

Karsten Suhre

List of Publications by Year in descending order

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Version: 2024-02-01

271
papers

22,697
citations

9786

73
h-index

11607

135
g-index

311
all docs

311
docs citations

311
times ranked

32018
citing authors

#	ARTICLE	IF	CITATIONS
1	SGL: automatic clinical subgroup identification in omics datasets. <i>Bioinformatics</i> , 2022, 38, 573-576.	4.1	1
2	First mitochondrial genome-wide association study with metabolomics. <i>Human Molecular Genetics</i> , 2022, 31, 3367-3376.	2.9	4
3	maplet: an extensible R toolbox for modular and reproducible metabolomics pipelines. <i>Bioinformatics</i> , 2022, 38, 1168-1170.	4.1	18
4	Metabolic and Metabo-Clinical Signatures of Type 2 Diabetes, Obesity, Retinopathy, and Dyslipidemia. <i>Diabetes</i> , 2022, 71, 184-205.	0.6	29
5	Advancing Cancer Treatment by Targeting Glutamine Metabolism—A Roadmap. <i>Cancers</i> , 2022, 14, 553.	3.7	40
6	TIGER: technical variation elimination for metabolomics data using ensemble learning architecture. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	15
7	Epigenetic scores for the circulating proteome as tools for disease prediction. <i>ELife</i> , 2022, 11, .	6.0	37
8	Qatar genome: Insights on genomics from the Middle East. <i>Human Mutation</i> , 2022, 43, 499-510.	2.5	29
9	Defining the landscape of metabolic dysregulations in cancer metastasis. <i>Clinical and Experimental Metastasis</i> , 2022, 39, 345-362.	3.3	8
10	A population study of clinically actionable genetic variation affecting drug response from the Middle East. <i>Npj Genomic Medicine</i> , 2022, 7, 10.	3.8	20
11	Analysis of incidental findings in Qatar genome participants reveals novel functional variants in <i>LMNA</i> and <i>DSP</i> . <i>Human Molecular Genetics</i> , 2022, , .	2.9	2
12	Matching Drug Metabolites from Non-Targeted Metabolomics to Self-Reported Medication in the Qatar Biobank Study. <i>Metabolites</i> , 2022, 12, 249.	2.9	7
13	Proteomic Analysis of Plasma Markers in Patients Maintained on Antipsychotics: Comparison to Patients Off Antipsychotics and Normal Controls. <i>Frontiers in Psychiatry</i> , 2022, 13, 809071.	2.6	1
14	Ratios of Acetaminophen Metabolites Identify New Loci of Pharmacogenetic Relevance in a Genome-Wide Association Study. <i>Metabolites</i> , 2022, 12, 496.	2.9	4
15	Detection of infiltrating fibroblasts by single-cell transcriptomics in human kidney allografts. <i>PLoS ONE</i> , 2022, 17, e0267704.	2.5	14
16	Integrative metabolomic and proteomic signatures define clinical outcomes in severe COVID-19. <i>IScience</i> , 2022, 25, 104612.	4.1	9
17	Variational autoencoders learn transferrable representations of metabolomics data. <i>Communications Biology</i> , 2022, 5, .	4.4	11
18	Cross-Sectional Blood Metabolite Markers of Hypertension: A Multicohort Analysis of 44,306 Individuals from the Consortium of METabolomics Studies. <i>Metabolites</i> , 2022, 12, 601.	2.9	6

