

Jean-michel Jault

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.

93
papers

3,040
citations

31
h-index

52
g-index

96
ext. papers

3,301
ext. citations

4.4
avg. IF

4.52
L-index

#	Paper	IF	Citations
93	Substrate-bound and substrate-free outward-facing structures of a multidrug ABC exporter.. <i>Science Advances</i> , 2022 , 8, eabg9215	14.3	4
92	Identification of a two-component regulatory system involved in antimicrobial peptide resistance in <i>Streptococcus pneumoniae</i> .. <i>PLoS Pathogens</i> , 2022 , 18, e1010458	7.6	1
91	Structural insights into the catalytic cycle of a bacterial multidrug ABC efflux pump.. <i>Journal of Molecular Biology</i> , 2022 , 167541	6.5	2
90	Functional Overexpression of Membrane Proteins in <i>E. coli</i> : The Good, the Bad, and the Ugly. <i>Methods in Molecular Biology</i> , 2022 , 41-58	1.4	
89	Antibiotic Drug Nanocarriers for Probing of Multidrug ABC Membrane Transporter of. <i>ACS Omega</i> , 2020 , 5, 1625-1633	3.9	6
88	Ubk is Involved in the Resistance of <i>Bacillus Subtilis</i> to Oxidative Stress. <i>Current Microbiology</i> , 2020 , 77, 4063-4071	2.4	3
87	Identification of novel inhibitors of the ABC transporter BmrA. <i>Bioorganic Chemistry</i> , 2020 , 105, 104452	5.1	0
86	Multidrug ABC transporters in bacteria. <i>Research in Microbiology</i> , 2019 , 170, 381-391	4	34
85	Flexible-to-rigid transition is central for substrate transport in the ABC transporter BmrA from. <i>Communications Biology</i> , 2019 , 2, 149	6.7	21
84	Functionality of membrane proteins overexpressed and purified from <i>E. coli</i> is highly dependent upon the strain. <i>Scientific Reports</i> , 2019 , 9, 2654	4.9	17
83	The Tyrosine-Autokinase UbK Is Required for Proper Cell Growth and Cell Morphology of. <i>Frontiers in Microbiology</i> , 2019 , 10, 1942	5.7	10
82	Repurposing bioactive aporphine alkaloids as efflux pump inhibitors. <i>Phytotherapy Research</i> , 2019 , 139, 104371	3.2	5
81	Assemblies of lauryl maltose neopentyl glycol (LMNG) and LMNG-solubilized membrane proteins. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2019 , 1861, 939-957	3.8	10
80	A multidrug ABC transporter with a taste for GTP. <i>Scientific Reports</i> , 2018 , 8, 2309	4.9	18
79	High concentrations of GTP induce conformational changes in the essential bacterial GTPase EngA and enhance its binding to the ribosome. <i>FEBS Journal</i> , 2018 , 285, 160-177	5.7	2
78	Quantification of Detergents Complexed with Membrane Proteins. <i>Scientific Reports</i> , 2017 , 7, 41751	4.9	43
77	Expanding the Kinome World: A New Protein Kinase Family Widely Conserved in Bacteria. <i>Journal of Molecular Biology</i> , 2017 , 429, 3056-3074	6.5	17

