

# Nathan E Lewis

## 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.

166  
papers

9,883  
citations

42  
h-index

98  
g-index

200  
ext. papers

13,167  
ext. citations

11.1  
avg, IF

6.44  
L-index

#	Paper	IF	Citations
166	Neural responses to affective speech, including motherese, map onto clinical and social eye tracking profiles in toddlers with ASD.. <i>Nature Human Behaviour</i> , <b>2022</b> ,	12.8	3
165	Valine feeding reduces ammonia production through rearrangement of metabolic fluxes in central carbon metabolism of CHO cells.. <i>Applied Microbiology and Biotechnology</i> , <b>2022</b> , 106, 1113	5.7	0
164	Elucidating Human Milk Oligosaccharide biosynthetic genes through network-based multi-omics integration.. <i>Nature Communications</i> , <b>2022</b> , 13, 2455	17.4	1
163	Type 2 Immunity and Age Modify Gene Expression of Coronavirus-induced Disease 2019 Receptors in Eosinophilic Gastrointestinal Disorders. <i>Journal of Pediatric Gastroenterology and Nutrition</i> , <b>2021</b> , 72, 718-722	2.8	4
162	Genome-wide screens uncover KDM2B as a modifier of protein binding to heparan sulfate. <i>Nature Chemical Biology</i> , <b>2021</b> , 17, 684-692	11.7	4
161	From omics to cellular mechanisms in mammalian cell factory development. <i>Current Opinion in Chemical Engineering</i> , <b>2021</b> , 32, 100688	5.4	0
160	Systems glycombiology for discovering drug targets, biomarkers, and rational designs for glyco-immunotherapy. <i>Journal of Biomedical Science</i> , <b>2021</b> , 28, 50	13.3	2
159	A Chinese hamster transcription start site atlas that enables targeted editing of CHO cells. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqab061	3.7	1
158	A metabolic CRISPR-Cas9 screen in Chinese hamster ovary cells identifies glutamine-sensitive genes. <i>Metabolic Engineering</i> , <b>2021</b> , 66, 114-122	9.7	6
157	Deciphering cell-cell interactions and communication from gene expression. <i>Nature Reviews Genetics</i> , <b>2021</b> , 22, 71-88	30.1	129
156	Systematically gap-filling the genome-scale metabolic model of CHO cells. <i>Biotechnology Letters</i> , <b>2021</b> , 43, 73-87	3	5
155	In situ detection of protein interactions for recombinant therapeutic enzymes. <i>Biotechnology and Bioengineering</i> , <b>2021</b> , 118, 890-904	4.9	1
154	Big-Data Glycomics: Tools to Connect Glycan Biosynthesis to Extracellular Communication. <i>Trends in Biochemical Sciences</i> , <b>2021</b> , 46, 284-300	10.3	11
153	Coordinate regulation of systemic and kidney tryptophan metabolism by the drug transporters OAT1 and OAT3. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 296, 100575	5.4	12
152	A Systems View of the Heparan Sulfate Interactome. <i>Journal of Histochemistry and Cytochemistry</i> , <b>2021</b> , 69, 105-119	3.4	17
151	The lytic polysaccharide monooxygenase CbpD promotes <i>Pseudomonas aeruginosa</i> virulence in systemic infection. <i>Nature Communications</i> , <b>2021</b> , 12, 1230	17.4	15
150	A genome-scale metabolic network model and machine learning predict amino acid concentrations in Chinese Hamster Ovary cell cultures. <i>Biotechnology and Bioengineering</i> , <b>2021</b> , 118, 2118-2123	4.9	14

