

# Milton H Saier Jr

## List of Publications by Year in descending order

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370  
papers

25,807  
citations

6233

80  
h-index

9311

143  
g-index

383  
all docs

383  
docs citations

383  
times ranked

20309  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparative Analyses of the Transport Proteins Encoded within the Genomes of nine <i>Bifidobacterium</i> Species. <i>Microbial Physiology</i> , 2022, 32, 30-44.	1.1	4
2	Insertion Sequence (IS) Element-Mediated Activating Mutations of the Cryptic Aromatic $\beta$ -Glucoside Utilization (BglGFB) Operon Are Promoted by the Anti-Terminator Protein (BglG) in <i>Escherichia coli</i> . <i>International Journal of Molecular Sciences</i> , 2022, 23, 1505.	1.8	2
3	Discovery and Characterization of the Phospholemman/SIMP/Vioporin Superfamily. <i>Microbial Physiology</i> , 2022, 32, 83-94.	1.1	0
4	A systems approach discovers the role and characteristics of seven LysR type transcription factors in <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2022, 12, 7274.	1.6	5
5	The Transporter Classification Database (TCDB): 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D461-D467.	6.5	192
6	Gut <i>Bacteroides</i> species in health and disease. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	383
7	Comparative population genomic analyses of transporters within the Asgard archaeal superphylum. <i>PLoS ONE</i> , 2021, 16, e0247806.	1.1	5
8	The Protein Interactome of Glycolysis in <i>Escherichia coli</i> . <i>Proteomes</i> , 2021, 9, 16.	1.7	3
9	Identification of a transcription factor, PunR, that regulates the purine and purine nucleoside transporter punC in <i>E. coli</i> . <i>Communications Biology</i> , 2021, 4, 991.	2.0	13
10	The SARS-Coronavirus Infection Cycle: A Survey of Viral Membrane Proteins, Their Functional Interactions and Pathogenesis. <i>International Journal of Molecular Sciences</i> , 2021, 22, 1308.	1.8	83
11	Protein-Protein Interactions in the Cytoplasmic Membrane of <i>Escherichia coli</i> : Influence of the Overexpression of Diverse Transporter-Encoding Genes on the Activities of PTS Sugar Uptake Systems. <i>Microbial Physiology</i> , 2020, 30, 36-49.	1.1	1
12	Comparative Genomics of the Transport Proteins of Ten <i>Lactobacillus</i> Strains. <i>Genes</i> , 2020, 11, 1234.	1.0	11
13	Systems Biology Analysis Reveals Eight SLC22 Transporter Subgroups, Including OATs, OCTs, and OCTNs. <i>International Journal of Molecular Sciences</i> , 2020, 21, 1791.	1.8	44
14	Expansion of the Major Facilitator Superfamily (MFS) to include novel transporters as well as transmembrane-acting enzymes. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2020, 1862, 183277.	1.4	40
15	Expansion of the Transporter-Opsonin-G protein-coupled receptor superfamily with five new protein families. <i>PLoS ONE</i> , 2020, 15, e0231085.	1.1	11
16	A Riboflavin Transporter in <i>Bdellovibrio exovorus</i> JSS. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2019, 29, 27-34.	1.0	3
17	Cryo-EM structure of OSCA1.2 from <i>Oryza sativa</i> elucidates the mechanical basis of potential membrane hyperosmolality gating. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 14309-14318.	3.3	71
18	Bacterial and Archaeal Cell Membranes. , 2019, , 333-333.		1

