

Milton H Saier Jr

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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	Major facilitator superfamily. <i>Microbiology and Molecular Biology Reviews</i> , 1998 , 62, 1-34	13.2	1423
364	A major superfamily of transmembrane facilitators that catalyse uniport, symport and antiport. <i>Trends in Biochemical Sciences</i> , 1993 , 18, 13-20	10.3	784
363	A functional-phylogenetic classification system for transmembrane solute transporters. <i>Microbiology and Molecular Biology Reviews</i> , 2000 , 64, 354-411	13.2	643
362	TCDB: the Transporter Classification Database for membrane transport protein analyses and information. <i>Nucleic Acids Research</i> , 2006 , 34, D181-6	20.1	622
361	The Transporter Classification Database (TCDB): recent advances. <i>Nucleic Acids Research</i> , 2016 , 44, D372-9	20.1	434
360	The Transporter Classification Database: recent advances. <i>Nucleic Acids Research</i> , 2009 , 37, D274-8	20.1	346
359	The transporter classification database. <i>Nucleic Acids Research</i> , 2014 , 42, D251-8	20.1	323
358	Type II protein secretion and its relationship to bacterial type IV pili and archaeal flagella. <i>Microbiology (United Kingdom)</i> , 2003 , 149, 3051-3072	2.9	297
357	The major facilitator superfamily (MFS) revisited. <i>FEBS Journal</i> , 2012 , 279, 2022-35	5.7	294
356	Microbial genome analyses: global comparisons of transport capabilities based on phylogenies, bioenergetics and substrate specificities. <i>Journal of Molecular Biology</i> , 1998 , 277, 573-92	6.5	262
355	Phylogeny of multidrug transporters. <i>Seminars in Cell and Developmental Biology</i> , 2001 , 12, 205-13	7.5	254
354	Microbial genome analyses: comparative transport capabilities in eighteen prokaryotes. <i>Journal of Molecular Biology</i> , 2000 , 301, 75-100	6.5	243
353	Families of transmembrane sugar transport proteins. <i>Molecular Microbiology</i> , 2000 , 35, 699-710	4.1	234
352	The SMR family: a novel family of multidrug efflux proteins involved with the efflux of lipophilic drugs. <i>Molecular Microbiology</i> , 1996 , 19, 1167-75	4.1	232
351	The drug/metabolite transporter superfamily. <i>FEBS Journal</i> , 2001 , 268, 3620-39		220
350	The amino acid/polyamine/organocation (APC) superfamily of transporters specific for amino acids, polyamines and organocations. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 8), 1797-1814	2.9	220
349	The transporter classification (TC) system, 2002. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2002 , 37, 287-337	8.7	219

348	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, 235-57	8.7	218
347	Comparative genomic analyses of the bacterial phosphotransferase system. <i>Microbiology and Molecular Biology Reviews</i> , 2005 , 69, 608-34	13.2	217
346	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> , 2001 , 39, 1366-81	4.1	200
345	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	2.9	198
344	Phylogenetic characterization of novel transport protein families revealed by genome analyses. <i>BBA - Biomembranes</i> , 1999 , 1422, 1-56		189
343	The multidrug/oligosaccharidyl-lipid/polysaccharide (MOP) exporter superfamily. <i>FEBS Journal</i> , 2003 , 270, 799-813		187
342	A novel protein kinase that controls carbon catabolite repression in bacteria. <i>Molecular Microbiology</i> , 1998 , 27, 1157-69	4.1	185
341	Two families of mechanosensitive channel proteins. <i>Microbiology and Molecular Biology Reviews</i> , 2003 , 67, 66-85, table of contents	13.2	182
340	Unified inventory of established and putative transporters encoded within the complete genome of <i>Saccharomyces cerevisiae</i> . <i>FEBS Letters</i> , 1998 , 430, 116-25	3.8	180
339	Transcriptome analysis of Crp-dependent catabolite control of gene expression in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2004 , 186, 3516-24	3.5	178
338	Novel proteins of the phosphotransferase system encoded within the rpoN operon of <i>Escherichia coli</i> . Enzyme IIANtr affects growth on organic nitrogen and the conditional lethality of an erats mutant. <i>Journal of Biological Chemistry</i> , 1995 , 270, 4822-39	5.4	178
337	A functional superfamily of sodium/solute symporters. <i>BBA - Biomembranes</i> , 1994 , 1197, 133-66		177
336	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , 1998 , 12, 265-274	0.9	174
335	Catabolite repression and inducer control in Gram-positive bacteria. <i>Microbiology (United Kingdom)</i> , 1996 , 142 (Pt 2), 217-230	2.9	170
334	Evolutionary origins of multidrug and drug-specific efflux pumps in bacteria. <i>FASEB Journal</i> , 1998 , 12, 265-74	0.9	169
333	P-type ATPases of eukaryotes and bacteria: sequence analyses and construction of phylogenetic trees. <i>Journal of Molecular Evolution</i> , 1994 , 38, 57-99	3.1	167
332	Families of transmembrane transporters selective for amino acids and their derivatives. <i>Microbiology (United Kingdom)</i> , 2000 , 146 (Pt 8), 1775-1795	2.9	162
331	Protein-translocating outer membrane porins of Gram-negative bacteria. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002 , 1562, 6-31	3.8	156

