Nathan E Lewis

List of Publications by Year
in descending order

148 papers	15,305 citations	50276 46 h-index	22832 112 g-index
200 all docs	200 docs citations	200 times ranked	15681 citing authors

#	Article	IF	Citations
1	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. Nature Protocols, 2011, 6, 1290-1307.	12.0	1,408
2	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	12.0	833
3	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	14.5	746
4	Constraining the metabolic genotype–phenotype relationship using a phylogeny of in silico methods. Nature Reviews Microbiology, 2012, 10, 291-305.	28.6	721
5	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. Nature Biotechnology, 2011, 29, 735-741.	17.5	699
6	Omic data from evolved *E. coli* are consistent with computed optimal growth from genome-scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
7	Deciphering cell–cell interactions and communication from gene expression. Nature Reviews Genetics, 2021, 22, 71-88.	16.3	575
8	Design and analysis of synthetic carbon fixation pathways. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8889-8894.	7.1	402
9	An enhanced CRISPR repressor for targeted mammalian gene regulation. Nature Methods, 2018, 15, 611-616.	19.0	361
10	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	3.2	344
11	Genomic landscapes of Chinese hamster ovary cell lines as revealed by the Cricetulus griseus draft genome. Nature Biotechnology, 2013, 31, 759-765.	17.5	340
12	Virus-Receptor Interactions of Glycosylated SARS-CoV-2 Spike and Human ACE2 Receptor. Cell Host and Microbe, 2020, 28, 586-601.e6.	11.0	334
13	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
14	Combinatorial CRISPR–Cas9 screens for de novo mapping of genetic interactions. Nature Methods, 2017, 14, 573-576.	19.0	287
15	The role of replicates for error mitigation in next-generation sequencing. Nature Reviews Genetics, 2014, 15, 56-62.	16.3	267
16	Network Context and Selection in the Evolution to Enzyme Specificity. Science, 2012, 337, 1101-1104.	12.6	249
17	Insight into human alveolar macrophage and *M. tuberculosis* interactions via metabolic reconstructions. Molecular Systems Biology, 2010, 6, 422.	7.2	246
18	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. Nature Biotechnology, 2010, 28, 1279-1285.	17.5	246

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19	Microbial laboratory evolution in the era of genome‐scale science. Molecular Systems Biology, 2011, 7, 509.	7.2	245
20	Recon 2.2: from reconstruction to model of human metabolism. Metabolomics, 2016, 12, 109.	3.0	243
21	In silico method for modelling metabolism and gene product expression at genome scale. Nature Communications, 2012, 3, 929.	12.8	238
22	RNA polymerase mutants found through adaptive evolution reprogram *Escherichia coli* for optimal growth in minimal media. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20500-20505.	7.1	219
23	The ASD Living Biology: from cell proliferation to clinical phenotype. Molecular Psychiatry, 2019, 24, 88-107.	7.9	210
24	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
25	Elimination of Thermodynamically Infeasible Loops in Steady-State Metabolic Models. Biophysical Journal, 2011, 100, 544-553.	0.5	203
26	Human milk oligosaccharide composition predicts risk of necrotising enterocolitis in preterm infants. Gut, 2018, 67, 1064-1070.	12.1	193
27	Rapid neurogenesis through transcriptional activation in human stem cells. Molecular Systems Biology, 2014, 10, 760.	7.2	187
28	A Systematic Evaluation of Methods for Tailoring Genome-Scale Metabolic Models. Cell Systems, 2017, 4, 318-329.e6.	6.2	178
29	Analysis of omics data with genome-scale models of metabolism. Molecular BioSystems, 2013, 9, 167-174.	2.9	176
30	Proteomic Analysis of Chinese Hamster Ovary Cells. Journal of Proteome Research, 2012, 11, 5265-5276.	3.7	168
31	The emerging CHO systems biology era: harnessing the ‘omics revolution for biotechnology. Current Opinion in Biotechnology, 2013, 24, 1102-1107.	6.6	159
32	Novel personalized pathway-based metabolomics models reveal key metabolic pathways for breast cancer diagnosis. Genome Medicine, 2016, 8, 34.	8.2	122
33	A Multiscale Map of the Stem Cell State in Pancreatic Adenocarcinoma. Cell, 2019, 177, 572-586.e22.	28.9	107
34	CRISPR/Cas9‐mediated genome engineering of CHO cell factories: Application and perspectives. Biotechnology Journal, 2015, 10, 979-994.	3.5	104
35	Prenatal Origins of ASD: The When, What, and How of ASD Development. Trends in Neurosciences, 2020, 43, 326-342.	8.6	100
36	A reference genome of the Chinese hamster based on a hybrid assembly strategy. Biotechnology and Bioengineering, 2018, 115, 2087-2100.	3.3	95