76	Gradient reconstitution of membrane proteins for solid-state NMR studies. <i>Journal of Biomolecular NMR</i> , 2017 , 69, 81-91	3	8
75	Structures and Transport Mechanisms of the ABC Efflux Pumps 2016 , 73-98		3
74	Two different centered monoclinic crystals of the E. coli outer-membrane protein OmpF originate from the same building block. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2016 , 1858, 326-32	3.8	7
73	Single Nanoparticle Plasmonic Spectroscopy for Study of the Efflux Function of Multidrug ABC Membrane Transporters of Single Live Cells. <i>RSC Advances</i> , 2016 , 6, 36794-36802	3.7	8
72	Diffraction anisotropy falloff in the direction of the detergent belt for two centered monoclinic crystals of OmpF. <i>Data in Brief</i> , 2016 , 7, 726-9	1.2	1
71	Overexpression, Membrane Preparation, and Purification of a Typical Multidrug ABC Transporter BmrA. <i>Methods in Molecular Biology</i> , 2016 , 1432, 133-42	1.4	
70	The C-terminal α helix of YsxC is essential for its binding to 50S ribosome and rRNAs. <i>FEBS Letters</i> , 2015 , 589, 2080-6	3.8	3
69	Interaction between Bacillus subtilis YsxC and ribosomes (or rRNAs). <i>FEBS Letters</i> , 2015 , 589, 1026-32	3.8	3
68	3D cryo-electron reconstruction of BmrA, a bacterial multidrug ABC transporter in an inward-facing conformation and in a lipidic environment. <i>Journal of Molecular Biology</i> , 2014 , 426, 2059-69	6.5	25
67	Efficient and stable reconstitution of the ABC transporter BmrA for solid-state NMR studies. <i>Frontiers in Molecular Biosciences</i> , 2014 , 1, 5	5.6	21
66	Stubborn contaminants: influence of detergents on the purity of the multidrug ABC transporter BmrA. <i>PLoS ONE</i> , 2014 , 9, e114864	3.7	18
65	Small angle neutron scattering for the study of solubilised membrane proteins. <i>European Physical Journal E</i> , 2013 , 36, 71	1.5	58
64	Characterization of hydrophobic peptides in the presence of detergent by photoionization mass spectrometry. <i>PLoS ONE</i> , 2013 , 8, e79033	3.7	19
63	Sedimentation velocity analytical ultracentrifugation in hydrogenated and deuterated solvents for the characterization of membrane proteins. <i>Methods in Molecular Biology</i> , 2013 , 1033, 219-51	1.4	9
62	PatA and PatB form a functional heterodimeric ABC multidrug efflux transporter responsible for the resistance of Streptococcus pneumoniae to fluoroquinolones. <i>Biochemistry</i> , 2012 , 51, 7755-65	3.2	45
61	Phosphorylation of CpgA protein enhances both its GTPase activity and its affinity for ribosome and is crucial for Bacillus subtilis growth and morphology. <i>Journal of Biological Chemistry</i> , 2012 , 287, 20830-8	5.4	14
60	Dynamics of a bacterial multidrug ABC transporter in the inward- and outward-facing conformations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 10832-6	11.5	84
59	Potassium acts as a GTPase-activating element on each nucleotide-binding domain of the essential Bacillus subtilis EngA. <i>PLoS ONE</i> , 2012 , 7, e46795	3.7	18

