

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	Major Facilitator Superfamily. <i>Microbiology and Molecular Biology Reviews</i> , 1998, 62, 1-34.	2.9	1,760
2	A major superfamily of transmembrane facilitators that catalyse uniport, symport and antiport. <i>Trends in Biochemical Sciences</i> , 1993, 18, 13-20.	3.7	909
3	TCDB: the Transporter Classification Database for membrane transport protein analyses and information. <i>Nucleic Acids Research</i> , 2006, 34, D181-D186.	6.5	774
4	A Functional-Phylogenetic Classification System for Transmembrane Solute Transporters. <i>Microbiology and Molecular Biology Reviews</i> , 2000, 64, 354-411.	2.9	773
5	The Transporter Classification Database (TCDB): recent advances. <i>Nucleic Acids Research</i> , 2016, 44, D372-D379.	6.5	711
6	The Transporter Classification Database. <i>Nucleic Acids Research</i> , 2014, 42, D251-D258.	6.5	437
7	The major facilitator superfamily (MFS) revisited. <i>FEBS Journal</i> , 2012, 279, 2022-2035.	2.2	402
8	The Transporter Classification Database: recent advances. <i>Nucleic Acids Research</i> , 2009, 37, D274-D278.	6.5	391
9	Gut <i>Bacteroides</i> species in health and disease. <i>Gut Microbes</i> , 2021, 13, 1-20.	4.3	383
10	Type II protein secretion and its relationship to bacterial type IV pili and archaeal flagella. <i>Microbiology (United Kingdom)</i> , 2003, 149, 3051-3072.	0.7	333
11	Microbial genome analyses: global comparisons of transport capabilities based on phylogenies, bioenergetics and substrate specificities 1 Edited by G. Von Heijne. <i>Journal of Molecular Biology</i> , 1998, 277, 573-592.	2.0	289
12	Phylogeny of multidrug transporters. <i>Seminars in Cell and Developmental Biology</i> , 2001, 12, 205-213.	2.3	288
13	The SMR family: a novel family of multidrug efflux proteins involved with the efflux of lipophilic drugs. <i>Molecular Microbiology</i> , 1996, 19, 1167-1175.	1.2	275
14	The drug/metabolite transporter superfamily. <i>FEBS Journal</i> , 2001, 268, 3620-3639.	0.2	270
15	Microbial genome analyses: comparative transport capabilities in eighteen prokaryotes 1 Edited by G. von Heijne. <i>Journal of Molecular Biology</i> , 2000, 301, 75-100.	2.0	265
16	Families of transmembrane sugar transport proteins. <i>Molecular Microbiology</i> , 2000, 35, 699-710.	1.2	260
17	The MIP Family of Integral Membrane Channel Proteins: Sequence Comparisons, Evolutionary Relationships, Reconstructed Pathway of Evolution, and Proposed Functional Differentiation of the Two Repeated Halves of the Proteins. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 1993, 28, 235-257.	2.3	255
18	The amino acid/polyamine/organocation (APC) superfamily of transporters specific for amino acids, polyamines and organocations. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1797-1814.	0.7	251

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19	Comparative Genomic Analyses of the Bacterial Phosphotransferase System. <i>Microbiology and Molecular Biology Reviews</i> , 2005, 69, 608-634.	2.9	246
20	The Transporter Classification (TC) System, 2002. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2002, 37, 287-337.	2.3	240
21	Catabolite repression mediated by the CcpA protein in <i>Bacillus subtilis</i> : novel modes of regulation revealed by whole-genome analyses. <i>Molecular Microbiology</i> , 2004, 39, 1366-1381.	1.2	223
22	Catabolite repression and inducer control in Gram-positive bacteria. <i>Microbiology (United Kingdom)</i> , 1996, 142, 217-230.	0.7	222
23	The multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) exporter superfamily. <i>FEBS Journal</i> , 2003, 270, 799-813.	0.2	218
24	Transcriptome Analysis of Crp-Dependent Catabolite Control of Gene Expression in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2004, 186, 3516-3524.	1.0	218
25	A functional superfamily of sodium/solute symporters. <i>BBA - Biomembranes</i> , 1994, 1197, 133-166.	7.9	216