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37	A Markov chain model for N-linked protein glycosylation â€" towards a low-parameter tool for model-driven glycoengineering. Metabolic Engineering, 2016, 33, 52-66.	7.0	86
38	The evolution of genome-scale models of cancer metabolism. Frontiers in Physiology, 2013, 4, 237.	2.8	79
39	Cell cycle networks link gene expression dysregulation, mutation, and brain maldevelopment in autistic toddlers. Molecular Systems Biology, 2015, 11, 841.	7.2	78
40	PinAPL-Py: A comprehensive web-application for the analysis of CRISPR/Cas9 screens. Scientific Reports, 2017, 7, 15854.	3.3	75
41	Genome-scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein secretion. Nature Communications, 2020, 11, 68.	12.8	74
42	A perturbed gene network containing PI3Kâ€"AKT, RASâ€"ERK and WNTâ€"Î²-catenin pathways in leukocytes is linked to ASD genetics and symptom severity. Nature Neuroscience, 2019, 22, 1624-1634.	14.8	71
43	Large-scale associations between the leukocyte transcriptome and BOLD responses to speech differ in autism early language outcome subtypes. Nature Neuroscience, 2018, 21, 1680-1688.	14.8	69
44	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
45	The emerging role of systems biology for engineering protein production in CHO cells. Current Opinion in Biotechnology, 2018, 51, 64-69.	6.6	67
46	Multiplex secretome engineering enhances recombinant protein production and purity. Nature Communications, 2020, 11, 1908.	12.8	63
47	Increasing consensus of context-specific metabolic models by integrating data-inferred cell functions. PLoS Computational Biology, 2019, 15, e1006867.	3.2	61
48	The Emerging Facets of Non-Cancerous Warburg Effect. Frontiers in Endocrinology, 2017, 8, 279.	3.5	59
49	The lytic polysaccharide monooxygenase CbpD promotes Pseudomonas aeruginosa virulence in systemic infection. Nature Communications, 2021, 12, 1230.	12.8	57
50	Systems analysis of hostâ€"parasite interactions. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2015, 7, 381-400.	6.6	55
51	Assessing key decisions for transcriptomic data integration in biochemical networks. PLoS Computational Biology, 2019, 15, e1007185.	3.2	52
52	Gene Expression Profiling and the Use of Genome-Scale In Silico Models of *Escherichia coli* for Analysis: Providing Context for Content. Journal of Bacteriology, 2009, 191, 3437-3444.	2.2	51
53	Minimizing Clonal Variation during Mammalian Cell Line Engineering for Improved Systems Biology Data Generation. ACS Synthetic Biology, 2018, 7, 2148-2159.	3.8	51
54	Deletion of Genes Encoding Cytochrome Oxidases and Quinol Monooxygenase Blocks the Aerobic-Anaerobic Shift in *Escherichia coli* K-12 MG1655. Applied and Environmental Microbiology, 2010, 76, 6529-6540.	3.1	49

