

Uwe Völker

List of Publications by Year in descending order

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Version: 2024-02-01

195
papers

28,761
citations

22153

59
h-index

7348

152
g-index

222
all docs

222
docs citations

222
times ranked

40545
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	21.4	2,421
3	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	27.8	1,855
4	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013, 45, 1238-1243.	21.4	1,544
5	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
6	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
7	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	21.4	1,104
8	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	21.4	924
9	Cohort Profile: The Study of Health in Pomerania. <i>International Journal of Epidemiology</i> , 2011, 40, 294-307.	1.9	876
10	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i> . <i>Science</i> , 2012, 335, 1103-1106.	12.6	809
11	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
12	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	21.4	590
13	Meta-Analysis of 28,141 Individuals Identifies Common Variants within Five New Loci That Influence Uric Acid Concentrations. <i>PLoS Genetics</i> , 2009, 5, e1000504.	3.5	572
14	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	21.4	552
15	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549
16	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020, 11, 163.	12.8	466
17	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
18	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. <i>Nature Communications</i> , 2016, 7, 10023.	12.8	412

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19	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
20	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	28.9	353
21	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	27.8	320
22	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
23	Insights in ChAdOx1 nCoV-19 vaccine-induced immune thrombotic thrombocytopenia. <i>Blood</i> , 2021, 138, 2256-2268.	1.4	228
24	A genome-wide association study of metabolic traits in human urine. <i>Nature Genetics</i> , 2011, 43, 565-569.	21.4	224
25	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	21.4	223
26	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. <i>Nature Communications</i> , 2019, 10, 2773.	12.8	183
27	<i>Staphylococcus aureus</i> Transcriptome Architecture: From Laboratory to Infection-Mimicking Conditions. <i>PLoS Genetics</i> , 2016, 12, e1005962.	3.5	170
28	NLRP3 Inflammasome Regulates Development of Systemic Inflammatory Response and Compensatory Anti-Inflammatory Response Syndromes in Mice With Acute Pancreatitis. <i>Gastroenterology</i> , 2020, 158, 253-269.e14.	1.3	162
29	Sigma Factor SigB Is Crucial to Mediate <i>Staphylococcus aureus</i> Adaptation during Chronic Infections. <i>PLoS Pathogens</i> , 2015, 11, e1004870.	4.7	150
30	Identification of Genetic Loci Associated With <i>Helicobacter pylori</i> Serologic Status. <i>JAMA - Journal of the American Medical Association</i> , 2013, 309, 1912.	7.4	142
31	A genome-wide association study identifies 6p21 as novel risk locus for dilated cardiomyopathy. <i>European Heart Journal</i> , 2014, 35, 1069-1077.	2.2	137
32	Large-scale reduction of the <i>Bacillus subtilis</i> genome: consequences for the transcriptional network, resource allocation, and metabolism. <i>Genome Research</i> , 2017, 27, 289-299.	5.5	137
33	Associations of circulating plasma microRNAs with age, body mass index and sex in a population-based study. <i>BMC Medical Genomics</i> , 2015, 8, 61.	1.5	133
34	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	12.8	133
35	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. <i>Diabetes</i> , 2016, 65, 803-817.	0.6	131
36	Genome-wide association study of chronic periodontitis in a general German population. <i>Journal of Clinical Periodontology</i> , 2013, 40, 977-985.	4.9	123

