

Samuel Deutsch

List of Publications by Year in descending order

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Version: 2024-02-01

49
papers

5,113
citations

182225

30
h-index

214428

50
g-index

51
all docs

51
docs citations

51
times ranked

11072
citing authors

#	ARTICLE	IF	CITATIONS
1	A Synthetic Gene Library Yields a Previously Unknown Glycoside Phosphorylase That Degrades and Assembles Poly- β -1,3-GlcNAc, Completing the Suite of β -Linked GlcNAc Polysaccharides. ACS Central Science, 2022, 8, 430-440.	5.3	7
2	Intersubunit Coupling Enables Fast CO ₂ -Fixation by Reductive Carboxylases. ACS Central Science, 2022, 8, 1091-1101.	5.3	10
3	A plant host, <i>Nicotiana benthamiana</i> , enables the production and study of fungal lignin-degrading enzymes. Communications Biology, 2021, 4, 1027.	2.0	5
4	An Integrated Computer-Aided Design and Manufacturing Workflow for Synthetic Biology. Methods in Molecular Biology, 2020, 2205, 3-18.	0.4	2
5	Engineered Root Bacteria Release Plant-Available Phosphate from Phytate. Applied and Environmental Microbiology, 2019, 85, .	1.4	41
6	Lessons from Two Design-Test-Learn Cycles of Dodecanol Production in <i>Escherichia coli</i> Aided by Machine Learning. ACS Synthetic Biology, 2019, 8, 1337-1351.	1.9	107
7	MAGI: A Method for Metabolite Annotation and Gene Integration. ACS Chemical Biology, 2019, 14, 704-714.	1.6	28
8	Chemical synthesis rewriting of a bacterial genome to achieve design flexibility and biological functionality. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 8070-8079.	3.3	69
9	An integrated workflow for phenazine-modifying enzyme characterization. Journal of Industrial Microbiology and Biotechnology, 2018, 45, 567-577.	1.4	6
10	A combinatorial approach to synthetic transcription factor-promoter combinations for yeast strain engineering. Yeast, 2018, 35, 273-280.	0.8	19
11	Streamlining the Design-to-Build Transition with Build-Optimization Software Tools. ACS Synthetic Biology, 2017, 6, 485-496.	1.9	48
12	Exploiting members of the BAHD acyltransferase family to synthesize multiple hydroxycinnamate and benzoate conjugates in yeast. Microbial Cell Factories, 2016, 15, 198.	1.9	32
13	Investigation of Proposed Ladderane Biosynthetic Genes from Anammox Bacteria by Heterologous Expression in <i>E. coli</i> . PLoS ONE, 2016, 11, e0151087.	1.1	26
14	Development of a High Throughput Platform for Screening Glycoside Hydrolases Based on Oxime-NIMS. Frontiers in Bioengineering and Biotechnology, 2015, 3, 153.	2.0	14
15	Genome Calligrapher: A Web Tool for Refactoring Bacterial Genome Sequences for <i>de Novo</i> DNA Synthesis. ACS Synthetic Biology, 2015, 4, 927-934.	1.9	16
16	Development of an orthogonal fatty acid biosynthesis system in <i>E. coli</i> for oleochemical production. Metabolic Engineering, 2015, 30, 1-6.	3.6	42
17	Domains of genome-wide gene expression dysregulation in Down's syndrome. Nature, 2014, 508, 345-350.	13.7	298
18	Phylogenomically Guided Identification of Industrially Relevant GH1 β -Glucosidases through DNA Synthesis and Nanostructure-Initiator Mass Spectrometry. ACS Chemical Biology, 2014, 9, 2082-2091.	1.6	78