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19	Understanding the Genetic Code. <i>Journal of Bacteriology</i> , 2019, 201, .	1.0	15
20	Comparative genomics of the transportome of Ten <i>Treponema</i> species. <i>Microbial Pathogenesis</i> , 2019, 132, 87-99.	1.3	12
21	Protein:Protein interactions in the cytoplasmic membrane apparently influencing sugar transport and phosphorylation activities of the <i>e. coli</i> phosphotransferase system. <i>PLoS ONE</i> , 2019, 14, e0219332.	1.1	6
22	Title is missing!. , 2019, 14, e0219332.		0
23	Title is missing!. , 2019, 14, e0219332.		0
24	Title is missing!. , 2019, 14, e0219332.		0
25	Title is missing!. , 2019, 14, e0219332.		0
26	The Nitrogen Regulatory PII Protein (GlnB) and <i>N</i> -Acetylglucosamine 6-Phosphate Epimerase (NanE) Allosterically Activate Glucosamine 6-Phosphate Deaminase (NagB) in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2018, 200, .	1.0	19
27	Comparative genomics of transport proteins in seven <i>Bacteroides</i> species. <i>PLoS ONE</i> , 2018, 13, e0208151.	1.1	34
28	The uridylyltransferase GlnD and tRNA modification GTPase MnmE allosterically control <i>Escherichia coli</i> folylpoly- $\beta$ -glutamate synthase FolC. <i>Journal of Biological Chemistry</i> , 2018, 293, 15725-15732.	1.6	11
29	Bioinformatic characterization of the Anoctamin Superfamily of Ca <sup>2+</sup> -activated ion channels and lipid scramblases. <i>PLoS ONE</i> , 2018, 13, e0192851.	1.1	52
30	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.	9.4	110
31	Characterization of the Tetraspan Junctional Complex (4JC) superfamily. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017, 1859, 402-414.	1.4	3
32	The phosphocarrier protein HPr of the bacterial phosphotransferase system globally regulates energy metabolism by directly interacting with multiple enzymes in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2017, 292, 14250-14257.	1.6	42
33	Comparative genomics of transport proteins in probiotic and pathogenic <i>Escherichia coli</i> and <i>Salmonella enterica</i> strains. <i>Microbial Pathogenesis</i> , 2017, 107, 106-115.	1.3	21
34	Comparative genomic analyses of transport proteins encoded within the red algae <i>Chondrus crispus</i> , <i>Galdieria sulphuraria</i> , and <i>Cyanidioschyzon merolae</i> 11. <i>Journal of Phycology</i> , 2017, 53, 503-521.	1.0	7
35	Difference distance map data of alternative crystal forms of UlaA. <i>Data in Brief</i> , 2017, 10, 198-201.	0.5	2
36	Comparative Analyses of Transport Proteins Encoded within the Genomes of <i>Bdellovibrio bacteriovorus</i> HD100 and <i>Bdellovibrio exovorus</i> JSS. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2017, 27, 332-349.	1.0	6

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37	The Membrane Attack Complex/Perforin Superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2017, 27, 252-267.	1.0	23
38	Science, Innovation and the Future of Humanity. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2017, 27, 128-132.	1.0	1
39	Hopping into a hot seat: Role of DNA structural features on IS5-mediated gene activation and inactivation under stress. <i>PLoS ONE</i> , 2017, 12, e0180156.	1.1	15
40	Transposon-mediated directed mutation in bacteria and eukaryotes. <i>Frontiers in Bioscience - Landmark</i> , 2017, 22, 1458-1468.	3.0	11
41	Environment-directed activation of the <i>Escherichia coli</i> flhDC operon by transposons. <i>Microbiology (United Kingdom)</i> , 2017, 163, 554-569.	0.7	17
42	Properties and Phylogeny of 76 Families of Bacterial and Eukaryotic Organellar Outer Membrane Pore-Forming Proteins. <i>PLoS ONE</i> , 2016, 11, e0152733.	1.1	22
43	Transposon-mediated activation of the <i>Escherichia coli</i> glpFK operon is inhibited by specific DNA-binding proteins: Implications for stress-induced transposition events. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2016, 793-794, 22-31.	0.4	9
44	The V-motifs facilitate the substrate capturing step of the PTS elevator mechanism. <i>Journal of Structural Biology</i> , 2016, 196, 496-502.	1.3	2
45	Analysis of 58 Families of Holins Using a Novel Program, PhyST. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2016, 26, 381-388.	1.0	3
46	Transport protein evolution deduced from analysis of sequence, topology and structure. <i>Current Opinion in Structural Biology</i> , 2016, 38, 9-17.	2.6	43
47	Comparative analyses of transport proteins encoded within the genomes of <i>Leptospira</i> species. <i>Microbial Pathogenesis</i> , 2016, 98, 118-131.	1.3	10
48	Time to Stop Holding the Elevator: A New Piece of the Transport Protein Mechanism Puzzle. <i>Structure</i> , 2016, 24, 845-846.	1.6	2
49	The Transporter Classification Database (TCDB): recent advances. <i>Nucleic Acids Research</i> , 2016, 44, D372-D379.	6.5	711
50	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the <i>Journal of Biological Databases and Curation</i> , 2015, 2015, bav063.	1.4	8
51	Conserved movement of TMS11 between occluded conformations of LacY and XylE of the major facilitator superfamily suggests a similar hinge-like mechanism. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 735-745.	1.5	5
52	The LysE Superfamily of Transport Proteins Involved in Cell Physiology and Pathogenesis. <i>PLoS ONE</i> , 2015, 10, e0137184.	1.1	25
53	Evolutionary Analysis and Classification of OATs, OCTs, OCTNs, and Other SLC22 Transporters: Structure-Function Implications and Analysis of Sequence Motifs. <i>PLoS ONE</i> , 2015, 10, e0140569.	1.1	63
54	Control of Transposon-Mediated Directed Mutation by the <i>Escherichia coli</i> Phosphoenolpyruvate: Sugar Phosphotransferase System. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2015, 25, 226-233.	1.0	5

