

Milton H Saier Jr

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

365
papers

21,300
citations

77
h-index

133
g-index

383
ext. papers

23,496
ext. citations

4.2
avg, IF

7.1
L-index

#	Paper	IF	Citations
365	Discovery and Characterization of the Phospholemman/SIMP/Vioporin Superfamily.. <i>Microbial Physiology</i> , 2022 , 1-12	0.8	
364	A systems approach discovers the role and characteristics of seven LysR type transcription factors in Escherichia coli.. <i>Scientific Reports</i> , 2022 , 12, 7274	4.9	
363	Comparative population genomic analyses of transporters within the Asgard archaeal superphylum. <i>PLoS ONE</i> , 2021 , 16, e0247806	3.7	0
362	The Protein Interactome of Glycolysis in. <i>Proteomes</i> , 2021 , 9,	4.6	2
361	The Transporter Classification Database (TCDB): 2021 update. <i>Nucleic Acids Research</i> , 2021 , 49, D461-D467.1	7.1	32
360	Gut species in health and disease. <i>Gut Microbes</i> , 2021 , 13, 1-20	8.8	57
359	Identification of a transcription factor, PunR, that regulates the purine and purine nucleoside transporter punC in E. coli. <i>Communications Biology</i> , 2021 , 4, 991	6.7	5
358	Comparative Analyses of the Transport Proteins Encoded within the Genomes of nine Bifidobacterium Species. <i>Microbial Physiology</i> , 2021 , 1-15	0.8	0
357	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,	6.3	35
356	Systems Biology Analysis Reveals Eight SLC22 Transporter Subgroups, Including OATs, OCTs, and OCTNs. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	23
355	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	3.8	22
354	Protein-Protein Interactions in the Cytoplasmic Membrane of Escherichia coli: 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	0.8	
353	Comparative Genomics of the Transport Proteins of Ten Strains. <i>Genes</i> , 2020 , 11,	4.2	3
352	Expansion of the Transporter-Opsin-G protein-coupled receptor superfamily with five new protein families. <i>PLoS ONE</i> , 2020 , 15, e0231085	3.7	8
351	A Riboflavin Transporter in Bdellovibrio exovorous JSS. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2019 , 29, 27-34	0.9	3
350	Cryo-EM structure of OSCA1.2 from 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	11.5	33
349	Bacterial and Archaeal Cell Membranes 2019 , 333-333		

348	Understanding the Genetic Code. <i>Journal of Bacteriology</i> , 2019 , 201,	3.5	5
347	Comparative genomics of the transportome of Ten <i>Treponema</i> species. <i>Microbial Pathogenesis</i> , 2019 , 132, 87-99	3.8	7
346	Protein:Protein interactions in the cytoplasmic membrane apparently influencing sugar transport and phosphorylation activities of the e. coli phosphotransferase system. <i>PLoS ONE</i> , 2019 , 14, e0219332	3.7	5
345	Protein:Protein interactions in the cytoplasmic membrane apparently influencing sugar transport and phosphorylation activities of the e. coli phosphotransferase system 2019 , 14, e0219332		
344	Protein:Protein interactions in the cytoplasmic membrane apparently influencing sugar transport and phosphorylation activities of the e. coli phosphotransferase system 2019 , 14, e0219332		
343	Protein:Protein interactions in the cytoplasmic membrane apparently influencing sugar transport and phosphorylation activities of the e. coli phosphotransferase system 2019 , 14, e0219332		
342	Protein:Protein interactions in the cytoplasmic membrane apparently influencing sugar transport and phosphorylation activities of the e. coli phosphotransferase system 2019 , 14, e0219332		
341	The uridylyltransferase GlnD and tRNA modification GTPase MnmE allosterically control fohlypoly- γ -glutamate synthase FolC. <i>Journal of Biological Chemistry</i> , 2018 , 293, 15725-15732	5.4	7
340	Bioinformatic characterization of the Anoctamin Superfamily of Ca ²⁺ -activated ion channels and lipid scramblases. <i>PLoS ONE</i> , 2018 , 13, e0192851	3.7	29
339	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018 , 36, 103-112	44.5	68
338	The Nitrogen Regulatory PII Protein (GlnB) and -Acetylglucosamine 6-Phosphate Epimerase (NanE) Allosterically Activate Glucosamine 6-Phosphate Deaminase (NagB) in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	9
337	Comparative genomics of transport proteins in seven <i>Bacteroides</i> species. <i>PLoS ONE</i> , 2018 , 13, e0208151	3.7	21
336	Characterization of the Tetraspan Junctional Complex (4JC) superfamily. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2017 , 1859, 402-414	3.8	3
335	The phosphocarrier protein HPr of the bacterial phosphotransferase system globally regulates energy metabolism by directly interacting with multiple enzymes in. <i>Journal of Biological Chemistry</i> , 2017 , 292, 14250-14257	5.4	20
334	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	3.8	14
333	Comparative genomic analyses of transport proteins encoded within the red algae <i>Chondrus crispus</i> , <i>Galdieria sulphuraria</i> , and <i>Cyanidioschyzon merolae</i> . <i>Journal of Phycology</i> , 2017 , 53, 503-521	3	6
332	Difference distance map data of alternative crystal forms of UlaA. <i>Data in Brief</i> , 2017 , 10, 198-201	1.2	2
331	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	3.7	6