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55	Ribosome profiling-guided depletion of an mRNA increases cell growth rate and protein secretion. Scientific Reports, 2017, 7, 40388.	3.3	48
56	Systems glycobiology for glycoengineering. Current Opinion in Biotechnology, 2014, 30, 218-224.	6.6	47
57	Optimizing eukaryotic cell hosts for protein production through systems biotechnology and genome‐scale modeling. Biotechnology Journal, 2015, 10, 939-949.	3.5	46
58	Proteomic atlas of organ vasculopathies triggered by Staphylococcus aureus sepsis. Nature Communications, 2019, 10, 4656.	12.8	46
59	What CHO is made of: Variations in the biomass composition of Chinese hamster ovary cell lines. Metabolic Engineering, 2020, 61, 288-300.	7.0	46
60	Dual RNA-seq identifies human mucosal immunity protein Mucin-13 as a hallmark of Plasmodium exoerythrocytic infection. Nature Communications, 2019, 10, 488.	12.8	45
61	Characterizing posttranslational modifications in prokaryotic metabolism using a multiscale workflow. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 11096-11101.	7.1	44
62	A Systems View of the Heparan Sulfate Interactome. Journal of Histochemistry and Cytochemistry, 2021, 69, 105-119.	2.5	44
63	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. Molecular Systems Biology, 2014, 10, 737.	7.2	41
64	Mitigating Clonal Variation in Recombinant Mammalian Cell Lines. Trends in Biotechnology, 2019, 37, 931-942.	9.3	41
65	Quantitative feature extraction from the Chinese hamster ovary bioprocess bibliome using a novel meta-analysis workflow. Biotechnology Advances, 2016, 34, 621-633.	11.7	40
66	Modeling Meets Metabolomics—The WormJam Consensus Model as Basis for Metabolic Studies in the Model Organism Caenorhabditis elegans. Frontiers in Molecular Biosciences, 2018, 5, 96.	3.5	40
67	Revealing Key Determinants of Clonal Variation in Transgene Expression in Recombinant CHO Cells Using Targeted Genome Editing. ACS Synthetic Biology, 2018, 7, 2867-2878.	3.8	39
68	Reduced apoptosis in Chinese hamster ovary cells via optimized CRISPR interference. Biotechnology and Bioengineering, 2019, 116, 1813-1819.	3.3	39
69	JSBML 1.0: providing a smorgasbord of options to encode systems biology models. Bioinformatics, 2015, 31, 3383-3386.	4.1	37
70	A genome‐scale metabolic network model and machine learning predict amino acid concentrations in Chinese Hamster Ovary cell cultures. Biotechnology and Bioengineering, 2021, 118, 2118-2123.	3.3	37
71	Dietary serine-microbiota interaction enhances chemotherapeutic toxicity without altering drug conversion. Nature Communications, 2020, 11, 2587.	12.8	37
72	Whole-Genome Sequencing of Invasion-Resistant Cells Identifies Laminin α2 as a Host Factor for Bacterial Invasion. MBio, 2017, 8, .	4.1	36

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73	A metabolic network-based approach for developing feeding strategies for CHO cells to increase monoclonal antibody production. Bioprocess and Biosystems Engineering, 2020, 43, 1381-1389.	3.4	36
74	Elucidation of the CHO Super-Ome (CHO-SO) by Proteoinformatics. Journal of Proteome Research, 2015, 14, 4687-4703.	3.7	35
75	Improvements in protein production in mammalian cells from targeted metabolic engineering. Current Opinion in Systems Biology, 2017, 6, 1-6.	2.6	34
76	Big-Data Glycomics: Tools to Connect Glycan Biosynthesis to Extracellular Communication. Trends in Biochemical Sciences, 2021, 46, 284-300.	7.5	34
77	Ptpn6 inhibits caspase-8- and Ripk3/Mlkl-dependent inflammation. Nature Immunology, 2020, 21, 54-64.	14.5	33
78	Systematic Evaluation of Site-Specific Recombinant Gene Expression for Programmable Mammalian Cell Engineering. ACS Synthetic Biology, 2019, 8, 758-774.	3.8	32
79	Context-aware deconvolution of cell–cell communication with Tensor-cell2cell. Nature Communications, 2022, 13, .	12.8	32
80	The role of cellular objectives and selective pressures in metabolic pathway evolution. Current Opinion in Biotechnology, 2011, 22, 595-600.	6.6	31
81	Immune response to intravenous immunoglobulin in patients with Kawasaki disease and MIS-C. Journal of Clinical Investigation, 2021, 131, .	8.2	31
82	ZNF263 is a transcriptional regulator of heparin and heparan sulfate biosynthesis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 9311-9317.	7.1	30
83	Increased Production of LIGHT by T Cells in Eosinophilic Esophagitis Promotes Differentiation of Esophageal Fibroblasts Toward an Inflammatory Phenotype. Gastroenterology, 2020, 159, 1778-1792.e13.	1.3	29
84	Predictive glycoengineering of biosimilars using a Markov chain glycosylation model. Biotechnology Journal, 2017, 12, 1600489.	3.5	28
85	From genotype to phenotype: augmenting deep learning with networks and systems biology. Current Opinion in Systems Biology, 2019, 15, 68-73.	2.6	27
86	Awakening dormant glycosyltransferases in CHO cells with CRISPRa. Biotechnology and Bioengineering, 2020, 117, 593-598.	3.3	27
87	Elucidating Human Milk Oligosaccharide biosynthetic genes through network-based multi-omics integration. Nature Communications, 2022, 13, 2455.	12.8	27
88	Coordinate regulation of systemic and kidney tryptophan metabolism by the drug transporters OAT1 and OAT3. Journal of Biological Chemistry, 2021, 296, 100575.	3.4	25
89	Model-based assessment of mammalian cell metabolic functionalities using omics data. Cell Reports Methods, 2021, 1, 100040.	2.9	25
90	Hierarchical cortical transcriptome disorganization in autism. Molecular Autism, 2017, 8, 29.	4.9	24

