

John E Walker

List of Publications by Year in descending order

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117
papers

16,587
citations

22153

59
h-index

23533

111
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120
all docs

120
docs citations

120
times ranked

9043
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure at 2.8 Å, resolution of F1-ATPase from bovine heart mitochondria. <i>Nature</i> , 1994, 370, 621-628.	27.8	3,138
2	Molecular Architecture of the Rotary Motor in ATP Synthase. <i>Science</i> , 1999, 286, 1700-1705.	12.6	1,224
3	The NADH:ubiquinone oxidoreductase (complex I) of respiratory chains. <i>Quarterly Reviews of Biophysics</i> , 1992, 25, 253-324.	5.7	738
4	The UNC operon nucleotide sequence, regulation and structure of ATP-synthase. <i>Biochimica Et Biophysica Acta - Reviews on Bioenergetics</i> , 1984, 768, 164-200.	0.2	505
5	The ATP synthase: the understood, the uncertain and the unknown. <i>Biochemical Society Transactions</i> , 2013, 41, 1-16.	3.4	499
6	Structure of Bovine Mitochondrial F1-ATPase with Nucleotide Bound to All Three Catalytic Sites. <i>Cell</i> , 2001, 106, 331-341.	28.9	452
7	Bioenergetic cost of making an adenosine triphosphate molecule in animal mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 16823-16827.	7.1	443
8	The structure of the central stalk in bovine F(1)-ATPase at 2.4 Å resolution. <i>Nature Structural Biology</i> , 2000, 7, 1055-1061.	9.7	427
9	Mechanism of inhibition of bovine F ₁ -ATPase by resveratrol and related polyphenols. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13632-13637.	7.1	342
10	Mitochondrial ATP synthase subunit storage in the ceroid-lipofuscinoses (Batten disease). <i>American Journal of Medical Genetics Part A</i> , 1992, 42, 561-567.	2.4	334
11	Internal sequence repeats and the path of polypeptide in mitochondrial ADP/ATP translocase. <i>FEBS Letters</i> , 1982, 144, 250-254.	2.8	297
12	ATP Synthesis by Rotary Catalysis (Nobel lecture). <i>Angewandte Chemie - International Edition</i> , 1998, 37, 2308-2319.	13.8	278
13	Structure and conformational states of the bovine mitochondrial ATP synthase by cryo-EM. <i>ELife</i> , 2015, 4, e10180.	6.0	264
14	The crystal structure of the nucleotide-free \hat{F}_1F_0 subcomplex of F1-ATPase from the thermophilic <i>Bacillus PS3</i> is a symmetric trimer. <i>Structure</i> , 1997, 5, 825-836.	3.3	241
15	How azide inhibits ATP hydrolysis by the F-ATPases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 8646-8649.	7.1	220
16	Persistence of the mitochondrial permeability transition in the absence of subunit c of human ATP synthase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3409-3414.	7.1	219
17	How the regulatory protein, IF ₁ , inhibits F ₁ -ATPase from bovine mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 15671-15676.	7.1	188
18	Identification of the subunits of F1F0-ATPase from bovine heart mitochondria. <i>Biochemistry</i> , 1991, 30, 5369-5378.	2.5	185