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19	Robust Huber-LASSO for improved prediction of protein, metabolite and gene expression levels relying on individual genotype data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	10
20	Genetics meets proteomics: perspectives for large population-based studies. <i>Nature Reviews Genetics</i> , 2021, 22, 19-37.	16.3	196
21	Metabolic Predictors of Equine Performance in Endurance Racing. <i>Metabolites</i> , 2021, 11, 82.	2.9	5
22	Omics Resources and Applications in Date Palm. <i>Compendium of Plant Genomes</i> , 2021, , 73-83.	0.5	0
23	Validation of Candidate Phospholipid Biomarkers of Chronic Kidney Disease in Hyperglycemic Individuals and Their Organ-Specific Exploration in Leptin Receptor-Deficient db/db Mouse. <i>Metabolites</i> , 2021, 11, 89.	2.9	10
24	Signal Transducer and Activator of Transcription 3 (STAT3) Suppresses STAT1/Interferon Signaling Pathway and Inflammation in Senescent Preadipocytes. <i>Antioxidants</i> , 2021, 10, 334.	5.1	12
25	Whole genome sequencing in the Middle Eastern Qatari population identifies genetic associations with 45 clinically relevant traits. <i>Nature Communications</i> , 2021, 12, 1250.	12.8	37
26	Revealing the role of the human blood plasma proteome in obesity using genetic drivers. <i>Nature Communications</i> , 2021, 12, 1279.	12.8	50
27	Genome-wide investigation identifies a rare copy-number variant burden associated with human spina bifida. <i>Genetics in Medicine</i> , 2021, 23, 1211-1218.	2.4	10
28	Deep sequencing of DNA from urine of kidney allograft recipients to estimate donor/recipient-specific DNA fractions. <i>PLoS ONE</i> , 2021, 16, e0249930.	2.5	0
29	Evidence of Recombination Suppression Blocks on the Y Chromosome of Date Palm (Phoenix) Tj ETQq1 1 0.784314 3.6 /Overlock 10 T	3.6	4
30	Connecting the epigenome, metabolome and proteome for a deeper understanding of disease. <i>Journal of Internal Medicine</i> , 2021, 290, 527-548.	6.0	5
31	Metabolic syndrome and the plasma proteome: from association to causation. <i>Cardiovascular Diabetology</i> , 2021, 20, 111.	6.8	19
32	Plasma Proteomics of Renal Function: A Transethnic Meta-Analysis and Mendelian Randomization Study. <i>Journal of the American Society of Nephrology: JASN</i> , 2021, 32, 1747-1763.	6.1	16
33	Salivary metabolites associated with a 5-year tooth loss identified in a population-based setting. <i>BMC Medicine</i> , 2021, 19, 161.	5.5	9
34	Kidney Allograft Function Is a Confounder of Urine Metabolite Profiles in Kidney Allograft Recipients. <i>Metabolites</i> , 2021, 11, 533.	2.9	6
35	Actionable genomic variants in 6045 participants from the Qatar Genome Program. <i>Human Mutation</i> , 2021, 42, 1584-1601.	2.5	13
36	Thousands of Qatari genomes inform human migration history and improve imputation of Arab haplotypes. <i>Nature Communications</i> , 2021, 12, 5929.	12.8	18

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37	The Proteomic Signature of Recombinant Growth Hormone in Recreational Athletes. <i>Journal of the Endocrine Society</i> , 2021, 5, bvab156.	0.2	3
38	Proteome-wide associations with short- and long-term weight loss and regain after Roux-en-Y gastric bypass surgery. <i>Obesity</i> , 2021, 30, 129.	3.0	7
39	Systems biology analysis of human genomes points to key pathways conferring spina bifida risk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	11
40	Epigenetics meets proteomics in an epigenome-wide association study with circulating blood plasma protein traits. <i>Nature Communications</i> , 2020, 11, 15.	12.8	57
41	Machine Learning Approaches Reveal Metabolic Signatures of Incident Chronic Kidney Disease in Individuals With Prediabetes and Type 2 Diabetes. <i>Diabetes</i> , 2020, 69, 2756-2765.	0.6	33
42	A strategy to incorporate prior knowledge into correlation network cutoff selection. <i>Nature Communications</i> , 2020, 11, 5153.	12.8	13
43	Identification of genetic variants controlling RNA editing and their effect on RNA structure stabilization. <i>European Journal of Human Genetics</i> , 2020, 28, 1753-1762.	2.8	5
44	Deletion of beta-fructofuranosidase (invertase) genes is associated with sucrose content in Date Palm fruit. <i>Plant Direct</i> , 2020, 4, e00214.	1.9	11
45	The metabolic footprint of compromised insulin sensitivity under fasting and hyperinsulinemic-euglycemic clamp conditions in an Arab population. <i>Scientific Reports</i> , 2020, 10, 17164.	3.3	5
46	STXBP6, reciprocally regulated with autophagy, reduces triple negative breast cancer aggressiveness. <i>Clinical and Translational Medicine</i> , 2020, 10, e147.	4.0	3
47	Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Diabetes</i> , 2020, 69, 2766-2778.	0.6	34
48	Circulating Protein Signatures and Causal Candidates for Type 2 Diabetes. <i>Diabetes</i> , 2020, 69, 1843-1853.	0.6	64
49	Effect of induced hypoglycemia on inflammation and oxidative stress in type 2 diabetes and control subjects. <i>Scientific Reports</i> , 2020, 10, 4750.	3.3	69
50	Metabolic Signatures of Tumor Responses to Doxorubicin Elucidated by Metabolic Profiling in Ovo. <i>Metabolites</i> , 2020, 10, 268.	2.9	19
51	Genome-Wide Association Study Reveals a Novel Association Between MYBPC3 Gene Polymorphism, Endurance Athlete Status, Aerobic Capacity and Steroid Metabolism. <i>Frontiers in Genetics</i> , 2020, 11, 595.	2.3	30
52	Proteome-wide assessment of diabetes mellitus in Qatari identifies IGFBP-2 as a risk factor already with early glycaemic disturbances. <i>Archives of Biochemistry and Biophysics</i> , 2020, 689, 108476.	3.0	7
53	Genetic studies of urinary metabolites illuminate mechanisms of detoxification and excretion in humans. <i>Nature Genetics</i> , 2020, 52, 167-176.	21.4	101
54	Genome-wide scan identifies novel genetic loci regulating salivary metabolite levels. <i>Human Molecular Genetics</i> , 2020, 29, 864-875.	2.9	13

