

# Ramneek Gupta

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/881160/publications.pdf>

Version: 2024-02-01

83  
papers

11,578  
citations

117625  
34  
h-index

98798  
67  
g-index

88  
all docs

88  
docs citations

88  
times ranked

21458  
citing authors

#	ARTICLE	IF	CITATIONS
1	Characteristics of white blood cell count in acute lymphoblastic leukemia: A COST LEGEND phenotypeâ€“genotype study. <i>Pediatric Blood and Cancer</i> , 2022, 69, e29582.	1.5	1
2	Information theoretic perspective on genome clustering. <i>Saudi Journal of Biological Sciences</i> , 2021, 28, 1867-1889.	3.8	2
3	Profiles of Glucose Metabolism in Different Prediabetes Phenotypes, Classified by Fasting Glycemia, 2-Hour OGTT, Glycated Hemoglobin, and 1-Hour OGTT: An IMI DIRECT Study. <i>Diabetes</i> , 2021, 70, 2092-2106.	0.6	17
4	Whole blood co-expression modules associate with metabolic traits and type 2 diabetes: an IMI-DIRECT study. <i>Genome Medicine</i> , 2020, 12, 109.	8.2	8
5	A reference map of potential determinants for the human serum metabolome. <i>Nature</i> , 2020, 588, 135-140.	27.8	230
6	The intestinal microbiome is a co-determinant of the postprandial plasma glucose response. <i>PLoS ONE</i> , 2020, 15, e0238648.	2.5	9
7	Polygenic risk score-analysis of thromboembolism in patients with acute lymphoblastic leukemia. <i>Thrombosis Research</i> , 2020, 196, 15-20.	1.7	3
8	Data integration for prediction of weight loss in randomized controlled dietary trials. <i>Scientific Reports</i> , 2020, 10, 20103.	3.3	10
9	Predicting and elucidating the etiology of fatty liver disease: A machine learning modeling and validation study in the IMI DIRECT cohorts. <i>PLoS Medicine</i> , 2020, 17, e1003149.	8.4	47
10	Prediction of Nephrotoxicity Associated With Cisplatin-Based Chemotherapy in Testicular Cancer Patients. <i>JNCI Cancer Spectrum</i> , 2020, 4, pkaa032.	2.9	13
11	Effects of germline DHFR and FPGS variants on methotrexate metabolism and relapse of leukemia. <i>Blood</i> , 2020, 136, 1161-1168.	1.4	9
12	Nationwide germline whole genome sequencing of 198 consecutive pediatric cancer patients reveals a high incidence of cancer prone syndromes. <i>PLoS Genetics</i> , 2020, 16, e1009231.	3.5	64
13	Title is missing!. , 2020, 16, e1009231.		0
14	Title is missing!. , 2020, 16, e1009231.		0
15	Title is missing!. , 2020, 16, e1009231.		0
16	Title is missing!. , 2020, 16, e1009231.		0
17	Title is missing!. , 2020, 17, e1003149.		0
18	Title is missing!. , 2020, 17, e1003149.		0

#	ARTICLE	IF	CITATIONS
19	Title is missing!. , 2020, 17, e1003149.		0
20	Title is missing!. , 2020, 17, e1003149.		0
21	Title is missing!. , 2020, 17, e1003149.		0
22	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: descriptive characteristics of the epidemiological studies within the IMI DIRECT Consortium. Diabetologia, 2019, 62, 1601-1615.	6.3	22
23	Candidate single nucleotide polymorphisms and thromboembolism in acute lymphoblastic leukemia â€“ A NOPHO ALL2008 study. Thrombosis Research, 2019, 184, 92-98.	1.7	20
24	Trypsin-encoding <i>PRSS1-PRSS2</i> variations influence the risk of asparaginase-associated pancreatitis in children with acute lymphoblastic leukemia: a Ponte di Legno toxicity working group report. Haematologica, 2019, 104, 556-563.	3.5	36
25	Genetic predisposition to <sc>PEG</sc>â€™asparaginase hypersensitivity in children treated according to <sc>NOPHO ALL</sc>2008. British Journal of Haematology, 2019, 184, 405-417.	2.5	33
26	Whole grain-rich diet reduces body weight and systemic low-grade inflammation without inducing major changes of the gut microbiome: a randomised cross-over trial. Gut, 2019, 68, 83-93.	12.1	278
27	Transcriptome analysis of rootâ€™nematode (<i>Meloidogyne incognita</i>)â€™infected tomato (<i>Solanum lycopersicum</i>) roots reveals complex gene expression profiles and metabolic networks of both host and nematode during susceptible and resistance responses. Molecular Plant Pathology, 2018, 19, 615-633.	4.2	127
28	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. Diabetologia, 2018, 61, 117-129.	6.3	32
29	A low-gluten diet induces changes in the intestinal microbiome of healthy Danish adults. Nature Communications, 2018, 9, 4630.	12.8	124
30	The governance structure for data access in the DIRECT consortium: an innovative medicines initiative (IMI) project. Life Sciences, Society and Policy, 2018, 14, 20.	3.2	7
31	NT5C2 germline variants alter thiopurine metabolism and are associated with acquired NT5C2 relapse mutations in childhood acute lymphoblastic leukaemia. Leukemia, 2018, 32, 2527-2535.	7.2	13
32	Integrative network analysis highlights biological processes underlying GLP-1 stimulated insulin secretion: A DIRECT study. PLoS ONE, 2018, 13, e0189886.	2.5	9
33	Obesity is associated with depot-specific alterations in adipocyte DNA methylation and gene expression. Adipocyte, 2017, 6, 124-133.	2.8	34
34	Meta-analysis of five genome-wide association studies identifies multiple new loci associated with testicular germ cell tumor. Nature Genetics, 2017, 49, 1141-1147.	21.4	105
35	Cerebellar mutism syndrome in children with brain tumours of the posterior fossa. BMC Cancer, 2017, 17, 439.	2.6	38
36	Sequencing and de novo assembly of 150 genomes from Denmark as a population reference. Nature, 2017, 548, 87-91.	27.8	130