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19	Sequences of 20 subunits of NADH: Ubiquinone oxidoreductase from bovine heart mitochondria. <i>Journal of Molecular Biology</i> , 1992, 226, 1051-1072.	4.2	185
20	The structure of bovine F1-ATPase in complex with its regulatory protein IF1. <i>Nature Structural and Molecular Biology</i> , 2003, 10, 744-750.	8.2	182
21	F0 Membrane Domain of ATP Synthase from Bovine Heart Mitochondria: Purification, Subunit Composition, and Reconstitution with F1-ATPase. <i>Biochemistry</i> , 1994, 33, 7971-7978.	2.5	180
22	On the structure of the stator of the mitochondrial ATP synthase. <i>EMBO Journal</i> , 2006, 25, 2911-2918.	7.8	178
23	Ground State Structure of F1-ATPase from Bovine Heart Mitochondria at 1.9 Å Resolution. <i>Journal of Biological Chemistry</i> , 2007, 282, 14238-14242.	3.4	176
24	Novel features of the rotary catalytic mechanism revealed in the structure of yeast F1 ATPase. <i>EMBO Journal</i> , 2006, 25, 5433-5442.	7.8	175
25	The peripheral stalk of the mitochondrial ATP synthase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2006, 1757, 286-296.	1.0	167
26	The structure of the membrane extrinsic region of bovine ATP synthase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21597-21601.	7.1	167
27	Modulation of the Oligomerization State of the Bovine F1-ATPase Inhibitor Protein, IF1, by pH. <i>Journal of Biological Chemistry</i> , 2000, 275, 25460-25464.	3.4	164
28	Structure of bovine mitochondrial F1-ATPase inhibited by Mg ²⁺ +ADP and aluminium fluoride. <i>Structure</i> , 2000, 8, 567-573.	3.3	163
29	Permeability transition in human mitochondria persists in the absence of peripheral stalk subunits of ATP synthase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 9086-9091.	7.1	163
30	The structure of bovine F1-ATPase inhibited by ADP and beryllium fluoride. <i>EMBO Journal</i> , 2004, 23, 2734-2744.	7.8	160
31	SIRT3 Deacetylates ATP Synthase F ₁ Complex Proteins in Response to Nutrient- and Exercise-Induced Stress. <i>Antioxidants and Redox Signaling</i> , 2014, 21, 551-564.	5.4	159
32	Homology between human bladder carcinoma oncogene product and mitochondrial ATP-synthase. <i>Nature</i> , 1983, 301, 262-264.	27.8	153
33	Assembly of the membrane domain of ATP synthase in human mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2988-2993.	7.1	152
34	Structure of the dimeric ATP synthase from bovine mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 23519-23526.	7.1	136
35	Structure of ATP synthase from <i>Paracoccus denitrificans</i> determined by X-ray crystallography at 4.0 Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13231-13236.	7.1	131
36	Assembly factors for the membrane arm of human complex I. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 18934-18939.	7.1	127

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37	E. coli F1-ATPase interacts with a membrane protein component of a proton channel. Nature, 1982, 298, 867-869.	27.8	121
38	Heat Stability of a Tetrameric Enzyme, D-Glyceraldehyde-3-Phosphate Dehydrogenase. FEBS Journal, 1980, 108, 581-586.	0.2	117
39	Lysine residue 199 of human serum albumin is modified by acetylsalicylic acid. FEBS Letters, 1976, 66, 173-175.	2.8	116
40	Cardiolipin binds selectively but transiently to conserved lysine residues in the rotor of metazoan ATP synthases. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 8687-8692.	7.1	116
41	Arrangement of subunits in intact mammalian mitochondrial ATP synthase determined by cryo-EM. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11675-11680.	7.1	112
42	A sixth subunit of ATP synthase, an F ₀ component, is encoded in the pea chloroplast genome. EMBO Journal, 1986, 5, 217-222.	7.8	109
43	Novel features in the structure of bovine ATP synthase. Journal of Molecular Biology, 1999, 290, 379-384.	4.2	109
44	Persistence of the permeability transition pore in human mitochondria devoid of an assembled ATP synthase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 12816-12821.	7.1	108
45	Dimerization of Bovine F1-ATPase by Binding the Inhibitor Protein, IF1. Journal of Biological Chemistry, 2000, 275, 28353-28355.	3.4	97
46	Bovine F1-ATPase covalently inhibited with 4-chloro-7-nitrobenzofurazan: the structure provides further support for a rotary catalytic mechanism. Structure, 1998, 6, 831-837.	3.3	95
47	Subunit equivalence in Escherichia coli and bovine heart mitochondrial F1 F0 ATPases. FEBS Letters, 1982, 146, 393-396.	2.8	94
48	Domain structure of bacteriophage fd adsorption protein. FEBS Letters, 1981, 135, 167-172.	2.8	91
49	ATP synthase from bovine mitochondria: sequences of imported precursors of oligomycin sensitivity conferral protein, factor 6, and adenosine triphosphatase inhibitor protein. Biochemistry, 1987, 26, 8613-8619.	2.5	91
50	Solid-Phase Sequence Analysis of Polypeptides Eluted from Polyacrylamide Gels. An Aid to Interpretation of DNA Sequences Exemplified by the Escherichia coli unc Operon and Bacteriophage Lambda. FEBS Journal, 1982, 123, 253-260.	0.2	83
51	Structural evidence of a new catalytic intermediate in the pathway of ATP hydrolysis by F ₁ -ATPase from bovine heart mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 11139-11143.	7.1	80
52	The ATPase Inhibitor Protein from Bovine Heart Mitochondria: The Minimal Inhibitory Sequence. Biochemistry, 1996, 35, 15618-15625.	2.5	79
53	D-Glyceraldehyde-3-Phosphate Dehydrogenase. Complete Amino-Acid Sequence of the Enzyme from Bacillus stearothermophilus. FEBS Journal, 1980, 108, 549-565.	0.2	76
54	The F1Fo-ATPase Complex from Bovine Heart Mitochondria: The Molar Ratio of the Subunits in the Stalk Region Linking the F1 and Fo Domains. Biochemistry, 1996, 35, 12640-12646.	2.5	76