26	A family of Gram-negative bacterial outer membrane factors that function in the export of proteins, carbohydrates, drugs and heavy metals from Gram-negative bacteria. <i>FEMS Microbiology Letters</i> , 1997, 156, 1-8.	0.7	215
27	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , 1998, 12, 265-274.	0.2	210
28	Two Families of Mechanosensitive Channel Proteins. <i>Microbiology and Molecular Biology Reviews</i> , 2003, 67, 66-85.	2.9	208
29	Phylogenetic characterization of novel transport protein families revealed by genome analyses. <i>BBA - Biomembranes</i> , 1999, 1422, 1-56.	7.9	207
30	A novel protein kinase that controls carbon catabolite repression in bacteria. <i>Molecular Microbiology</i> , 1998, 27, 1157-1169.	1.2	205
31	Unified inventory of established and putative transporters encoded within the complete genome of <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 1998, 430, 116-125.	1.3	203
32	The Transporter Classification Database (TCDB): 2021 update. <i>Nucleic Acids Research</i> , 2021, 49, D461-D467.	6.5	192
33	Novel Proteins of the Phosphotransferase System Encoded within the rpoN Operon of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1995, 270, 4822-4839.	1.6	190
34	Families of transmembrane transporters selective for amino acids and their derivatives The information presented in this review was initially prepared for presentation at the FASEB meeting on amino acid transport held in Copper Mountain, Colorado, June 26–July 1, 1999 and was updated in January 2000 following the meeting of the Transport Nomenclature Panel of the International Union of Biochemistry and Molecular Biology (IUBMB) in Geneva, November 28–30, 1999. The system of classification described in this. <i>Microbiology (United Kingdom)</i> , 2000, 146, 1775-1795.	0.7	188
35	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , 1998, 12, 265-274.	0.2	184
36	The Phosphoenolpyruvate: Sugar Phosphotransferase System in Gram-Positive Bacteria: Properties, Mechanism, and Regulation. <i>CRC Critical Reviews in Microbiology</i> , 1988, 15, 297-338.	4.8	183

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37	P-type ATPases of eukaryotes and bacteria: Sequence analyses and construction of phylogenetic trees. <i>Journal of Molecular Evolution</i> , 1994, 38, 57-99.	0.8	177
38	Protein-translocating outer membrane porins of Gram-negative bacteria. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002, 1562, 6-31.	1.4	176
39	The Mitochondrial Carrier Family of Transport Proteins: Structural, Functional, and Evolutionary Relationships. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 1993, 28, 209-233.	2.3	168
40	Protein phosphorylation and regulation of carbon metabolism in Gram-negative versus Gram-positive bacteria. <i>Trends in Biochemical Sciences</i> , 1995, 20, 267-271.	3.7	164
41	Sequence and phylogenetic analyses of the twin-arginine targeting (Tat) protein export system. <i>Archives of Microbiology</i> , 2002, 177, 441-450.	1.0	159
42	Phylogeny as a guide to structure and function of membrane transport proteins (Review). <i>Molecular Membrane Biology</i> , 2004, 21, 171-181.	2.0	157
43	Computer-based analyses of the protein constituents of transport systems catalysing export of complex carbohydrates in bacteria. <i>Microbiology (United Kingdom)</i> , 1997, 143, 2685-2699.	0.7	152
44	A new subfamily of bacterial ABC-type transport systems catalyzing export of drugs and carbohydrates. <i>Protein Science</i> , 1992, 1, 1326-1332.	3.1	151
45	The global regulatory protein FruR modulates the direction of carbon flow in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1995, 16, 1157-1169.	1.2	151
46	Export of l-Isoleucine from <i>Corynebacterium glutamicum</i> : a Two-Gene-Encoded Member of a New Translocator Family. <i>Journal of Bacteriology</i> , 2002, 184, 3947-3956.	1.0	148
47	Multidrug-Resistant Transport Proteins in Yeast: Complete Inventory and Phylogenetic Characterization of Yeast Open Reading Frames within the Major Facilitator Superfamily. , 1997, 13, 43-54.		137