149	An integrated modular framework for modeling the effect of ammonium on the sialylation process of monoclonal antibodies produced by CHO cells. <i>Biotechnology Journal</i> , <b>2021</b> , 16, e2100019	5.6	4
148	Model-based assessment of mammalian cell metabolic functionalities using omics data. <i>Cell Reports Methods</i> , <b>2021</b> , 1, 100040-100040		3
147	Systematic evaluation of parameters for genome-scale metabolic models of cultured mammalian cells. <i>Metabolic Engineering</i> , <b>2021</b> , 66, 21-30	9.7	3
146	A unique esophageal extracellular matrix proteome alters normal fibroblast function in severe eosinophilic esophagitis. <i>Journal of Allergy and Clinical Immunology</i> , <b>2021</b> , 148, 486-494	11.5	5
145	Correcting for sparsity and interdependence in glycomics by accounting for glycan biosynthesis. <i>Nature Communications</i> , <b>2021</b> , 12, 4988	17.4	3
144	An optimized genome-wide, virus-free CRISPR screen for mammalian cells.. <i>Cell Reports Methods</i> , <b>2021</b> , 1, 100062-100062		1
143	Immune response to intravenous immunoglobulin in patients with Kawasaki disease and MIS-C. <i>Journal of Clinical Investigation</i> , <b>2021</b> , 131,	15.9	7
142	Atypical genomic cortical patterning in autism with poor early language outcome. <i>Science Advances</i> , <b>2021</b> , 7, eabh1663	14.3	1
141	Synergisms of machine learning and constraint-based modeling of metabolism for analysis and optimization of fermentation parameters. <i>Biotechnology Journal</i> , <b>2021</b> , 16, e2100212	5.6	0
140	Endothelial Heparan Sulfate Mediates Hepatic Neutrophil Trafficking and Injury during Staphylococcus aureus Sepsis. <i>MBio</i> , <b>2021</b> , 12, e0118121	7.8	0
139	Dysregulation of the secretory pathway connects Alzheimer's disease genetics to aggregate formation. <i>Cell Systems</i> , <b>2021</b> , 12, 873-884.e4	10.6	1
138	Multiple freeze-thaw cycles lead to a loss of consistency in poly(A)-enriched RNA sequencing. <i>BMC Genomics</i> , <b>2021</b> , 22, 69	4.5	3
137	LIGHT controls distinct homeostatic and inflammatory gene expression profiles in esophageal fibroblasts via differential HVEM and LTB-mediated mechanisms.. <i>Mucosal Immunology</i> , <b>2021</b> ,	9.2	2
136	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1007764	5	6
135	A metabolic network-based approach for developing feeding strategies for CHO cells to increase monoclonal antibody production. <i>Bioprocess and Biosystems Engineering</i> , <b>2020</b> , 43, 1381-1389	3.7	17
134	What CHO is made of: Variations in the biomass composition of Chinese hamster ovary cell lines. <i>Metabolic Engineering</i> , <b>2020</b> , 61, 288-300	9.7	18
133	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , <b>2020</b> , 38, 272-276	11.5	121
132	A Markov model of glycosylation elucidates isozyme specificity and glycosyltransferase interactions for glycoengineering. <i>Current Research in Biotechnology</i> , <b>2020</b> , 2, 22-36	4.8	12

