Samuel Deutsch

List of Publications by Year
in descending order

49 papers	5,113 citations	159585 30 h-index	189892 50 g-index
51 all docs	51 docs citations	51 times ranked	9829 citing authors

#	Article	IF	Citations
1	A Synthetic Gene Library Yields a Previously Unknown Glycoside Phosphorylase That Degrades and Assembles Poly-Î²-1,3-GlcNAc, Completing the Suite of Î²-Linked GlcNAc Polysaccharides. ACS Central Science, 2022, 8, 430-440.	11.3	7
2	Intersubunit Coupling Enables Fast CO₂-Fixation by Reductive Carboxylases. ACS Central Science, 2022, 8, 1091-1101.	11.3	10
3	A plant host, Nicotiana benthamiana, enables the production and study of fungal lignin-degrading enzymes. Communications Biology, 2021, 4, 1027.	4.4	5
4	An Integrated Computer-Aided Design and Manufacturing Workflow for Synthetic Biology. Methods in Molecular Biology, 2020, 2205, 3-18.	0.9	2
5	Engineered Root Bacteria Release Plant-Available Phosphate from Phytate. Applied and Environmental Microbiology, 2019, 85, .	3.1	41
6	Lessons from Two Designâ€“Buildâ€“Testâ€“Learn Cycles of Dodecanol Production in Escherichia coli Aided by Machine Learning. ACS Synthetic Biology, 2019, 8, 1337-1351.	3.8	107
7	MAGI: A Method for Metabolite Annotation and Gene Integration. ACS Chemical Biology, 2019, 14, 704-714.	3.4	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.	7.1	69
9	An integrated workflow for phenazine-modifying enzyme characterization. Journal of Industrial Microbiology and Biotechnology, 2018, 45, 567-577.	3.0	6
10	A combinatorial approach to synthetic transcription factorâ€promoter combinations for yeast strain engineering. Yeast, 2018, 35, 273-280.	1.7	19
11	Streamlining the Design-to-Build Transition with Build-Optimization Software Tools. ACS Synthetic Biology, 2017, 6, 485-496.	3.8	48
12	Exploiting members of the BAHD acyltransferase family to synthesize multiple hydroxycinnamate and benzoate conjugates in yeast. Microbial Cell Factories, 2016, 15, 198.	4.0	32
13	Investigation of Proposed Ladderane Biosynthetic Genes from Anammox Bacteria by Heterologous Expression in E. coli. PLoS ONE, 2016, 11, e0151087.	2.5	26
14	Development of a High Throughput Platform for Screening Glycoside Hydrolases Based on Oxime-NIMS. Frontiers in Bioengineering and Biotechnology, 2015, 3, 153.	4.1	14
15	Genome Calligrapher: A Web Tool for Refactoring Bacterial Genome Sequences for de Novo DNA Synthesis. ACS Synthetic Biology, 2015, 4, 927-934.	3.8	16
16	Development of an orthogonal fatty acid biosynthesis system in E. coli for oleochemical production. Metabolic Engineering, 2015, 30, 1-6.	7.0	42
17	Domains of genome-wide gene expression dysregulation in Downâ€™s syndrome. Nature, 2014, 508, 345-350.	27.8	298
18	Phylogenomically Guided Identification of Industrially Relevant GH1 Î²-Glucosidases through DNA Synthesis and Nanostructure-Initiator Mass Spectrometry. ACS Chemical Biology, 2014, 9, 2082-2091.	3.4	78