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19	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. <i>Genome Research</i> , 2014, 24, 1517-1525.	2.4	332
20	The complex SNP and CNV genetic architecture of the increased risk of congenital heart defects in Down syndrome. <i>Genome Research</i> , 2013, 23, 1410-1421.	2.4	65
21	Extensive Natural Variation for Cellular Hydrogen Peroxide Release Is Genetically Controlled. <i>PLoS ONE</i> , 2012, 7, e43566.	1.1	5
22	Identification of <i>cis</i> - and <i>trans</i> -regulatory variation modulating microRNA expression levels in human fibroblasts. <i>Genome Research</i> , 2011, 21, 68-73.	2.4	70
23	A new mouse model for the trisomy of the <i>Abcg1</i> – <i>U2af1</i> region reveals the complexity of the combinatorial genetic code of down syndrome. <i>Human Molecular Genetics</i> , 2009, 18, 4756-4769.	1.4	101
24	Common Regulatory Variation Impacts Gene Expression in a Cell Type–Dependent Manner. <i>Science</i> , 2009, 325, 1246-1250.	6.0	694
25	Transcriptional and post-transcriptional profile of human chromosome 21. <i>Genome Research</i> , 2009, 19, 1471-1479.	2.4	2
26	Genetic and epigenetic analysis of SSAT gene dysregulation in suicidal behavior. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2009, 150B, 799-807.	1.1	57
27	DYRK1A-Dosage Imbalance Perturbs NRSF/REST Levels, Deregulating Pluripotency and Embryonic Stem Cell Fate in Down Syndrome. <i>American Journal of Human Genetics</i> , 2008, 83, 388-400.	2.6	139
28	Genomic determinants of the efficiency of internal ribosomal entry sites of viral and cellular origin. <i>Nucleic Acids Research</i> , 2008, 36, 6918-6925.	6.5	13
29	In Vitro Whole-Genome Analysis Identifies a Susceptibility Locus for HIV-1. <i>PLoS Biology</i> , 2008, 6, e32.	2.6	63
30	Islands of euchromatin-like sequence and expressed polymorphic sequences within the short arm of human chromosome 21. <i>Genome Research</i> , 2007, 17, 1690-1696.	2.4	25
31	Promoter polymorphisms and allelic imbalance in ABCB1 expression. <i>Pharmacogenetics and Genomics</i> , 2007, 17, 951-959.	0.7	23
32	Genomewide Linkage Scan for Split-Hand/Foot Malformation with Long-Bone Deficiency in a Large Arab Family Identifies Two Novel Susceptibility Loci on Chromosomes 1q42.2-q43 and 6q14.1. <i>American Journal of Human Genetics</i> , 2007, 80, 105-111.	2.6	30
33	Natural Gene-Expression Variation in Down Syndrome Modulates the Outcome of Gene-Dosage Imbalance. <i>American Journal of Human Genetics</i> , 2007, 81, 252-263.	2.6	187
34	Human microRNA-155 on Chromosome 21 Differentially Interacts with Its Polymorphic Target in the AGTR1 3' Untranslated Region: A Mechanism for Functional Single-Nucleotide Polymorphisms Related to Phenotypes. <i>American Journal of Human Genetics</i> , 2007, 81, 405-413.	2.6	335
35	Ectrodactyly with aplasia of long bones (OMIM; 119100) in a large inbred Arab family with an apparent autosomal dominant inheritance and reduced penetrance: Clinical and genetic analysis. <i>American Journal of Medical Genetics, Part A</i> , 2006, 140A, 1440-1446.	0.7	19
36	Pathogenic mutations and polymorphisms in the lipoprotein receptor-related protein 5 reveal a new biological pathway for the control of bone mass. <i>Current Opinion in Lipidology</i> , 2005, 16, 207-214.	1.2	47

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37	A response to Suzuki et al. ?How pathogenic is the p.D104N/endostatin polymorphic allele ofCOL18A1 in Knobloch syndrome??. Human Mutation, 2005, 25, 316-316.	1.1	2
38	Genome-Wide Associations of Gene Expression Variation in Humans. PLoS Genetics, 2005, 1, e78.	1.5	467
39	Gene expression variation and expression quantitative trait mapping of human chromosome 21 genes. Human Molecular Genetics, 2005, 14, 3741-3749.	1.4	99
40	Chromosome 21 and Down syndrome: from genomics to pathophysiology. Nature Reviews Genetics, 2004, 5, 725-738.	7.7	582
41	Knobloch syndrome: Novel mutations inCOL18A1, evidence for genetic heterogeneity, and a functionally impaired polymorphism in endostatin. Human Mutation, 2004, 23, 77-84.	1.1	89
42	Gene Expression From the Aneuploid Chromosome in a Trisomy Mouse Model of Down Syndrome. Genome Research, 2004, 14, 1268-1274.	2.4	183
43	Polymorphisms in the Low-Density Lipoprotein Receptor-Related Protein 5 (LRP5) Gene Are Associated with Variation in Vertebral Bone Mass, Vertebral Bone Size, and Stature in Whites. American Journal of Human Genetics, 2004, 74, 866-875.	2.6	226
44	Asp1424Asn MYH9 mutation results in an unstable protein responsible for the phenotypes in May-Hegglin anomaly/Fechtner syndrome. Blood, 2003, 102, 529-534.	0.6	43
45	Nineteen Additional Unpredicted Transcripts from Human Chromosome 21. Genomics, 2002, 79, 824-832.	1.3	46
46	Numerous potentially functional but non-genic conserved sequences on human chromosome 21. Nature, 2002, 420, 578-582.	13.7	226
47	Chromosome 21: a small land of fascinating disorders with unknown pathophysiology. International Journal of Developmental Biology, 2002, 46, 89-96.	0.3	11
48	From PREDs and Open Reading Frames to cDNA Isolation: Revisiting the Human Chromosome 21 Transcription Map. Genomics, 2001, 78, 46-54.	1.3	37
49	A cSNP Map and Database for Human Chromosome 21. Genome Research, 2001, 11, 300-307.	2.4	46