# **David Scott Wishart**

## List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

410 papers **62,704** citations

100 h-index 248 g-index

429 ext. papers

77,013 ext. citations

8.1 avg, IF

8.29 L-index

#	Paper	IF	Citations
410	DrugBank 5.0: a major update to the DrugBank database for 2018. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D10	07 <u>24</u> -₽1	<b>0<u>87</u>62</b>
409	DrugBank: a comprehensive resource for in silico drug discovery and exploration. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D668-72	20.1	2266
408	HMDB 3.0The Human Metabolome Database in 2013. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D801-7	20.1	2210
407	MetaboAnalyst 4.0: towards more transparent and integrative metabolomics analysis. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, W486-W494	20.1	2157
406	MetaboAnalyst 3.0making metabolomics more meaningful. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W251-7	20.1	2067
405	1H, 13C and 15N chemical shift referencing in biomolecular NMR. <i>Journal of Biomolecular NMR</i> , <b>1995</b> , 6, 135-40	3	2054
404	HMDB: the Human Metabolome Database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D521-6	20.1	2021
403	HMDB 4.0: the human metabolome database for 2018. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D608-D617	20.1	1832
402	DrugBank: a knowledgebase for drugs, drug actions and drug targets. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D901-6	20.1	1770
401	PHASTER: a better, faster version of the PHAST phage search tool. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, W1	<b>6<u>2</u>2)1</b> 1	1573
400	DrugBank 4.0: shedding new light on drug metabolism. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D1091-7	20.1	1490
399	1H, 13C and 15N random coil NMR chemical shifts of the common amino acids. I. Investigations of nearest-neighbor effects. <i>Journal of Biomolecular NMR</i> , <b>1995</b> , 5, 67-81	3	1487
398	HMDB: a knowledgebase for the human metabolome. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D603-10	20.1	1431
397	PHAST: a fast phage search tool. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, W347-52	20.1	1392
396	DrugBank 3.0: a comprehensive resource for RomicsRresearch on drugs. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D1035-41	20.1	1355
395	MetaboAnalyst: a web server for metabolomic data analysis and interpretation. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, W652-60	20.1	1202
394	The human serum metabolome. <i>PLoS ONE</i> , <b>2011</b> , 6, e16957	3.7	1118

# (2010-2016)

393	Heatmapper: web-enabled heat mapping for all. Nucleic Acids Research, 2016, 44, W147-53	20.1	957
392	Using MetaboAnalyst 3.0 for Comprehensive Metabolomics Data Analysis. <i>Current Protocols in Bioinformatics</i> , <b>2016</b> , 55, 14.10.1-14.10.91	24.2	957
391	MetaboAnalyst 2.0a comprehensive server for metabolomic data analysis. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W127-33	20.1	935
390	Using MetaboAnalyst 4.0 for Comprehensive and Integrative Metabolomics Data Analysis. <i>Current Protocols in Bioinformatics</i> , <b>2019</b> , 68, e86	24.2	928
389	The human urine metabolome. <i>PLoS ONE</i> , <b>2013</b> , 8, e73076	3.7	862
388	Chemical shifts as a tool for structure determination. <i>Methods in Enzymology</i> , <b>1994</b> , 239, 363-92	1.7	744
387	Web-based inference of biological patterns, functions and pathways from metabolomic data using MetaboAnalyst. <i>Nature Protocols</i> , <b>2011</b> , 6, 743-60	18.8	718
386	Emerging applications of metabolomics in drug discovery and precision medicine. <i>Nature Reviews Drug Discovery</i> , <b>2016</b> , 15, 473-84	64.1	694
385	VADAR: a web server for quantitative evaluation of protein structure quality. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3316-9	20.1	602
384	Translational biomarker discovery in clinical metabolomics: an introductory tutorial. <i>Metabolomics</i> , <b>2013</b> , 9, 280-299	4.7	594
383	Circular genome visualization and exploration using CGView. <i>Bioinformatics</i> , <b>2005</b> , 21, 537-9	7.2	590
382	Escherichia coli K-12: a cooperatively developed annotation snapshot2005. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, 1-9	20.1	525
381	The future of NMR-based metabolomics. Current Opinion in Biotechnology, 2017, 43, 34-40	11.4	500
380	Metabolomics: applications to food science and nutrition research. <i>Trends in Food Science and Technology</i> , <b>2008</b> , 19, 482-493	15.3	476
379	SuperPose: a simple server for sophisticated structural superposition. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, W590-4	20.1	471
378	Rapid and accurate calculation of protein 1H, 13C and 15N chemical shifts. <i>Journal of Biomolecular NMR</i> , <b>2003</b> , 26, 215-40	3	452
377	SHIFTX2: significantly improved protein chemical shift prediction. <i>Journal of Biomolecular NMR</i> , <b>2011</b> , 50, 43-57	3	449
376	MetPA: a web-based metabolomics tool for pathway analysis and visualization. <i>Bioinformatics</i> , <b>2010</b> , 26, 2342-4	7.2	447