58	Binding, reconstitution and 2D crystallization of membrane or soluble proteins onto functionalized lipid layer observed in situ by reflected light microscopy. <i>Journal of Structural Biology</i> , 2011 , 174, 307-14 ³⁻⁴	6
57	Structuring detergents for extracting and stabilizing functional membrane proteins. <i>PLoS ONE</i> , 2011 , 6, e18036	3-7 71
56	Optimized purification of a heterodimeric ABC transporter in a highly stable form amenable to 2-D crystallization. <i>PLoS ONE</i> , 2011 , 6, e19677	3-7 29
55	Crenarchaeal CdvA forms double-helical filaments containing DNA and interacts with ESCRT-III-like CdvB. <i>PLoS ONE</i> , 2011 , 6, e21921	3-7 35
54	Hijacking of the pleiotropic cytokine interferon- β by the type III secretion system of <i>Yersinia pestis</i> . <i>PLoS ONE</i> , 2010 , 5, e15242	3-7 5
53	Probing the conformation of the resting state of a bacterial multidrug ABC transporter, BmrA, by a site-directed spin labeling approach. <i>Protein Science</i> , 2009 , 18, 1507-20	6-3 12
52	The YheI/YheH heterodimer from <i>Bacillus subtilis</i> is a multidrug ABC transporter. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2009 , 1788, 615-22	3-8 26
51	The ATPase activity of an essential <i>Bacillus subtilis</i> enzyme, YdiB, is required for its cellular function and is modulated by oligomerization. <i>Microbiology (United Kingdom)</i> , 2009 , 155, 944-956	2-9 18
50	Conformational change induced by ATP binding in the multidrug ATP-binding cassette transporter BmrA. <i>Biochemistry</i> , 2008 , 47, 2404-12	3-2 48
49	Interactions of an essential <i>Bacillus subtilis</i> GTPase, YsxC, with ribosomes. <i>Journal of Bacteriology</i> , 2008 , 190, 681-90	3-5 24
48	Tyrosine-kinase Wzc from <i>Escherichia coli</i> possesses an ATPase activity regulated by autophosphorylation. <i>FEMS Microbiology Letters</i> , 2007 , 274, 252-9	2-9 23
47	<i>Staphylococcus aureus</i> operates protein-tyrosine phosphorylation through a specific mechanism. <i>Journal of Biological Chemistry</i> , 2006 , 281, 14048-56	5-4 48
46	Multiple GTPases participate in the assembly of the large ribosomal subunit in <i>Bacillus subtilis</i> . <i>Journal of Bacteriology</i> , 2006 , 188, 8252-8	3-5 61
45	The ABC transporter BmrA from <i>Bacillus subtilis</i> is a functional dimer when in a detergent-solubilized state. <i>Biochemical Journal</i> , 2006 , 395, 345-53	3-8 49
44	Time-resolved fluorescence resonance energy transfer shows that the bacterial multidrug ABC half-transporter BmrA functions as a homodimer. <i>Biochemistry</i> , 2005 , 44, 4312-21	3-2 23
43	The Q-loop disengages from the first intracellular loop during the catalytic cycle of the multidrug ABC transporter BmrA. <i>Journal of Biological Chemistry</i> , 2005 , 280, 36857-64	5-4 42
42	Two FHA domains on an ABC transporter, Rv1747, mediate its phosphorylation by PknF, a Ser/Thr protein kinase from <i>Mycobacterium tuberculosis</i> . <i>FEMS Microbiology Letters</i> , 2004 , 234, 215-223	2-9 76
41	Characterization of YvcC (BmrA), a multidrug ABC transporter constitutively expressed in <i>Bacillus subtilis</i> . <i>Biochemistry</i> , 2004 , 43, 7491-502	3-2 103

