

Uwe Völker

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5119179/publications.pdf>

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	Gene-mapping study of extremes of cerebral small vessel disease reveals TRIM47 as a strong candidate. <i>Brain</i> , 2022, 145, 1992-2007.	7.6	6
2	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
3	Tissue-specific multi-omics analysis of atrial fibrillation. <i>Nature Communications</i> , 2022, 13, 441.	12.8	17
4	Pathogenesis of vaccine-induced immune thrombotic thrombocytopenia (VITT). <i>Seminars in Hematology</i> , 2022, 59, 97-107.	3.4	30
5	Serum starvation induces sexual dimorphisms in secreted proteins of human umbilical vein endothelial cells (HUVECs) from twin pairs. <i>Proteomics</i> , 2022, 22, e2100168.	2.2	2
6	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
7	Cohort Profile Update: The Study of Health in Pomerania (SHIP). <i>International Journal of Epidemiology</i> , 2022, 51, e372-e383.	1.9	73
8	Plasma circulating micro-RNAs associated with alexithymia reflect a high overlap on neuropsychiatric outcomes. <i>Journal of Affective Disorders</i> , 2022, 305, 206-212.	4.1	3
9	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
10	Overexpression of Renin-B Induces Warburg-like Effects That Are Associated with Increased AKT/mTOR Signaling. <i>Cells</i> , 2022, 11, 1459.	4.1	1
11	Comparative proteome analysis of the tegument of male and female adult <i>Schistosoma mansoni</i> . <i>Scientific Reports</i> , 2022, 12, 7569.	3.3	3
12	Fetal Zone Steroids Show Discrete Effects on Hyperoxia-Induced Attenuation of Migration in Cultured Oligodendrocyte Progenitor Cells. <i>Oxidative Medicine and Cellular Longevity</i> , 2022, 2022, 1-19.	4.0	0
13	APOE ϵ 4 in Depression-Associated Memory Impairment—Evidence from Genetic and MicroRNA Analyses. <i>Biomedicines</i> , 2022, 10, 1560.	3.2	7
14	The <i>Vibrio vulnificus</i> stressosome is an oxygen-sensor involved in regulating iron metabolism. <i>Communications Biology</i> , 2022, 5, .	4.4	6
15	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
16	Analysis of DCM associated protein alterations of human right and left ventricles. <i>Journal of Proteomics</i> , 2021, 231, 104018.	2.4	1
17	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. <i>Kidney International</i> , 2021, 99, 926-939.	5.2	42
18	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

#	ARTICLE	IF	CITATIONS
19	Bottom-Up Community Proteome Analysis of Samples and Swabs by Data-Dependent Acquisition Nano LC-MS/MS Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021, 2327, 221-238.	0.9	2
20	Large-scale association analyses identify host factors influencing human gut microbiome composition. <i>Nature Genetics</i> , 2021, 53, 156-165.	21.4	676
21	Major Determinants of Airway Epithelial Cell Sensitivity to <i>S. aureus</i> Alpha-Toxin: Disposal of Toxin Heptamers by Extracellular Vesicle Formation and Lysosomal Degradation. <i>Toxins</i> , 2021, 13, 173.	3.4	0
22	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
23	Energy Metabolites as Biomarkers in Ischemic and Dilated Cardiomyopathy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1999.	4.1	20
24	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
25	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
26	Multi-ancestry genome-wide gene-sleep interactions identify novel loci for blood pressure. <i>Molecular Psychiatry</i> , 2021, 26, 6293-6304.	7.9	13
27	Sputum Proteome Signatures of Mechanically Ventilated Intensive Care Unit Patients Distinguish Samples with or without Anti-pneumococcal Activity. <i>MSystems</i> , 2021, 6, .	3.8	4
28	The association between genetically determined ABO blood types and major depressive disorder. <i>Psychiatry Research</i> , 2021, 299, 113837.	3.3	4
29	Fetal Zone Steroids and Estrogen Show Sex Specific Effects on Oligodendrocyte Precursor Cells in Response to Oxidative Damage. <i>International Journal of Molecular Sciences</i> , 2021, 22, 6586.	4.1	4
30	Association between different dimensions of childhood traumatization and plasma micro-RNA levels in a clinical psychiatric sample. <i>Journal of Psychiatric Research</i> , 2021, 139, 113-119.	3.1	4
31	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
32	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
33	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021, 8, 5531-5541.	3.1	11
34	Insights in ChAdOx1 nCoV-19 vaccine-induced immune thrombotic thrombocytopenia. <i>Blood</i> , 2021, 138, 2256-2268.	1.4	228
35	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
36	Host-pathogen interactions of clinical <i>S. aureus</i> isolates to induce infective endocarditis. <i>Virulence</i> , 2021, 12, 2073-2087.	4.4	9