330	The phosphoenolpyruvate:sugar phosphotransferase system in gram-positive bacteria: properties, mechanism, and regulation. <i>CRC Critical Reviews in Microbiology</i> , 1988 , 15, 297-338		156
329	Sequence and phylogenetic analyses of the twin-arginine targeting (Tat) protein export system. <i>Archives of Microbiology</i> , 2002 , 177, 441-50	3	148
328	Protein phosphorylation and regulation of carbon metabolism in gram-negative versus gram-positive bacteria. <i>Trends in Biochemical Sciences</i> , 1995 , 20, 267-71	10.3	146
327	The mitochondrial carrier family of transport proteins: structural, functional, and evolutionary relationships. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 1993 , 28, 209-33	8.7	140
326	Computer-based analyses of the protein constituents of transport systems catalysing export of complex carbohydrates in bacteria. <i>Microbiology (United Kingdom)</i> , 1997 , 143 (Pt 8), 2685-2699	2.9	139
325	A new subfamily of bacterial ABC-type transport systems catalyzing export of drugs and carbohydrates. <i>Protein Science</i> , 1992 , 1, 1326-32	6.3	138
324	Phylogeny as a guide to structure and function of membrane transport proteins. <i>Molecular Membrane Biology</i> , 2004 , 21, 171-81	3.4	135
323	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, 3947-56	3.5	132
322	The global regulatory protein FruR modulates the direction of carbon flow in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1995 , 16, 1157-69	4.1	128
321	Tracing pathways of transport protein evolution. <i>Molecular Microbiology</i> , 2003 , 48, 1145-56	4.1	125
320	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	6.5	125
319	Ser/Thr/Tyr protein phosphorylation in bacteria - for long time neglected, now well established. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2005 , 9, 125-31	0.9	120
318	Multidrug-resistant transport proteins in yeast: complete inventory and phylogenetic characterization of yeast open reading frames with the major facilitator superfamily. <i>Yeast</i> , 1997 , 13, 43-54	3.4	113
317	Phylogenetic and structural analyses of the oxa1 family of protein translocases. <i>FEMS Microbiology Letters</i> , 2001 , 204, 223-31	2.9	113
316	The general protein secretory pathway: phylogenetic analyses leading to evolutionary conclusions. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003 , 1609, 115-25	3.8	112
315	Structural and evolutionary relationships among the immunophilins: two ubiquitous families of peptidyl-prolyl cis-trans isomerases. <i>FASEB Journal</i> , 1992 , 6, 3410-20	0.9	108
314	Gap junctional proteins of animals: the innexin/pannexin superfamily. <i>Progress in Biophysics and Molecular Biology</i> , 2007 , 94, 5-14	4.7	106
313	Functional interactions between the carbon and iron utilization regulators, Crp and Fur, in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 2005 , 187, 980-90	3.5	104