375	MSEA: a web-based tool to identify biologically meaningful patterns in quantitative metabolomic data. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W71-7	20.1	412
374	Mass-spectrometry-based metabolomics: limitations and recommendations for future progress with particular focus on nutrition research. <i>Metabolomics</i> , <b>2009</b> , 5, 435-458	4.7	412
373	Quantitative metabolomics using NMR. TrAC - Trends in Analytical Chemistry, 2008, 27, 228-237	14.6	411
372	Phenol-Explorer 3.0: a major update of the Phenol-Explorer database to incorporate data on the effects of food processing on polyphenol content. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bat070	5	402
371	RefDB: a database of uniformly referenced protein chemical shifts. <i>Journal of Biomolecular NMR</i> , <b>2003</b> , 25, 173-95	3	357
370	Applications of Machine Learning in Cancer Prediction and Prognosis. <i>Cancer Informatics</i> , <b>2006</b> , 2, 1176	59 <b>3</b> 5 <sub>4</sub> 10	60,03200
369	The food metabolome: a window over dietary exposure. <i>American Journal of Clinical Nutrition</i> , <b>2014</b> , 99, 1286-308	7	335
368	NMR Spectroscopy for Metabolomics Research. <i>Metabolites</i> , <b>2019</b> , 9,	5.6	330
367	ClassyFire: automated chemical classification with a comprehensive, computable taxonomy. <i>Journal of Cheminformatics</i> , <b>2016</b> , 8, 61	8.6	327
366	Metabolomics enables precision medicine: "A White Paper, Community Perspective". <i>Metabolomics</i> , <b>2016</b> , 12, 149	4.7	327
365	A simple method to predict protein flexibility using secondary chemical shifts. <i>Journal of the American Chemical Society</i> , <b>2005</b> , 127, 14970-1	16.4	325
364	Use of chemical shifts in macromolecular structure determination. <i>Methods in Enzymology</i> , <b>2001</b> , 338, 3-34	1.7	296
363	CFM-ID: a web server for annotation, spectrum prediction and metabolite identification from tandem mass spectra. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W94-9	20.1	278
362	METAGENassist: a comprehensive web server for comparative metagenomics. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, W88-95	20.1	267
361	The human cerebrospinal fluid metabolome. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , <b>2008</b> , 871, 164-73	3.2	256
360	BASys: a web server for automated bacterial genome annotation. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, W4.	552 <b>9</b> .1	254
359	Competitive fragmentation modeling of ESI-MS/MS spectra for putative metabolite identification. <i>Metabolomics</i> , <b>2015</b> , 11, 98-110	4.7	237
358	Systems Biology and Multi-Omics Integration: Viewpoints from the Metabolomics Research Community. <i>Metabolites.</i> <b>2019</b> . 9.	5.6	236