131	ZNF263 is a transcriptional regulator of heparin and heparan sulfate biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2020</b> , 117, 9311-9317	11.5	11
130	Prenatal Origins of ASD: The When, What, and How of ASD Development. <i>Trends in Neurosciences</i> , <b>2020</b> , 43, 326-342	13.3	34
129	CHOmics: A web-based tool for multi-omics data analysis and interactive visualization in CHO cell lines. <i>PLoS Computational Biology</i> , <b>2020</b> , 16, e1008498	5	1
128	Dietary serine-microbiota interaction enhances chemotherapeutic toxicity without altering drug conversion. <i>Nature Communications</i> , <b>2020</b> , 11, 2587	17.4	18
127	Virus-Receptor Interactions of Glycosylated SARS-CoV-2 Spike and Human ACE2 Receptor <b>2020</b> ,		9
126	Bacterial modification of the host glycosaminoglycan heparan sulfate modulates SARS-CoV-2 infectivity <b>2020</b> ,		14
125	Awakening dormant glycosyltransferases in CHO cells with CRISPRa. <i>Biotechnology and Bioengineering</i> , <b>2020</b> , 117, 593-598	4.9	17
124	Genome-scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein secretion. <i>Nature Communications</i> , <b>2020</b> , 11, 68	17.4	37
123	Ptpn6 inhibits caspase-8- and Ripk3/Mlkl-dependent inflammation. <i>Nature Immunology</i> , <b>2020</b> , 21, 54-64	19.1	16
122	Virus-Receptor Interactions of Glycosylated SARS-CoV-2 Spike and Human ACE2 Receptor. <i>Cell Host and Microbe</i> , <b>2020</b> , 28, 586-601.e6	23.4	192
121	Increased Production of LIGHT by T Cells in Eosinophilic Esophagitis Promotes Differentiation of Esophageal Fibroblasts Toward an Inflammatory Phenotype. <i>Gastroenterology</i> , <b>2020</b> , 159, 1778-1792.e1333	13.3	8
120	A consensus-based and readable extension of near de facto reaction rules (LiCoRR). <i>Beilstein Journal of Organic Chemistry</i> , <b>2020</b> , 16, 2645-2662	2.5	8
119	Multiplex secretome engineering enhances recombinant protein production and purity. <i>Nature Communications</i> , <b>2020</b> , 11, 1908	17.4	26
118	StanDep: Capturing transcriptomic variability improves context-specific metabolic models <b>2020</b> , 16, e1007764		
117	StanDep: Capturing transcriptomic variability improves context-specific metabolic models <b>2020</b> , 16, e1007764		
116	StanDep: Capturing transcriptomic variability improves context-specific metabolic models <b>2020</b> , 16, e1007764		
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112	CHOmics: A web-based tool for multi-omics data analysis and interactive visualization in CHO cell lines <b>2020</b> , 16, e1008498		
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108	CHOmics: A web-based tool for multi-omics data analysis and interactive visualization in CHO cell lines <b>2020</b> , 16, e1008498		
107	CHOmics: A web-based tool for multi-omics data analysis and interactive visualization in CHO cell lines <b>2020</b> , 16, e1008498		
106	Increased mAb production in amplified CHO cell lines is associated with increased interaction of CREB1 with transgene promoter. <i>Current Research in Biotechnology</i> , <b>2019</b> , 1, 49-57	4.8	4
105	Dual RNA-seq identifies human mucosal immunity protein Mucin-13 as a hallmark of Plasmodium exoerythrocytic infection. <i>Nature Communications</i> , <b>2019</b> , 10, 488	17.4	27
104	Increasing consensus of context-specific metabolic models by integrating data-inferred cell functions. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1006867	5	37
103	Combating viral contaminants in CHO cells by engineering innate immunity. <i>Scientific Reports</i> , <b>2019</b> , 9, 8827	4.9	8
102	Proteogenomic Annotation of Chinese Hamsters Reveals Extensive Novel Translation Events and Endogenous Retroviral Elements. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 2433-2445	5.6	12
101	Reduced apoptosis in Chinese hamster ovary cells via optimized CRISPR interference. <i>Biotechnology and Bioengineering</i> , <b>2019</b> , 116, 1813-1819	4.9	23
100	Mitigating Clonal Variation in Recombinant Mammalian Cell Lines. <i>Trends in Biotechnology</i> , <b>2019</b> , 37, 931-942	15.1	17
99	A Multiscale Map of the Stem Cell State in Pancreatic Adenocarcinoma. <i>Cell</i> , <b>2019</b> , 177, 572-586.e22	56.2	56
98	From Genotype to Phenotype: Augmenting Deep Learning with Networks and Systems Biology. <i>Current Opinion in Systems Biology</i> , <b>2019</b> , 15, 68-73	3.2	17
97	Systematic Evaluation of Site-Specific Recombinant Gene Expression for Programmable Mammalian Cell Engineering. <i>ACS Synthetic Biology</i> , <b>2019</b> , 8, 758-774	5.7	13
96	The ASD Living Biology: from cell proliferation to clinical phenotype. <i>Molecular Psychiatry</i> , <b>2019</b> , 24, 88-107.1	107.1	127