40	Structural insight into the cooperativity between catalytic and noncatalytic sites of F1-ATPase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2004 , 1658, 133-40	4.6	12
39	Two FHA domains on an ABC transporter, Rv1747, mediate its phosphorylation by PknF, a Ser/Thr protein kinase from <i>Mycobacterium tuberculosis</i> . <i>FEMS Microbiology Letters</i> , 2004 , 234, 215-23	2.9	36
38	The conserved glutamate residue adjacent to the Walker-B motif is the catalytic base for ATP hydrolysis in the ATP-binding cassette transporter BmrA. <i>Journal of Biological Chemistry</i> , 2003 , 278, 4700-4	5.4	141
37	Regulation and mutational analysis of the HPr kinase/phosphorylase from <i>Bacillus subtilis</i> . <i>Biochemistry</i> , 2003 , 42, 6762-71	3.2	10
36	A new family of phosphotransferases with a P-loop motif. <i>Journal of Biological Chemistry</i> , 2002 , 277, 11362-7	5.4	24
35	Insights into the functioning of <i>Bacillus subtilis</i> HPr kinase/phosphatase: affinity for its protein substrates and role of cations and phosphate. <i>Biochemistry</i> , 2002 , 41, 6218-25	3.2	10
34	Three-dimensional structure by cryo-electron microscopy of YvcC, an homodimeric ATP-binding cassette transporter from <i>Bacillus subtilis</i> . <i>Journal of Molecular Biology</i> , 2002 , 315, 1075-85	6.5	66
33	Highly efficient over-production in <i>E. coli</i> of YvcC, a multidrug-like ATP-binding cassette transporter from <i>Bacillus subtilis</i> . <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2002 , 1565, 1-5	3.8	38
32	A common mechanism for ATP hydrolysis in ABC transporter and helicase superfamilies. <i>Trends in Biochemical Sciences</i> , 2001 , 26, 539-44	10.3	80
31	Protein kinase C effectors bind to multidrug ABC transporters and inhibit their activity. <i>Biochemistry</i> , 2001 , 40, 2564-71	3.2	53
30	The "catalytic" triad of isocitrate dehydrogenase kinase/phosphatase from <i>E. coli</i> and its relationship with that found in eukaryotic protein kinases. <i>Biochemistry</i> , 2001 , 40, 3047-55	3.2	10
29	Sequence requirements of the ATP-binding site within the C-terminal nucleotide-binding domain of mouse P-glycoprotein: structure-activity relationships for flavonoid binding. <i>Biochemistry</i> , 2001 , 40, 10382-91	3.2	41
28	The HPr kinase from <i>Bacillus subtilis</i> is a homo-oligomeric enzyme which exhibits strong positive cooperativity for nucleotide and fructose 1,6-bisphosphate binding. <i>Journal of Biological Chemistry</i> , 2000 , 275, 1773-80	5.4	82
27	Evidence for a second nucleotide binding site in rat elongation factor eEF-2 specific for adenylic nucleotides. <i>Biochemistry</i> , 2000 , 39, 13558-64	3.2	8
26	Prenyl-flavonoids as potent inhibitors of the Pdr5p multidrug ABC transporter from <i>Saccharomyces cerevisiae</i> . <i>Biochemistry</i> , 2000 , 39, 6910-7	3.2	57
25	The isocitrate dehydrogenase kinase/phosphatase from <i>Escherichia coli</i> is highly sensitive to in-vitro oxidative conditions role of cysteine67 and cysteine108 in the formation of a disulfide-bonded homodimer. <i>FEBS Journal</i> , 1999 , 262, 224-9		9
24	Inactivation of isocitrate dehydrogenase kinase/phosphatase by 5P[p-(fluorosulfonyl)benzoyl]adenosine is not due to the labeling of the invariant lysine residue found in the protein kinase family. <i>FEBS Journal</i> , 1998 , 258, 579-85		10
23	Flavonoids: a class of modulators with bifunctional interactions at vicinal ATP- and steroid-binding sites on mouse P-glycoprotein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1998 , 95, 9831-6	11.5	348