## (2006-2014)

357	SMPDB 2.0: big improvements to the Small Molecule Pathway Database. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D478-84	20.1	216
356	SMPDB: The Small Molecule Pathway Database. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D480-7	20.1	213
355	Applications of machine learning in cancer prediction and prognosis. <i>Cancer Informatics</i> , <b>2007</b> , 2, 59-77	2.4	212
354	Advances in metabolite identification. <i>Bioanalysis</i> , <b>2011</b> , 3, 1769-82	2.1	208
353	The blood exposome and its role in discovering causes of disease. <i>Environmental Health Perspectives</i> , <b>2014</b> , 122, 769-74	8.4	203
352	Intermolecular transmission of superoxide dismutase 1 misfolding in living cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 16398-403	11.5	198
351	Metabolomics for Investigating Physiological and Pathophysiological Processes. <i>Physiological Reviews</i> , <b>2019</b> , 99, 1819-1875	47.9	196
350	PolySearch: a web-based text mining system for extracting relationships between human diseases, genes, mutations, drugs and metabolites. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, W399-405	20.1	180
349	An NMR approach to structural proteomics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2002</b> , 99, 1825-30	11.5	180
348	CS23D: a web server for rapid protein structure generation using NMR chemical shifts and sequence data. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, W496-502	20.1	177
347	Standardizing the experimental conditions for using urine in NMR-based metabolomic studies with a particular focus on diagnostic studies: a review. <i>Metabolomics</i> , <b>2015</b> , 11, 872-894	4.7	171
346	Interpreting protein chemical shift data. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , <b>2011</b> , 58, 62-87	10.4	171
345	Protein chemical shift analysis: a practical guide. <i>Biochemistry and Cell Biology</i> , <b>1998</b> , 76, 153-163	3.6	168
344	T3DB: the toxic exposome database. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D928-34	20.1	162
343	pE-DB: a database of structural ensembles of intrinsically disordered and of unfolded proteins. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D326-35	20.1	159
342	Current progress in computational metabolomics. <i>Briefings in Bioinformatics</i> , <b>2007</b> , 8, 279-93	13.4	159
341	Modulation of structure and antibacterial and hemolytic activity by ring size in cyclic gramicidin S analogs. <i>Journal of Biological Chemistry</i> , <b>1996</b> , 271, 25261-8	5.4	159
340	PREDITOR: a web server for predicting protein torsion angle restraints. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W63-9	20.1	158

339	The CyberCell Database (CCDB): a comprehensive, self-updating, relational database to coordinate and facilitate in silico modeling of Escherichia coli. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D293-5	20.1	156
338	Databases on food phytochemicals and their health-promoting effects. <i>Journal of Agricultural and Food Chemistry</i> , <b>2011</b> , 59, 4331-48	5.7	151
337	MetaboMinersemi-automated identification of metabolites from 2D NMR spectra of complex biofluids. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 507	3.6	150
336	Accurate, fully-automated NMR spectral profiling for metabolomics. <i>PLoS ONE</i> , <b>2015</b> , 10, e0124219	3.7	149
335	YMDB: the Yeast Metabolome Database. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D815-20	20.1	147
334	MyCompoundID: using an evidence-based metabolome library for metabolite identification. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 3401-8	7.8	143
333	The human saliva metabolome. <i>Metabolomics</i> , <b>2015</b> , 11, 1864-1883	4.7	142
332	Applications of metabolomics in drug discovery and development. <i>Drugs in R and D</i> , <b>2008</b> , 9, 307-22	3.4	142
331	BioTransformer: a comprehensive computational tool for small molecule metabolism prediction and metabolite identification. <i>Journal of Cheminformatics</i> , <b>2019</b> , 11, 2	8.6	142
330	Livestock metabolomics and the livestock metabolome: A systematic review. <i>PLoS ONE</i> , <b>2017</b> , 12, e017	76 <i>.7</i> 5	140
329	Metabolomics: the principles and potential applications to transplantation. <i>American Journal of Transplantation</i> , <b>2005</b> , 5, 2814-20	8.7	139
328	Predictive models for breast cancer susceptibility from multiple single nucleotide polymorphisms. <i>Clinical Cancer Research</i> , <b>2004</b> , 10, 2725-37	12.9	131
327	Gramicidin S is active against both gram-positive and gram-negative bacteria. <i>International Journal of Peptide and Protein Research</i> , <b>1996</b> , 47, 460-6		130
326	CFM-ID 3.0: Significantly Improved ESI-MS/MS Prediction and Compound Identification. <i>Metabolites</i> , <b>2019</b> , 9,	5.6	126
325	Metabolomics reveals unhealthy alterations in rumen metabolism with increased proportion of cereal grain in the diet of dairy cows. <i>Metabolomics</i> , <b>2010</b> , 6, 583-594	4.7	125
324	Metabolomic data processing, analysis, and interpretation using MetaboAnalyst. <i>Current Protocols in Bioinformatics</i> , <b>2011</b> , Chapter 14, Unit 14.10	24.2	124
323	Improved Glucose Homeostasis in Obese Mice Treated With Resveratrol Is Associated With Alterations in the Gut Microbiome. <i>Diabetes</i> , <b>2017</b> , 66, 418-425	0.9	121
322	INMEXa web-based tool for integrative meta-analysis of expression data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, W63-70	20.1	119

