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	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
2	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
3	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
4	Multiplex genome editing of mammalian cells for producing recombinant heparin. Metabolic Engineering, 2022, 70, 155-165.	7.0	5
5	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
6	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
7	Elucidating Human Milk Oligosaccharide biosynthetic genes through network-based multi-omics integration. Nature Communications, 2022, 13, 2455.	12.8	27
8	Artificial intelligence in the analysis of glycosylation data. Biotechnology Advances, 2022, 60, 108008.	11.7	7
9	Context-aware deconvolution of cell–cell communication with Tensor-cell2cell. Nature Communications, 2022, 13, .	12.8	32
10	What are housekeeping genes?. PLoS Computational Biology, 2022, 18, e1010295.	3.2	24
11	Deciphering cell–cell interactions and communication from gene expression. Nature Reviews Genetics, 2021, 22, 71-88.	16.3	575
12	Systematically gap-filling the genome-scale metabolic model of CHO cells. Biotechnology Letters, 2021, 43, 73-87.	2.2	10
13	In situ detection of protein interactions for recombinant therapeutic enzymes. Biotechnology and Bioengineering, 2021, 118, 890-904.	3.3	1
14	Big-Data Glycomics: Tools to Connect Glycan Biosynthesis to Extracellular Communication. Trends in Biochemical Sciences, 2021, 46, 284-300.	7.5	34
15	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
16	A Systems View of the Heparan Sulfate Interactome. Journal of Histochemistry and Cytochemistry, 2021, 69, 105-119.	2.5	44
17	The lytic polysaccharide monooxygenase CbpD promotes Pseudomonas aeruginosa virulence in systemic infection. Nature Communications, 2021, 12, 1230.	12.8	57
18	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

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19	Genome-wide screens uncover KDM2B as a modifier of protein binding to heparan sulfate. Nature Chemical Biology, 2021, 17, 684-692.	8.0	14
20	From omics to cellular mechanisms in mammalian cell factory development. Current Opinion in Chemical Engineering, 2021, 32, 100688.	7.8	5
21	Systems glycobiology for discovering drug targets, biomarkers, and rational designs for glyco-immunotherapy. Journal of Biomedical Science, 2021, 28, 50.	7.0	5
22	A Chinese hamster transcription start site atlas that enables targeted editing of CHO cells. NAR Genomics and Bioinformatics, 2021, 3, lqab061.	3.2	7
23	A metabolic CRISPR-Cas9 screen in Chinese hamster ovary cells identifies glutamine-sensitive genes. Metabolic Engineering, 2021, 66, 114-122.	7.0	17
24	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
25	Model-based assessment of mammalian cell metabolic functionalities using omics data. Cell Reports Methods, 2021, 1, 100040.	2.9	25
26	Systematic evaluation of parameters for genome-scale metabolic models of cultured mammalian cells. Metabolic Engineering, 2021, 66, 21-30.	7.0	16
27	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
28	Correcting for sparsity and interdependence in glycomics by accounting for glycan biosynthesis. Nature Communications, 2021, 12, 4988.	12.8	22
29	An optimized genome-wide, virus-free CRISPR screen for mammalian cells. Cell Reports Methods, 2021, 1, 100062.	2.9	14
30	Immune response to intravenous immunoglobulin in patients with Kawasaki disease and MIS-C. Journal of Clinical Investigation, 2021, 131, .	8.2	31
31	Atypical genomic cortical patterning in autism with poor early language outcome. Science Advances, 2021, 7, eabh1663.	10.3	21
32	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
33	Endothelial Heparan Sulfate Mediates Hepatic Neutrophil Trafficking and Injury during Staphylococcus aureus Sepsis. MBio, 2021, 12, e0118121.	4.1	8
34	Dysregulation of the secretory pathway connects Alzheimer's disease genetics to aggregate formation. Cell Systems, 2021, 12, 873-884.e4.	6.2	11
35	Multiple freeze-thaw cycles lead to a loss of consistency in poly(A)-enriched RNA sequencing. BMC Genomics, 2021, 22, 69.	2.8	12
36	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