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55	The Bacterial Phosphotransferase System: New Frontiers 50 Years after Its Discovery. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2015, 25, 73-78.	1.0	70
56	Comparative Genomic Analysis of Integral Membrane Transport Proteins in Ciliates. <i>Journal of Eukaryotic Microbiology</i> , 2015, 62, 167-187.	0.8	4
57	Comparative genomic analyses of transport proteins encoded within the genomes of <i>Leptospira</i> species. <i>Microbial Pathogenesis</i> , 2015, 88, 52-64.	1.3	7
58	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. <i>Briefings in Bioinformatics</i> , 2015, 16, 865-872.	3.2	6
59	Key challenges for the creation and maintenance of specialist protein resources. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 1005-1013.	1.5	13
60	Holins in Bacteria, Eukaryotes, and Archaea: Multifunctional Xenologues with Potential Biotechnological and Biomedical Applications. <i>Journal of Bacteriology</i> , 2015, 197, 7-17.	1.0	105
61	Overall Transport Capabilities of <i>Bacillus subtilis</i> . , 2014, , 111-128.		7
62	Regulation of <i>crp</i> Gene Expression by the Catabolite Repressor/Activator, Cra, in <i>Escherichia coli</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2014, 24, 135-141.	1.0	23
63	Establishing homology between mitochondrial calcium uniporters, prokaryotic magnesium channels and chlamydial IncA proteins. <i>Microbiology (United Kingdom)</i> , 2014, 160, 1679-1689.	0.7	6
64	Transposon-mediated directed mutation controlled by DNA binding proteins in <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2014, 5, 390.	1.5	10
65	The Transporter Classification Database. <i>Nucleic Acids Research</i> , 2014, 42, D251-D258.	6.5	437
66	Reliability of Nine Programs of Topological Predictions and Their Application to Integral Membrane Channel and Carrier Proteins. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2014, 24, 161-190.	1.0	19
67	Psychobiotics and Their Involvement in Mental Health. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2014, 24, 211-214.	1.0	16
68	Major Facilitator Superfamily (MFS) evolved without 3-transmembrane segment unit rearrangements. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1162-3.	3.3	11
69	The involvement of transport proteins in transcriptional and metabolic regulation. <i>Current Opinion in Microbiology</i> , 2014, 18, 8-15.	2.3	45
70	Major Facilitator Superfamily Porters, LacY, FucP and XylE of <i>Escherichia coli</i> Appear to Have Evolved Positionally Dissimilar Catalytic Residues without Rearrangement of 3-TMS Repeat Units. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2014, 24, 82-90.	1.0	13
71	Bioinformatic analyses of integral membrane transport proteins encoded within the genome of the planctomycetes species, <i>Rhodopirellula baltica</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014, 1838, 193-215.	1.4	14
72	Evolutionary relationship between 5+5 and 7+7 inverted repeat folds within the amino acid-polyamine-organocation superfamily. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 336-346.	1.5	48