#	ARTICLE	IF	CITATIONS
37	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
38	The Thyroid Hormone Transporter Mct8 Restricts Cathepsin-Mediated Thyroglobulin Processing in Male Mice through Thyroid Auto-Regulatory Mechanisms That Encompass Autophagy. <i>International Journal of Molecular Sciences</i> , 2021, 22, 462.	4.1	5
39	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
40	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. <i>Nature Communications</i> , 2021, 12, 5647.	12.8	61
41	Cytokine-Mediated Alterations of Human Cardiac Fibroblast's Secretome. <i>International Journal of Molecular Sciences</i> , 2021, 22, 12262.	4.1	8
42	Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. <i>Nature Communications</i> , 2021, 12, 7173.	12.8	8
43	Differences in Cell-Intrinsic Inflammatory Programs of Yolk Sac and Bone Marrow Macrophages. <i>Cells</i> , 2021, 10, 3564.	4.1	4
44	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
45	Copy number variants in lipid metabolism genes are associated with gallstones disease in men. <i>European Journal of Human Genetics</i> , 2020, 28, 264-273.	2.8	6
46	Technical report: xMAPr – High-dynamic-range (HDR) quantification of antigen-specific antibody binding. <i>Journal of Proteomics</i> , 2020, 212, 103577.	2.4	7
47	Hfq modulates global protein pattern and stress response in <i>Bordetella pertussis</i> . <i>Journal of Proteomics</i> , 2020, 211, 103559.	2.4	5
48	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
49	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
50	Arsenic and gallbladder cancer risk: Mendelian randomization analysis of European prospective data. <i>International Journal of Cancer</i> , 2020, 146, 2648-2650.	5.1	6
51	Association of proteome and metabolome signatures with severity in patients with community-acquired pneumonia. <i>Journal of Proteomics</i> , 2020, 214, 103627.	2.4	6
52	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
53	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	28.9	388
54	Exploring metal availability in the natural niche of <i>Streptococcus pneumoniae</i> to discover potential vaccine antigens. <i>Virulence</i> , 2020, 11, 1310-1328.	4.4	8

#	ARTICLE	IF	CITATIONS
55	Associations of plasma YKL-40 concentrations with heel ultrasound parameters and bone turnover markers in the general adult population. <i>Bone</i> , 2020, 141, 115675.	2.9	2
56	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
57	Impact of Storage Conditions on the Breast Milk Peptidome. <i>Nutrients</i> , 2020, 12, 2733.	4.1	7
58	The Membrane Transporter OAT7 (SLC22A9) Is Not a Susceptibility Factor for Osteoporosis in Europeans. <i>Frontiers in Endocrinology</i> , 2020, 11, 532.	3.5	2
59	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
60	Cerebral small vessel disease genomics and its implications across the lifespan. <i>Nature Communications</i> , 2020, 11, 6285.	12.8	89
61	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
62	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
63	The Involvement of the McsB Arginine Kinase in Clp-Dependent Degradation of the MgsR Regulator in <i>Bacillus subtilis</i> . <i>Frontiers in Microbiology</i> , 2020, 11, 900.	3.5	5
64	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	12.8	59
65	Adenosine Triphosphate Neutralizes Pneumolysin-Induced Neutrophil Activation. <i>Journal of Infectious Diseases</i> , 2020, 222, 1702-1712.	4.0	8
66	Screening for New Markers to Assess Thyroid Hormone Action by OMICs Analysis of Human Samples. <i>Experimental and Clinical Endocrinology and Diabetes</i> , 2020, 128, 479-487.	1.2	2
67	CD5L Constitutes a Novel Biomarker for Integrated Hepatic Thyroid Hormone Action. <i>Thyroid</i> , 2020, 30, 908-923.	4.5	8
68	<i>S. aureus</i> alpha-toxin monomer binding and heptamer formation in host cell membranes – Do they determine sensitivity of airway epithelial cells toward the toxin?. <i>PLoS ONE</i> , 2020, 15, e0233854.	2.5	4
69	Interaction of <i>Staphylococcus aureus</i> and Host Cells upon Infection of Bronchial Epithelium during Different Stages of Regeneration. <i>ACS Infectious Diseases</i> , 2020, 6, 2279-2290.	3.8	4
70	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
71	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
72	Polygenic Architecture of Human Neuroanatomical Diversity. <i>Cerebral Cortex</i> , 2020, 30, 2307-2320.	2.9	16