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55	Structural Comparisons of Superoxide Dismutases. <i>FEBS Journal</i> , 1980, 106, 297-303.	0.2	76
56	Pathway of binding of the intrinsically disordered mitochondrial inhibitor protein to F ₁ -ATPase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11305-11310.	7.1	75
57	The role of the stalk in the coupling mechanism of F ₁ F ₀ -ATPases. <i>FEBS Letters</i> , 1994, 346, 39-43.	2.8	72
58	Structure of the mitochondrial ATP synthase from <i>Pichia angusta</i> determined by electron cryo-microscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 12709-12714.	7.1	66
59	A gelsolin-like Ca ²⁺ -dependent actin-binding domain in villin. <i>Nature</i> , 1985, 315, 248-250.	27.8	65
60	Sequences of the human and bovine genes for the mitochondrial 2-oxoglutarate carrier. <i>DNA Sequence</i> , 1992, 3, 79-88.	0.7	60
61	Binding of the Inhibitor Protein IF1 to Bovine F ₁ -ATPase. <i>Journal of Molecular Biology</i> , 2011, 406, 443-453.	4.2	59
62	ATP Synthase from Bovine Heart Mitochondria. <i>Journal of Molecular Biology</i> , 1994, 242, 408-421.	4.2	52
63	Asymmetric Structure of the Yeast F ₁ ATPase in the Absence of Bound Nucleotides. <i>Journal of Biological Chemistry</i> , 2009, 284, 10546-10551.	3.4	52
64	Regulation of bovine kidney branched-chain 2-oxoacid dehydrogenase complex by reversible phosphorylation. <i>FEBS Journal</i> , 1984, 145, 587-591.	0.2	51
65	How release of phosphate from mammalian F ₁ -ATPase generates a rotary substep. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 6009-6014.	7.1	51
66	Regulation of the thermoalkaliphilic F ₁ -ATPase from <i>Caldalkalibacillus thermarum</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10860-10865.	7.1	51
67	Association of two proteolipids of unknown function with ATP synthase from bovine heart mitochondria. <i>FEBS Letters</i> , 2007, 581, 3145-3148.	2.8	50
68	The affinity purification and characterization of ATP synthase complexes from mitochondria. <i>Open Biology</i> , 2013, 3, 120160.	3.6	50
69	Human METTL20 Methylates Lysine Residues Adjacent to the Recognition Loop of the Electron Transfer Flavoprotein in Mitochondria. <i>Journal of Biological Chemistry</i> , 2014, 289, 24640-24651.	3.4	48
70	Homoserine Kinase from <i>Escherichia coli</i> K12. <i>FEBS Journal</i> , 1976, 62, 519-526.	0.2	46
71	Solution structure of a C-terminal coiled-coil domain from bovine IF1: the inhibitor protein of F ₁ ATPase. Edited by M. F. Summers. <i>Journal of Molecular Biology</i> , 2001, 308, 325-339.	4.2	46
72	Model of the c-subunit oligomer in the membrane domain of F ₁ -ATPases. <i>FEBS Letters</i> , 1997, 410, 117-123.	2.8	44

