## Reza M Salek

## List of Publications by Year in Descending Order

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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.

88
papers
4,075
citations

34
h-index

63
g-index

109
ext. papers

7.1
avg, IF

L-index

#	Paper	IF	Citations
88	Networks and Graphs Discovery in Metabolomics Data Analysis and Interpretation <i>Frontiers in Molecular Biosciences</i> , <b>2022</b> , 9, 841373	5.6	2
87	ELIXIR and Toxicology: a community in development. F1000Research, 2021, 10, 1129	3.6	O
86	Emerging technologies and their impact on regulatory science. <i>Experimental Biology and Medicine</i> , <b>2021</b> , 15353702211052280	3.7	3
85	Metabolomics: The Stethoscope for the Twenty-First Century. <i>Medical Principles and Practice</i> , <b>2021</b> , 30, 301-310	2.1	17
84	Information Retrieval Using Machine Learning for Biomarker Curation in the Exposome-Explorer. Frontiers in Research Metrics and Analytics, 2021, 6, 689264	1.3	O
83	A New Pipeline for the Normalization and Pooling of Metabolomics Data. <i>Metabolites</i> , <b>2021</b> , 11,	5.6	1
82	The Disruptive 4IR in the Life Sciences: Metabolomics. <i>Lecture Notes in Electrical Engineering</i> , <b>2020</b> , 227	-256	1
81	NMR-based plasma metabolic profiling in patients with unstable angina. <i>Iranian Journal of Basic Medical Sciences</i> , <b>2020</b> , 23, 311-320	1.8	2
80	Exposome-Explorer 2.0: an update incorporating candidate dietary biomarkers and dietary associations with cancer risk. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D908-D912	20.1	15
79	The ABRF Metabolomics Research Group 2016 Exploratory Study: Investigation of Data Analysis Methods for Untargeted Metabolomics. <i>Metabolites</i> , <b>2020</b> , 10,	5.6	2
78	The metaRbolomics Toolbox in Bioconductor and beyond. <i>Metabolites</i> , <b>2019</b> , 9,	5.6	38
77	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 3302-3310	7.8	27
76	A Tool to Encourage Minimum Reporting Guideline Uptake for Data Analysis in Metabolomics. <i>Metabolites</i> , <b>2019</b> , 9,	5.6	12
75	Interoperable and scalable data analysis with microservices: applications in metabolomics. <i>Bioinformatics</i> , <b>2019</b> , 35, 3752-3760	7.2	15
74	Metabolomics in early detection and prognosis of acute coronary syndrome. <i>Clinica Chimica Acta</i> , <b>2019</b> , 495, 43-53	6.2	20
73	Metabolome Analysis <b>2019</b> , 396-409		0
72	Use cases, best practice and reporting standards for metabolomics in regulatory toxicology. <i>Nature Communications</i> , <b>2019</b> , 10, 3041	17.4	62