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55	Abstract 21: Deciphering the Plasma Proteome of Type 2 Diabetes. <i>Circulation</i> , 2020, 141, .	1.6	1
56	Urinary cell transcriptomics and acute rejection in human kidney allografts. <i>JCI Insight</i> , 2020, 5, .	5.0	25
57	<i>MoDentify</i> : phenotype-driven module identification in metabolomics networks at different resolutions. <i>Bioinformatics</i> , 2019, 35, 532-534.	4.1	13
58	Association of childhood traumatization and neuropsychiatric outcomes with altered plasma micro RNA-levels. <i>Neuropsychopharmacology</i> , 2019, 44, 2030-2037.	5.4	21
59	A Systems-level Characterization of the Differentiation of Human Embryonic Stem Cells into Mesenchymal Stem Cells*[S]. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 1950-1966.	3.8	13
60	Fine-Mapping of the Human Blood Plasma N-Glycome onto Its Proteome. <i>Metabolites</i> , 2019, 9, 122.	2.9	10
61	Alterations in long noncoding RNAs in women with and without polycystic ovarian syndrome. <i>Clinical Endocrinology</i> , 2019, 91, 793-797.	2.4	15
62	Metabolomic profiling identifies novel associations with Electrolyte and Acid-Base Homeostatic patterns. <i>Scientific Reports</i> , 2019, 9, 15088.	3.3	7
63	Unraveling the functional role of the orphan solute carrier, SLC22A24 in the transport of steroid conjugates through metabolomic and genome-wide association studies. <i>PLoS Genetics</i> , 2019, 15, e1008208.	3.5	23
64	Novel subpopulations in date palm (<i>Phoenix dactylifera</i>) identified by population-wide organellar genome sequencing. <i>BMC Genomics</i> , 2019, 20, 498.	2.8	26
65	Characterization of Bulk Phosphatidylcholine Compositions in Human Plasma Using Side-Chain Resolving Lipidomics. <i>Metabolites</i> , 2019, 9, 109.	2.9	15
66	The Saliva Metabolome in Association to Oral Health Status. <i>Journal of Dental Research</i> , 2019, 98, 642-651.	5.2	59
67	Defining the genetic control of human blood plasma N-glycome using genome-wide association study. <i>Human Molecular Genetics</i> , 2019, 28, 2062-2077.	2.9	40
68	Metabolic profiling of elite athletes with different cardiovascular demand. <i>Scandinavian Journal of Medicine and Science in Sports</i> , 2019, 29, 933-943.	2.9	23
69	Metabolomics Identifies Novel Blood Biomarkers of Pulmonary Function and COPD in the General Population. <i>Metabolites</i> , 2019, 9, 61.	2.9	30
70	Metabolomics of Dynamic Changes in Insulin Resistance Before and After Exercise in PCOS. <i>Frontiers in Endocrinology</i> , 2019, 10, 116.	3.5	29
71	Metabolic GWAS of elite athletes reveals novel genetically-influenced metabolites associated with athletic performance. <i>Scientific Reports</i> , 2019, 9, 19889.	3.3	33
72	Metabolic and proteomic signatures of hypoglycaemia in type 2 diabetes. <i>Diabetes, Obesity and Metabolism</i> , 2019, 21, 909-919.	4.4	20