95	Assessing key decisions for transcriptomic data integration in biochemical networks. <i>PLoS Computational Biology</i> , <b>2019</b> , 15, e1007185	5	26
94	Enhancing Product and Bioprocess Attributes Using Genome-Scale Models of CHO Metabolism <b>2019</b> , 73-95		1
93	Adaption of Generic Metabolic Models to Specific Cell Lines for Improved Modeling of Biopharmaceutical Production and Prediction of Processes <b>2019</b> , 127-162		
92	Proteomic atlas of organ vasculopathies triggered by <i>Staphylococcus aureus</i> sepsis. <i>Nature Communications</i> , <b>2019</b> , 10, 4656	17.4	20
91	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. <i>Nature Protocols</i> , <b>2019</b> , 14, 639-702	18.8	385
90	A perturbed gene network containing PI3K-AKT, RAS-ERK and WNT- $\beta$ -catenin pathways in leukocytes is linked to ASD genetics and symptom severity. <i>Nature Neuroscience</i> , <b>2019</b> , 22, 1624-1634	25.5	31
89	A reference genome of the Chinese hamster based on a hybrid assembly strategy. <i>Biotechnology and Bioengineering</i> , <b>2018</b> , 115, 2087-2100	4.9	55
88	Human milk oligosaccharide composition predicts risk of necrotising enterocolitis in preterm infants. <i>Gut</i> , <b>2018</b> , 67, 1064-1070	19.2	123
87	Minimizing Clonal Variation during Mammalian Cell Line Engineering for Improved Systems Biology Data Generation. <i>ACS Synthetic Biology</i> , <b>2018</b> , 7, 2148-2159	5.7	19
86	An enhanced CRISPR repressor for targeted mammalian gene regulation. <i>Nature Methods</i> , <b>2018</b> , 15, 611-616	11.6	192
85	Functional interrogation of <i>Plasmodium</i> genus metabolism identifies species- and stage-specific differences in nutrient essentiality and drug targeting. <i>PLoS Computational Biology</i> , <b>2018</b> , 14, e1005895	5	18
84	A novel systems-level approach to unravel the regulation and biosynthetic steps of glycosylation. <i>FASEB Journal</i> , <b>2018</b> , 32, 544.23	0.9	
83	Encoding and Estimating the Remarkable Diversity of Possible Sialyltrisaccharides in Nature. <i>FASEB Journal</i> , <b>2018</b> , 32, 673.22	0.9	
82	Genome-scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein synthesis and secretion. <i>FASEB Journal</i> , <b>2018</b> , 32, 526.18	0.9	
81	The emerging role of systems biology for engineering protein production in CHO cells. <i>Current Opinion in Biotechnology</i> , <b>2018</b> , 51, 64-69	11.4	46
80	Large-scale associations between the leukocyte transcriptome and BOLD responses to speech differ in autism early language outcome subtypes. <i>Nature Neuroscience</i> , <b>2018</b> , 21, 1680-1688	25.5	32
79	Revealing Key Determinants of Clonal Variation in Transgene Expression in Recombinant CHO Cells Using Targeted Genome Editing. <i>ACS Synthetic Biology</i> , <b>2018</b> , 7, 2867-2878	5.7	23
78	Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 11096-11101	11.5	28

77	Modeling Meets Metabolomics-The WormJam Consensus Model as Basis for Metabolic Studies in the Model Organism. <i>Frontiers in Molecular Biosciences</i> , <b>2018</b> , 5, 96	5.6	23
76	Ribosome profiling-guided depletion of an mRNA increases cell growth rate and protein secretion. <i>Scientific Reports</i> , <b>2017</b> , 7, 40388	4.9	39
75	Whole-Genome Sequencing of Invasion-Resistant Cells Identifies Laminin $\alpha$ as a Host Factor for Bacterial Invasion. <i>MBio</i> , <b>2017</b> , 8,	7.8	21
74	A Systematic Evaluation of Methods for Tailoring Genome-Scale Metabolic Models. <i>Cell Systems</i> , <b>2017</b> , 4, 318-329.e6	10.6	107
73	Improvements in protein production in mammalian cells from targeted metabolic engineering. <i>Current Opinion in Systems Biology</i> , <b>2017</b> , 6, 1-6	3.2	23
72	Combinatorial CRISPR-Cas9 screens for de novo mapping of genetic interactions. <i>Nature Methods</i> , <b>2017</b> , 14, 573-576	21.6	209
71	PinAPL-Py: A comprehensive web-application for the analysis of CRISPR/Cas9 screens. <i>Scientific Reports</i> , <b>2017</b> , 7, 15854	4.9	38
70	Hierarchical cortical transcriptome disorganization in autism. <i>Molecular Autism</i> , <b>2017</b> , 8, 29	6.5	18
69	Predictive glycoengineering of biosimilars using a Markov chain glycosylation model. <i>Biotechnology Journal</i> , <b>2017</b> , 12, 1600489	5.6	22
68	The Emerging Facets of Non-Cancerous Warburg Effect. <i>Frontiers in Endocrinology</i> , <b>2017</b> , 8, 279	5.7	35
67	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D515-22	20.1	430
66	Recon 2.2: from reconstruction to model of human metabolism. <i>Metabolomics</i> , <b>2016</b> , 12, 109	4.7	184
65	Modulating carbohydrate-protein interactions through glycoengineering of monoclonal antibodies to impact cancer physiology. <i>Current Opinion in Structural Biology</i> , <b>2016</b> , 40, 104-111	8.1	15
64	Novel personalized pathway-based metabolomics models reveal key metabolic pathways for breast cancer diagnosis. <i>Genome Medicine</i> , <b>2016</b> , 8, 34	14.4	80
63	Quantitative feature extraction from the Chinese hamster ovary bioprocess bibliome using a novel meta-analysis workflow. <i>Biotechnology Advances</i> , <b>2016</b> , 34, 621-633	17.8	30
62	A Markov chain model for N-linked protein glycosylation--towards a low-parameter tool for model-driven glycoengineering. <i>Metabolic Engineering</i> , <b>2016</b> , 33, 52-66	9.7	66
61	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. <i>Cell Systems</i> , <b>2016</b> , 3, 434-443.e8	10.6	145
60	Elucidation of the CHO Super-Ome (CHO-SO) by Proteoinformatics. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 4687-703	5.6	29