71 Measurement Technologies **2019**, 35-72

Nuclear Magnetic Resonance Spectroscopy Data Processing 2019, 101-128  Nuclear Magnetic Resonance Spectroscopy Data Processing 2019, 101-128  Nuclear Magnetic Resonance Spectroscopy Data Processing 2019, 101-128  PhenoMeNal: processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8, 7,6 41  PhenoMeNal: processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8, 7,6 41  PhenoMeNal: processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8, 7,6 41  PhenoMeNal: processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8, 7,6 41  PhenoMeNal: Processing and analysis of metabolomics data in the cloud. GigaScience, 2019, 8, 7,6 41  PhenoMeNal: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. Analytical Chemistry, 2018, 90, 649-656  Improving sample classification by harnessing the potential of H-NMR signal chemical shifts. 49 3  Improving sample classification by harnessing the potential of H-NMR signal chemical shifts. 49 3  Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-40686 26  Mind the Gap: Mapping Mass Spectral Databases in Genome-Scale Metabolic Networks Reveals Poolty Covered Areas. Metabolomics, 2018, 8, 8  Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. Metabolomics, 2017, 13, 12  Global open data management in metabolomics. Current Opinion in Chemical Biology, 2017, 36, 58-63 97 26  mzML2ISA & mmrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. Bioinformatics, 2017, 33, 2598-2600  Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409  Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409  The Human Proteome Organization-Proteomics, Standards Initiative Quality Control Working Gro	71 	Measurement Technologies <b>2019</b> , 35-72		
Overview of Metabolomics 2019, 1-13  PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , 2019, 8, 7.6 41  Progress in Standardization of Metabolic Phenotyping Data 2019, 369-384  Toolphin: a GUI R package for proficient automatic profiling of 1D H-NMR spectra of study datasets. 47 35  Metabolomics, 2018, 14, 24  Annimic A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. <i>Analytical Chemistry</i> , 2018, 90, 649-656  Improving sample classification by harnessing the potential of H-NMR signal chemical shifts. 50/610/616 Scientific Reports, 2018, 8, 11886  Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-40696 26  Mind the Gap: Mapping Mass Spectral Databases in Genome-Scale Metabolic Networks Reveals Poorly Covered Areas. <i>Metabolites</i> , 2018, 8, 1886  Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. <i>Metabolomics</i> , 2017, 13, 12  Global open data management in metabolomics. <i>Current Opinion in Chemical Biology</i> , 2017, 36, 58-63 9,7 26  mzML2ISA & mnrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. <i>Bioinformatics</i> , 2017, 33, 2598-2600  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Croup. Making Quality Control More Accessible for Biological Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 4474-4479  35 Automated assembly of species metabolomes through data submission into a public repository. 61 8 61 61 61 61 61 61 61 61 61 61 61 61 61	70	Data Sharing and Standards <b>2019</b> , 235-252		O
PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , 2019, 8, 7.6 41  Progress in Standardization of Metabolic Phenotyping Data 2019, 369-384  Toolphin: a GUI R package for proficient automatic profiling of 1D H-NMR spectra of study datasets. 47 35  Metabolomics, 2018, 14, 24  Improving Sample classification by harnessing the potential of H-NMR signal chemical shifts. 49 3  Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4069.6 26  Mind the Gap: Mapping Mass Spectral Databases in Genome-Scale Metabolic Networks Reveals Poorly Covered Areas. <i>Metabolites</i> , 2018, 8, 188  Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. <i>Metabolomics</i> , 2017, 13, 12 47 52  Global open data management in metabolomics. <i>Current Opinion in Chemical Biology</i> , 2017, 36, 58-63 9,7 26  mzML2ISA & nmrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. <i>Bioinformatics</i> , 2017, 33, 2598-2600 445 105  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. 7.6 8	69	Nuclear Magnetic Resonance Spectroscopy Data Processing <b>2019</b> , 101-128		
rDolphin: a GUI R package for proficient automatic profiling of 1D H-NMR spectra of study datasets.  ### Acommunity Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. **Analytical Chemistry, 2018, 90, 649-656**    Improving sample classification by harnessing the potential of H-NMR signal chemical shifts. Scientific Reports, 2018, 8, 11886**   Expanding the Use of Spectral Libraries in Proteomics. **Journal of Proteome Research, 2018, 17, 4051-4069.6**   Mind the Gap: Mapping Mass Spectral Databases in Genome-Scale Metabolic Networks Reveals Poorly Covered Areas. **Metabolites, 2018, 8, 1886**    Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. **Metabolomics, 2017, 13, 12**   Global open data management in metabolomics. **Current Opinion in Chemical Biology, 2017, 36, 58-63**   Discovering and linking public omics data sets using the Omics Discovery Index. **Nature Biotechnology, 2017, 33, 42598-2600**   Discovering and linking public omics data sets using the Omics Discovery Index. **Nature Biotechnology, 2017, 33, 406-409**   The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. **Analytical Chemistry, 2017, 8, 4474-4479**   Automated assembly of species metabolomes through data submission into a public repository. **GigaScience, 2017, 6, 1-4**	68	Overview of Metabolomics <b>2019</b> , 1-13		