48	Tracing pathways of transport protein evolution. <i>Molecular Microbiology</i> , 2003, 48, 1145-1156.	1.2	137
49	In Vitro Binding of the Pleiotropic Transcriptional Regulatory Protein, FruR, to the fru, pps, ace, pts and icd Operons of <i>Escherichia coli</i> and <i>Salmonella typhimurium</i> . <i>Journal of Molecular Biology</i> , 1993, 234, 28-44.	2.0	135
50	Gap junctional proteins of animals: The innexin/pannexin superfamily. <i>Progress in Biophysics and Molecular Biology</i> , 2007, 94, 5-14.	1.4	131
51	Ser/Thr/Tyr Protein Phosphorylation in Bacteria – For Long Time Neglected, Now Well Established. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2005, 9, 125-131.	1.0	130
52	Functional Interactions between the Carbon and Iron Utilization Regulators, Crp and Fur, in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005, 187, 980-990.	1.0	129
53	Phylogenetic and structural analyses of the oxa1 family of protein translocases. <i>FEMS Microbiology Letters</i> , 2001, 204, 223-231.	0.7	128
54	A family of Gram-negative bacterial outer membrane factors that function in the export of proteins, carbohydrates, drugs and heavy metals from Gram-negative bacteria. <i>FEMS Microbiology Letters</i> , 2006, 156, 1-8.	0.7	125

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55	Structural and evolutionary relationships among the immunophilins: two ubiquitous families of peptidyl-prolyl <i>cis</i> - <i>trans</i> isomerases. <i>FASEB Journal</i> , 1992, 6, 3410-3120.	0.2	121
56	Molecular Phylogeny as a Basis for the Classification of Transport Proteins from Bacteria, Archaea and Eukarya. <i>Advances in Microbial Physiology</i> , 1998, 40, 81-136.	1.0	120
57	The general protein secretory pathway: phylogenetic analyses leading to evolutionary conclusions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003, 1609, 115-125.	1.4	120
58	A novel family of channel-forming, autotransporting, bacterial virulence factors. <i>Molecular Membrane Biology</i> , 1997, 14, 113-123.	2.0	114
59	Overexpression of the <i>Escherichia coli</i> <i>sugE</i> Gene Confers Resistance to a Narrow Range of Quaternary Ammonium Compounds. <i>Journal of Bacteriology</i> , 2002, 184, 2543-2545.	1.0	114
60	Structure and evolution of a multidomain multiphosphoryl transfer protein. <i>Journal of Molecular Biology</i> , 1990, 213, 687-703.	2.0	110
61	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018, 36, 103-112.	9.4	110
62	Transport capabilities of eleven gram-positive bacteria: Comparative genomic analyses. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007, 1768, 1342-1366.	1.4	106
63	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
64	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
65	The P-Type ATPase Superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010, 19, 5-104.	1.0	103
66	In Silico and Transcriptional Analysis of Carbohydrate Uptake Systems of <i>Streptomyces coelicolor</i> A3(2). <i>Journal of Bacteriology</i> , 2004, 186, 1362-1373.	1.0	102
67	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
68	The ion transporter superfamily. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003, 1618, 79-92.	1.4	101
69	Protein Secretion and Membrane Insertion Systems in Gram-Negative Bacteria. <i>Journal of Membrane Biology</i> , 2006, 214, 75-90.	1.0	99
70	Enzyme INtr from <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1999, 274, 26185-26191.	1.6	97
71	The Amino Acid-Polyamine-Organocation Superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2012, 22, 105-113.	1.0	97
72	Novel phosphotransferase system genes revealed by genome analysis – the complete complement of PTS proteins encoded within the genome of <i>Bacillus subtilis</i> . <i>Microbiology (United Kingdom)</i> , 1999, 145, 3419-3429.	0.7	96

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73	TRAP transporters: an ancient family of extracytoplasmic solute- receptor-dependent secondary active transporters. <i>Microbiology (United Kingdom)</i> , 1999, 145, 3431-3445.	0.7	94