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37	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. <i>Nature Communications</i> , 2018, 9, 5141.	12.8	119
38	Rare and low-frequency coding variants in CXCR2 and other genes are associated with hematological traits. <i>Nature Genetics</i> , 2014, 46, 629-634.	21.4	113
39	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	3.5	107
40	Large-scale genome-wide analysis identifies genetic variants associated with cardiac structure and function. <i>Journal of Clinical Investigation</i> , 2017, 127, 1798-1812.	8.2	106
41	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. <i>Nature Genetics</i> , 2020, 52, 167-176.	21.4	101
42	Genome-wide association study in 8,956 German individuals identifies influence of ABO histo-blood groups on gut microbiome. <i>Nature Genetics</i> , 2021, 53, 147-155.	21.4	101
43	Aureo Wiki – The repository of the <i>Staphylococcus aureus</i> research and annotation community. <i>International Journal of Medical Microbiology</i> , 2018, 308, 558-568.	3.6	99
44	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	3.3	98
45	Long-term instability of the intestinal microbiome is associated with metabolic liver disease, low microbiota diversity, diabetes mellitus and impaired exocrine pancreatic function. <i>Gut</i> , 2021, 70, 522-530.	12.1	96
46	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	12.8	89
47	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. <i>Current Biology</i> , 2019, 29, 120-127.e5.	3.9	86
48	Comparative evaluation of saliva collection methods for proteome analysis. <i>Clinica Chimica Acta</i> , 2013, 419, 42-46.	1.1	85
49	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
50	Adaptation of <i>Bacillus subtilis</i> carbon core metabolism to simultaneous nutrient limitation and osmotic challenge: a multi-omics perspective. <i>Environmental Microbiology</i> , 2014, 16, 1898-1917.	3.8	83
51	Genome-Wide Association Study with Targeted and Non-targeted NMR Metabolomics Identifies 15 Novel Loci of Urinary Human Metabolic Individuality. <i>PLoS Genetics</i> , 2015, 11, e1005487.	3.5	83
52	Genomewide meta-analysis identifies loci associated with IGF and IGFBP levels with impact on age-related traits. <i>Aging Cell</i> , 2016, 15, 811-824.	6.7	83
53	Fucosyltransferase 2 (FUT2) non-secretor status and blood group B are associated with elevated serum lipase activity in asymptomatic subjects, and an increased risk for chronic pancreatitis: a genetic association study. <i>Gut</i> , 2015, 64, 646-656.	12.1	82
54	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	6.2	82

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55	A structured weight loss program increases gut microbiota phylogenetic diversity and reduces levels of <i>Collinsella</i> in obese type 2 diabetics: A pilot study. <i>PLoS ONE</i> , 2019, 14, e0219489.	2.5	82
56	Genome-wide meta-analysis of muscle weakness identifies 15 susceptibility loci in older men and women. <i>Nature Communications</i> , 2021, 12, 654.	12.8	75
57	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. <i>Gastroenterology</i> , 2016, 151, 351-363.e28.	1.3	74
58	Impaired Exocrine Pancreatic Function Associates With Changes in Intestinal Microbiota Composition and Diversity. <i>Gastroenterology</i> , 2019, 156, 1010-1015.	1.3	74
59	Cohort Profile Update: The Study of Health in Pomerania (SHIP). <i>International Journal of Epidemiology</i> , 2022, 51, e372-e383.	1.9	73
60	Analyzing Illumina Gene Expression Microarray Data from Different Tissues: Methodological Aspects of Data Analysis in the MetaXpress Consortium. <i>PLoS ONE</i> , 2012, 7, e50938.	2.5	71
61	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018, 9, 2904.	12.8	71
62	Characterization of the Human Myocardial Proteome in Inflammatory Dilated Cardiomyopathy by Label-free Quantitative Shotgun Proteomics of Heart Biopsies. <i>Journal of Proteome Research</i> , 2011, 10, 2161-2171.	3.7	66
63	Myocardial gene expression profiles and cardiodepressant autoantibodies predict response of patients with dilated cardiomyopathy to immunoabsorption therapy. <i>European Heart Journal</i> , 2013, 34, 666-675.	2.2	64
64	Genetic correlations and genome-wide associations of cortical structure in general population samples of 22,824 adults. <i>Nature Communications</i> , 2020, 11, 4796.	12.8	61
65	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. <i>Nature Communications</i> , 2021, 12, 5647.	12.8	61
66	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	12.8	59
67	Effects of <i>Staphylococcus aureus</i> -hemolysin A on calcium signalling in immortalized human airway epithelial cells. <i>Cell Calcium</i> , 2009, 45, 165-176.	2.4	56
68	<sc>GWAS</sc> analysis of handgrip and lower body strength in older adults in the <sc>CHARGE</sc> consortium. <i>Aging Cell</i> , 2016, 15, 792-800.	6.7	51
69	Specific serum IgG at diagnosis of <i>Staphylococcus aureus</i> bloodstream invasion is correlated with disease progression. <i>Journal of Proteomics</i> , 2015, 128, 1-7.	2.4	49
70	HDAC (Histone Deacetylase) Inhibitor Valproic Acid Attenuates Atrial Remodeling and Delays the Onset of Atrial Fibrillation in Mice. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2019, 12, e007071.	4.8	49
71	<i>Helicobacter pylori</i> infection associates with fecal microbiota composition and diversity. <i>Scientific Reports</i> , 2019, 9, 20100.	3.3	49
72	The Gut Microbiome in Patients With Chronic Pancreatitis Is Characterized by Significant Dysbiosis and Overgrowth by Opportunistic Pathogens. <i>Clinical and Translational Gastroenterology</i> , 2020, 11, e00232.	2.5	49