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73	ProGeM: a framework for the prioritization of candidate causal genes at molecular quantitative trait loci. <i>Nucleic Acids Research</i> , 2019, 47, e3-e3.	14.5	90
74	Single nucleotide variant counts computed from RNA sequencing and cellular traffic into human kidney allografts. <i>American Journal of Transplantation</i> , 2018, 18, 2429-2442.	4.7	11
75	Whole-exome sequencing identifies common and rare variant metabolic QTLs in a Middle Eastern population. <i>Nature Communications</i> , 2018, 9, 333.	12.8	63
76	Deep molecular phenotypes link complex disorders and physiological insult to CpG methylation. <i>Human Molecular Genetics</i> , 2018, 27, 1106-1121.	2.9	30
77	A comprehensive metabolomic data set of date palm fruit. <i>Data in Brief</i> , 2018, 18, 1313-1321.	1.0	18
78	Metabolite ratios as potential biomarkers for type 2 diabetes: a DIRECT study. <i>Diabetologia</i> , 2018, 61, 117-129.	6.3	32
79	Characterization of missing values in untargeted MS-based metabolomics data and evaluation of missing data handling strategies. <i>Metabolomics</i> , 2018, 14, 128.	3.0	138
80	Genotyping-by-sequencing identifies date palm clone preference in agronomics of the State of Qatar. <i>PLoS ONE</i> , 2018, 13, e0207299.	2.5	14
81	Metabolomics profiling of xenobiotics in elite athletes: relevance to supplement consumption. <i>Journal of the International Society of Sports Nutrition</i> , 2018, 15, 48.	3.9	28
82	Genus-wide sequencing supports a two-locus model for sex-determination in Phoenix. <i>Nature Communications</i> , 2018, 9, 3969.	12.8	86
83	Overview of the Meso-NH model version 5.4 and its applications. <i>Geoscientific Model Development</i> , 2018, 11, 1929-1969.	3.6	194
84	Metabolic changes of the blood metabolome after a date fruit challenge. <i>Journal of Functional Foods</i> , 2018, 49, 267-276.	3.4	10
85	Accelerated lipid catabolism and autophagy are cancer survival mechanisms under inhibited glutaminolysis. <i>Cancer Letters</i> , 2018, 430, 133-147.	7.2	54
86	Ldlr and ApoE mice better mimic the human metabolite signature of increased carotid intima media thickness compared to other animal models of cardiovascular disease. <i>Atherosclerosis</i> , 2018, 276, 140-147.	0.8	13
87	A pilot study comparing the metabolic profiles of elite-level athletes from different sporting disciplines. <i>Sports Medicine - Open</i> , 2018, 4, 2.	3.1	94
88	Genome-wide mapping of plasma protein QTLs identifies putatively causal genes and pathways for cardiovascular disease. <i>Nature Communications</i> , 2018, 9, 3268.	12.8	221
89	Genomic atlas of the human plasma proteome. <i>Nature</i> , 2018, 558, 73-79.	27.8	1,180
90	Improvement of myocardial infarction risk prediction via inflammation-associated metabolite biomarkers. <i>Heart</i> , 2017, 103, 1278-1285.	2.9	38