rDolphin: a GUI R package for proficient automatic profiling of 1D H-NMR spectra of study datasets.  Metabolomics, 2018, 14, 24  At 35  mnrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. Analytical Chemistry, 2018, 90, 649-656  Improving sample classification by harnessing the potential of H-NMR signal chemical shifts.  Scientific Reports, 2018, 8, 11886  Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-40696  Mind the Gap: Mapping Mass Spectral Databases in Genome-Scale Metabolic Networks Reveals Poorly Covered Areas. Metabolites, 2018, 8,  Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. Metabolomics, 2017, 13, 12  Global open data management in metabolomics. Current Opinion in Chemical Biology, 2017, 36, 58-63  MZML2ISA & nmrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. Bioinformatics, 2017, 33, 2598-2600  Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical Chemistry, 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. GigaScience, 2017, 6, 1-4	67	PhenoMeNal: processing and analysis of metabolomics data in the cloud. <i>GigaScience</i> , <b>2019</b> , 8,	7.6	41
nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. Analytical Chemistry, 2018, 90, 649-656  Improving sample classification by harnessing the potential of H-NMR signal chemical shifts. Scientific Reports, 2018, 8, 11886  Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-40696 26  Mind the Gap: Mapping Mass Spectral Databases in Genome-Scale Metabolic Networks Reveals Poorly Covered Areas. Metabolites, 2018, 8,  Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. Metabolomics, 2017, 13, 12  47 52  Global open data management in metabolomics. Current Opinion in Chemical Biology, 2017, 36, 58-63  piscovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 33, 2598-2600  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical 7.8 12  Automated assembly of species metabolomes through data submission into a public repository. GigaScience, 2017, 6, 1-4	66	Progress in Standardization of Metabolic Phenotyping Data <b>2019</b> , 369-384		
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Scientific Reports, 2018, 8, 11886  Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-40696  Mind the Gap: Mapping Mass Spectral Databases in Genome-Scale Metabolic Networks Reveals Poorly Covered Areas. Metabolites, 2018, 8,  Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. Metabolomics, 2017, 13, 12  Global open data management in metabolomics. Current Opinion in Chemical Biology, 2017, 36, 58-63  mzML2ISA & nmrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. Bioinformatics, 2017, 33, 2598-2600  Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical Chemistry, 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. GigaScience, 2017, 6, 1-4	64		7.8	37
Mind the Gap: Mapping Mass Spectral Databases in Genome-Scale Metabolic Networks Reveals Poorly Covered Areas. Metabolites, 2018, 8,  Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. Metabolomics, 2017, 13, 12  47 52  Global open data management in metabolomics. Current Opinion in Chemical Biology, 2017, 36, 58-63  mzML2ISA & nmrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. Bioinformatics, 2017, 33, 2598-2600  7.2 9  Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical Chemistry, 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. GigaScience, 2017, 6, 1-4	63		4.9	3
Poorly Covered Areas. Metabolites, 2018, 8,  Computational tools and workflows in metabolomics: An international survey highlights the opportunity for harmonisation through Galaxy. Metabolomics, 2017, 13, 12  Global open data management in metabolomics. Current Opinion in Chemical Biology, 2017, 36, 58-63  mzML2ISA & nmrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. Bioinformatics, 2017, 33, 2598-2600  Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical Chemistry, 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. GigaScience, 2017, 6, 1-4	62	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4051-40	0 <b>69</b> .6	26
opportunity for harmonisation through Galaxy. <i>Metabolomics</i> , <b>2017</b> , 13, 12  4.7 52  Global open data management in metabolomics. <i>Current Opinion in Chemical Biology</i> , <b>2017</b> , 36, 58-63  mzML2ISA & nmrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. <i>Bioinformatics</i> , <b>2017</b> , 33, 2598-2600  Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 406-409  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2017</b> , 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. <i>GigaScience</i> , <b>2017</b> , 6, 1-4	61		5.6	38
mzML2ISA & nmrML2ISA: generating enriched ISA-Tab metadata files from metabolomics XML data. <i>Bioinformatics</i> , 2017, 33, 2598-2600  Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. <i>Analytical Chemistry</i> , 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. <i>GigaScience</i> , 2017, 6, 1-4	60		4.7	52
data. Bioinformatics, 2017, 33, 2598-2600  Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409  The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical Chemistry, 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. GigaScience, 2017, 6, 1-4	59	Global open data management in metabolomics. Current Opinion in Chemical Biology, 2017, 36, 58-63	9.7	26
The Human Proteome Organization-Proteomics Standards Initiative Quality Control Working Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical Chemistry, 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository.  GigaScience, 2017, 6, 1-4	58		7.2	9
Group: Making Quality Control More Accessible for Biological Mass Spectrometry. Analytical 7.8 12 Chemistry, 2017, 89, 4474-4479  Automated assembly of species metabolomes through data submission into a public repository. GigaScience, 2017, 6, 1-4	57		44.5	105
55 GigaScience, <b>2017</b> , 6, 1-4	56	Group: Making Quality Control More Accessible for Biological Mass Spectrometry. <i>Analytical</i>	7.8	12
Navigating freely-available software tools for metabolomics analysis. <i>Metabolomics</i> , <b>2017</b> , 13, 106 4.7 131	55		7.6	8
	54	Navigating freely-available software tools for metabolomics analysis. <i>Metabolomics</i> , <b>2017</b> , 13, 106	4.7	131