#	ARTICLE	IF	CITATIONS
37	Common Genetic Variants in Trypsin Regulating Genes Are Associated with Asparaginase-Associated Pancreatitis in Children with Acute Lymphoblastic Leukemia: A Ponte Di Legno Toxicity Working Group Study. <i>Blood</i> , 2017, 130, 885-885.	1.4	0
38	Integrative analysis of miRNA and gene expression reveals regulatory networks in tamoxifen-resistant breast cancer. <i>Oncotarget</i> , 2016, 7, 57239-57253.	1.8	30
39	Ranking factors involved in diabetes remission after bariatric surgery using machine-learning integrating clinical and genomic biomarkers. <i>Npj Genomic Medicine</i> , 2016, 1, 16035.	3.8	21
40	Colonic transit time is related to bacterial metabolism and mucosal turnover in the gut. <i>Nature Microbiology</i> , 2016, 1, 16093.	13.3	321
41	Investigation of Human Cancers for Retrovirus by Low-Stringency Target Enrichment and High-Throughput Sequencing. <i>Scientific Reports</i> , 2015, 5, 13201.	3.3	34
42	Acquisition of docetaxel resistance in breast cancer cells reveals upregulation of ABCB1 expression as a key mediator of resistance accompanied by discrete upregulation of other specific genes and pathways. <i>Tumor Biology</i> , 2015, 36, 4327-4338.	1.8	36
43	Novel variation and de novo mutation rates in population-wide de novo assembled Danish trios. <i>Nature Communications</i> , 2015, 6, 5969.	12.8	164
44	Eukaryotic Glycosylation: Online Methods for Site Prediction on Protein Sequences. <i>Methods in Molecular Biology</i> , 2015, 1273, 127-137.	0.9	13
45	Inherited coding variants at the CDKN2A locus influence susceptibility to acute lymphoblastic leukaemia in children. <i>Nature Communications</i> , 2015, 6, 7553.	12.8	72
46	Establishment and characterization of models of chemotherapy resistance in colorectal cancer: Towards a predictive signature of chemoresistance. <i>Molecular Oncology</i> , 2015, 9, 1169-1185.	4.6	91
47	Transcriptome profiling of brown adipose tissue during cold exposure reveals extensive regulation of glucose metabolism. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2015, 308, E380-E392.	3.5	105
48	Germ Cell Cancer and Multiple Relapses: Toxicity and Survival. <i>Journal of Clinical Oncology</i> , 2015, 33, 3116-3123.	1.6	29
49	Germ cell cancer and multiple relapses: Toxicity and survival.. <i>Journal of Clinical Oncology</i> , 2015, 33, 4533-4533.	1.6	0
50	Host genome variations and risk of infections during induction treatment for childhood acute lymphoblastic leukaemia. <i>European Journal of Haematology</i> , 2014, 92, 321-330.	2.2	7
51	The genome of a Late Pleistocene human from a Clovis burial site in western Montana. <i>Nature</i> , 2014, 506, 225-229.	27.8	500
52	A genome-wide association study identifies CDHR3 as a susceptibility locus for early childhood asthma with severe exacerbations. <i>Nature Genetics</i> , 2014, 46, 51-55.	21.4	497
53	Choice of bacterial DNA extraction method from fecal material influences community structure as evaluated by metagenomic analysis. <i>Microbiome</i> , 2014, 2, 19.	11.1	228
54	Discovery of biomarkers for glycaemic deterioration before and after the onset of type 2 diabetes: rationale and design of the epidemiological studies within the IMI DIRECT Consortium. <i>Diabetologia</i> , 2014, 57, 1132-1142.	6.3	48