#	ARTICLE	IF	CITATIONS
73	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. <i>Nature Genetics</i> , 2020, 52, 167-176.	21.4	101
74	Genome-wide scan identifies novel genetic loci regulating salivary metabolite levels. <i>Human Molecular Genetics</i> , 2020, 29, 864-875.	2.9	13
75	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
76	Analyses of competent and non-competent subpopulations of <i>Bacillus subtilis</i> reveal <i>yhfW</i> , <i>yhxC</i> and ncRNAs as novel players in competence. <i>Environmental Microbiology</i> , 2020, 22, 2312-2328.	3.8	13
77	A MicroRNA Network Controls <i>Legionella pneumophila</i> Replication in Human Macrophages via LGALS8 and MX1. <i>MBio</i> , 2020, 11, .	4.1	14
78	Nup133 and ER1± mediate the differential effects of hyperoxia-induced damage in male and female OPCs. <i>Molecular and Cellular Pediatrics</i> , 2020, 7, 10.	1.8	7
79	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
80	Title is missing!. , 2020, 15, e0233854.		0
81	Title is missing!. , 2020, 15, e0233854.		0
82	Title is missing!. , 2020, 15, e0233854.		0
83	Title is missing!. , 2020, 15, e0233854.		0
84	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
85	Association of childhood traumatization and neuropsychiatric outcomes with altered plasma micro RNA-levels. <i>Neuropsychopharmacology</i> , 2019, 44, 2030-2037.	5.4	21
86	Shotgun proteomic analysis of <i>Bordetella parapertussis</i> provides insights into the physiological response to iron starvation and potential new virulence determinants absent in <i>Bordetella pertussis</i> . <i>Journal of Proteomics</i> , 2019, 206, 103448.	2.4	4
87	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
88	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
89	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
90	Global plasma protein profiling reveals DCM characteristic protein signatures. <i>Journal of Proteomics</i> , 2019, 209, 103508.	2.4	3

#	ARTICLE	IF	CITATIONS
91	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. <i>BMC Cardiovascular Disorders</i> , 2019, 19, 240.	1.7	22
92	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	12.8	84
93	T51ASSOCIATION OF CHILDHOOD TRAUMATIZATION AND NEUROPSYCHIATRIC OUTCOMES WITH ALTERED PLASMA MICRO RNA-LEVELS. <i>European Neuropsychopharmacology</i> , 2019, 29, S243.	0.7	0
94	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
95	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
96	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
97	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	12.8	133
98	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
99	Variants in ABCG8 and TRAF3 genes confer risk for gallstone disease in admixed Latinos with Mapuche Native American ancestry. <i>Scientific Reports</i> , 2019, 9, 772.	3.3	30
100	Genome-wide analysis of dental caries and periodontitis combining clinical and self-reported data. <i>Nature Communications</i> , 2019, 10, 2773.	12.8	183
101	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
102	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
103	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
104	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
105	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
106	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
107	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
108	Impaired Exocrine Pancreatic Function Associates With Changes in Intestinal Microbiota Composition and Diversity. <i>Gastroenterology</i> , 2019, 156, 1010-1015.	1.3	74