59	JSBML 1.0: providing a smorgasbord of options to encode systems biology models. <i>Bioinformatics</i> , <b>2015</b> , 31, 3383-6	7.2	31
58	CRISPR/Cas9-mediated genome engineering of CHO cell factories: Application and perspectives. <i>Biotechnology Journal</i> , <b>2015</b> , 10, 979-94	5.6	82
57	Systems analysis of host-parasite interactions. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , <b>2015</b> , 7, 381-400	6.6	15
56	Do genome-scale models need exact solvers or clearer standards?. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 831	12.2	41
55	Cell cycle networks link gene expression dysregulation, mutation, and brain maldevelopment in autistic toddlers. <i>Molecular Systems Biology</i> , <b>2015</b> , 11, 841	12.2	53
54	A novel low-parameter computational model to aid in-silico glycoengineering. <i>BMC Proceedings</i> , <b>2015</b> , 9,	2.3	78
53	Optimizing eukaryotic cell hosts for protein production through systems biotechnology and genome-scale modeling. <i>Biotechnology Journal</i> , <b>2015</b> , 10, 939-49	5.6	37
52	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. <i>PLoS Computational Biology</i> , <b>2015</b> , 11, e1004321	5	187
51	The role of replicates for error mitigation in next-generation sequencing. <i>Nature Reviews Genetics</i> , <b>2014</b> , 15, 56-62	30.1	192
50	Systems glycobiology for glycoengineering. <i>Current Opinion in Biotechnology</i> , <b>2014</b> , 30, 218-24	11.4	47
49	Multi-tissue computational modeling analyzes pathophysiology of type 2 diabetes in MKR mice. <i>PLoS ONE</i> , <b>2014</b> , 9, e102319	3.7	10
48	From random mutagenesis to systems biology in metabolic engineering of mammalian cells. <i>Pharmaceutical Bioprocessing</i> , <b>2014</b> , 2, 355-358		8
47	Rapid neurogenesis through transcriptional activation in human stem cells. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 760	12.2	130
46	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 737	12.2	31
45	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the <i>Cricetulus griseus</i> draft genome. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 759-65	44.5	289
44	Reconstruction of Genome-Scale Metabolic Networks <b>2013</b> , 229-250		
43	The emerging CHO systems biology era: harnessing the 'omics revolution for biotechnology. <i>Current Opinion in Biotechnology</i> , <b>2013</b> , 24, 1102-7	11.4	138
42	Analysis of omics data with genome-scale models of metabolism. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 167-74		143