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73	Advanced tool for characterization of microbial cultures by combining cytomics and proteomics. <i>Applied Microbiology and Biotechnology</i> , 2010, 88, 575-584.	3.6	44
74	Cohort profile: Greifswald approach to individualized medicine (GANI_MED). <i>Journal of Translational Medicine</i> , 2014, 12, 144.	4.4	43
75	Sequential organ failure assessment score is an excellent operationalization of disease severity of adult patients with hospitalized community acquired pneumonia – results from the prospective observational PROGRESS study. <i>Critical Care</i> , 2019, 23, 110.	5.8	43
76	A global <i>Staphylococcus aureus</i> proteome resource applied to the in vivo characterization of host-pathogen interactions. <i>Scientific Reports</i> , 2017, 7, 9718.	3.3	42
77	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.	5.2	42
78	Role of Platelet Size Revisited – Function and Protein Composition of Large and Small Platelets. <i>Thrombosis and Haemostasis</i> , 2019, 119, 407-420.	3.4	41
79	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	38
80	Comparative analysis of ChAdOx1 nCoV-19 and Ad26.COV2.S SARS-CoV-2 vector vaccines. <i>Haematologica</i> , 2022, 107, 947-957.	3.5	37
81	Characterization of human and <i>Staphylococcus aureus</i> proteins in respiratory mucosa by in vivo- and immunoproteomics. <i>Journal of Proteomics</i> , 2017, 155, 31-39.	2.4	36
82	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. <i>Hypertension</i> , 2017, 70, 743-750.	2.7	34
83	A new, accurate predictive model for incident hypertension. <i>Journal of Hypertension</i> , 2013, 31, 2142-2150.	0.5	32
84	Comparative proteome analysis reveals conserved and specific adaptation patterns of <i>Staphylococcus aureus</i> after internalization by different types of human non-professional phagocytic host cells. <i>Frontiers in Microbiology</i> , 2014, 5, 392.	3.5	32
85	Metabolic Cross-talk Between Human Bronchial Epithelial Cells and Internalized <i>Staphylococcus aureus</i> as a Driver for Infection*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 892a-908.	3.8	32
86	Variants in <i>ABCG8</i> and <i>TRAF3</i> genes confer risk for gallstone disease in admixed Latinos with Mapuche Native American ancestry. <i>Scientific Reports</i> , 2019, 9, 772.	3.3	30
87	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. <i>Neurology</i> , 2019, 92, .	1.1	30
88	Pathogenesis of vaccine-induced immune thrombotic thrombocytopenia (VITT). <i>Seminars in Hematology</i> , 2022, 59, 97-107.	3.4	30
89	3,5-T2 alters murine genes relevant for xenobiotic, steroid, and thyroid hormone metabolism. <i>Journal of Molecular Endocrinology</i> , 2016, 56, 311-323.	2.5	28
90	Essentiality of c-di-AMP in <i>Bacillus subtilis</i> : Bypassing mutations converge in potassium and glutamate homeostasis. <i>PLoS Genetics</i> , 2021, 17, e1009092.	3.5	28