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37	Awakening dormant glycosyltransferases in CHO cells with CRISPRa. Biotechnology and Bioengineering, 2020, 117, 593-598.	3.3	27
38	Genome-scale reconstructions of the mammalian secretory pathway predict metabolic costs and limitations of protein secretion. Nature Communications, 2020, 11, 68.	12.8	74
39	Ptpn6 inhibits caspase-8- and Ripk3/Mlkl-dependent inflammation. Nature Immunology, 2020, 21, 54-64.	14.5	33
40	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
41	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
42	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
43	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. PLoS Computational Biology, 2020, 16, e1007764.	3.2	20
44	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
45	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
46	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	17.5	314
47	A Markov model of glycosylation elucidates isozyme specificity and glycosyltransferase interactions for glycoengineering. Current Research in Biotechnology, 2020, 2, 22-36.	3.7	17
48	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
49	Prenatal Origins of ASD: The When, What, and How of ASD Development. Trends in Neurosciences, 2020, 43, 326-342.	8.6	100
50	Multiplex secretome engineering enhances recombinant protein production and purity. Nature Communications, 2020, 11, 1908.	12.8	63
51	Dietary serine-microbiota interaction enhances chemotherapeutic toxicity without altering drug conversion. Nature Communications, 2020, 11, 2587.	12.8	37
52	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
53	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
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55	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
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57	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
58	StanDep: Capturing transcriptomic variability improves context-specific metabolic models. , 2020, 16, e1007764.		0
59	Title is missing!. , 2020, 16, e1008498.		0
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62	Title is missing!. , 2020, 16, e1008498.		0
63	Title is missing!. , 2020, 16, e1008498.		0
64	Title is missing!. , 2020, 16, e1008498.		0
65	The ASD Living Biology: from cell proliferation to clinical phenotype. Molecular Psychiatry, 2019, 24, 88-107.	7.9	210
66	Assessing key decisions for transcriptomic data integration in biochemical networks. PLoS Computational Biology, 2019, 15, e1007185.	3.2	52
67	Proteomic atlas of organ vasculopathies triggered by Staphylococcus aureus sepsis. Nature Communications, 2019, 10, 4656.	12.8	46
68	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
69	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
70	Increasing consensus of context-specific metabolic models by integrating data-inferred cell functions. PLoS Computational Biology, 2019, 15, e1006867.	3.2	61
71	Combating viral contaminants in CHO cells by engineering innate immunity. Scientific Reports, 2019, 9, 8827.	3.3	13
72	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

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73	Reduced apoptosis in Chinese hamster ovary cells via optimized CRISPR interference. Biotechnology and Bioengineering, 2019, 116, 1813-1819.	3.3	39
74	Mitigating Clonal Variation in Recombinant Mammalian Cell Lines. Trends in Biotechnology, 2019, 37, 931-942.	9.3	41
75	A Multiscale Map of the Stem Cell State in Pancreatic Adenocarcinoma. Cell, 2019, 177, 572-586.e22.	28.9	107
76	From genotype to phenotype: augmenting deep learning with networks and systems biology. Current Opinion in Systems Biology, 2019, 15, 68-73.	2.6	27
77	Systematic Evaluation of Site-Specific Recombinant Gene Expression for Programmable Mammalian Cell Engineering. ACS Synthetic Biology, 2019, 8, 758-774.	3.8	32
78	Creation and analysis of biochemical constraint-based models using the COBRA Toolbox v.3.0. Nature Protocols, 2019, 14, 639-702.	12.0	833
79	A perturbed gene network containing PI3K–AKT, RAS–ERK and WNT–β-catenin pathways in leukocytes is linked to ASD genetics and symptom severity. Nature Neuroscience, 2019, 22, 1624-1634.	14.8	71