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73	Organization of Subunits in the Membrane Domain of the Bovine F-ATPase Revealed by Covalent Cross-linking. <i>Journal of Biological Chemistry</i> , 2015, 290, 13308-13320.	3.4	44
74	The topography of the purple membrane. <i>Nature</i> , 1979, 278, 653-654.	27.8	43
75	NDUF5 Hydroxylates NDUF7 at an Early Stage in the Assembly of Human Complex I. <i>Journal of Biological Chemistry</i> , 2016, 291, 14851-14860.	3.4	43
76	The structure of F ₁ -ATPase from <i>Saccharomyces cerevisiae</i> inhibited by its regulatory protein IF ₁ . <i>Open Biology</i> , 2013, 3, 120164.	3.6	40
77	ATP synthase from bovine heart mitochondria: reconstitution into unilamellar phospholipid vesicles of the pure enzyme in a functional state. <i>Biochemical Journal</i> , 1996, 318, 351-357.	3.7	39
78	The structure of the catalytic domain of the ATP synthase from <i>Mycobacterium smegmatis</i> is a target for developing antitubercular drugs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 4206-4211.	7.1	38
79	Measurement of the molecular masses of hydrophilic and hydrophobic subunits of ATP synthase and complex I in a single experiment. <i>Analytical Biochemistry</i> , 2009, 395, 249-255.	2.4	36
80	The structure and nucleotide occupancy of bovine mitochondrial F ₁ -ATPase are not influenced by crystallisation at high concentrations of nucleotide. <i>FEBS Letters</i> , 2001, 494, 11-14.	2.8	35
81	Important mitochondrial proteins in human omental adipose tissue show reduced expression in obesity. <i>Journal of Proteomics</i> , 2015, 124, 79-87.	2.4	35
82	D-Glyceraldehyde-3-Phosphate Dehydrogenase. The Purification and Characterisation of the Enzyme from the Thermophiles <i>Bacillus stearothermophilus</i> and <i>Thermus aquaticus</i> . <i>FEBS Journal</i> , 1980, 108, 535-547.	0.2	34
83	Human METTL12 is a mitochondrial methyltransferase that modifies citrate synthase. <i>FEBS Letters</i> , 2017, 591, 1641-1652.	2.8	32
84	How the N-terminal Domain of the OSCP Subunit of Bovine F ₁ F _o -ATP Synthase Interacts with the N-terminal Region of an Alpha Subunit. <i>Journal of Molecular Biology</i> , 2007, 368, 310-318.	4.2	30
85	Isolation of a novel calcium-binding protein from <i>Streptomyces erythreus</i> . <i>FEBS Letters</i> , 1984, 178, 157-160.	2.8	28
86	Conservation of Complete Trimethylation of Lysine-43 in the Rotor Ring of c-Subunits of Metazoan Adenosine Triphosphate (ATP) Synthases*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 828-840.	3.8	27
87	ATP synthase from <i>Trypanosoma brucei</i> has an elaborated canonical F ₁ -domain and conventional catalytic sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2102-2107.	7.1	27
88	Structure of the ATP synthase from <i>Mycobacterium smegmatis</i> provides targets for treating tuberculosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	27
89	Interface mobility between monomers in dimeric bovine ATP synthase participates in the ultrastructure of inner mitochondrial membranes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	26
90	Extrinsic conditions influence the self-association and structure of IF ₁ , the regulatory protein of mitochondrial ATP synthase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10354-10359.	7.1	25