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91	The quest for bacterial allergens. <i>International Journal of Medical Microbiology</i> , 2018, 308, 738-750.	3.6	27
92	Metaproteomics analysis of microbial diversity of human saliva and tongue dorsum in young healthy individuals. <i>Journal of Oral Microbiology</i> , 2019, 11, 1654786.	2.7	27
93	<i>S. aureus</i> haemolysin A-induced IL-8 and IL-6 release from human airway epithelial cells is mediated by activation of p38- and Erk-MAP kinases and additional, cell type-specific signalling mechanisms. <i>Cellular Microbiology</i> , 2013, 15, 1253-1265.	2.1	26
94	Improving Proteome Coverage for Small Sample Amounts: An Advanced Method for Proteomics Approaches with Low Bacterial Cell Numbers. <i>Proteomics</i> , 2019, 19, e1900192.	2.2	26
95	In vivo proteomics identifies the competence regulon and AliB oligopeptide transporter as pathogenic factors in pneumococcal meningitis. <i>PLoS Pathogens</i> , 2019, 15, e1007987.	4.7	25
96	A Comprehensive View on the Human Antibody Repertoire Against <i>Staphylococcus aureus</i> Antigens in the General Population. <i>Frontiers in Immunology</i> , 2021, 12, 651619.	4.8	24
97	A description of large-scale metabolomics studies: increasing value by combining metabolomics with genome-wide SNP genotyping and transcriptional profiling. <i>Journal of Endocrinology</i> , 2012, 215, 17-28.	2.6	23
98	Changes of myocardial gene expression and protein composition in patients with dilated cardiomyopathy after immunoadsorption with subsequent immunoglobulin substitution. <i>Basic Research in Cardiology</i> , 2016, 111, 53.	5.9	23
99	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. <i>BMC Cardiovascular Disorders</i> , 2019, 19, 240.	1.7	22
100	Sex-specific differences in the intracellular proteome of human endothelial cells from dizygotic twins. <i>Journal of Proteomics</i> , 2019, 201, 48-56.	2.4	22
101	Virus-induced dilated cardiomyopathy is characterized by increased levels of fibrotic extracellular matrix proteins and reduced amounts of energy-producing enzymes. <i>Proteomics</i> , 2011, 11, 4310-4320.	2.2	21
102	Impact of blood sample collection methods on blood protein profiling studies. <i>Clinica Chimica Acta</i> , 2017, 471, 128-134.	1.1	21
103	Association of childhood traumatization and neuropsychiatric outcomes with altered plasma micro RNA-levels. <i>Neuropsychopharmacology</i> , 2019, 44, 2030-2037.	5.4	21
104	Alternative fluorescent labeling strategies for characterizing gram-positive pathogenic bacteria: Flow cytometry supported counting, sorting, and proteome analysis of <i>Staphylococcus aureus</i> retrieved from infected host cells. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2016, 89, 932-940.	1.5	20
105	Energy Metabolites as Biomarkers in Ischemic and Dilated Cardiomyopathy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1999.	4.1	20
106	Characterization of the Genetic Program Linked to the Development of Atrial Fibrillation in CREM-1 ^{fl} C-X Mice. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2017, 10, .	4.8	19
107	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002037.	3.6	19
108	Carrying asymptomatic gallstones is not associated with changes in intestinal microbiota composition and diversity but cholecystectomy with significant dysbiosis. <i>Scientific Reports</i> , 2021, 11, 6677.	3.3	19