80	A reference genome of the Chinese hamster based on a hybrid assembly strategy. Biotechnology and Bioengineering, 2018, 115, 2087-2100.	3.3	95
81	Human milk oligosaccharide composition predicts risk of necrotising enterocolitis in preterm infants. Gut, 2018, 67, 1064-1070.	12.1	193
82	The emerging role of systems biology for engineering protein production in CHO cells. Current Opinion in Biotechnology, 2018, 51, 64-69.	6.6	67
83	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
84	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
85	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
86	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
87	Minimizing Clonal Variation during Mammalian Cell Line Engineering for Improved Systems Biology Data Generation. ACS Synthetic Biology, 2018, 7, 2148-2159.	3.8	51
88	An enhanced CRISPR repressor for targeted mammalian gene regulation. Nature Methods, 2018, 15, 611-616.	19.0	361
89	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
90	Can we capture an accurate view of tissue metabolism from an expression profile?. FASEB Journal, 2018, 32, .	0.5	0

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91	A novel systems–level approach to unravel the regulation and biosynthetic steps of glycosylation. FASEB Journal, 2018, 32, 544.23.	0.5	0
92	Encoding and Estimating the Remarkable Diversity of Possible Sialyltrisaccharides in Nature. FASEB Journal, 2018, 32, 673.22.	0.5	0
93	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
94	Ribosome profiling-guided depletion of an mRNA increases cell growth rate and protein secretion. Scientific Reports, 2017, 7, 40388.	3.3	48
95	Whole-Genome Sequencing of Invasion-Resistant Cells Identifies Laminin α2 as a Host Factor for Bacterial Invasion. MBio, 2017, 8, .	4.1	36
96	A Systematic Evaluation of Methods for Tailoring Genome-Scale Metabolic Models. Cell Systems, 2017, 4, 318-329.e6.	6.2	178
97	Improvements in protein production in mammalian cells from targeted metabolic engineering. Current Opinion in Systems Biology, 2017, 6, 1-6.	2.6	34
98	Combinatorial CRISPR–Cas9 screens for de novo mapping of genetic interactions. Nature Methods, 2017, 14, 573-576.	19.0	287
99	PinAPL-Py: A comprehensive web-application for the analysis of CRISPR/Cas9 screens. Scientific Reports, 2017, 7, 15854.	3.3	75
100	Hierarchical cortical transcriptome disorganization in autism. Molecular Autism, 2017, 8, 29.	4.9	24
101	Predictive glycoengineering of biosimilars using a Markov chain glycosylation model. Biotechnology Journal, 2017, 12, 1600489.	3.5	28
102	The Emerging Facets of Non-Cancerous Warburg Effect. Frontiers in Endocrinology, 2017, 8, 279.	3.5	59
103	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
104	Recon 2.2: from reconstruction to model of human metabolism. Metabolomics, 2016, 12, 109.	3.0	243
105	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
106	Novel personalized pathway-based metabolomics models reveal key metabolic pathways for breast cancer diagnosis. Genome Medicine, 2016, 8, 34.	8.2	122
107	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
108	A Markov chain model for N-linked protein glycosylation – towards a low-parameter tool for model-driven glycoengineering. Metabolic Engineering, 2016, 33, 52-66.	7.0	86

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109	BiGG Models: A platform for integrating, standardizing and sharing genome-scale models. Nucleic Acids Research, 2016, 44, D515-D522.	14.5	746
110	CRISPR/Cas9â€mediated genome engineering of CHO cell factories: Application and perspectives. Biotechnology Journal, 2015, 10, 979-994.	3.5	104
111	Systems analysis of hostâ€"parasite interactions. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2015, 7, 381-400.	6.6	55
112	Do genomeâ€scale models need exact solvers or clearer standards?. Molecular Systems Biology, 2015, 11, 831.	7.2	68
113	Cell cycle networks link gene expression dysregulation, mutation, and brain maldevelopment in autistic toddlers. Molecular Systems Biology, 2015, 11, 841.	7.2	78
114	A novel low-parameter computational model to aid in-silico glycoengineering. BMC Proceedings, 2015, 9, .	1.6	0