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91	Connecting genetic risk to disease end points through the human blood plasma proteome. <i>Nature Communications</i> , 2017, 8, 14357.	12.8	460
92	Metabolic network failures in Alzheimer's disease: A biochemical road map. <i>Alzheimer's and Dementia</i> , 2017, 13, 965-984.	0.8	362
93	Nesting of colon and ovarian cancer cells in the endothelial niche is associated with alterations in glycan and lipid metabolism. <i>Scientific Reports</i> , 2017, 7, 39999.	3.3	26
94	Evidence for Stress-like Alterations in the HPA-Axis in Women Taking Oral Contraceptives. <i>Scientific Reports</i> , 2017, 7, 14111.	3.3	51
95	Large Scale Metabolic Profiling identifies Novel Steroids linked to Rheumatoid Arthritis. <i>Scientific Reports</i> , 2017, 7, 9137.	3.3	28
96	Genetic variants including markers from the exome chip and metabolite traits of type 2 diabetes. <i>Scientific Reports</i> , 2017, 7, 6037.	3.3	12
97	Advanced glycation end products among patients maintained on antipsychotics. <i>International Clinical Psychopharmacology</i> , 2017, 32, 256-261.	1.7	1
98	Sex-specific metabolic profiles of androgens and its main binding protein SHBG in a middle aged population without diabetes. <i>Scientific Reports</i> , 2017, 7, 2235.	3.3	12
99	PopPANTe: population and pedigree association testing for quantitative data. <i>BMC Genomics</i> , 2017, 18, 150.	2.8	6
100	Complementarity of SOMAscan to LC-MS/MS and RNA-seq for quantitative profiling of human embryonic and mesenchymal stem cells. <i>Journal of Proteomics</i> , 2017, 150, 86-97.	2.4	46
101	Phenotype-driven identification of modules in a hierarchical map of multifluid metabolic correlations. <i>Npj Systems Biology and Applications</i> , 2017, 3, 28.	3.0	21
102	From Discovery to Translation: Characterization of C-Mannosyltryptophan and Pseudouridine as Markers of Kidney Function. <i>Scientific Reports</i> , 2017, 7, 17400.	3.3	31
103	pulver: an R package for parallel ultra-rapid p-value computation for linear regression interaction terms. <i>BMC Bioinformatics</i> , 2017, 18, 429.	2.6	1
104	The association between various smoking behaviors, cotinine biomarkers and skin autofluorescence, a marker for advanced glycation end product accumulation. <i>PLoS ONE</i> , 2017, 12, e0179330.	2.5	30
105	Alterations in Lipid and Inositol Metabolisms in Two Dopaminergic Disorders. <i>PLoS ONE</i> , 2016, 11, e0147129.	2.5	31
106	The Pharmacogenetic Footprint of ACE Inhibition: A Population-Based Metabolomics Study. <i>PLoS ONE</i> , 2016, 11, e0153163.	2.5	13
107	Non-truncating <i>LIFR</i> mutation: causal for prominent congenital pain insensitivity phenotype with progressive vertebral destruction?. <i>Clinical Genetics</i> , 2016, 89, 210-216.	2.0	9
108	A Web Server for Visualization and Annotation of Genetic Variants Using Genomic Data from Qatar. , 2016, , .		0