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109	Signatures of cytoplasmic proteins in the exoproteome distinguish community- and hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> USA300 lineages. <i>Virulence</i> , 2017, 8, 891-907.	4.4	19
110	Regression of Polypoid Nasal Mucosa after Systemic Corticosteroid Therapy: A Proteomics Study. <i>American Journal of Rhinology and Allergy</i> , 2009, 23, 480-485.	2.0	18
111	Metabolic Fingerprints of Circulating IGF-1 and the IGF-1/IGFBP-3 Ratio: A Multifluid Metabolomics Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016, 101, 4730-4742.	3.6	18
112	Changes of DNA topology affect the global transcription landscape and allow rapid growth of a <i>Bacillus subtilis</i> mutant lacking carbon catabolite repression. <i>Metabolic Engineering</i> , 2018, 45, 171-179.	7.0	18
113	Correlation of gene expression and clinical parameters identifies a set of genes reflecting LV systolic dysfunction and morphological alterations. <i>Physiological Genomics</i> , 2019, 51, 356-367.	2.3	18
114	Management of Osmoprotectant Uptake Hierarchy in <i>Bacillus subtilis</i> via a SigB-Dependent Antisense RNA. <i>Frontiers in Microbiology</i> , 2020, 11, 622.	3.5	18
115	Cross-Sectional Association of Salivary Proteins with Age, Sex, Body Mass Index, Smoking, and Education. <i>Journal of Proteome Research</i> , 2017, 16, 2273-2281.	3.7	17
116	Endomyocardial proteomic signature corresponding to the response of patients with dilated cardiomyopathy to immunoadsorption therapy. <i>Journal of Proteomics</i> , 2017, 150, 121-129.	2.4	17
117	From the genome sequence via the proteome to cell physiology – Pathoproteomics and pathophysiology of <i>Staphylococcus aureus</i> . <i>International Journal of Medical Microbiology</i> , 2018, 308, 545-557.	3.6	17
118	Tissue-specific multi-omics analysis of atrial fibrillation. <i>Nature Communications</i> , 2022, 13, 441.	12.8	17
119	Genetic Determinants of Electrocardiographic P-Wave Duration and Relation to Atrial Fibrillation. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 387-395.	3.6	16
120	Polygenic Architecture of Human Neuroanatomical Diversity. <i>Cerebral Cortex</i> , 2020, 30, 2307-2320.	2.9	16
121	Dynamic adaptation of myocardial proteome during heart failure development. <i>PLoS ONE</i> , 2017, 12, e0185915.	2.5	16
122	PROGRESS – prospective observational study on hospitalized community acquired pneumonia. <i>BMC Pulmonary Medicine</i> , 2016, 16, 108.	2.0	15
123	Global secretome analysis of resident cardiac progenitor cells from wild-type and transgenic heart failure mice: Why ambience matters. <i>Journal of Cellular Physiology</i> , 2019, 234, 10111-10122.	4.1	15
124	Biallelic CCM3 mutations cause a clonogenic survival advantage and endothelial cell stiffening. <i>Journal of Cellular and Molecular Medicine</i> , 2019, 23, 1771-1783.	3.6	15
125	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. <i>JCI Insight</i> , 2019, 4, .	5.0	15
126	Thyroid Related Quality of Life in Elderly with Subclinical Hypothyroidism and Improvement on Levothyroxine is Distinct from that in Young Patients (TSAGE). <i>Hormone and Metabolic Research</i> , 2019, 51, 568-574.	1.5	14