312	A novel family of channel-forming, autotransporting, bacterial virulence factors. <i>Molecular Membrane Biology</i> , 1997 , 14, 113-23	3.4	102
311	Structure and evolution of a multidomain multiphosphoryl transfer protein. Nucleotide sequence of the fruB(HI) gene in <i>Rhodobacter capsulatus</i> and comparisons with homologous genes from other organisms. <i>Journal of Molecular Biology</i> , 1990 , 213, 687-703	6.5	98
310	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	2.9	95
309	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	4.4	94
308	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
307	Protein secretion and membrane insertion systems in gram-negative bacteria. <i>Journal of Membrane Biology</i> , 2006 , 214, 75-90	2.3	91
306	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
305	The ion transporter superfamily. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003 , 1618, 79-92	3.8	89
304	Enzyme I(Ntr) from <i>Escherichia coli</i> . A novel enzyme of the phosphoenolpyruvate-dependent phosphotransferase system exhibiting strict specificity for its phosphoryl acceptor, NPr. <i>Journal of Biological Chemistry</i> , 1999 , 274, 26185-91	5.4	88
303	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	4.2	88
302	The p-type ATPase superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2010 , 19, 5-104	0.9	87
301	Conjugal type IV macromolecular transfer systems of Gram-negative bacteria: organismal distribution, structural constraints and evolutionary conclusions. <i>Microbiology (United Kingdom)</i> , 2001 , 147, 3201-14	2.9	87
300	TRAP transporters: an ancient family of extracytoplasmic solute-receptor-dependent secondary active transporters. <i>Microbiology (United Kingdom)</i> , 1999 , 145 (Pt 12), 3431-3445	2.9	86
299	Transport capabilities of eleven gram-positive bacteria: comparative genomic analyses. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2007 , 1768, 1342-66	3.8	83
298	The beta-barrel finder (BBF) program, allowing identification of outer membrane beta-barrel proteins encoded within prokaryotic genomes. <i>Protein Science</i> , 2002 , 11, 2196-207	6.3	82
297	The amino acid-polyamine-organocation superfamily. <i>Journal of Molecular Microbiology and Biotechnology</i> , 2012 , 22, 105-13	0.9	81
296	CHR, a novel family of prokaryotic proton motive force-driven transporters probably containing chromate/sulfate antiporters. <i>Journal of Bacteriology</i> , 1998 , 180, 5799-802	3.5	80
295	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 (Pt 12), 3419-3429	2.9	80

294	In silico and transcriptional analysis of carbohydrate uptake systems of <i>Streptomyces coelicolor</i> A3(2). <i>Journal of Bacteriology</i> , 2004 , 186, 1362-73	3.5	79
293	Is Nuclear Energy the Solution?. <i>Water, Air, and Soil Pollution</i> , 2010 , 208, 1-3	2.6	78
292	The Crisis in Haiti, 2010: What to be done?. <i>Water, Air, and Soil Pollution</i> , 2010 , 212, 1-2	2.6	78
291	A broad-specificity multidrug efflux pump requiring a pair of homologous SMR-type proteins. <i>Journal of Bacteriology</i> , 2000 , 182, 2311-3	3.5	78
290	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	2.9	77
289	Catabolite repression and activation in <i>Bacillus subtilis</i> : dependency on CcpA, HPr, and HprK. <i>Journal of Bacteriology</i> , 2005 , 187, 7826-39	3.5	77
288	Protein secretion systems of <i>Pseudomonas aeruginosa</i> and <i>P. fluorescens</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003 , 1611, 223-33	3.8	76
287	Phylogenetic, structural and functional analyses of the LacI-GalR family of bacterial transcription factors. <i>FEBS Letters</i> , 1995 , 377, 98-102	3.8	76
286	Overexpression of the <i>Escherichia coli</i> sugE gene confers resistance to a narrow range of quaternary ammonium compounds. <i>Journal of Bacteriology</i> , 2002 , 184, 2543-5	3.5	75
285	Vectorial metabolism and the evolution of transport systems. <i>Journal of Bacteriology</i> , 2000 , 182, 5029-35	3.5	75
284	A proposed link between nitrogen and carbon metabolism involving protein phosphorylation in bacteria. <i>Protein Science</i> , 1992 , 1, 722-6	6.3	73
283	A functional-phylogenetic system for the classification of transport proteins. <i>Journal of Cellular Biochemistry</i> , 1999 , Suppl 32-33, 84-94	4.7	72
282	Cyclic AMP-independent catabolite repression in bacteria. <i>FEMS Microbiology Letters</i> , 1996 , 138, 97-103	2.9	72
281	Modular multidomain phosphoryl transfer proteins of bacteria. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 407-15	8.1	70
280	Multiple mechanisms controlling carbon metabolism in bacteria. <i>Biotechnology and Bioengineering</i> , 1998 , 58, 170-4	4.9	70
279	Evidence for the evolutionary relatedness of the proteins of the bacterial phosphoenolpyruvate:sugar phosphotransferase system. <i>Journal of Cellular Biochemistry</i> , 1985 , 27, 43-56	4.7	70
278	Mammalian integral membrane receptors are homologous to facilitators and antiporters of yeast, fungi, and eubacteria. <i>Protein Science</i> , 1993 , 2, 20-30	6.3	68
277	Global landscape of cell envelope protein complexes in <i>Escherichia coli</i> . <i>Nature Biotechnology</i> , 2018 , 36, 103-112	44.5	68