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91	PINK1 rendered temperature sensitive by disease-associated and engineered mutations. Human Molecular Genetics, 2013, 22, 2572-2589.	2.9	23
92	The purification and characterization of ATP synthase complexes from the mitochondria of four fungal species. Biochemical Journal, 2015, 468, 167-175.	3.7	23
93	Sequence and pattern of expression of a bovine homologue of a human mitochondrial transport protein associated with Grave's disease. DNA Sequence, 1992, 3, 71-78.	0.7	22
94	The F ₁ -ATPase from <i>Trypanosoma brucei</i> is elaborated by three copies of an additional p18 subunit. FEBS Journal, 2018, 285, 614-628.	4.7	20
95	Assembly of the peripheral stalk of ATP synthase in human mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 29602-29608.	7.1	19
96	TMEM70 and TMEM242 help to assemble the rotor ring of human ATP synthase and interact with assembly factors for complex I. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	19
97	Reply to Bernardi: The mitochondrial permeability transition pore and the ATP synthase. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 2745-2746.	7.1	18
98	Coupling capacity of solid phase sequencing supports. FEBS Letters, 1977, 81, 403-405.	2.8	15
99	Structure, Mechanism and Regulation of ATP Synthases. Chemical Biology, 2017, , 338-373.	0.2	15
100	Structure and genes of ATP synthase. Biochemical Society Transactions, 1987, 15, 104-106.	3.4	14
101	Electrospray ionization mass spectrometric analysis of subunits of NADH:ubiquinone oxidoreductase (complex I) from bovine heart mitochondria. Biochemical Society Transactions, 1994, 22, 551-555.	3.4	13
102	Purification, characterization and crystallization of the F-ATPase from <i>Paracoccus denitrificans</i> . Open Biology, 2015, 5, 150119.	3.6	13
103	The Amino-Acid Sequence of a Fragment of Human-Serum Albumin Containing Two of Its Antigenic Determinants. FEBS Journal, 1976, 69, 517-526.	0.2	12
104	Comment on "Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry". Science, 2019, 366, .	12.6	10
105	Structure of a catalytic dimer of the \hat{F}_1 - and \hat{F}_2 -subunits of the F-ATPase from <i>Paracoccus denitrificans</i> at 2.3 Å resolution. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 1309-1317.	0.8	9
106	Altered chromatographic behaviour of mitochondrial ADP/ATP translocase induced by stabilization of the protein by binding of 6-O-fluorescein-actyloside. Biochemical Journal, 2003, 376, 757-763.	3.7	8
107	Overlapping Genes in Bacteriophages ϕ X174 and G4. Biochemical Society Transactions, 1978, 6, 63-67.	3.4	7
108	Inhibition of F ₁ -ATPase from <i>Trypanosoma brucei</i> by its regulatory protein inhibitor Tb IF 1. FEBS Journal, 2018, 285, 4413-4423.	4.7	5

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109	Important mitochondrial proteins in human omental adipose tissue show reduced expression in obesity. <i>Data in Brief</i> , 2015, 4, 40-43.	1.0	4
110	Structure of F ₁ -ATPase from the obligate anaerobe <i>Fusobacterium nucleatum</i> . <i>Open Biology</i> , 2019, 9, 190066.	3.6	3
111	Genes for bacterial and mitochondrial ATP synthase. <i>Biochemical Society Transactions</i> , 1984, 12, 234-235.	3.4	2
112	ATP Synthesis by Rotary Catalysis (Nobel lecture). , 1998, 37, 2308.		2
113	Modular Assembly of ATP Synthase. , 2019, , 119-134.		2
114	ATP Synthesis by Rotary Catalysis (Nobel lecture). , 1998, 37, 2308.		1
115	ROTARY MECHANISM OF ATP SYNTHESIS. <i>Biochemical Society Transactions</i> , 2000, 28, A97-A97.	3.4	0
116	Regulation, functional analysis and assembly of dimeric ATP synthases in mitochondria. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, e2-e3.	1.0	0
117	Deletion of subunits of human ATP synthase and impact on the mitochondrial permeability transition. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2018, 1859, e111.	1.0	0