#	ARTICLE	IF	CITATIONS
109	Helicobacter pylori infection associates with fecal microbiota composition and diversity. Scientific Reports, 2019, 9, 20100.	3.3	49
110	Association of alcohol consumption with allergic disease and asthma: a multi-centre Mendelian randomization analysis. Addiction, 2019, 114, 216-225.	3.3	14
111	Global secretome analysis of resident cardiac progenitor cells from wild-type and transgenic heart failure mice: Why ambience matters. Journal of Cellular Physiology, 2019, 234, 10111-10122.	4.1	15
112	Genetic and lifestyle risk factors for MRI-defined brain infarcts in a population-based setting. Neurology, 2019, 92, .	1.1	30
113	Metabolic niche adaptation of community- and hospital-associated methicillin-resistant Staphylococcus aureus. Journal of Proteomics, 2019, 193, 154-161.	2.4	12
114	Neandertal Introgression Sheds Light on Modern Human Endocranial Globularity. Current Biology, 2019, 29, 120-127.e5.	3.9	86
115	Biallelic CCM3 mutations cause a clonogenic survival advantage and endothelial cell stiffening. Journal of Cellular and Molecular Medicine, 2019, 23, 1771-1783.	3.6	15
116	KCND3 potassium channel gene variant confers susceptibility to electrocardiographic early repolarization pattern. JCI Insight, 2019, 4, .	5.0	15
117	From the genome sequence via the proteome to cell physiology – Pathoproteomics and pathophysiology of Staphylococcus aureus. International Journal of Medical Microbiology, 2018, 308, 545-557.	3.6	17
118	Comparative analysis of Salivette® and paraffin gum preparations for establishment of a metaproteomics analysis pipeline for stimulated human saliva. Journal of Oral Microbiology, 2018, 10, 1428006.	2.7	10
119	Aureo Wiki – The repository of the Staphylococcus aureus research and annotation community. International Journal of Medical Microbiology, 2018, 308, 558-568.	3.6	99
120	Plasma protein profiling of patients with intraductal papillary mucinous neoplasm of the pancreas as potential precursor lesions of pancreatic cancer. Clinica Chimica Acta, 2018, 477, 127-134.	1.1	9
121	The quest for bacterial allergens. International Journal of Medical Microbiology, 2018, 308, 738-750.	3.6	27
122	Changes of DNA topology affect the global transcription landscape and allow rapid growth of a Bacillus subtilis mutant lacking carbon catabolite repression. Metabolic Engineering, 2018, 45, 171-179.	7.0	18
123	Circulating proteomic patterns in AF related left atrial remodeling indicate involvement of coagulation and complement cascade. PLoS ONE, 2018, 13, e0198461.	2.5	11
124	GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. Nature Communications, 2018, 9, 5141.	12.8	119
125	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
126	Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. Circulation Genomic and Precision Medicine, 2018, 11, e002037.	3.6	19

#	ARTICLE	IF	CITATIONS
127	Analysis of <i>Staphylococcus aureus</i> proteins secreted inside infected human epithelial cells. <i>International Journal of Medical Microbiology</i> , 2018, 308, 664-674.	3.6	4
128	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
129	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	21.4	552
130	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
131	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
132	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
133	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. <i>Scientific Reports</i> , 2017, 7, 45040.	3.3	98
134	Impact of blood sample collection methods on blood protein profiling studies. <i>Clinica Chimica Acta</i> , 2017, 471, 128-134.	1.1	21
135	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
136	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
137	Data on the impact of the blood sample collection methods on blood protein profiling studies. <i>Data in Brief</i> , 2017, 14, 313-319.	1.0	4
138	Characterization of the Genetic Program Linked to the Development of Atrial Fibrillation in CREM-Ib1 ^{Cre} C-X Mice. <i>Circulation: Arrhythmia and Electrophysiology</i> , 2017, 10, .	4.8	19
139	Fifteen Genetic Loci Associated With the Electrocardiographic P Wave. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	38
140	Transcriptome-Wide Analysis Identifies Novel Associations With Blood Pressure. <i>Hypertension</i> , 2017, 70, 743-750.	2.7	34
141	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
142	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
143	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
144	Dynamic adaptation of myocardial proteome during heart failure development. <i>PLoS ONE</i> , 2017, 12, e0185915.	2.5	16