330	Transposon-mediated directed mutation in bacteria and eukaryotes. <i>Frontiers in Bioscience - Landmark</i> , 2017 , 22, 1458-1468	2.8	7
329	Comparative Analyses of Transport Proteins Encoded within the Genomes of Bdellovibrio bacteriovorus HD100 and Bdellovibrio exovorus JSS. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2017 , 27, 332-349	0.9	5
328	The Membrane Attack Complex/Perforin Superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2017 , 27, 252-267	0.9	16
327	Environment-directed activation of the Escherichia coli flhDC operon by transposons. <i>Microbiology (United Kingdom)</i> , 2017 , 163, 554-569	2.9	8
326	Transport protein evolution deduced from analysis of sequence, topology and structure. <i>Current Opinion in Structural Biology</i> , 2016 , 38, 9-17	8.1	32
325	Comparative analyses of transport proteins encoded within the genomes of Leptospira species. <i>Microbial Pathogenesis</i> , 2016 , 98, 118-31	3.8	4
324	Time to Stop Holding the Elevator: A New Piece of the Transport Protein Mechanism Puzzle. <i>Structure</i> , 2016 , 24, 845-6	5.2	2
323	The Transporter Classification Database (TCDB): recent advances. <i>Nucleic Acids Research</i> , 2016 , 44, D3722-9	20.1	434
322	Properties and Phylogeny of 76 Families of Bacterial and Eukaryotic Organellar Outer Membrane Pore-Forming Proteins. <i>PLoS ONE</i> , 2016 , 11, e0152733	3.7	16
321	Transposon-mediated activation of the Escherichia coli 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	3.3	6
320	The V-motifs facilitate the substrate capturing step of the PTS elevator mechanism. <i>Journal of Structural Biology</i> , 2016 , 196, 496-502	3.4	2
319	Analysis of 58 Families of Holins Using a Novel Program, PhyST. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2016 , 26, 381-388	0.9	3
318	Comparative genomic analysis of integral membrane transport proteins in ciliates. <i>Journal of Eukaryotic Microbiology</i> , 2015 , 62, 167-87	3.6	2
317	Comparative genomic analyses of transport proteins encoded within the genomes of Leptospira species. <i>Microbial Pathogenesis</i> , 2015 , 88, 52-64	3.8	7
316	The complexity, challenges and benefits of comparing two transporter classification systems in TCDB and Pfam. <i>Briefings in Bioinformatics</i> , 2015 , 16, 865-72	13.4	5
315	Holins in bacteria, eukaryotes, and archaea: multifunctional xenologues with potential biotechnological and biomedical applications. <i>Journal of Bacteriology</i> , 2015 , 197, 7-17	3.5	64
314	Lactic Acid Bacteria 2015 , 55-79		
313	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav063	5	5