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73	Expansion of the APC superfamily of secondary carriers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2797-2811.	1.5	82
74	Conformational Transition Pathway in the Inhibitor Binding Process of Human Monoacylglycerol Lipase. <i>Protein Journal</i> , 2014, 33, 503-511.	0.7	5
75	Transport proteins promoting <i>Escherichia coli</i> pathogenesis. <i>Microbial Pathogenesis</i> , 2014, 71-72, 41-55.	1.3	20
76	Genetic Implication of a Novel Thiamine Transporter in Human Hypertension. <i>Journal of the American College of Cardiology</i> , 2014, 63, 1542-1555.	1.2	36
77	Microcompartments and Protein Machines in Prokaryotes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013, 23, 243-269.	1.0	28
78	Evolutionary relationships of ATP-Binding Cassette (ABC) uptake porters. <i>BMC Microbiology</i> , 2013, 13, 98.	1.3	30
79	Membranous Organelles in Bacteria. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013, 23, 5-12.	1.0	13
80	Comparative genomics of transport proteins in developmental bacteria: <i>Myxococcus xanthus</i> and <i>Streptomyces coelicolor</i> . <i>BMC Microbiology</i> , 2013, 13, 279.	1.3	21
81	Topological and phylogenetic analyses of bacterial holin families and superfamilies. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2654-2671.	1.4	61
82	Subcellular Localization and Logistics of Integral Membrane Protein Biogenesis in <i>Escherichia coli</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013, 23, 24-34.	1.0	8
83	The transporter "opsin" <sc>G</sc> protein-coupled receptor (<sc>TOG</sc>) superfamily. <i>FEBS Journal</i> , 2013, 280, 5780-5800.	2.2	46
84	Transposon Mutagenesis in Disease, Drug Discovery, and Bacterial Evolution. , 2013, , 59-77.		2
85	Lipid dependencies, biogenesis and cytoplasmic micellar forms of integral membrane sugar transport proteins of the bacterial phosphotransferase system. <i>Microbiology (United Kingdom)</i> , 2013, 159, 2213-2224.	0.7	13
86	Bioinformatic Analyses of Bacterial Mercury Ion (Hg <sup>2+</sup> ) Transporters. <i>Water, Air, and Soil Pollution</i> , 2012, 223, 4443-4457.	1.1	9
87	Genetic Engineering of the Phosphocarrier Protein NPr of the <i>Escherichia coli</i> Phosphotransferase System Selectively Improves Sugar Uptake Activity. <i>Journal of Biological Chemistry</i> , 2012, 287, 29931-29939.	1.6	4
88	Comparative analyses of transport proteins encoded within the genomes of <i>Mycobacterium tuberculosis</i> and <i>Mycobacterium leprae</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 776-797.	1.4	24
89	Bioinformatic characterization of the 4-Toluene Sulfonate Uptake Permease (TSUP) family of transmembrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 703-717.	1.4	20
90	The Amino Acid-Polyamine-Organocation Superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2012, 22, 105-113.	1.0	97