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91	Functional interrogation of Plasmodium genus metabolism identifies species- and stage-specific differences in nutrient essentiality and drug targeting. PLoS Computational Biology, 2018, 14, e1005895.	3.2	24
92	What are housekeeping genes?. PLoS Computational Biology, 2022, 18, e1010295.	3.2	24
93	Correcting for sparsity and interdependence in glycomics by accounting for glycan biosynthesis. Nature Communications, 2021, 12, 4988.	12.8	22
94	A proof for loop-law constraints in stoichiometric metabolic networks. BMC Systems Biology, 2012, 6, 140.	3.0	21
95	Modulating carbohydrate–protein interactions through glycoengineering of monoclonal antibodies to impact cancer physiology. Current Opinion in Structural Biology, 2016, 40, 104-111.	5.7	21
96	Atypical genomic cortical patterning in autism with poor early language outcome. Science Advances, 2021, 7, eabh1663.	10.3	21
97	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. PLoS Computational Biology, 2020, 16, e1007764.	3.2	20
98	Synergisms of machine learning and constraint–based modeling of metabolism for analysis and optimization of fermentation parameters. Biotechnology Journal, 2021, 16, e2100212.	3.5	18
99	A Markov model of glycosylation elucidates isozyme specificity and glycosyltransferase interactions for glycoengineering. Current Research in Biotechnology, 2020, 2, 22-36.	3.7	17
100	A metabolic CRISPR-Cas9 screen in Chinese hamster ovary cells identifies glutamine-sensitive genes. Metabolic Engineering, 2021, 66, 114-122.	7.0	17
101	Systematic evaluation of parameters for genome-scale metabolic models of cultured mammalian cells. Metabolic Engineering, 2021, 66, 21-30.	7.0	16
102	Multi-Tissue Computational Modeling Analyzes Pathophysiology of Type 2 Diabetes in MKR Mice. PLoS ONE, 2014, 9, e102319.	2.5	15
103	Proteogenomic Annotation of Chinese Hamsters Reveals Extensive Novel Translation Events and Endogenous Retroviral Elements. Journal of Proteome Research, 2019, 18, 2433-2445.	3.7	15
104	A consensus-based and readable extension of *Li*near *Co*de for *R*eaction *R*ules (LiCoRR). Beilstein Journal of Organic Chemistry, 2020, 16, 2645-2662.	2.2	14
105	Genome-wide screens uncover KDM2B as a modifier of protein binding to heparan sulfate. Nature Chemical Biology, 2021, 17, 684-692.	8.0	14
106	A unique esophageal extracellular matrix proteome alters normal fibroblast function in severe eosinophilic esophagitis. Journal of Allergy and Clinical Immunology, 2021, 148, 486-494.	2.9	14
107	An optimized genome-wide, virus-free CRISPR screen for mammalian cells. Cell Reports Methods, 2021, 1, 100062.	2.9	14
108	Neural responses to affective speech, including motherese, map onto clinical and social eye tracking profiles in toddlers with ASD. Nature Human Behaviour, 2022, 6, 443-454.	12.0	14