41	The evolution of genome-scale models of cancer metabolism. <i>Frontiers in Physiology</i> , <b>2013</b> , 4, 237	4.6	63
40	Proteomic analysis of Chinese hamster ovary cells. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 5265-76	5.6	128
39	Constraining the metabolic genotype-phenotype relationship using a phylogeny of in silico methods. <i>Nature Reviews Microbiology</i> , <b>2012</b> , 10, 291-305	22.2	571
38	Network context and selection in the evolution to enzyme specificity. <i>Science</i> , <b>2012</b> , 337, 1101-4	33.3	204
37	In silico method for modelling metabolism and gene product expression at genome scale. <i>Nature Communications</i> , <b>2012</b> , 3, 929	17.4	194
36	A proof for loop-law constraints in stoichiometric metabolic networks. <i>BMC Systems Biology</i> , <b>2012</b> , 6, 140	3.5	17
35	Elimination of thermodynamically infeasible loops in steady-state metabolic models. <i>Biophysical Journal</i> , <b>2011</b> , 100, 544-553	2.9	143
34	Microbial laboratory evolution in the era of genome-scale science. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 509	12.2	210
33	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. <i>Nature Protocols</i> , <b>2011</b> , 6, 1290-307	18.8	1061
32	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , <b>2011</b> , 29, 735-41	44.5	584
31	The role of cellular objectives and selective pressures in metabolic pathway evolution. <i>Current Opinion in Biotechnology</i> , <b>2011</b> , 22, 595-600	11.4	26
30	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 1279-85	44.5	206
29	RNA polymerase mutants found through adaptive evolution reprogram Escherichia coli for optimal growth in minimal media. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 20500-5	11.5	153
28	Omic data from evolved E. coli are consistent with computed optimal growth from genome-scale models. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 390	12.2	419
27	Deletion of genes encoding cytochrome oxidases and quinol monooxygenase blocks the aerobic-anaerobic shift in Escherichia coli K-12 MG1655. <i>Applied and Environmental Microbiology</i> , <b>2010</b> , 76, 6529-40	4.8	41
26	Design and analysis of synthetic carbon fixation pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 8889-94	11.5	321
25	Insight into human alveolar macrophage and M. tuberculosis interactions via metabolic reconstructions. <i>Molecular Systems Biology</i> , <b>2010</b> , 6, 422	12.2	204
24	Gene expression profiling and the use of genome-scale in silico models of Escherichia coli for analysis: providing context for content. <i>Journal of Bacteriology</i> , <b>2009</b> , 191, 3437-44	3.5	43

23	Genome-scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein secretion	3
22	A consensus-based and readable extension of Linear Code for Reaction Rules (LiCoRR)	1
21	Hierarchical cortical transcriptome disorganization in autism	5
20	Systemic post-translational control of bacterial metabolism regulates adaptation in dynamic environments	1
19	Systematically gap-filling the genome-scale metabolic model of CHO cells	2
18	Multiple freeze-thaw cycles lead to a loss of consistency in poly(A)-enriched RNA sequencing	1
17	What does your cell really do? Model-based assessment of mammalian cells metabolic functionalities using omics data	3
16	A metabolic CRISPR-Cas9 screen in Chinese hamster ovary cells identifies glutamine-sensitive genes	2
15	Using targeted genome integration for virus-free genome-wide mammalian CRISPR screen	1
14	Systematic evaluation of parameters for genome-scale metabolic models of cultured mammalian cells	2
13	Dysregulation of the secretory pathway connects Alzheimer's disease genetics to aggregate formation	1
12	Elucidating Human Milk Oligosaccharide biosynthetic genes through network-based multiomics integration	2
11	A genome-scale metabolic network model and machine learning predict amino acid concentrations in Chinese Hamster Ovary cell cultures	2
10	Inferring a spatial code of cell-cell interactions across a whole animal body	8
9	Assessing key decisions for transcriptomic data integration in biochemical networks	5
8	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite	26
7	A perturbed gene network containing PI3K/AKT, RAS/ERK, WNT/ $\beta$ -catenin pathways in leukocytes is linked to ASD genetics and symptom severity	3
6	StanDep: capturing transcriptomic variability improves context-specific metabolic models	1

5	Multiplex secretome engineering enhances recombinant protein production and purity	3
4	On the impact of biomass composition in constraint-based flux analysis	5
3	Correcting for sparsity and non-independence in glycomic data through a systems biology framework	4
2	A metabolic network-based approach for developing feeding strategies for CHO cells to increase monoclonal antibody production	2
1	Context-aware deconvolution of cell-cell communication with Tensor-cell2cell	3