321	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-70	5.2	117
320	Computational systems biology in drug discovery and development: methods and applications. <i>Drug Discovery Today</i> , <b>2007</b> , 12, 295-303	8.8	112
319	A review on human fecal metabolomics: Methods, applications and the human fecal metabolome database. <i>Analytica Chimica Acta</i> , <b>2018</b> , 1030, 1-24	6.6	111
318	Comparison of SDS- and methanol-assisted protein solubilization and digestion methods for Escherichia coli membrane proteome analysis by 2-D LC-MS/MS. <i>Proteomics</i> , <b>2007</b> , 7, 484-493	4.8	107
317	Nutrimetabolomics: An Integrative Action for Metabolomic Analyses in Human Nutritional Studies. <i>Molecular Nutrition and Food Research</i> , <b>2019</b> , 63, e1800384	5.9	107
316	Metabolomic fingerprint of heart failure with preserved ejection fraction. <i>PLoS ONE</i> , <b>2015</b> , 10, e012484	<b>4</b> 3.7	106
315	Towards automatic metabolomic profiling of high-resolution one-dimensional proton NMR spectra. Journal of Biomolecular NMR, <b>2011</b> , 49, 307-23	3	105
314	Phenol-Explorer 2.0: a major update of the Phenol-Explorer database integrating data on polyphenol metabolism and pharmacokinetics in humans and experimental animals. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2012</b> , 2012, bas031	5	105
313	Unusual beta-sheet periodicity in small cyclic peptides. <i>Nature Structural Biology</i> , <b>1998</b> , 5, 284-8		104
312	CSI 3.0: a web server for identifying secondary and super-secondary structure in proteins using NMR chemical shifts. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W370-7	20.1	100
311	Multi-platform characterization of the human cerebrospinal fluid metabolome: a comprehensive and quantitative update. <i>Genome Medicine</i> , <b>2012</b> , 4, 38	14.4	100
310	ECMDB: the E. coli Metabolome Database. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D625-30	20.1	95
309	Recommendations and Standardization of Biomarker Quantification Using NMR-Based Metabolomics with Particular Focus on Urinary Analysis. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 360-73	5.6	94
308	T3DB: a comprehensively annotated database of common toxins and their targets. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D781-6	20.1	94
307	Improving the accuracy of protein secondary structure prediction using structural alignment. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 301	3.6	94
306	Fatty acid composition of developing sea buckthorn (Hippophae rhamnoides L.) berry and the transcriptome of the mature seed. <i>PLoS ONE</i> , <b>2012</b> , 7, e34099	3.7	93
305	PolySearch2: a significantly improved text-mining system for discovering associations between human diseases, genes, drugs, metabolites, toxins and more. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, W535-42	20.1	92
304	Identification of bacteria using tandem mass spectrometry combined with a proteome database and statistical scoring. <i>Analytical Chemistry</i> , <b>2004</b> , 76, 2355-66	7.8	90