312	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, 735-45	4.2	5
311	The LysE Superfamily of Transport Proteins Involved in Cell Physiology and Pathogenesis. <i>PLoS ONE</i> , 2015 , 10, e0137184	3.7	18
310	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	3.7	53
309	Control of Transposon-Mediated Directed Mutation by the Escherichia coli Phosphoenolpyruvate: Sugar Phosphotransferase System. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2015 , 25, 226-33	0.9	4
308	The Bacterial Phosphotransferase System: New Frontiers 50 Years after Its Discovery. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2015 , 25, 73-8	0.9	43
307	Major facilitator superfamily porters, LacY, FucP and Xyle of Escherichia coli 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	0.9	12
306	Bioinformatic analyses of integral membrane transport proteins encoded within the genome of the planctomycetes species, Rhodopirellula baltica. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2014 , 1838, 193-215	3.8	13
305	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, 336-46	4.2	36
304	Expansion of the APC superfamily of secondary carriers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 2797-811	4.2	53
303	Conformational transition pathway in the inhibitor binding process of human monoacylglycerol lipase. <i>Protein Journal</i> , 2014 , 33, 503-11	3.9	3
302	Transport proteins promoting Escherichia coli pathogenesis. <i>Microbial Pathogenesis</i> , 2014 , 71-72, 41-55	3.8	15
301	Genetic implication of a novel thiamine transporter in human hypertension. <i>Journal of the American College of Cardiology</i> , 2014 , 63, 1542-55	15.1	27
300	Overall Transport Capabilities of Bacillus subtilis 2014 , 111-128		6
299	Regulation of crp gene expression by the catabolite repressor/activator, Cra, in Escherichia coli. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2014 , 24, 135-41	0.9	19
298	Establishing homology between mitochondrial calcium uniporters, prokaryotic magnesium channels and chlamydial IncA proteins. <i>Microbiology (United Kingdom)</i> , 2014 , 160, 1679-1689	2.9	6
297	Transposon-mediated directed mutation controlled by DNA binding proteins in Escherichia coli. <i>Frontiers in Microbiology</i> , 2014 , 5, 390	5.7	7
296	The transporter classification database. <i>Nucleic Acids Research</i> , 2014 , 42, D251-8	20.1	323
295	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, 161-90	0.9	15

294	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	11.5	10
293	The involvement of transport proteins in transcriptional and metabolic regulation. <i>Current Opinion in Microbiology</i> , 2014 , 18, 8-15	7.9	34
292	Microcompartments and protein machines in prokaryotes. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013 , 23, 243-69	0.9	21
291	Evolutionary relationships of ATP-Binding Cassette (ABC) uptake porters. <i>BMC Microbiology</i> , 2013 , 13, 98	4.5	25
290	Membranous organelles in bacteria. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2013 , 23, 5-12	0.9	13
289	Comparative genomics of transport proteins in developmental bacteria: <i>Myxococcus xanthus</i> and <i>Streptomyces coelicolor</i> . <i>BMC Microbiology</i> , 2013 , 13, 279	4.5	17
288	Topological and phylogenetic analyses of bacterial holin families and superfamilies. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 2654-71	3.8	42
287	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	0.9	7
286	Deducing Transport Protein Evolution Based on Sequence, Structure, and Function 2013 , 315-339		1
285	The transporter-opsin-G protein-coupled receptor (TOG) superfamily. <i>FEBS Journal</i> , 2013 , 280, 5780-800	5.7	42
284	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	2.9	8
283	Transposon Mutagenesis in Disease, Drug Discovery, and Bacterial Evolution 2013 , 59-77		1
282	The major facilitator superfamily (MFS) revisited. <i>FEBS Journal</i> , 2012 , 279, 2022-35	5.7	294
281	BioV Suite--a collection of programs for the study of transport protein evolution. <i>FEBS Journal</i> , 2012 , 279, 2036-46	5.7	49
280	Bioinformatic Analyses of Bacterial Mercury Ion (Hg ²⁺) Transporters. <i>Water, Air, and Soil Pollution</i> , 2012 , 223, 4443-4457	2.6	8
279	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, 29931-9	5.4	4
278	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, 776-97	3.8	19
277	Bioinformatic characterization of the 4-Toluene Sulfonate Uptake Permease (TSUP) family of transmembrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012 , 1818, 703-17	3.8	16