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127	Association of alcohol consumption with allergic disease and asthma: a multi-centre Mendelian randomization analysis. <i>Addiction</i> , 2019, 114, 216-225.	3.3	14
128	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. <i>Biological Psychiatry</i> , 2020, 88, 470-479.	1.3	14
129	Impact of high salinity and the compatible solute glycine betaine on gene expression of <i>Bacillus subtilis</i> . <i>Environmental Microbiology</i> , 2020, 22, 3266-3286.	3.8	14
130	A MicroRNA Network Controls <i>Legionella pneumophila</i> Replication in Human Macrophages via LGALS8 and MX1. <i>MBio</i> , 2020, 11, .	4.1	14
131	Labeling of the pathogenic bacterium <i>Staphylococcus aureus</i> with gold or ferric oxide-core nanoparticles highlights new capabilities for investigation of host-pathogen interactions. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2014, 85, 140-150.	1.5	13
132	Two Functionally Deviating Type 6 Secretion Systems Occur in the Nitrogen-Fixing Endophyte <i>Azoarcus olearius</i> BH72. <i>Frontiers in Microbiology</i> , 2019, 10, 459.	3.5	13
133	Fumarate dependent protein composition under aerobic and anaerobic growth conditions in <i>Escherichia coli</i> . <i>Journal of Proteomics</i> , 2020, 212, 103583.	2.4	13
134	Genome-wide scan identifies novel genetic loci regulating salivary metabolite levels. <i>Human Molecular Genetics</i> , 2020, 29, 864-875.	2.9	13
135	Analyses of competent and non-competent subpopulations of <i>Bacillus subtilis</i> reveal <i>yhfw</i> , <i>yhc</i> and <i>ncRNAs</i> as novel players in competence. <i>Environmental Microbiology</i> , 2020, 22, 2312-2328.	3.8	13
136	Multi-ancestry genome-wide gene-gene interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	7.9	13
137	Extracellular Vesicle Separation Techniques Impact Results from Human Blood Samples: Considerations for Diagnostic Applications. <i>International Journal of Molecular Sciences</i> , 2021, 22, 9211.	4.1	13
138	A Thyroid Hormone-Independent Molecular Fingerprint of 3,5-Diiodothyronine Suggests a Strong Relationship with Coffee Metabolism in Humans. <i>Thyroid</i> , 2019, 29, 1743-1754.	4.5	12
139	Metabolic niche adaptation of community- and hospital-associated methicillin-resistant <i>Staphylococcus aureus</i> . <i>Journal of Proteomics</i> , 2019, 193, 154-161.	2.4	12
140	Genome-Wide Association Study for Endothelial Growth Factors. <i>Circulation: Cardiovascular Genetics</i> , 2015, 8, 389-397.	5.1	11
141	Circulating proteomic patterns in AF related left atrial remodeling indicate involvement of coagulation and complement cascade. <i>PLoS ONE</i> , 2018, 13, e0198461.	2.5	11
142	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	3.1	11
143	NMR Metabolomics Reveal Urine Markers of Microbiome Diversity and Identify Benzoate Metabolism as a Mediator between High Microbial Alpha Diversity and Metabolic Health. <i>Metabolites</i> , 2022, 12, 308.	2.9	11
144	SHIP-MR and Radiology: 12 Years of Whole-Body Magnetic Resonance Imaging in a Single Center. <i>Healthcare (Switzerland)</i> , 2022, 10, 33.	2.0	11

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145	Comparative analysis of Salivette® and paraffin gum preparations for establishment of a metaproteomics analysis pipeline for stimulated human saliva. <i>Journal of Oral Microbiology</i> , 2018, 10, 1428006.	2.7	10
146	From heterogeneous healthcare data to disease-specific biomarker networks: A hierarchical Bayesian network approach. <i>PLoS Computational Biology</i> , 2021, 17, e1008735.	3.2	10
147	Immunogenicity and protective efficacy of a <i>Streptococcus suis</i> vaccine composed of six conserved immunogens. <i>Veterinary Research</i> , 2021, 52, 112.	3.0	10
148	Plasma protein profiling of patients with intraductal papillary mucinous neoplasm of the pancreas as potential precursor lesions of pancreatic cancer. <i>Clinica Chimica Acta</i> , 2018, 477, 127-134.	1.1	9
149	Associations between adipose tissue volume and small molecules in plasma and urine among asymptomatic subjects from the general population. <i>Scientific Reports</i> , 2020, 10, 1487.	3.3	9
150	ABCB1/4 gallbladder cancer risk variants identified in India also show strong effects in Chileans. <i>Cancer Epidemiology</i> , 2020, 65, 101643.	1.9	9
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