Susumu Goto

List of Publications by Year
in descending order

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	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
2	Taxon Richness of â€œMegaviridaeâ€•Exceeds those of Bacteria and Archaea in the Ocean. Microbes and Environments, 2018, 33, 162-171.	0.7	83
3	Discriminating the reaction types of plant type III polyketide synthases. Bioinformatics, 2017, 33, 1937-1943.	1.8	7
4	ViPTree: the viral proteomic tree server. Bioinformatics, 2017, 33, 2379-2380.	1.8	415
5	Environmental Viral Genomes Shed New Light on Virus-Host Interactions in the Ocean. MSphere, 2017, 2, .	1.3	114
6	Typeâ€…III Polyketide Synthases: Functional Classification and Phylogenomics. ChemBioChem, 2017, 18, 50-65.	1.3	104
7	Revealing phenotype-associated functional differences by genome-wide scan of ancient haplotype blocks. PLoS ONE, 2017, 12, e0176530.	1.1	0
8	Linking Virus Genomes with Host Taxonomy. Viruses, 2016, 8, 66.	1.5	295
9	An automated system for evaluation of the potential functionome: MAPLE version 2.1.0. DNA Research, 2016, 23, 467-475.	1.5	66
10	DINIES: drugâ€“target interaction network inference engine based on supervised analysis. Nucleic Acids Research, 2014, 42, W39-W45.	6.5	97
11	Data, information, knowledge and principle: back to metabolism in KEGG. Nucleic Acids Research, 2014, 42, D199-D205.	6.5	2,846
12	Virus proteins similar to human proteins as possible disturbance on human pathways. Systems and Synthetic Biology, 2014, 8, 283-295.	1.0	2
13	Pharmacoepidemiological characterization of drug-induced adverse reaction clusters towards understanding of their mechanisms. Computational Biology and Chemistry, 2014, 50, 50-59.	1.1	10
14	Modular Architecture of Metabolic Pathways Revealed by Conserved Sequences of Reactions. Journal of Chemical Information and Modeling, 2013, 53, 613-622.	2.5	73
15	Drug target prediction using adverse event report systems: a pharmacogenomic approach. Bioinformatics, 2012, 28, i611-i618.	1.8	107
16	KEGG for integration and interpretation of large-scale molecular data sets. Nucleic Acids Research, 2012, 40, D109-D114.	6.5	4,174
17	Evaluation method for the potential functionome harbored in the genome and metagenome. BMC Genomics, 2012, 13, 699.	1.2	65
18	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

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19	MUCHA: multiple chemical alignment algorithm to identify building block substructures of orphan secondary metabolites. BMC Bioinformatics, 2011, 12, S1.	1.2	1
20	SIMCOMP/SUBCOMP: chemical structure search servers for network analyses. Nucleic Acids Research, 2010, 38, W652-W656.	6.5	125
21	KEGG for representation and analysis of molecular networks involving diseases and drugs. Nucleic Acids Research, 2010, 38, D355-D360.	6.5	1,999
22	Drug-target interaction prediction from chemical, genomic and pharmacological data in an integrated framework. Bioinformatics, 2010, 26, i246-i254.	1.8	396
23	varDB: A database of antigenic variant sequencesâ€"Current status and future prospects. Acta Tropica, 2010, 114, 144-151.	0.9	5
24	Bioinformatics Strategies for the Analysis of Lipids. , 2009, 580, 339-368.		23
25	varDB: a pathogen-specific sequence database of protein families involved in antigenic variation. Bioinformatics, 2008, 24, 2564-2565.	1.8	18
26	KEGG for linking genomes to life and the environment. Nucleic Acids Research, 2007, 36, D480-D484.	6.5	5,451
27	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
28	Prediction of missing enzyme genes in a bacterial metabolic network. FEBS Journal, 2007, 274, 2262-2273.	2.2	30
29	Regulation of metabolic networks by small molecule metabolites. BMC Bioinformatics, 2007, 8, 88.	1.2	23
30	KEGG Bioinformatics Resource for Plant Genomics Research. , 2007, 406, 437-458.		27
31	Extraction of phylogenetic network modules from the metabolic network. BMC Bioinformatics, 2006, 7, 130.	1.2	44
32	Effects of post-electrophoretic analysis on variance in gel-based proteomics. Expert Review of Proteomics, 2006, 3, 129-142.	1.3	36
33	The KEGG resource for deciphering the genome. Nucleic Acids Research, 2004, 32, 277D-280.	6.5	4,093
34	Extraction of phylogenetic network modules from prokayrote metabolic pathways. Genome Informatics, 2004, 15, 249-58.	0.4	12
35	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
36	The KEGG databases at GenomeNet. Nucleic Acids Research, 2002, 30, 42-46.	6.5	1,202

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37	LIGAND: database of chemical compounds and reactions in biological pathways. Nucleic Acids Research, 2002, 30, 402-404.	6.5	255