53	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 4288-4298	5.6	61
52	Assessing Public Metabolomics Metadata, Towards Improving Quality. <i>Journal of Integrative Bioinformatics</i> , <b>2017</b> , 14,	3.8	9
51	Compliance with minimum information guidelines in public metabolomics repositories. <i>Scientific Data</i> , <b>2017</b> , 4, 170137	8.2	43
50	A decade after the metabolomics standards initiative it's time for a revision. Scientific Data, 2017, 4, 170	0 <u>83</u> 8	45
49	The future of metabolomics in ELIXIR. F1000Research, 2017, 6,	3.6	18
48	The future of metabolomics in ELIXIR. <i>F1000Research</i> , <b>2017</b> , 6, 1649	3.6	10
47	NMR Spectroscopy of Tissues, 1H MAS <b>2017</b> , 254-259		
46	SPLASH, a hashed identifier for mass spectra. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 1099-1101	44.5	48
45	Infection Susceptibility in Gastric Intrinsic Factor (Vitamin B12)-Defective Mice Is Subject to Maternal Influences. <i>MBio</i> , <b>2016</b> , 7,	7.8	4
44	MetaboLights: An Open-Access Database Repository for Metabolomics Data. <i>Current Protocols in Bioinformatics</i> , <b>2016</b> , 53, 14.13.1-14.13.18	24.2	111
43	Data standards can boost metabolomics research, and if there is a will, there is a way. <i>Metabolomics</i> , <b>2016</b> , 12, 14	4.7	85
42	From Databases to Big Data <b>2016</b> , 317-331		4
41	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
40	Mass spectral databases for LC/MS- and GC/MS-based metabolomics: State of the field and future prospects. <i>TrAC - Trends in Analytical Chemistry</i> , <b>2016</b> , 78, 23-35	14.6	295
39	The Time Is Right to Focus on Model Organism Metabolomes. <i>Metabolites</i> , <b>2016</b> , 6,	5.6	43
38	Embedding standards in metabolomics: the Metabolomics Society data standards task group. <i>Metabolomics</i> , <b>2015</b> , 11, 782-783	4.7	12
37	Behavioural and molecular endophenotypes in psychotic disorders reveal heritable abnormalities in glutamatergic neurotransmission. <i>Translational Psychiatry</i> , <b>2015</b> , 5, e540	8.6	9
36	SpeckTackle: JavaScript charts for spectroscopy. <i>Journal of Cheminformatics</i> , <b>2015</b> , 7, 17	8.6	10