#	ARTICLE	IF	CITATIONS
145	Staphylococcus aureus Transcriptome Architecture: From Laboratory to Infection-Mimicking Conditions. PLoS Genetics, 2016, 12, e1005962.	3.5	170
146	Four Susceptibility Loci for Gallstone Disease Identified in a Meta-analysis of Genome-Wide Association Studies. Gastroenterology, 2016, 151, 351-363.e28.	1.3	74
147	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
148	PROGRESS " prospective observational study on hospitalized community acquired pneumonia. BMC Pulmonary Medicine, 2016, 16, 108.	2.0	15
149	<scp>GWAS</scp> analysis of handgrip and lower body strength in older adults in the <scp>CHARGE</scp> consortium. Aging Cell, 2016, 15, 792-800.	6.7	51
150	Genomewide meta-analysis identifies loci associated with <scp>IGF</scp> and <scp>IGFBP</scp> levels with impact on age-related traits. Aging Cell, 2016, 15, 811-824.	6.7	83
151	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
152	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. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 932-940.	1.5	20
153	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
154	Changes of myocardial gene expression and protein composition in patients with dilated cardiomyopathy after immunoadsorption with subsequent immunoglobulin substitution. Basic Research in Cardiology, 2016, 111, 53.	5.9	23
155	Metabolic Fingerprints of Circulating IGF-1 and the IGF-1/IGFBP-3 Ratio: A Multifluid Metabolomics Study. Journal of Clinical Endocrinology and Metabolism, 2016, 101, 4730-4742.	3.6	18
156	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
157	3,5-T2 alters murine genes relevant for xenobiotic, steroid, and thyroid hormone metabolism. Journal of Molecular Endocrinology, 2016, 56, 311-323.	2.5	28
158	Genome-wide Association Studies Identify Genetic Loci Associated With Albuminuria in Diabetes. Diabetes, 2016, 65, 803-817.	0.6	131
159	Genetic associations at 53 loci highlight cell types and biological pathways relevant for kidney function. Nature Communications, 2016, 7, 10023.	12.8	412
160	Associations of circulating plasma microRNAs with age, body mass index and sex in a population-based study. BMC Medical Genomics, 2015, 8, 61.	1.5	133
161	Genome-Wide Association Study with Targeted and Non-targeted NMR Metabolomics Identifies 15 Novel Loci of Urinary Human Metabolic Individuality. PLoS Genetics, 2015, 11, e1005487.	3.5	83
162	Genome-Wide Association Study for Endothelial Growth Factors. Circulation: Cardiovascular Genetics, 2015, 8, 389-397.	5.1	11

#	ARTICLE	IF	CITATIONS
163	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
164	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
165	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
166	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
167	A Meta-analysis of Gene Expression Signatures of Blood Pressure and Hypertension. <i>PLoS Genetics</i> , 2015, 11, e1005035.	3.5	107
168	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
169	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
170	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
171	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
172	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
173	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
174	Cohort profile: Greifswald approach to individualized medicine (GANI_MED). <i>Journal of Translational Medicine</i> , 2014, 12, 144.	4.4	43
175	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
176	Systematic identification of trans eQTLs as putative drivers of known disease associations. <i>Nature Genetics</i> , 2013, 45, 1238-1243.	21.4	1,544
177	Comparative evaluation of saliva collection methods for proteome analysis. <i>Clinica Chimica Acta</i> , 2013, 419, 42-46.	1.1	85
178	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
179	A new, accurate predictive model for incident hypertension. <i>Journal of Hypertension</i> , 2013, 31, 2142-2150.	0.5	32
180	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

#	ARTICLE	IF	CITATIONS
181	<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
182	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	27.8	320
183	Condition-Dependent Transcriptome Reveals High-Level Regulatory Architecture in <i>Bacillus subtilis</i> . <i>Science</i> , 2012, 335, 1103-1106.	12.6	809
184	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
185	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
186	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
187	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	27.8	1,855
188	A genome-wide association study of metabolic traits in human urine. <i>Nature Genetics</i> , 2011, 43, 565-569.	21.4	224
189	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
190	Cohort Profile: The Study of Health in Pomerania. <i>International Journal of Epidemiology</i> , 2011, 40, 294-307.	1.9	876
191	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
192	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
193	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
194	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	21.4	1,104
195	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