74	A Broad-Specificity Multidrug Efflux Pump Requiring a Pair of Homologous SMR-Type Proteins. <i>Journal of Bacteriology</i> , 2000, 182, 2311-2313.	1.0	94
75	The β -barrel finder (BBF) program, allowing identification of outer membrane β -barrel proteins encoded within prokaryotic genomes. <i>Protein Science</i> , 2009, 11, 2196-2207.	3.1	94
76	Protein secretion systems of <i>Pseudomonas aeruginosa</i> and <i>P. fluorescens</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003, 1611, 223-233.	1.4	92
77	Mechanism, regulation and physiological significance of the loop diuretic-sensitive NaCl/KCl symport system in animal cells. <i>Molecular and Cellular Biochemistry</i> , 1984, 59, 11-32.	1.4	91
78	Catabolite Repression and Activation in <i>Bacillus subtilis</i> : Dependency on CcpA, HPr, and HprK. <i>Journal of Bacteriology</i> , 2005, 187, 7826-7839.	1.0	91
79	Conjugal type IV macromolecular transfer systems of Gram-negative bacteria: organismal distribution, structural constraints and evolutionary conclusions. <i>Microbiology (United Kingdom)</i> , 2001, 147, 3201-3214.	0.7	91
80	CHR, a Novel Family of Prokaryotic Proton Motive Force-Driven Transporters Probably Containing Chromate/Sulfate Antiporters. <i>Journal of Bacteriology</i> , 1998, 180, 5799-5802.	1.0	90
81	Phylogenetic, structural and functional analyses of the LacI-GalR family of bacterial transcription factors. <i>FEBS Letters</i> , 1995, 377, 98-102.	1.3	86
82	Mammalian integral membrane receptors are homologous to facilitators and antiporters of yeast, fungi, and eubacteria. <i>Protein Science</i> , 1993, 2, 20-30.	3.1	85
83	The tripartite tricarboxylate transporter (TTT) family. <i>Research in Microbiology</i> , 2003, 154, 457-465.	1.0	85
84	A proposed link between nitrogen and carbon metabolism involving protein phosphorylation in bacteria. <i>Protein Science</i> , 1992, 1, 722-726.	3.1	83
85	Cyclic AMP-independent catabolite repression in bacteria. <i>FEMS Microbiology Letters</i> , 1996, 138, 97-103.	0.7	83
86	Multiple mechanisms controlling carbon metabolism in bacteria. , 1998, 58, 170-174.		83
87	Vectorial Metabolism and the Evolution of Transport Systems. <i>Journal of Bacteriology</i> , 2000, 182, 5029-5035.	1.0	83
88	The principal chloroquine resistance protein of <i>Plasmodium falciparum</i> is a member of the drug/metabolite transporter superfamily. <i>Microbiology (United Kingdom)</i> , 2004, 150, 1-3.	0.7	83
89	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
90	Expansion of the APC superfamily of secondary carriers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014, 82, 2797-2811.	1.5	82

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91	A functional-phylogenetic system for the classification of transport proteins. , 1999, 75, 84-94.		79
92	Functional Taxonomy of Bacterial Hyperstructures. Microbiology and Molecular Biology Reviews, 2007, 71, 230-253.	2.9	79
93	Bioinformatic Characterization of P-Type ATPases Encoded Within the Fully Sequenced Genomes of 26 Eukaryotes. Journal of Membrane Biology, 2009, 229, 115-130.	1.0	79
94	Evidence for the evolutionary relatedness of the proteins of the bacterial phosphoenolpyruvate: Sugar phosphotransferase system. Journal of Cellular Biochemistry, 1985, 27, 43-56.	1.2	78
95	Modular multidomain phosphoryl transfer proteins of bacteria. Current Opinion in Structural Biology, 1997, 7, 407-415.	2.6	75
96	Membrane Porters of ATP-Binding Cassette Transport Systems Are Polyphyletic. Journal of Membrane Biology, 2009, 231, 1-9.	1.0	75
97	Discovering lactic acid bacteria by genomics. , 2002, 82, 29-58.		74
98	The Ascorbate Transporter of Escherichia coli. Journal of Bacteriology, 2003, 185, 2243-2250.	1.0	73
99	Novel phosphotransferase genes revealed by bacterial genome sequencing: a gene cluster encoding a putative N-acetylgalactosamine metabolic pathway in Escherichia coli. Microbiology (United Kingdom), 1996, 142, 231-250.	0.7	73