303	Computational strategies for metabolite identification in metabolomics. <i>Bioanalysis</i> , <b>2009</b> , 1, 1579-96	2.1	89
302	Probing the structural determinants of type IIRbeta-turn formation in peptides and proteins. <i>Journal of the American Chemical Society</i> , <b>2002</b> , 124, 1203-13	16.4	88
301	Synthesis and evaluation of keto-glutamine analogues as potent inhibitors of severe acute respiratory syndrome 3CLpro. <i>Journal of Medicinal Chemistry</i> , <b>2004</b> , 47, 6113-6	8.3	87
300	Application of the random coil index to studying protein flexibility. <i>Journal of Biomolecular NMR</i> , <b>2008</b> , 40, 31-48	3	86
299	Solution structure of carnobacteriocin B2 and implications for structure-activity relationships among type IIa bacteriocins from lactic acid bacteria. <i>Biochemistry</i> , <b>1999</b> , 38, 15438-47	3.2	86
298	Metabolomics and first-trimester prediction of early-onset preeclampsia. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , <b>2012</b> , 25, 1840-7	2	85
297	Cancer Metabolomics and the Human Metabolome Database. <i>Metabolites</i> , <b>2016</b> , 6,	5.6	84
296	Current and Future Perspectives on the Structural Identification of Small Molecules in Biological Systems. <i>Metabolites</i> , <b>2016</b> , 6,	5.6	84
295	YMDB 2.0: a significantly expanded version of the yeast metabolome database. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D440-D445	20.1	83
294	Automated 1H and 13C chemical shift prediction using the BioMagResBank. <i>Journal of Biomolecular NMR</i> , <b>1997</b> , 10, 329-36	3	81
293	Proteome Analyst: custom predictions with explanations in a web-based tool for high-throughput proteome annotations. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, W365-71	20.1	80
292	Detailed biophysical characterization of the acid-induced PrP(c) to PrP(I)conversion process. <i>Biochemistry</i> , <b>2011</b> , 50, 1162-73	3.2	79
291	Exposome-Explorer: a manually-curated database on biomarkers of exposure to dietary and environmental factors. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D979-D984	20.1	77
290	Computational Prediction of Electron Ionization Mass Spectra to Assist in GC/MS Compound Identification. <i>Analytical Chemistry</i> , <b>2016</b> , 88, 7689-97	7.8	76
289	The Bovine Ruminal Fluid Metabolome. <i>Metabolomics</i> , <b>2013</b> , 9, 360-378	4.7	75
288	Is Cancer a Genetic Disease or a Metabolic Disease?. <i>EBioMedicine</i> , <b>2015</b> , 2, 478-9	8.8	73
287	ECMDB 2.0: A richer resource for understanding the biochemistry of E. coli. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D495-501	20.1	73
286	PROSESS: a protein structure evaluation suite and server. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, W633-40	20.1	72