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91	Transformative research: definitions, approaches and consequences. <i>Theory in Biosciences</i> , 2012, 131, 117-123.	0.6	23
92	The major facilitator superfamily (MFS) revisited. <i>FEBS Journal</i> , 2012, 279, 2022-2035.	2.2	402
93	BioV Suite – a collection of programs for the study of transport protein evolution. <i>FEBS Journal</i> , 2012, 279, 2036-2046.	2.2	55
94	Identifying Relevant Data for a Biological Database: Handcrafted Rules versus Machine Learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011, 8, 851-857.	1.9	10
95	Pathways of transport protein evolution: recent advances. <i>Biological Chemistry</i> , 2011, 392, 5-12.	1.2	24
96	Transposon-Mediated Adaptive and Directed Mutations and Their Potential Evolutionary Benefits. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 21, 59-70.	1.0	37
97	Comparative genomics of the pathogenic ciliate <i>Ichthyophthirius multifiliis</i> , its free-living relatives and a host species provide insights into adoption of a parasitic lifestyle and prospects for disease control. <i>Genome Biology</i> , 2011, 12, R100.	13.9	102
98	Thermodynamic perspectives on genetic instructions, the laws of biology and diseased states. <i>Comptes Rendus - Biologies</i> , 2011, 334, 1-5.	0.1	11
99	Biophysical Studies of the Membrane-Embedded and Cytoplasmic Forms of the Glucose-Specific Enzyme II of the <i>E. coli</i> Phosphotransferase System (PTS). <i>PLoS ONE</i> , 2011, 6, e24088.	1.1	10
100	Rebuttal to “A Vaccine Against Arrogance” by W. M. Briggs, W. Soon, D. Legates, and R. M. Carter. <i>Water, Air, and Soil Pollution</i> , 2011, 220, 7-8.	1.1	0
101	Evolution of the Oligopeptide Transporter Family. <i>Journal of Membrane Biology</i> , 2011, 240, 89-110.	1.0	43
102	Bioinformatic Characterization of the Trimeric Intracellular Cation-Specific Channel Protein Family. <i>Journal of Membrane Biology</i> , 2011, 241, 77-101.	1.0	17
103	Did Adaptive and Directed Mutation Evolve to Accelerate Stress-Induced Evolutionary Change?. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 21, 5-7.	1.0	4
104	Phylogenetic Characterization of Transport Protein Superfamilies: Superiority of SuperfamilyTree Programs over Those Based on Multiple Alignments. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011, 21, 83-96.	1.0	44
105	A new direction for directed mutation?. <i>Trends in Evolutionary Biology</i> , 2011, 3, 3.	0.4	1
106	The P-Type ATPase Superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010, 19, 5-104.	1.0	103
107	Defense Against Cannibalism: The Sdpl Family of Bacterial Immunity/Signal Transduction Proteins. <i>Journal of Membrane Biology</i> , 2010, 235, 145-162.	1.0	10
108	Water Crises. <i>Water, Air, and Soil Pollution</i> , 2010, 205, 27-28.	1.1	0

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109	Goinâ€™ Fishinâ€™. <i>Water, Air, and Soil Pollution</i> , 2010, 205, 29-30.	1.1	0
110	Desertification and Migration. <i>Water, Air, and Soil Pollution</i> , 2010, 205, 31-32.	1.1	3
111	Our Human Population and the Planet. <i>Water, Air, and Soil Pollution</i> , 2010, 205, 33-33.	1.1	0
112	Real Sustainability. <i>Water, Air, and Soil Pollution</i> , 2010, 205, 67-68.	1.1	0
113	Education for Humanity. <i>Water, Air, and Soil Pollution</i> , 2010, 206, 1-2.	1.1	5
114	Is Nuclear Energy the Solution?. <i>Water, Air, and Soil Pollution</i> , 2010, 208, 1-3.	1.1	0
115	UN Climate Change Conference, Copenhagen 2009: Whatever Works?. <i>Water, Air, and Soil Pollution</i> , 2010, 207, 1-3.	1.1	3
116	The Crisis in Haiti, 2010: Whatâ€™s to be done?. <i>Water, Air, and Soil Pollution</i> , 2010, 212, 1-2.	1.1	0
117	Animal Ca <sup>2+</sup> release-activated Ca <sup>2+</sup> (CRAC) channels appear to be homologous to and derived from the ubiquitous cation diffusion facilitators. <i>BMC Research Notes</i> , 2010, 3, 158.	0.6	17
118	The Bacterial Intimins and Invasins: A Large and Novel Family of Secreted Proteins. <i>PLoS ONE</i> , 2010, 5, e14403.	1.1	50
119	The Autoinducer-2 Exporter Superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010, 18, 195-205.	1.0	19
120	Functional Promiscuity of Homologues of the Bacterial ArsA ATPases. <i>International Journal of Microbiology</i> , 2010, 2010, 1-21.	0.9	37
121	Precise Excision of IS <i>5</i> from the Intergenic Region between the <i>fucPIK</i> and the <i>fucAO</i> Operons and Mutational Control of <i>fucPIK</i> Operon Expression in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2010, 192, 2013-2019.	1.0	19
122	Bacterial Adaptor Membrane Fusion Proteins and the Structurally Dissimilar Outer Membrane Auxiliary Proteins Have Exchanged Central Domains in $\pm$ -Proteobacteria. <i>International Journal of Microbiology</i> , 2010, 2010, 1-5.	0.9	7
123	Multidrug Resistance: Phylogenetic Characterization of Superfamilies of Secondary Carriers that Include Drug Exporters. <i>Methods in Molecular Biology</i> , 2010, 637, 47-64.	0.4	50
124	Molecular archeological studies of transmembrane transport systems. , 2010, , 29-43.		1
125	Bioinformatic Analyses of Transmembrane Transport: Novel Software for Deducing Protein Phylogeny, Topology, and Evolution. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009, 17, 163-176.	1.0	47
126	The Transporter Classification Database: recent advances. <i>Nucleic Acids Research</i> , 2009, 37, D274-D278.	6.5	391