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109	Combating viral contaminants in CHO cells by engineering innate immunity. Scientific Reports, 2019, 9, 8827.	3.3	13
110	Harnessing secretory pathway differences between HEK293 and CHO to rescue production of difficult to express proteins. Metabolic Engineering, 2022, 72, 171-187.	7.0	13
111	Increased mAb production in amplified CHO cell lines is associated with increased interaction of CREB1 with transgene promoter. Current Research in Biotechnology, 2019, 1, 49-57.	3.7	12
112	Multiple freeze-thaw cycles lead to a loss of consistency in poly(A)-enriched RNA sequencing. BMC Genomics, 2021, 22, 69.	2.8	12
113	Type 2 Immunity and Age Modify Gene Expression of Coronavirus-induced Disease 2019 Receptors in Eosinophilic Gastrointestinal Disorders. Journal of Pediatric Gastroenterology and Nutrition, 2021, 72, 718-722.	1.8	12
114	Dysregulation of the secretory pathway connects Alzheimer's disease genetics to aggregate formation. Cell Systems, 2021, 12, 873-884.e4.	6.2	11
115	Restoration of DNA repair mitigates genome instability and increases productivity of Chinese hamster ovary cells. Biotechnology and Bioengineering, 2022, 119, 963-982.	3.3	11
116	From random mutagenesis to systems biology in metabolic engineering of mammalian cells. Pharmaceutical Bioprocessing, 2014, 2, 355-358.	0.8	10
117	Systematically gap-filling the genome-scale metabolic model of CHO cells. Biotechnology Letters, 2021, 43, 73-87.	2.2	10
118	Endothelial Heparan Sulfate Mediates Hepatic Neutrophil Trafficking and Injury during Staphylococcus aureus Sepsis. MBio, 2021, 12, e0118121.	4.1	8
119	LIGHT controls distinct homeostatic and inflammatory gene expression profiles in esophageal fibroblasts via differential HVEM and LTβR-mediated mechanisms. Mucosal Immunology, 2022, 15, 327-337.	6.0	8
120	A Chinese hamster transcription start site atlas that enables targeted editing of CHO cells. NAR Genomics and Bioinformatics, 2021, 3, lqab061.	3.2	7
121	An integrated modular framework for modeling the effect of ammonium on the sialylation process of monoclonal antibodies produced by CHO cells. Biotechnology Journal, 2021, 16, e2100019.	3.5	7
122	Artificial intelligence in the analysis of glycosylation data. Biotechnology Advances, 2022, 60, 108008.	11.7	7
123	Metabolic Systems Biology. , 2009, , 5535-5552.		6
124	From omics to cellular mechanisms in mammalian cell factory development. Current Opinion in Chemical Engineering, 2021, 32, 100688.	7.8	5
125	Systems glycobiology for discovering drug targets, biomarkers, and rational designs for glyco-immunotherapy. Journal of Biomedical Science, 2021, 28, 50.	7.0	5
126	Multiplex genome editing of mammalian cells for producing recombinant heparin. Metabolic Engineering, 2022, 70, 155-165.	7.0	5

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127	CHOmics: A web-based tool for multi-omics data analysis and interactive visualization in CHO cell lines. PLoS Computational Biology, 2020, 16, e1008498.	3.2	4
128	Valine feeding reduces ammonia production through rearrangement of metabolic fluxes in central carbon metabolism of CHO cells. Applied Microbiology and Biotechnology, 2022, 106, 1113-1126.	3.6	4
129	Reconstruction of Genome-Scale Metabolic Networks. , 2013, , 229-250.		1
130	In situ detection of protein interactions for recombinant therapeutic enzymes. Biotechnology and Bioengineering, 2021, 118, 890-904.	3.3	1
131	A novel low-parameter computational model to aid in-silico glycoengineering. BMC Proceedings, 2015, 9, .	1.6	0
132	Systemic Post-Translational Control of Bacterial Metabolism Regulates Adaptation in Dynamic Environments. SSRN Electronic Journal, 0, , .	0.4	0
133	Can we capture an accurate view of tissue metabolism from an expression profile?. FASEB Journal, 2018, 32, .	0.5	0
134	A novel systems‐level approach to unravel the regulation and biosynthetic steps of glycosylation. FASEB Journal, 2018, 32, 544.23.	0.5	0
135	Encoding and Estimating the Remarkable Diversity of Possible Sialyltrisaccharides in Nature. FASEB Journal, 2018, 32, 673.22.	0.5	0
136	Genome‐scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein synthesis and secretion. FASEB Journal, 2018, 32, 526.18.	0.5	0
137	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
138	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
139	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
140	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
141	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
142	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
143	Title is missing!. , 2020, 16, e1008498.		0
144	Title is missing!. , 2020, 16, e1008498.		0

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145	Title is missing!. , 2020, 16, e1008498.		0
146	Title is missing!. , 2020, 16, e1008498.		0
147	Title is missing!. , 2020, 16, e1008498.		0
148	Title is missing!. , 2020, 16, e1008498.		0