276	The amino acid-polyamine-organocation superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2012 , 22, 105-13	0.9	81
275	Transformative research: definitions, approaches and consequences. <i>Theory in Biosciences</i> , 2012 , 131, 117-23	1.3	17
274	Pathways of transport protein evolution: recent advances. <i>Biological Chemistry</i> , 2011 , 392, 5-12	4.5	22
273	Transposon-mediated adaptive and directed mutations and their potential evolutionary benefits. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011 , 21, 59-70	0.9	25
272	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	18.3	89
271	Thermodynamic perspectives on genetic instructions, the laws of biology and diseased states. <i>Comptes Rendus - Biologies</i> , 2011 , 334, 1-5	1.4	4
270	Biophysical studies of the membrane-embedded and cytoplasmic forms of the glucose-specific Enzyme II of the E. coli phosphotransferase system (PTS). <i>PLoS ONE</i> , 2011 , 6, e24088	3.7	6
269	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	2.6	
268	Evolution of the oligopeptide transporter family. <i>Journal of Membrane Biology</i> , 2011 , 240, 89-110	2.3	37
267	Bioinformatic characterization of the trimeric intracellular cation-specific channel protein family. <i>Journal of Membrane Biology</i> , 2011 , 241, 77-101	2.3	14
266	Identifying relevant data for a biological database: handcrafted rules versus machine learning. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 851-7	3	6
265	Did adaptive and directed mutation evolve to accelerate stress-induced evolutionary change?. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2011 , 21, 5-7	0.9	3
264	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	0.9	38
263	A new direction for directed mutation?. <i>Trends in Evolutionary Biology</i> , 2011 , 3, 3		1
262	The bacterial intimins and invasins: a large and novel family of secreted proteins. <i>PLoS ONE</i> , 2010 , 5, e14403	3.7	44
261	The autoinducer-2 exporter superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010 , 18, 195-205	0.9	14
260	Functional Promiscuity of Homologues of the Bacterial ArsA ATPases. <i>International Journal of Microbiology</i> , 2010 , 2010, 187373	3.6	27
259	Precise excision of IS5 from the intergenic region between the fucPIK and the fucAO operons and mutational control of fucPIK operon expression in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2010 , 192, 2013-9	3.5	13