276	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
275	Functional taxonomy of bacterial hyperstructures. <i>Microbiology and Molecular Biology Reviews</i> , 2007 , 71, 230-53	13.2	67
274	Discovering lactic acid bacteria by genomics. <i>Antonie Van Leeuwenhoek</i> , 2002 , 82, 29-58	2.1	67
273	The tripartite tricarboxylate transporter (TTT) family. <i>Research in Microbiology</i> , 2003 , 154, 457-65	4	66
272	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
271	Membrane Porters of ATP-Binding Cassette Transport Systems Are Polyphyletic. <i>Journal of Membrane Biology</i> , 2009 , 231, 1-9	2.3	64
270	Growth regulation and amino acid transport in epithelial cells: influence of culture conditions and transformation on A, ASC, and L transport activities. <i>Journal of Cellular Physiology</i> , 1982 , 113, 240-6	7	63
269	The ascorbate transporter of Escherichia coli. <i>Journal of Bacteriology</i> , 2003 , 185, 2243-50	3.5	62
268	Novel phosphotransferase genes revealed by bacterial genome sequencing: a gene cluster encoding a putative N-acetylgalactosamine metabolic pathway in Escherichia coli. <i>Microbiology (United Kingdom)</i> , 1996 , 142 (Pt 2), 231-250	2.9	62
267	Solution structure of the phosphocarrier protein HPr from Bacillus subtilis by two-dimensional NMR spectroscopy. <i>Protein Science</i> , 1992 , 1, 1363-76	6.3	59
266	Homologues of archaeal rhodopsins in plants, animals and fungi: structural and functional predications for a putative fungal chaperone protein. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2001 , 1511, 206-23	3.8	58
265	Regulation of bacterial physiological processes by three types of protein phosphorylating systems. <i>Trends in Biochemical Sciences</i> , 1990 , 15, 391-5	10.3	58
264	Gut species in health and disease. <i>Gut Microbes</i> , 2021 , 13, 1-20	8.8	57
263	The bile/arsenite/riboflavin transporter (BART) superfamily. <i>FEBS Journal</i> , 2007 , 274, 612-29	5.7	56
262	Regulation of competence development and sugar utilization in Haemophilus influenzae Rd by a phosphoenolpyruvate:fructose phosphotransferase system. <i>Molecular Microbiology</i> , 1996 , 21, 941-52	4.1	56
261	Multiple phosphorylation of SacY, a Bacillus subtilis transcriptional antiterminator negatively controlled by the phosphotransferase system. <i>Journal of Biological Chemistry</i> , 1997 , 272, 17230-7	5.4	55
260	Expansion of the APC superfamily of secondary carriers. <i>Proteins: Structure, Function and Bioinformatics</i> , 2014 , 82, 2797-811	4.2	53
259	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

258	Lysophospholipid flipping across the Escherichia coli inner membrane catalyzed by a transporter (LplT) belonging to the major facilitator superfamily. <i>Journal of Biological Chemistry</i> , 2005 , 280, 12028-34	5.4	51
257	Genome archeology leading to the characterization and classification of transport proteins. <i>Current Opinion in Microbiology</i> , 1999 , 2, 555-61	7.9	51
256	In vitro reconstitution of transcriptional antitermination by the SacT and SacY proteins of Bacillus subtilis. <i>Journal of Biological Chemistry</i> , 1996 , 271, 18966-72	5.4	51
255	Toward a hyperstructure taxonomy. <i>Annual Review of Microbiology</i> , 2007 , 61, 309-29	17.5	50
254	A transporter of Escherichia coli 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	3	50
253	BioV Suite--a collection of programs for the study of transport protein evolution. <i>FEBS Journal</i> , 2012 , 279, 2036-46	5.7	49
252	Regulation of sigL expression by the catabolite control protein CcpA involves a roadblock mechanism in Bacillus subtilis: potential connection between carbon and nitrogen metabolism. <i>Journal of Bacteriology</i> , 2005 , 187, 6856-61	3.5	48
251	Identification of regulatory network topological units coordinating the genome-wide transcriptional response to glucose in Escherichia coli. <i>BMC Microbiology</i> , 2007 , 7, 53	4.5	47
250	The IUBMB-endorsed transporter classification system. <i>Molecular Biotechnology</i> , 2004 , 27, 253-62	3	47
249	Regulatory interactions involving the proteins of the phosphotransferase system in enteric bacteria. <i>Journal of Cellular Biochemistry</i> , 1993 , 51, 62-8	4.7	47
248	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	9.9	46
247	The amoebapore superfamily. <i>BBA - Biomembranes</i> , 2000 , 1469, 87-99		46
246	CcpB, a novel transcription factor implicated in catabolite repression in Bacillus subtilis. <i>Journal of Bacteriology</i> , 1998 , 180, 491-7	3.5	46
245	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, 169-76	0.9	45
244	The bacterial intimins and invasins: a large and novel family of secreted proteins. <i>PLoS ONE</i> , 2010 , 5, e14403	3.7	44
243	Sec61beta--a component of the archaeal protein secretory system. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 170-1	10.3	44
242	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, 308-15	7	44
241	Characterization of glucose-specific catabolite repression-resistant mutants of Bacillus subtilis: identification of a novel hexose:H ⁺ symporter. <i>Journal of Bacteriology</i> , 1998 , 180, 498-504	3.5	44