## (2004-2011)

285	calculation of local water densities in biological systems: a comparison of molecular dynamics simulations and the 3D-RISM-KH molecular theory of solvation. <i>Journal of Physical Chemistry B</i> , <b>2011</b> , 115, 319-28	3.4	72
284	PHAST, PHASTER and PHASTEST: Tools for finding prophage in bacterial genomes. <i>Briefings in Bioinformatics</i> , <b>2019</b> , 20, 1560-1567	13.4	71
283	Chemical Composition of Commercial Cowß Milk. <i>Journal of Agricultural and Food Chemistry</i> , <b>2019</b> , 67, 4897-4914	5.7	70
282	Recommended strategies for spectral processing and post-processing of 1D H-NMR data of biofluids with a particular focus on urine. <i>Metabolomics</i> , <b>2018</b> , 14, 31	4.7	70
281	Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , <b>2011</b> , 10, 661-9	64.1	69
280	Informatics and Data Analytics to Support Exposome-Based Discovery for Public Health. <i>Annual Review of Public Health</i> , <b>2017</b> , 38, 279-294	20.6	68
279	NMR metabolomics: A look ahead. <i>Journal of Magnetic Resonance</i> , <b>2019</b> , 306, 155-161	3	68
278	Improving early drug discovery through ADME modelling: an overview. <i>Drugs in R and D</i> , <b>2007</b> , 8, 349-62	2 3.4	67
277	The metabolomic profile of umbilical cord blood in neonatal hypoxic ischaemic encephalopathy. <i>PLoS ONE</i> , <b>2012</b> , 7, e50520	3.7	66
276	NMR: prediction of protein flexibility. <i>Nature Protocols</i> , <b>2006</b> , 1, 683-8	18.8	65
276	NMR: prediction of protein flexibility. <i>Nature Protocols</i> , <b>2006</b> , 1, 683-8  HMDB 5.0: the Human Metabolome Database for 2022 <i>Nucleic Acids Research</i> , <b>2022</b> , 50, D622-D631	18.8	<ul><li>65</li><li>65</li></ul>
275	HMDB 5.0: the Human Metabolome Database for 2022 <i>Nucleic Acids Research</i> , <b>2022</b> , 50, D622-D631  Dynamic relationships among type IIa bacteriocins: temperature effects on antimicrobial activity and on structure of the C-terminal amphipathic alpha helix as a receptor-binding region.	20.1	65
<sup>2</sup> 75	HMDB 5.0: the Human Metabolome Database for 2022 <i>Nucleic Acids Research</i> , <b>2022</b> , 50, D622-D631  Dynamic relationships among type IIa bacteriocins: temperature effects on antimicrobial activity and on structure of the C-terminal amphipathic alpha helix as a receptor-binding region. <i>Biochemistry</i> , <b>2004</b> , 43, 9009-20  Combining traditional dietary assessment methods with novel metabolomics techniques: present	20.1	65 64
<sup>2</sup> 75 <sup>2</sup> 74 <sup>2</sup> 73	HMDB 5.0: the Human Metabolome Database for 2022 <i>Nucleic Acids Research</i> , <b>2022</b> , 50, D622-D631  Dynamic relationships among type IIa bacteriocins: temperature effects on antimicrobial activity and on structure of the C-terminal amphipathic alpha helix as a receptor-binding region. <i>Biochemistry</i> , <b>2004</b> , 43, 9009-20  Combining traditional dietary assessment methods with novel metabolomics techniques: present efforts by the Food Biomarker Alliance. <i>Proceedings of the Nutrition Society</i> , <b>2017</b> , 76, 619-627  Small molecule inhibitors of ERCC1-XPF protein-protein interaction synergize alkylating agents in	20.1 3.2 2.9	65 64 62
275 274 273 272	HMDB 5.0: the Human Metabolome Database for 2022 <i>Nucleic Acids Research</i> , <b>2022</b> , 50, D622-D631  Dynamic relationships among type IIa bacteriocins: temperature effects on antimicrobial activity and on structure of the C-terminal amphipathic alpha helix as a receptor-binding region. <i>Biochemistry</i> , <b>2004</b> , 43, 9009-20  Combining traditional dietary assessment methods with novel metabolomics techniques: present efforts by the Food Biomarker Alliance. <i>Proceedings of the Nutrition Society</i> , <b>2017</b> , 76, 619-627  Small molecule inhibitors of ERCC1-XPF protein-protein interaction synergize alkylating agents in cancer cells. <i>Molecular Pharmacology</i> , <b>2013</b> , 84, 12-24  Identification of novel and known oocyte-specific genes using complementary DNA subtraction and	20.1 3.2 2.9 4.3	<ul><li>65</li><li>64</li><li>62</li><li>61</li></ul>
275 274 273 272 271	HMDB 5.0: the Human Metabolome Database for 2022 <i>Nucleic Acids Research</i> , <b>2022</b> , 50, D622-D631  Dynamic relationships among type IIa bacteriocins: temperature effects on antimicrobial activity and on structure of the C-terminal amphipathic alpha helix as a receptor-binding region. <i>Biochemistry</i> , <b>2004</b> , 43, 9009-20  Combining traditional dietary assessment methods with novel metabolomics techniques: present efforts by the Food Biomarker Alliance. <i>Proceedings of the Nutrition Society</i> , <b>2017</b> , 76, 619-627  Small molecule inhibitors of ERCC1-XPF protein-protein interaction synergize alkylating agents in cancer cells. <i>Molecular Pharmacology</i> , <b>2013</b> , 84, 12-24  Identification of novel and known oocyte-specific genes using complementary DNA subtraction and microarray analysis in three different species. <i>Biology of Reproduction</i> , <b>2005</b> , 73, 63-71	20.1 3.2 2.9 4.3	<ul><li>65</li><li>64</li><li>62</li><li>61</li><li>60</li></ul>

