Susumu Goto

List of Publications by Year
in descending order

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37 papers	22,840 citations	218381 26 h-index	377514 34 g-index
38 all docs	38 docs citations	38 times ranked	35467 citing authors

#	Article	IF	Citations
1	KEGG for linking genomes to life and the environment. Nucleic Acids Research, 2007, 36, D480-D484.	6.5	5,451
2	KEGG for integration and interpretation of large-scale molecular data sets. Nucleic Acids Research, 2012, 40, D109-D114.	6.5	4,174
3	The KEGG resource for deciphering the genome. Nucleic Acids Research, 2004, 32, 277D-280.	6.5	4,093
4	Data, information, knowledge and principle: back to metabolism in KEGG. Nucleic Acids Research, 2014, 42, D199-D205.	6.5	2,846
5	KEGG for representation and analysis of molecular networks involving diseases and drugs. Nucleic Acids Research, 2010, 38, D355-D360.	6.5	1,999
6	The KEGG databases at GenomeNet. Nucleic Acids Research, 2002, 30, 42-46.	6.5	1,202
7	Development of a Chemical Structure Comparison Method for Integrated Analysis of Chemical and Genomic Information in the Metabolic Pathways. Journal of the American Chemical Society, 2003, 125, 11853-11865.	6.6	423
8	ViPTree: the viral proteomic tree server. Bioinformatics, 2017, 33, 2379-2380.	1.8	415
9	Drug-target interaction prediction from chemical, genomic and pharmacological data in an integrated framework. Bioinformatics, 2010, 26, i246-i254.	1.8	396
10	Linking Virus Genomes with Host Taxonomy. Viruses, 2016, 8, 66.	1.5	295
11	LIGAND: database of chemical compounds and reactions in biological pathways. Nucleic Acids Research, 2002, 30, 402-404.	6.5	255
12	SIMCOMP/SUBCOMP: chemical structure search servers for network analyses. Nucleic Acids Research, 2010, 38, W652-W656.	6.5	125
13	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. MSphere, 2017, 2, .	1.3	114
14	Drug target prediction using adverse event report systems: a pharmacogenomic approach. Bioinformatics, 2012, 28, i611-i618.	1.8	107
15	The KEGG Databases and Tools Facilitating Omics Analysis: Latest Developments Involving Human Diseases and Pharmaceuticals. Methods in Molecular Biology, 2012, 802, 19-39.	0.4	104
16	Typeâ€…III Polyketide Synthases: Functional Classification and Phylogenomics. ChemBioChem, 2017, 18, 50-65.	1.3	104
17	DINIES: drugâ€“target interaction network inference engine based on supervised analysis. Nucleic Acids Research, 2014, 42, W39-W45.	6.5	97
18	Taxon Richness of â€œMegaviridaeâ€•Exceeds those of Bacteria and Archaea in the Ocean. Microbes and Environments, 2018, 33, 162-171.	0.7	83

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19	MAPLE 2.3.0: an improved system for evaluating the functionomes of genomes and metagenomes. Bioscience, Biotechnology and Biochemistry, 2018, 82, 1515-1517.	0.6	80
20	Modular Architecture of Metabolic Pathways Revealed by Conserved Sequences of Reactions. Journal of Chemical Information and Modeling, 2013, 53, 613-622.	2.5	73
21	An automated system for evaluation of the potential functionome: MAPLE version 2.1.0. DNA Research, 2016, 23, 467-475.	1.5	66
22	Evaluation method for the potential functionome harbored in the genome and metagenome. BMC Genomics, 2012, 13, 699.	1.2	65
23	Extraction of phylogenetic network modules from the metabolic network. BMC Bioinformatics, 2006, 7, 130.	1.2	44
24	Effects of post-electrophoretic analysis on variance in gel-based proteomics. Expert Review of Proteomics, 2006, 3, 129-142.	1.3	36
25	EGENES: Transcriptome-Based Plant Database of Genes with Metabolic Pathway Information and Expressed Sequence Tag Indices in KEGG. Plant Physiology, 2007, 144, 857-866.	2.3	35
26	Prediction of missing enzyme genes in a bacterial metabolic network. FEBS Journal, 2007, 274, 2262-2273.	2.2	30
27	KEGG Bioinformatics Resource for Plant Genomics Research. , 2007, 406, 437-458.		27
28	Regulation of metabolic networks by small molecule metabolites. BMC Bioinformatics, 2007, 8, 88.	1.2	23
29	Bioinformatics Strategies for the Analysis of Lipids. , 2009, 580, 339-368.		23
30	varDB: a pathogen-specific sequence database of protein families involved in antigenic variation. Bioinformatics, 2008, 24, 2564-2565.	1.8	18
31	Extraction of phylogenetic network modules from prokayrote metabolic pathways. Genome Informatics, 2004, 15, 249-58.	0.4	12
32	Pharmacoepidemiological characterization of drug-induced adverse reaction clusters towards understanding of their mechanisms. Computational Biology and Chemistry, 2014, 50, 50-59.	1.1	10
33	Discriminating the reaction types of plant type III polyketide synthases. Bioinformatics, 2017, 33, 1937-1943.	1.8	7
34	varDB: A database of antigenic variant sequencesâ€"Current status and future prospects. Acta Tropica, 2010, 114, 144-151.	0.9	5
35	Virus proteins similar to human proteins as possible disturbance on human pathways. Systems and Synthetic Biology, 2014, 8, 283-295.	1.0	2
36	MUCHA: multiple chemical alignment algorithm to identify building block substructures of orphan secondary metabolites. BMC Bioinformatics, 2011, 12, S1.	1.2	1

#	Article	IF	Citations
37	Revealing phenotype-associated functional differences by genome-wide scan of ancient haplotype blocks. PLoS ONE, 2017, 12, e0176530.	1.1	0