240	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
239	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
238	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	0.9	43
237	Topological and phylogenetic analyses of bacterial holin families and superfamilies. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2013 , 1828, 2654-71	3.8	42
236	The transporter-opsin-G protein-coupled receptor (TOG) superfamily. <i>FEBS Journal</i> , 2013 , 280, 5780-8005	7	42
235	A novel mechanism of transposon-mediated gene activation. <i>PLoS Genetics</i> , 2009 , 5, e1000689	6	41
234	Evolution of bacterial type III protein secretion systems. <i>Trends in Microbiology</i> , 2004 , 12, 113-5	12.4	41
233	Phylogeny of phosphoryl transfer proteins of the phosphoenolpyruvate-dependent sugar-transporting phosphotransferase system. <i>Research in Microbiology</i> , 2002 , 153, 405-15	4	41
232	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, 2478-86	6.3	41
231	Size comparisons among integral membrane transport protein homologues in bacteria, Archaea, and Eucarya. <i>Journal of Bacteriology</i> , 2001 , 183, 1012-21	3.5	40
230	Low resolution solution structure of the Bacillus subtilis glucose permease IIA domain derived from heteronuclear three-dimensional NMR spectroscopy. <i>FEBS Letters</i> , 1992 , 296, 148-52	3.8	40
229	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, 506-21	6.3	40
228	The structure of an energy-coupling protein from bacteria, IIBcellobiose, reveals similarity to eukaryotic protein tyrosine phosphatases. <i>Structure</i> , 1997 , 5, 217-25	5.2	39
227	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
226	Eukaryotic transmembrane solute transport systems. <i>International Review of Cytology</i> , 1999 , 190, 61-136	13	38
225	Evolution of the oligopeptide transporter family. <i>Journal of Membrane Biology</i> , 2011 , 240, 89-110	2.3	37
224	Introduction: protein phosphorylation and signal transduction in bacteria. <i>Journal of Cellular Biochemistry</i> , 1993 , 51, 1-6	4.7	37
223	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

222	Extra domains in secondary transport carriers and channel proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2006 , 1758, 1557-79	3.8	36
221	Molecular modeling of the bacterial outer membrane receptor energizer, ExbBD/TonB, based on homology with the flagellar motor, MotAB. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2003 , 1614, 201-10	3.8	36
220	Genes involved in control of galactose uptake in <i>Lactobacillus brevis</i> and reconstitution of the regulatory system in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2001 , 183, 3224-36	3.5	35
219	Unique regulation of carbohydrate chemotaxis in <i>Bacillus subtilis</i> by the phosphoenolpyruvate-dependent phosphotransferase system and the methyl-accepting chemotaxis protein McpC. <i>Journal of Bacteriology</i> , 1998 , 180, 4475-80	3.5	35
218	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
217	The involvement of transport proteins in transcriptional and metabolic regulation. <i>Current Opinion in Microbiology</i> , 2014 , 18, 8-15	7.9	34
216	Domain analysis of transcriptional regulators bearing PTS regulatory domains. <i>Research in Microbiology</i> , 2002 , 153, 519-26	4	34
215	The <i>Escherichia coli</i> ABC transporters: an update. <i>Molecular Microbiology</i> , 1999 , 32, 887-9	4.1	34
214	Differential codon usage: a safeguard against inappropriate expression of specialized genes?. <i>FEBS Letters</i> , 1995 , 362, 1-4	3.8	34
213	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
212	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
211	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
210	Decrease in protein content and cell volume of cultured dog kidney epithelial cells during growth. <i>In Vitro</i> , 1982 , 18, 196-202		33
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