115	Optimizing eukaryotic cell hosts for protein production through systems biotechnology and genomeâ€scale modeling. Biotechnology Journal, 2015, 10, 939-949.	3.5	46
116	Escher: A Web Application for Building, Sharing, and Embedding Data-Rich Visualizations of Biological Pathways. PLoS Computational Biology, 2015, 11, e1004321.	3.2	344
117	Elucidation of the CHO Super-Ome (CHO-SO) by Proteoinformatics. Journal of Proteome Research, 2015, 14, 4687-4703.	3.7	35
118	JSBML 1.0: providing a smorgasbord of options to encode systems biology models. Bioinformatics, 2015, 31, 3383-3386.	4.1	37
119	Multi-Tissue Computational Modeling Analyzes Pathophysiology of Type 2 Diabetes in MKR Mice. PLoS ONE, 2014, 9, e102319.	2.5	15
120	From random mutagenesis to systems biology in metabolic engineering of mammalian cells. Pharmaceutical Bioprocessing, 2014, 2, 355-358.	0.8	10
121	Rapid neurogenesis through transcriptional activation in human stem cells. Molecular Systems Biology, 2014, 10, 760.	7.2	187
122	Minimal metabolic pathway structure is consistent with associated biomolecular interactions. Molecular Systems Biology, 2014, 10, 737.	7.2	41
123	The role of replicates for error mitigation in next-generation sequencing. Nature Reviews Genetics, 2014, 15, 56-62.	16.3	267
124	Systems glycobiology for glycoengineering. Current Opinion in Biotechnology, 2014, 30, 218-224.	6.6	47
125	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
126	Reconstruction of Genome-Scale Metabolic Networks. , 2013, , 229-250.		1

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127	The emerging CHO systems biology era: harnessing the â€˜omics revolution for biotechnology. Current Opinion in Biotechnology, 2013, 24, 1102-1107.	6.6	159
128	Analysis of omics data with genome-scale models of metabolism. Molecular BioSystems, 2013, 9, 167-174.	2.9	176
129	The evolution of genome-scale models of cancer metabolism. Frontiers in Physiology, 2013, 4, 237.	2.8	79
130	Proteomic Analysis of Chinese Hamster Ovary Cells. Journal of Proteome Research, 2012, 11, 5265-5276.	3.7	168
131	Constraining the metabolic genotypeâ€"phenotype relationship using a phylogeny of in silico methods. Nature Reviews Microbiology, 2012, 10, 291-305.	28.6	721
132	Network Context and Selection in the Evolution to Enzyme Specificity. Science, 2012, 337, 1101-1104.	12.6	249
133	In silico method for modelling metabolism and gene product expression at genome scale. Nature Communications, 2012, 3, 929.	12.8	238
134	A proof for loop-law constraints in stoichiometric metabolic networks. BMC Systems Biology, 2012, 6, 140.	3.0	21
135	Elimination of Thermodynamically Infeasible Loops in Steady-State Metabolic Models. Biophysical Journal, 2011, 100, 544-553.	0.5	203
136	Microbial laboratory evolution in the era of genomeâ€scale science. Molecular Systems Biology, 2011, 7, 509.	7.2	245
137	Quantitative prediction of cellular metabolism with constraint-based models: the COBRA Toolbox v2.0. Nature Protocols, 2011, 6, 1290-1307.	12.0	1,408
138	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. Nature Biotechnology, 2011, 29, 735-741.	17.5	699
139	The role of cellular objectives and selective pressures in metabolic pathway evolution. Current Opinion in Biotechnology, 2011, 22, 595-600.	6.6	31
140	Insight into human alveolar macrophage and *M. tuberculosis* interactions via metabolic reconstructions. Molecular Systems Biology, 2010, 6, 422.	7.2	246
141	Large-scale in silico modeling of metabolic interactions between cell types in the human brain. Nature Biotechnology, 2010, 28, 1279-1285.	17.5	246
142	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
143	Omic data from evolved *E. coli* are consistent with computed optimal growth from genomeâ€scale models. Molecular Systems Biology, 2010, 6, 390.	7.2	615
144	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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145	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
146	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
147	Metabolic Systems Biology. , 2009, , 5535-5552.		6
148	Systemic Post-Translational Control of Bacterial Metabolism Regulates Adaptation in Dynamic Environments. SSRN Electronic Journal, 0, , .	0.4	0