258	Bacterial Adaptor Membrane Fusion Proteins and the Structurally Dissimilar Outer Membrane Auxiliary Proteins Have Exchanged Central Domains in alpha-Proteobacteria. <i>International Journal of Microbiology</i> , 2010 , 2010, 589391	3.6	6
257	The p-type ATPase superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010 , 19, 5-104	0.9	87
256	Defense against cannibalism: the Sdpl family of bacterial immunity/signal transduction proteins. <i>Journal of Membrane Biology</i> , 2010 , 235, 145-62	2.3	8
255	Desertification and Migration. <i>Water, Air, and Soil Pollution</i> , 2010 , 205, 31-32	2.6	2
254	Real Sustainability. <i>Water, Air, and Soil Pollution</i> , 2010 , 205, 67-68	2.6	
253	Education for Humanity. <i>Water, Air, and Soil Pollution</i> , 2010 , 206, 1-2	2.6	2
252	Is Nuclear Energy the Solution?. <i>Water, Air, and Soil Pollution</i> , 2010 , 208, 1-3	2.6	78
251	UN Climate Change Conference, Copenhagen 2009: Whatever Works?. <i>Water, Air, and Soil Pollution</i> , 2010 , 207, 1-3	2.6	3
250	The Crisis in Haiti, 2010: What to be done?. <i>Water, Air, and Soil Pollution</i> , 2010 , 212, 1-2	2.6	78
249	Animal Ca ²⁺ release-activated Ca ²⁺ (CRAC) channels appear to be homologous to and derived from the ubiquitous cation diffusion facilitators. <i>BMC Research Notes</i> , 2010 , 3, 158	2.3	15
248	Multidrug resistance: phylogenetic characterization of superfamilies of secondary carriers that include drug exporters. <i>Methods in Molecular Biology</i> , 2010 , 637, 47-64	1.4	43
247	Molecular archeological studies of transmembrane transport systems 2010 , 29-43		1
246	Bioinformatic analyses of transmembrane transport: novel software for deducing protein phylogeny, topology, and evolution. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2009 , 17, 163-76	0.9	46
245	The Transporter Classification Database: recent advances. <i>Nucleic Acids Research</i> , 2009 , 37, D274-8	20.1	346
244	A novel mechanism of transposon-mediated gene activation. <i>PLoS Genetics</i> , 2009 , 5, e1000689	6	41
243	Global Pollution: How Much Is Too Much?. <i>Water, Air, and Soil Pollution</i> , 2009 , 204, 1-3	2.6	
242	Comprehensive analyses of transport proteins encoded within the genome of "Aromatoleum aromaticum" strain EbN1. <i>Journal of Membrane Biology</i> , 2009 , 229, 53-90	2.3	10
241	Bioinformatic characterization of p-type ATPases encoded within the fully sequenced genomes of 26 eukaryotes. <i>Journal of Membrane Biology</i> , 2009 , 229, 115-30	2.3	67

240	Membrane Porters of ATP-Binding Cassette Transport Systems Are Polyphyletic. <i>Journal of Membrane Biology</i> , 2009 , 231, 1-9	2.3	64
239	A mechanism of transposon-mediated directed mutation. <i>Molecular Microbiology</i> , 2009 , 74, 29-43	4.1	24
238	A stochastic automaton shows how enzyme assemblies may contribute to metabolic efficiency. <i>BMC Systems Biology</i> , 2008 , 2, 27	3.5	23
237	A genomic analysis of the archaeal system <i>Ignicoccus hospitalis</i> - <i>Nanoarchaeum equitans</i> . <i>Genome Biology</i> , 2008 , 9, R158	18.3	92
236	Protein secretion and membrane insertion systems in bacteria and eukaryotic organelles. <i>Advances in Applied Microbiology</i> , 2008 , 65, 141-97	4.9	16
235	The bacterial chromosome. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2008 , 43, 89-134	8.7	26
234	The phagosomal nutrient transporter (Pht) family. <i>Microbiology (United Kingdom)</i> , 2008 , 154, 42-53	2.9	31
233	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	2.7	4
232	Learning to Find Relevant Biological Articles without Negative Training Examples. <i>Lecture Notes in Computer Science</i> , 2008 , 202-213	0.9	6
231	The bile/arsenite/riboflavin transporter (BART) superfamily. <i>FEBS Journal</i> , 2007 , 274, 612-29	5.7	56
230	Identification of regulatory network topological units coordinating the genome-wide transcriptional response to glucose in <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2007 , 7, 53	4.5	47
229	Gap junctional proteins of animals: the innexin/pannexin superfamily. <i>Progress in Biophysics and Molecular Biology</i> , 2007 , 94, 5-14	4.7	106
228	Mercury Transport in Bacteria. <i>Water, Air, and Soil Pollution</i> , 2007 , 182, 219	2.6	16
227	Functional taxonomy of bacterial hyperstructures. <i>Microbiology and Molecular Biology Reviews</i> , 2007 , 71, 230-53	13.2	67
226	Active transport in communication, protection and nutrition. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2007 , 12, 161-4	0.9	7
225	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, 263-8	0.9	4
224	Comprehensive analysis of transport proteins encoded within the genome of <i>Bdellovibrio bacteriovorus</i> . <i>Genomics</i> , 2007 , 90, 424-46	4.3	24
223	Transport capabilities of eleven gram-positive bacteria: comparative genomic analyses. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 1342-66	3.8	83