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19	Methane yield phenotypes linked to differential gene expression in the sheep rumen microbiome. Genome Research, 2014, 24, 1517-1525.	5.5	332
20	The complex SNP and CNV genetic architecture of the increased risk of congenital heart defects in Down syndrome. Genome Research, 2013, 23, 1410-1421.	5.5	65
21	Extensive Natural Variation for Cellular Hydrogen Peroxide Release Is Genetically Controlled. PLoS ONE, 2012, 7, e43566.	2.5	5
22	Identification of cis- and trans-regulatory variation modulating microRNA expression levels in human fibroblasts. Genome Research, 2011, 21, 68-73.	5.5	70
23	A new mouse model for the trisomy of the Abcg1â€“U2af1 region reveals the complexity of the combinatorial genetic code of down syndrome. Human Molecular Genetics, 2009, 18, 4756-4769.	2.9	101
24	Common Regulatory Variation Impacts Gene Expression in a Cell Typeâ€“Dependent Manner. Science, 2009, 325, 1246-1250.	12.6	694
25	Transcriptional and post-transcriptional profile of human chromosome 21. Genome Research, 2009, 19, 1471-1479.	5.5	2
26	Genetic and epigenetic analysis of SSAT gene dysregulation in suicidal behavior. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2009, 150B, 799-807.	1.7	57
27	DYRK1A-Dosage Imbalance Perturbs NRSF/REST Levels, Deregulating Pluripotency and Embryonic Stem Cell Fate in Down Syndrome. American Journal of Human Genetics, 2008, 83, 388-400.	6.2	139
28	Genomic determinants of the efficiency of internal ribosomal entry sites of viral and cellular origin. Nucleic Acids Research, 2008, 36, 6918-6925.	14.5	13
29	In Vitro Whole-Genome Analysis Identifies a Susceptibility Locus for HIV-1. PLoS Biology, 2008, 6, e32.	5.6	63
30	Islands of euchromatin-like sequence and expressed polymorphic sequences within the short arm of human chromosome 21. Genome Research, 2007, 17, 1690-1696.	5.5	25
31	Promoter polymorphisms and allelic imbalance in ABCB1 expression. Pharmacogenetics and Genomics, 2007, 17, 951-959.	1.5	23
32	Genomewide Linkage Scan for Splitâ€“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. American Journal of Human Genetics, 2007, 80, 105-111.	6.2	30
33	Natural Gene-Expression Variation in Down Syndrome Modulates the Outcome of Gene-Dosage Imbalance. American Journal of Human Genetics, 2007, 81, 252-263.	6.2	187
34	Human microRNA-155 on Chromosome 21 Differentially Interacts with Its Polymorphic Target in the AGTR1 3â€² Untranslated Region: A Mechanism for Functional Single-Nucleotide Polymorphisms Related to Phenotypes. American Journal of Human Genetics, 2007, 81, 405-413.	6.2	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. American Journal of Medical Genetics, Part A, 2006, 140A, 1440-1446.	1.2	19
36	Pathogenic mutations and polymorphisms in the lipoprotein receptor-related protein 5 reveal a new biological pathway for the control of bone mass. Current Opinion in Lipidology, 2005, 16, 207-214.	2.7	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.	2.5	2
38	Genome-Wide Associations of Gene Expression Variation in Humans. PLoS Genetics, 2005, 1, e78.	3.5	467
39	Gene expression variation and expression quantitative trait mapping of human chromosome 21 genes. Human Molecular Genetics, 2005, 14, 3741-3749.	2.9	99
40	Chromosome 21 and Down syndrome: from genomics to pathophysiology. Nature Reviews Genetics, 2004, 5, 725-738.	16.3	582
41	Knobloch syndrome: Novel mutations inCOL18A1, evidence for genetic heterogeneity, and a functionally impaired polymorphism in endostatin. Human Mutation, 2004, 23, 77-84.	2.5	89
42	Gene Expression From the Aneuploid Chromosome in a Trisomy Mouse Model of Down Syndrome. Genome Research, 2004, 14, 1268-1274.	5.5	183
43	Polymorphisms in the Low-Density Lipoprotein Receptorâ€“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.	6.2	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.	1.4	43
45	Nineteen Additional Unpredicted Transcripts from Human Chromosome 21. Genomics, 2002, 79, 824-832.	2.9	46
46	Numerous potentially functional but non-genic conserved sequences on human chromosome 21. Nature, 2002, 420, 578-582.	27.8	226
47	Chromosome 21: a small land of fascinating disorders with unknown pathophysiology. International Journal of Developmental Biology, 2002, 46, 89-96.	0.6	11
48	From PREDs and Open Reading Frames to cDNA Isolation: Revisiting the Human Chromosome 21 Transcription Map. Genomics, 2001, 78, 46-54.	2.9	37
49	A cSNP Map and Database for Human Chromosome 21. Genome Research, 2001, 11, 300-307.	5.5	46