations | 566801 15 h-index | 676716 22 g-index |
| 32 all docs | 32 docs citations | 32 times ranked | 7824 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The Allelic Landscape of Human Blood Cell Trait Variation and Links to Common Complex Disease. Cell, 2016, 167, 1415-1429.e19. | 13.5 | 1,052 |
| 2 | Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24. | 13.5 | 573 |
| 3 | The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11. | 13.5 | 388 |
| 4 | Shared genetic effects on chromatin and gene expression indicate a role for enhancer priming in immune response. Nature Genetics, 2018, 50, 424-431. | 9.4 | 253 |
| 5 | A map of transcriptional heterogeneity and regulatory variation in human microglia. Nature Genetics, 2021, 53, 861-868. | 9.4 | 115 |
| 6 | Freiburg RNA tools: a central online resource for RNA-focused research and teaching. Nucleic Acids Research, 2018, 46, W25-W29. | 6.5 | 107 |
| 7 | Tumors induce de novo steroid biosynthesis in T cells to evade immunity. Nature Communications, 2020, 11, 3588. | 5.8 | 54 |
| 8 | Mitochondrial DNA variants modulate N-formylmethionine, proteostasis and risk of late-onset human diseases. Nature Medicine, 2021, 27, 1564-1575. | 15.2 | 40 |
| 9 | MoDPepInt: an interactive web server for prediction of modular domainâ€“peptide interactions. Bioinformatics, 2014, 30, 2668-2669. | 1.8 | 37 |
| 10 | Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. Nature Communications, 2018, 9, 4674. | 5.8 | 33 |
| 11 | Genetic perturbation of PU.1 binding and chromatin looping at neutrophil enhancers associates with autoimmune disease. Nature Communications, 2021, 12, 2298. | 5.8 | 32 |
| 12 | Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893. | 2.6 | 28 |
| 13 | Semi-Supervised Prediction of SH2-Peptide Interactions from Imbalanced High-Throughput Data. PLoS ONE, 2013, 8, e62732. | 1.1 | 27 |
| 14 | Genetic associations at regulatory phenotypes improve fine-mapping of causal variants for 12 immune-mediated diseases. Nature Genetics, 2022, 54, 251-262. | 9.4 | 23 |
| 15 | Whole-exome sequencing identifies rare genetic variants associated with human plasma metabolites. American Journal of Human Genetics, 2022, 109, 1038-1054. | 2.6 | 17 |
| 16 | Cluster based prediction of PDZ-peptide interactions. BMC Genomics, 2014, 15, S5. | 1.2 | 16 |
| 17 | A graph kernel approach for alignment-free domain-peptide interaction prediction with an application to human SH3 domains. Bioinformatics, 2013, 29, i335-i343. | 1.8 | 15 |
| 18 | GRIN3B missense mutation as an inherited risk factor for schizophrenia: whole-exome sequencing in a family with a familiar history of psychotic disorders. Genetical Research, 2017, 99, e1. | 0.3 | 15 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851. | 2.6 | 14 |
| 20 | The influence of rare variants in circulating metabolic biomarkers. PLoS Genetics, 2020, 16, e1008605. | 1.5 | 9 |
| 21 | Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations. Scientific Reports, 2022, 12, 1131. | 1.6 | 2 |
| 22 | An Efficient Semi-supervised Learning Approach to Predict SH2 Domain Mediated Interactions. Methods in Molecular Biology, 2017, 1555, 83-97. | 0.4 | 0 |