22	Binding of steroid modulators to recombinant cytosolic domain from mouse P-glycoprotein in close proximity to the ATP site. <i>Biochemistry</i> , 1997 , 36, 15208-15	3.2	64
21	Recombinant N-terminal nucleotide-binding domain from mouse P-glycoprotein. Overexpression, purification, and role of cysteine 430. <i>Journal of Biological Chemistry</i> , 1996 , 271, 11652-8	5.4	60
20	An attempt to convert noncatalytic nucleotide binding site of F1-ATPase to the catalytic site: hydrolysis of tethered ATP by mutated alpha subunits in the enzyme. <i>Biochemical and Biophysical Research Communications</i> , 1996 , 220, 94-7	3.4	5
19	Does the gamma subunit move to an abortive position of ATP hydrolysis when the F1.ADP.Mg complex isomerizes to the inactive F1*.ADP.Mg complex?. <i>Journal of Bioenergetics and Biomembranes</i> , 1996 , 28, 433-8	3.7	7
18	The alpha3beta3gamma subcomplex of the F1-ATPase from the thermophilic bacillus PS3 with the betaT165S substitution does not entrap inhibitory MgADP in a catalytic site during turnover. <i>Journal of Biological Chemistry</i> , 1996 , 271, 28818-24	5.4	58
17	The alpha 3 beta 3 gamma complex of the F1-ATPase from thermophilic Bacillus PS3 containing the alpha D261N substitution fails to dissociate inhibitory MgADP from a catalytic site when ATP binds to noncatalytic sites. <i>Biochemistry</i> , 1995 , 34, 16412-8	3.2	68
16	A model for ATP hydrolysis catalysed by F1-ATPases based on kinetic and structural considerations. <i>Biochemical Society Transactions</i> , 1995 , 23, 752-6	5.1	12
15	Cytomegalovirus infection induces high levels of cyclins, phosphorylated Rb, and p53, leading to cell cycle arrest. <i>Journal of Virology</i> , 1995 , 69, 6697-704	6.6	232
14	Preparation of highly phosphorylating mitochondria from the yeast <i>Schizosaccharomyces pombe</i> . <i>Journal of Bioenergetics and Biomembranes</i> , 1994 , 26, 447-56	3.7	9
13	Probing the specificity of nucleotide binding to the F1-ATPase from thermophilic Bacillus PS3 and its isolated alpha and beta subunits with 2-N3-[beta, gamma-32P]ATP. <i>Archives of Biochemistry and Biophysics</i> , 1994 , 310, 282-8	4.1	16
12	Catalytic cooperativity of beef heart mitochondrial F1-ATPase revealed by using 2P3PO-(2,4,6-trinitrophenyl)-ATP as a substrate; an indication of mutually activating catalytic sites. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1994 , 1188, 108-16	4.6	6
11	ADP tethered to tyrosine-beta 345 at the catalytic site of the bovine heart F1-ATPase is converted to tethered AMP by Mg(2+)-dependent hydrolysis when the enzyme is photoinactivated with 2-N3-ADP. <i>FEBS Letters</i> , 1994 , 347, 13-6	3.8	5
10	Lowered temperature or binding of pyrophosphate to sites for noncatalytic nucleotides modulates the ATPase activity of the beef heart mitochondrial F1-ATPase by decreasing the affinity of a catalytic site for inhibitory MgADP. <i>Biochemistry</i> , 1994 , 33, 14979-85	3.2	18
9	Glutamine 170 to tyrosine substitution in yeast mitochondrial F1 beta-subunit increases catalytic site interaction with GDP and IDP and produces negative cooperativity of GTP and ITP hydrolysis. <i>Journal of Biological Chemistry</i> , 1993 , 268, 20762-7	5.4	8
8	Slow binding of ATP to noncatalytic nucleotide binding sites which accelerates catalysis is responsible for apparent negative cooperativity exhibited by the bovine mitochondrial F1-ATPase. <i>Journal of Biological Chemistry</i> , 1993 , 268, 1558-66	5.4	95
7	Functional sites in F1-ATPases: location and interactions. <i>Journal of Bioenergetics and Biomembranes</i> , 1992 , 24, 469-77	3.7	40
6	Alteration of apparent negative cooperativity of ATPase activity by alpha-subunit glutamine 173 mutation in yeast mitochondrial F1. Correlation with impaired nucleotide interaction at a regulatory site. <i>Journal of Biological Chemistry</i> , 1991 , 266, 8073-8	5.4	17
5	Purification from a yeast mutant of mitochondrial F1 with modified beta-subunit. High affinity for nucleotides and high negative cooperativity of ATPase activity. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1989 , 975, 119-26	4.6	11

4	A yeast strain with mutated beta-subunits of mitochondrial ATPase-ATP synthase: high azide and bicarbonate sensitivity of the ATPase activity. <i>Biochemical and Biophysical Research Communications</i> , 1989 , 158, 392-9	3.4	13
3	Structure-function relationships of mitochondrial ATPase-ATP synthase using <i>Schizosaccharomyces pombe</i> yeast mutants with altered F1 subunits. <i>Biochimie</i> , 1989 , 71, 931-40	4.6	9
2	Revertant of the yeast <i>Schizosaccharomyces pombe</i> with modified alpha subunits of mitochondrial ATPase-ATP synthase: impaired nucleotide interactions with soluble and membrane-bound enzyme. <i>Biochemical and Biophysical Research Communications</i> , 1987 , 148, 1182-8	3.4	13
1	Drug-bound and -free outward-facing structures of a multidrug ABC exporter point to a swing mechanism		2