#	ARTICLE	IF	CITATIONS
55	TIMP1 overexpression mediates resistance of MCF-7 human breast cancer cells to fulvestrant and down-regulates progesterone receptor expression. <i>Tumor Biology</i> , 2013, 34, 3839-3851.	1.8	18
56	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. <i>Nature Genetics</i> , 2013, 45, 902-906.	21.4	221
57	TIMP-1 Increases Expression and Phosphorylation of Proteins Associated with Drug Resistance in Breast Cancer Cells. <i>Journal of Proteome Research</i> , 2013, 12, 4136-4151.	3.7	36
58	Precision mapping of the human O-GalNAc glycoproteome through SimpleCell technology. <i>EMBO Journal</i> , 2013, 32, 1478-1488.	7.8	1,130
59	Genome-Wide Assessment of the Association of Rare and Common Copy Number Variations to Testicular Germ Cell Cancer. <i>Frontiers in Endocrinology</i> , 2013, 4, 2.	3.5	14
60	HExpoChem: a systems biology resource to explore human exposure to chemicals. <i>Bioinformatics</i> , 2013, 29, 1231-1232.	4.1	9
61	Prediction of Disease Causing Non-Synonymous SNPs by the Artificial Neural Network Predictor NetDiseaseSNP. <i>PLoS ONE</i> , 2013, 8, e68370.	2.5	20
62	Colorectal cancer cell lines made resistant to SN38 and Oxaliplatin: Roles of altered ion transporter function in resistance?. <i>FASEB Journal</i> , 2013, 27, lb452.	0.5	0
63	A genome-wide association study of men with symptoms of testicular dysgenesis syndrome and its network biology interpretation. <i>Journal of Medical Genetics</i> , 2012, 49, 58-65.	3.2	96
64	Genome-wide analysis of cytogenetic aberrations in <i>ETV6</i> / <i>RUNX1</i> -positive childhood acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2012, 157, 476-482.	2.5	25
65	Host Genomic Variants and Risk of Infections During Induction Treatment in Childhood Acute Lymphoblastic Leukemia. <i>Blood</i> , 2012, 120, 1382-1382.	1.4	0
66	Cost-effective multiplexing before capture allows screening of 25,000 clinically relevant SNPs in childhood acute lymphoblastic leukemia. <i>Leukemia</i> , 2011, 25, 1001-1006.	7.2	20
67	Heterozygous deletion at the <i>RLN1</i> locus in a family with testicular germ cell cancer identified by integrating copy number variation data with phenome and interactome information. <i>Journal of Developmental and Physical Disabilities</i> , 2011, 34, e122-32.	3.6	7
68	An Aboriginal Australian Genome Reveals Separate Human Dispersals into Asia. <i>Science</i> , 2011, 334, 94-98.	12.6	675
69	Protein annotation in the era of personal genomics. <i>Current Opinion in Structural Biology</i> , 2010, 20, 335-341.	5.7	1
70	Ancient human genome sequence of an extinct Palaeo-Eskimo. <i>Nature</i> , 2010, 463, 757-762.	27.8	750
71	Relating genomic variation to drug response in childhood acute lymphoblastic leukemia by multiplexed targeted sequencing. <i>Genome Biology</i> , 2010, 11, P41.	9.6	0
72	In silico determination of intracellular glycosylation and phosphorylation sites in human selectins: Implications for biological function. <i>Journal of Cellular Biochemistry</i> , 2007, 100, 1558-1572.	2.6	11

#	ARTICLE	IF	CITATIONS
73	Prediction, conservation analysis, and structural characterization of mammalian mucin-type O-glycosylation sites. <i>Glycobiology</i> , 2005, 15, 153-164.	2.5	825
74	Analysis and prediction of leucine-rich nuclear export signals. <i>Protein Engineering, Design and Selection</i> , 2004, 17, 527-536.	2.1	721
75	Prediction of post-translational glycosylation and phosphorylation of proteins from the amino acid sequence. <i>Proteomics</i> , 2004, 4, 1633-1649.	2.2	1,784
76	<i>Plasmodium falciparum</i> merozoite surface protein 1. Glycosylation and localization to low-density, detergent-resistant membranes in the parasitized erythrocyte. <i>FEBS Journal</i> , 2003, 270, 366-375.	0.2	16
77	Prediction of human protein function according to Gene Ontology categories. <i>Bioinformatics</i> , 2003, 19, 635-642.	4.1	233
78	NESbase version 1.0: a database of nuclear export signals. <i>Nucleic Acids Research</i> , 2003, 31, 393-396.	14.5	195
79	Prediction of Human Protein Function from Post-translational Modifications and Localization Features. <i>Journal of Molecular Biology</i> , 2002, 319, 1257-1265.	4.2	312
80	Prediction of glycosylation across the human proteome and the correlation to protein function. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2002, , 310-22.	0.7	246
81	Prediction of glycosylation across the human proteome and the correlation to protein function. , 2001, , .		276
82	Scanning the available <i>Dictyostelium discoideum</i> proteome for O-linked GlcNAc glycosylation sites using neural networks. <i>Glycobiology</i> , 1999, 9, 1009-1022.	2.5	99
83	O-GLYCBASE version 4.0: a revised database of O-glycosylated proteins. <i>Nucleic Acids Research</i> , 1999, 27, 370-372.	14.5	213