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185 184		5.6 3·3	21
	Test for the Detection of Colonic Adenomatous Polyps. <i>Metabolites</i> , <b>2017</b> , 7,		
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184	Test for the Detection of Colonic Adenomatous Polyps. <i>Metabolites</i> , <b>2017</b> , 7,  Molecular signatures of end-stage heart failure. <i>Journal of Cardiac Failure</i> , <b>2011</b> , 17, 867-74  Relative and regional stabilities of the hamster, mouse, rabbit, and bovine prion proteins toward urea unfolding assessed by nuclear magnetic resonance and circular dichroism spectroscopies. <i>Biochemistry</i> , <b>2011</b> , 50, 7536-45  Comparative analysis of essential collective dynamics and NMR-derived flexibility profiles in	3.3	21
184 183	Test for the Detection of Colonic Adenomatous Polyps. <i>Metabolites</i> , <b>2017</b> , 7,  Molecular signatures of end-stage heart failure. <i>Journal of Cardiac Failure</i> , <b>2011</b> , 17, 867-74  Relative and regional stabilities of the hamster, mouse, rabbit, and bovine prion proteins toward urea unfolding assessed by nuclear magnetic resonance and circular dichroism spectroscopies. <i>Biochemistry</i> , <b>2011</b> , 50, 7536-45  Comparative analysis of essential collective dynamics and NMR-derived flexibility profiles in evolutionarily diverse prion proteins. <i>Prion</i> , <b>2011</b> , 5, 188-200  PepTool and GeneTool: platform-independent tools for biological sequence analysis. <i>Methods in</i>	3.2	21 21 21
184 183 182	Test for the Detection of Colonic Adenomatous Polyps. <i>Metabolites</i> , <b>2017</b> , 7,  Molecular signatures of end-stage heart failure. <i>Journal of Cardiac Failure</i> , <b>2011</b> , 17, 867-74  Relative and regional stabilities of the hamster, mouse, rabbit, and bovine prion proteins toward urea unfolding assessed by nuclear magnetic resonance and circular dichroism spectroscopies. <i>Biochemistry</i> , <b>2011</b> , 50, 7536-45  Comparative analysis of essential collective dynamics and NMR-derived flexibility profiles in evolutionarily diverse prion proteins. <i>Prion</i> , <b>2011</b> , 5, 188-200  PepTool and GeneTool: platform-independent tools for biological sequence analysis. <i>Methods in Molecular Biology</i> , <b>2000</b> , 132, 93-113  Improved synthetic methods for the selective deuteration of aromatic amino acids: applications of selective protonation towards the identification of protein folding intermediates through nuclear	3.2	21 21 21 21

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