100	Cryo-EM structure of OSCA1.2 from <i>Oryza sativa</i> elucidates the mechanical basis of potential membrane hyperosmolality gating. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14309-14318.	3.3	71
101	Regulation of competence development and sugar utilization in Haemophilus influenzae Rd by a phosphoenolpyruvate:fructose phosphotransferase system. Molecular Microbiology, 1996, 21, 941-952.	1.2	70
102	The Bacterial Phosphotransferase System: New Frontiers 50 Years after Its Discovery. Journal of Molecular Microbiology and Biotechnology, 2015, 25, 73-78.	1.0	70
103	Homologues of archaeal rhodopsins in plants, animals and fungi: structural and functional predications for a putative fungal chaperone protein. Biochimica Et Biophysica Acta - Biomembranes, 2001, 1511, 206-223.	1.4	68
104	Growth regulation and amino acid transport in epithelial cells: Influence of culture conditions and transformation on A, ASC, and I transport activities. Journal of Cellular Physiology, 1982, 113, 240-246.	2.0	67
105	Multiple Phosphorylation of SacY, a Bacillus subtilis Transcriptional Antiterminator Negatively Controlled by the Phosphotransferase System. Journal of Biological Chemistry, 1997, 272, 17230-17237.	1.6	66
106	Solution structure of the phosphocarrier protein HPr from <i>Bacillus subtilis</i> by two-dimensional NMR spectroscopy. Protein Science, 1992, 1, 1363-1376.	3.1	65
107	The bile/arsenite/riboflavin transporter (BART) superfamily. FEBS Journal, 2007, 274, 612-629.	2.2	65
108	In Vitro Reconstitution of Transcriptional Antitermination by the SacT and SacY Proteins of Bacillus subtilis. Journal of Biological Chemistry, 1996, 271, 18966-18972.	1.6	64

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109	Toward a Hyperstructure Taxonomy. <i>Annual Review of Microbiology</i> , 2007, 61, 309-329.	2.9	63
110	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
111	Regulation of sigL Expression by the Catabolite Control Protein CcpA Involves a Roadblock Mechanism in <i>Bacillus subtilis</i> : Potential Connection between Carbon and Nitrogen Metabolism. <i>Journal of Bacteriology</i> , 2005, 187, 6856-6861.	1.0	61
112	Topological and phylogenetic analyses of bacterial holin families and superfamilies. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013, 1828, 2654-2671.	1.4	61
113	CcpB, a Novel Transcription Factor Implicated in Catabolite Repression in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 1998, 180, 491-497.	1.0	60
114	Regulation of bacterial physiological processes by three types of protein phosphorylating systems. <i>Trends in Biochemical Sciences</i> , 1990, 15, 391-395.	3.7	59
115	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.	1.3	59
116	The IUBMB-Endorsed Transporter Classification System. <i>Molecular Biotechnology</i> , 2004, 27, 253-262.	1.3	58
117	Lysophospholipid Flipping across the <i>Escherichia coli</i> Inner Membrane Catalyzed by a Transporter (LpIT) Belonging to the Major Facilitator Superfamily. <i>Journal of Biological Chemistry</i> , 2005, 280, 12028-12034.	1.6	58
118	Genome archeology leading to the characterization and classification of transport proteins. <i>Current Opinion in Microbiology</i> , 1999, 2, 555-561.	2.3	56
119	A transporter of <i>Escherichia coli</i> specific for l- and d-methionine is the prototype for a new family within the ABC superfamily. <i>Archives of Microbiology</i> , 2003, 180, 88-100.	1.0	55
120	Carbonic Anhydrases Fused to Anion Transporters of the SulP Family: Evidence for a Novel Type of Bicarbonate Transporter. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2004, 8, 169-176.	1.0	55
121	BioV Suite "a collection of programs for the study of transport protein evolution. <i>FEBS Journal</i> , 2012, 279, 2036-2046.	2.2	55
122	Regulatory interactions involving the proteins of the phosphotransferase system in enteric bacteria. <i>Journal of Cellular Biochemistry</i> , 1993, 51, 62-68.	1.2	53