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127	A Novel Mechanism of Transposon-Mediated Gene Activation. <i>PLoS Genetics</i> , 2009, 5, e1000689.	1.5	51
128	Watchdogs and Whistleblowers. <i>Water, Air, and Soil Pollution</i> , 2009, 199, 1-2.	1.1	0
129	Global Pollution: How Much Is Too Much?. <i>Water, Air, and Soil Pollution</i> , 2009, 204, 1-3.	1.1	1
130	Comprehensive Analyses of Transport Proteins Encoded Within the Genome of <i>Aromatoleum aromaticum</i> Strain EbN1. <i>Journal of Membrane Biology</i> , 2009, 229, 53-90.	1.0	11
131	Bioinformatic Characterization of P-Type ATPases Encoded Within the Fully Sequenced Genomes of 26 Eukaryotes. <i>Journal of Membrane Biology</i> , 2009, 229, 115-130.	1.0	79
132	Membrane Porters of ATP-Binding Cassette Transport Systems Are Polyphyletic. <i>Journal of Membrane Biology</i> , 2009, 231, 1-9.	1.0	75
133	A mechanism of transposon-mediated directed mutation. <i>Molecular Microbiology</i> , 2009, 74, 29-43.	1.2	32
134	The $\beta$ -barrel finder (BBF) program, allowing identification of outer membrane $\beta$ -barrel proteins encoded within prokaryotic genomes. <i>Protein Science</i> , 2009, 11, 2196-2207.	3.1	94
135	Are Megacities Sustainable?. <i>Water, Air, and Soil Pollution</i> , 2008, 191, 1-3.	1.1	12
136	Characterization of the <i>E. coli</i> glucose permease fused to the maltose-binding protein. <i>Journal of Basic Microbiology</i> , 2008, 48, 3-9.	1.8	5
137	A stochastic automaton shows how enzyme assemblies may contribute to metabolic efficiency. <i>BMC Systems Biology</i> , 2008, 2, 27.	3.0	30
138	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008, 9, R158.	3.8	104
139	Protein Secretion and Membrane Insertion Systems in Bacteria and Eukaryotic Organelles. <i>Advances in Applied Microbiology</i> , 2008, 65, 141-197.	1.3	20
140	The Bacterial Chromosome. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2008, 43, 89-134.	2.3	32
141	The phagosomal nutrient transporter (Pht) family. <i>Microbiology (United Kingdom)</i> , 2008, 154, 42-53.	0.7	37
142	Learning to Find Relevant Biological Articles without Negative Training Examples. <i>Lecture Notes in Computer Science</i> , 2008, , 202-213.	1.0	10
143	Functional Taxonomy of Bacterial Hyperstructures. <i>Microbiology and Molecular Biology Reviews</i> , 2007, 71, 230-253.	2.9	79
144	Active Transport in Communication, Protection and Nutrition. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2007, 12, 161-164.	1.0	7

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145	In vitro Interconversion of the Soluble and Membrane- Integrated Forms of the <i>Escherichia coli</i> Glucose Enzyme II of the Phosphoenolpyruvate-Dependent Sugar-Transporting Phosphotransferase System. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2007, 12, 263-268.	1.0	4
146	Comprehensive analysis of transport proteins encoded within the genome of <i>Bdellovibrio bacteriovorus</i> . <i>Genomics</i> , 2007, 90, 424-446.	1.3	28
147	Transport capabilities of eleven gram-positive bacteria: Comparative genomic analyses. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 1342-1366.	1.4	106
148	Evolutionary origins of members of a superfamily of integral membrane cytochrome c biogenesis proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 2164-2181.	1.4	41
149	Toward a Hyperstructure Taxonomy. <i>Annual Review of Microbiology</i> , 2007, 61, 309-329.	2.9	63
150	The bile/arsenite/riboflavin transporter (BART) superfamily. <i>FEBS Journal</i> , 2007, 274, 612-629.	2.2	65
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