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109	Guest Editorial: Special issue on metabolomics. Archives of Biochemistry and Biophysics, 2016, 589, 1-3.	3.0	1
110	Metabolomics enables precision medicine: a White Paper, Community Perspective. Metabolomics, 2016, 12, 149.	3.0	434
111	Identification of putative biomarkers for type 2 diabetes using metabolomics in the Korea Association REsource (KARE) cohort. Metabolomics, 2016, 12, 1.	3.0	23
112	Genome-wide association study of caffeine metabolites provides new insights to caffeine metabolism and dietary caffeine-consumption behavior. Human Molecular Genetics, 2016, 25, ddw334.	2.9	107
113	Comprehensive transcriptomic and proteomic characterization of human mesenchymal stem cells reveals source specific cellular markers. Scientific Reports, 2016, 6, 21507.	3.3	101
114	Characterization of the metabolic profile associated with serum 25-hydroxyvitamin D: a cross-sectional analysis in population-based data. International Journal of Epidemiology, 2016, 45, 1469-1481.	1.9	19
115	Metformin Effect on Nontargeted Metabolite Profiles in Patients With Type 2 Diabetes and in Multiple Murine Tissues. Diabetes, 2016, 65, 3776-3785.	0.6	49
116	Measurement of 1,5-anhydroglucitol in blood and saliva: from non-targeted metabolomics to biochemical assay. Journal of Translational Medicine, 2016, 14, 140.	4.4	28
117	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
118	Mendelian inheritance of trimodal CpG methylation sites suggests distal cis-acting genetic effects. Clinical Epigenetics, 2016, 8, 124.	4.1	16
119	Diagnostic and Prognostic Metabolites Identified for Joint Symptoms in the KORA Population. Journal of Proteome Research, 2016, 15, 554-562.	3.7	2
120	Epigenetic associations of type 2 diabetes and BMI in an Arab population. Clinical Epigenetics, 2016, 8, 13.	4.1	110
121	A graph based method for depicting population characteristics using Genome Wide Data. Journal of Computational Science, 2016, 15, 11-17.	2.9	2
122	Indigenous Arabs are descendants of the earliest split from ancient Eurasian populations. Genome Research, 2016, 26, 151-162.	5.5	89
123	Metabolic switch during adipogenesis: From branched chain amino acid catabolism to lipid synthesis. Archives of Biochemistry and Biophysics, 2016, 589, 93-107.	3.0	63
124	A Metabolome-Wide Association Study of Kidney Function and Disease in the General Population. Journal of the American Society of Nephrology: JASN, 2016, 27, 1175-1188.	6.1	159
125	Biochemical insights from population studies with genetics and metabolomics. Archives of Biochemistry and Biophysics, 2016, 589, 168-176.	3.0	46
126	Type 2 diabetes is associated with postprandial amino acid measures. Archives of Biochemistry and Biophysics, 2016, 589, 138-144.	3.0	30

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127	Urine Metabolite Profiles Predictive of Human Kidney Allograft Status. <i>Journal of the American Society of Nephrology: JASN</i> , 2016, 27, 626-636.	6.1	58
128	Genetic Influences on Metabolite Levels: A Comparison across Metabolomic Platforms. <i>PLoS ONE</i> , 2016, 11, e0153672.	2.5	69
129	Specific Metabolic Markers Are Associated with Future Waist-Gaining Phenotype in Women. <i>PLoS ONE</i> , 2016, 11, e0157733.	2.5	5
130	Metabolomics profiling reveals novel markers for leukocyte telomere length. <i>Aging</i> , 2016, 8, 77-86.	3.1	33
131	Date-Pathogen Pipeline: A Pipeline to Detect Pathogenic DNA in Date Palm Cultivars. , 2016, , .		0
132	Copy number variations in the genome of the Qatari population. <i>BMC Genomics</i> , 2015, 16, 834.	2.8	9
133	Metabolic signatures differentiate ovarian from colon cancer cell lines. <i>Journal of Translational Medicine</i> , 2015, 13, 223.	4.4	34
134	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
135	Bipolar disorders in the Arab world: a critical review. <i>Annals of the New York Academy of Sciences</i> , 2015, 1345, 59-66.	3.8	5
136	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
137	MetaRNA-Seq: An Interactive Tool to Browse and Annotate Metadata from RNA-Seq Studies. <i>BioMed Research International</i> , 2015, 2015, 1-6.	1.9	4
138	Association of DNA methylation with age, gender, and smoking in an Arab population. <i>Clinical Epigenetics</i> , 2015, 7, 6.	4.1	78
139	Genome-wide association study identifies novel genetic variants contributing to variation in blood metabolite levels. <i>Nature Communications</i> , 2015, 6, 7208.	12.8	178
140	Metabolomics of dates (<i>Phoenix dactylifera</i>) reveals a highly dynamic ripening process accounting for major variation in fruit composition. <i>BMC Plant Biology</i> , 2015, 15, 291.	3.6	41
141	Gender-specific pathway differences in the human serum metabolome. <i>Metabolomics</i> , 2015, 11, 1815-1833.	3.0	218
142	A Genome-Wide Survey of Date Palm Cultivars Supports Two Major Subpopulations in <i>Phoenix dactylifera</i> . <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1429-1438.	1.8	58
143	DI-HCR-FT-MS-based high-throughput deep metabotyping: a case study of the <i>Caenorhabditis elegans</i> "Pseudomonas aeruginosa" infection model. <i>Analytical and Bioanalytical Chemistry</i> , 2015, 407, 1059-1073.	3.7	26
144	<i>SNiPA</i> : an interactive, genetic variant-centered annotation browser. <i>Bioinformatics</i> , 2015, 31, 1334-1336.	4.1	273