123	Characterization of Glucose-Specific Catabolite Repression-Resistant Mutants of <i>Bacillus subtilis</i> : Identification of a Novel Hexose:H + Symporter. <i>Journal of Bacteriology</i> , 1998, 180, 498-504.	1.0	53
124	The amoebapore superfamily. <i>BBA - Biomembranes</i> , 2000, 1469, 87-99.	7.9	52
125	Bioinformatic characterization of the Anoctamin Superfamily of Ca ²⁺ -activated ion channels and lipid scramblases. <i>PLoS ONE</i> , 2018, 13, e0192851.	1.1	52
126	Sequence analyses and evolutionary relationships among the energy-coupling proteins enzyme I and HPr of the bacterial phosphoenolpyruvate: Sugar phosphotransferase system. <i>Protein Science</i> , 1993, 2, 506-521.	3.1	51

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127	A Novel Mechanism of Transposon-Mediated Gene Activation. <i>PLoS Genetics</i> , 2009, 5, e1000689.	1.5	51
128	The Bacterial Intimins and Invasins: A Large and Novel Family of Secreted Proteins. <i>PLoS ONE</i> , 2010, 5, e14403.	1.1	50
129	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
130	Sec61 ¹² is a component of the archaeal protein secretory system. <i>Trends in Biochemical Sciences</i> , 2002, 27, 170-171.	3.7	49
131	Adaptive regulatory control of system a transport activity in a kidney epithelial cell line (MDCK) and in a transformed variant (MDCK-T1). <i>Journal of Cellular Physiology</i> , 1985, 122, 308-315.	2.0	48
132	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
133	Low resolution solution structure of the <i>Bacillus subtilis</i> glucose permease IIA domain derived from heteronuclear three-dimensional NMR spectroscopy. <i>FEBS Letters</i> , 1992, 296, 148-152.	1.3	47
134	Phylogeny of phosphoryl transfer proteins of the phosphoenolpyruvate-dependent sugar-transporting phosphotransferase system. <i>Research in Microbiology</i> , 2002, 153, 405-415.	1.0	47
135	Evolution of bacterial type III protein secretion systems. <i>Trends in Microbiology</i> , 2004, 12, 113-115.	3.5	47
136	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
137	The transporter-opsin coupled protein-coupled receptor (TOG) superfamily. <i>FEBS Journal</i> , 2013, 280, 5780-5800.	2.2	46
138	The involvement of transport proteins in transcriptional and metabolic regulation. <i>Current Opinion in Microbiology</i> , 2014, 18, 8-15.	2.3	45
139	Eukaryotic Transmembrane Solute Transport Systems. <i>International Review of Cytology</i> , 1999, 190, 61-136.	6.2	44
140	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
141	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
142	Phosphorylation of serine-46 in HPr, a key regulatory protein in bacteria, results in stabilization of its solution structure. <i>Protein Science</i> , 1995, 4, 2478-2486.	3.1	43
143	Differential codon usage: a safeguard against inappropriate expression of specialized genes?. <i>FEBS Letters</i> , 1995, 362, 1-4.	1.3	43
144	Cra-mediated regulation of <i>Escherichia coli</i> adenylate cyclase. <i>Microbiology (United Kingdom)</i> , 1997, 143, 785-792.	0.7	43

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145	The structure of an energy-coupling protein from bacteria, IIBcellobiose, reveals similarity to eukaryotic protein tyrosine phosphatases. <i>Structure</i> , 1997, 5, 217-225.	1.6	43
146	Evolution of the Oligopeptide Transporter Family. <i>Journal of Membrane Biology</i> , 2011, 240, 89-110.	1.0	43
147	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
148	A web-based Tree View (TV) program for the visualization of phylogenetic trees. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2002, 4, 69-70.	1.0	43
149	Size Comparisons among Integral Membrane Transport Protein Homologues in Bacteria , Archaea , and Eucarya. <i>Journal of Bacteriology</i> , 2001, 183, 1012-1021.	1.0	42
150	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
151	Topological analysis of integral membrane constituents of prokaryotic ABC efflux systems. <i>Research in Microbiology</i> , 2005, 156, 270-277.	1.0	41
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