## (2012-2015)

35	Dolphin 1D: Improving Automation of Targeted Metabolomics in Multi-matrix Datasets of (^1)H-NMR Spectra. <i>Advances in Intelligent Systems and Computing</i> , <b>2015</b> , 59-67	0.4	2
34	COordination of Standards in MetabOlomicS (COSMOS): facilitating integrated metabolomics data access. <i>Metabolomics</i> , <b>2015</b> , 11, 1587-1597	4.7	109
33	Metabolomics continues to expand: highlights from the 2015 metabolomics conference. <i>Metabolomics</i> , <b>2015</b> , 11, 1036-1040	4.7	13
32	Getting the right answers: understanding metabolomics challenges. <i>Expert Review of Molecular Diagnostics</i> , <b>2015</b> , 15, 97-109	3.8	35
31	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
30	Metabolic differences in ripening of Solanum lycopersicum 'Ailsa Craig' and three monogenic mutants. <i>Scientific Data</i> , <b>2014</b> , 1, 140029	8.2	9
29	Dolphin: a tool for automatic targeted metabolite profiling using 1D and 2D (1)H-NMR data. <i>Analytical and Bioanalytical Chemistry</i> , <b>2014</b> , 406, 7967-76	4.4	40
28	Genome-wide association study of metabolic traits reveals novel gene-metabolite-disease links. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004132	6	70
27	The mzTab data exchange format: communicating mass-spectrometry-based proteomics and metabolomics experimental results to a wider audience. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2765-75	7.6	96
26	Expanding natural product chemistry resources at the EBI. Journal of Cheminformatics, 2013, 5,	8.6	78
25	Biomarkers of food intake and metabolite differences between plasma and red blood cell matrices; a human metabolomic profile approach. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 1411-22		21
24	NMR-based metabolomics in human disease diagnosis: applications, limitations, and recommendations. <i>Metabolomics</i> , <b>2013</b> , 9, 1048-1072	4.7	165
23	MetaboLightsan open-access general-purpose repository for metabolomics studies and associated meta-data. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D781-6	20.1	483
22	The MetaboLights repository: curation challenges in metabolomics. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bat029	5	40
21	MetaboLights: towards a new COSMOS of metabolomics data management. <i>Metabolomics</i> , <b>2012</b> , 8, 757	-7. <del>6</del> 0	64
20	Metabolomics of human breast cancer: new approaches for tumor typing and biomarker discovery. <i>Genome Medicine</i> , <b>2012</b> , 4, 37	14.4	74
19	Remodeling of central metabolism in invasive breast cancer compared to normal breast tissue - a GC-TOFMS based metabolomics study. <i>BMC Genomics</i> , <b>2012</b> , 13, 334	4.5	102
18	A metabolomic strategy defines the regulation of lipid content and global metabolism by <b>9</b> desaturases in Caenorhabditis elegans. <i>BMC Genomics</i> , <b>2012</b> , 13, 36	4.5	22

17	The study of mammalian metabolism through NMR-based metabolomics. <i>Methods in Enzymology</i> , <b>2011</b> , 500, 337-51	1.7	15
16	A metabolomic comparison of mouse models of the Neuronal Ceroid Lipofuscinoses. <i>Journal of Biomolecular NMR</i> , <b>2011</b> , 49, 175-84	3	9
15	A Metadata description of the data in "A metabolomic comparison of urinary changes in type 2 diabetes in mouse, rat, and human.". <i>BMC Research Notes</i> , <b>2011</b> , 4, 272	2.3	15
14	IH nuclear magnetic resonance spectroscopy characterisation of metabolic phenotypes in the medulloblastoma of the SMO transgenic mice. <i>British Journal of Cancer</i> , <b>2010</b> , 103, 1297-304	8.7	20
13	1 H MAS NMR Spectroscopy of Tissues <b>2010</b> , 925-930		1
12	A metabolomic study of the CRND8 transgenic mouse model of Alzheimer's disease.  Neurochemistry International, <b>2010</b> , 56, 937-47	4.4	112
11	A metabolomic study of brain tissues from aged mice with low expression of the vesicular monoamine transporter 2 (VMAT2) gene. <i>Neurochemical Research</i> , <b>2008</b> , 33, 292-300	4.6	21
10	Metabolomic applications to neuroscience: more challenges than chances?. <i>Expert Review of Proteomics</i> , <b>2007</b> , 4, 435-7	4.2	11
9	Metabolomic investigation of CLN6 neuronal ceroid lipofuscinosis in affected South Hampshire sheep. <i>Journal of Neuroscience Research</i> , <b>2007</b> , 85, 3494-504	4.4	21
8	A metabolomic comparison of urinary changes in type 2 diabetes in mouse, rat, and human. <i>Physiological Genomics</i> , <b>2007</b> , 29, 99-108	3.6	315
7	Backbone resonance assignments of the 25kD N-terminal ATPase domain from the Hsp90 chaperone. <i>Journal of Biomolecular NMR</i> , <b>2002</b> , 23, 327-8	3	19
6	Metabolomics		4
5	Interoperable and scalable data analysis with microservices: Applications in Metabolomics		2
4	PhenoMeNal: Processing and analysis of Metabolomics data in the Cloud		1
3	Information Retrieval using Machine Learning for Biomarker Curation in the Exposome-Explorer		1
2	Omics Discovery Index - Discovering and Linking Public Omics Datasets		2
1	Galaxy-Kubernetes integration: scaling bioinformatics workflows in the cloud		9