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145	Genetics of human metabolism: an update. <i>Human Molecular Genetics</i> , 2015, 24, R93-R101.	2.9	117
146	Sex differences in urine metabolites related with risk of diabetes using NMR spectroscopy: results of the study of health in pomerania. <i>Metabolomics</i> , 2015, 11, 1405-1415.	3.0	18
147	Multi-omic signature of body weight change: results from a population-based cohort study. <i>BMC Medicine</i> , 2015, 13, 48.	5.5	69
148	Effects of Metformin on Metabolite Profiles and LDL Cholesterol in Patients With Type 2 Diabetes. <i>Diabetes Care</i> , 2015, 38, 1858-1867.	8.6	97
149	A systems view of type 2 diabetes-associated metabolic perturbations in saliva, blood and urine at different timescales of glycaemic control. <i>Diabetologia</i> , 2015, 58, 1855-1867.	6.3	80
150	Metabolomic Identification of a Novel Pathway of Blood Pressure Regulation Involving Hexadecanedioate. <i>Hypertension</i> , 2015, 66, 422-429.	2.7	90
151	Response to Comment on Xu et al. Effects of Metformin on Metabolite Profiles and LDL Cholesterol in Patients With Type 2 Diabetes. <i>Diabetes Care</i> 2015;38:1858-1867. <i>Diabetes Care</i> , 2015, 38, e216-e217.	8.6	8
152	Network-Based Approach for Analyzing Intra- and Interfluid Metabolite Associations in Human Blood, Urine, and Saliva. <i>Journal of Proteome Research</i> , 2015, 14, 1183-1194.	3.7	40
153	Metformin Supports the Antidiabetic Effect of a Sodium Glucose Cotransporter 2 Inhibitor by Suppressing Endogenous Glucose Production in Diabetic Mice. <i>Diabetes</i> , 2015, 64, 284-290.	0.6	35
154	The Human Blood Metabolome-Transcriptome Interface. <i>PLoS Genetics</i> , 2015, 11, e1005274.	3.5	99
155	Systems Biology Analysis Merging Phenotype, Metabolomic and Genomic Data Identifies Non-SMC Condensin I Complex, Subunit G (NCAPG) and Cellular Maintenance Processes as Major Contributors to Genetic Variability in Bovine Feed Efficiency. <i>PLoS ONE</i> , 2015, 10, e0124574.	2.5	62
156	Mapping the Genetic Architecture of Gene Regulation in Whole Blood. <i>PLoS ONE</i> , 2014, 9, e93844.	2.5	31
157	Metabolic profiling in diabetes. <i>Journal of Endocrinology</i> , 2014, 221, R75-R85.	2.6	83
158	Evaluation of SNP calling using single and multiple-sample calling algorithms by validation against array base genotyping and Mendelian inheritance. <i>BMC Research Notes</i> , 2014, 7, 747.	1.4	17
159	Novel genetic associations with serum level metabolites identified by phenotype set enrichment analyses. <i>Human Molecular Genetics</i> , 2014, 23, 5847-5857.	2.9	26
160	Epigenetics meets metabolomics: an epigenome-wide association study with blood serum metabolic traits. <i>Human Molecular Genetics</i> , 2014, 23, 534-545.	2.9	169
161	Mesenchymal cell interaction with ovarian cancer cells induces a background dependent pro-metastatic transcriptomic profile. <i>Journal of Translational Medicine</i> , 2014, 12, 59.	4.4	28
162	Interrogating causal pathways linking genetic variants, small molecule metabolites, and circulating lipids. <i>Genome Medicine</i> , 2014, 6, 25.	8.2	17

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163	Metabolite profiling reveals new insights into the regulation of serum urate in humans. <i>Metabolomics</i> , 2014, 10, 141-151.	3.0	51
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