222	Evolutionary origins of members of a superfamily of integral membrane cytochrome c biogenesis proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 2164-81	3.8	33
221	Toward a hyperstructure taxonomy. <i>Annual Review of Microbiology</i> , 2007 , 61, 309-29	17.5	50
220	Evolution of the Bacterial Flagellum. <i>Microbe Magazine</i> , 2007 , 2, 335-340		6
219	Finding Transport Proteins in a General Protein Database. <i>Lecture Notes in Computer Science</i> , 2007 , 54-66.9		7
218	Protein secretion and membrane insertion systems in gram-negative bacteria. <i>Journal of Membrane Biology</i> , 2006 , 214, 75-90	2.3	91
217	TCDB: the Transporter Classification Database for membrane transport protein analyses and information. <i>Nucleic Acids Research</i> , 2006 , 34, D181-6	20.1	622
216	Bioinformatic Analyses of Gram-Negative Bacterial OstA Outer Membrane Assembly Homologues. <i>Current Genomics</i> , 2006 , 7, 447-461	2.6	7
215	The iron/lead transporter superfamily of Fe/Pb ²⁺ uptake systems. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2006 , 11, 1-9	0.9	26
214	Protein-translocating trimeric autotransporters of gram-negative bacteria. <i>Journal of Bacteriology</i> , 2006 , 188, 5655-67	3.5	21
213	Mechanism of CcpA-mediated glucose repression of the resABCDE operon of <i>Bacillus subtilis</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2006 , 11, 104-10	0.9	5
212	Engineering transport protein function: theoretical and technical considerations using the sugar-transporting phosphotransferase system of <i>Escherichia coli</i> as a model system. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2006 , 11, 302-7	0.9	4
211	Topological predictions for integral membrane permeases of the phosphoenolpyruvate:sugar phosphotransferase system. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2006 , 11, 345-60	0.9	33
210	Evolutionary appearance of H ⁺ -translocating pyrophosphatases. <i>Microbiology (United Kingdom)</i> , 2006 , 152, 1243-1247	2.9	19
209	The cecropin superfamily of toxic peptides. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2006 , 11, 94-103	0.9	25
208	Extra domains in secondary transport carriers and channel proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2006 , 1758, 1557-79	3.8	36
207	Our precarious planet. <i>The Environmentalist</i> , 2006 , 26, 321-324		
206	Protein Secretion Systems in Gram-Negative Bacteria. <i>Microbe Magazine</i> , 2006 , 1, 414-419		10
205	Modelling Bacterial Hyperstructures with Cellular Automata 2006 , 147-156		1

204	The bestrophin family of anion channels: identification of prokaryotic homologues. <i>Molecular Membrane Biology</i> , 2005 , 22, 291-302	3.4	11
203	Biochemical characterization of phosphoryl transfer involving HPr of the phosphoenolpyruvate-dependent phosphotransferase system in <i>Treponema denticola</i> , an organism that lacks PTS permeases. <i>Biochemistry</i> , 2005 , 44, 598-608	3.2	14
202	Topological analysis of integral membrane constituents of prokaryotic ABC efflux systems. <i>Research in Microbiology</i> , 2005 , 156, 270-7	4	22
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