

John E Walker

List of Publications by Year in descending order

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117
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16,587
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22153

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all docs

120
docs citations

120
times ranked

9043
citing authors

#	ARTICLE	IF	CITATIONS
1	Interface mobility between monomers in dimeric bovine ATP synthase participates in the ultrastructure of inner mitochondrial membranes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	26
2	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
3	Structure of the ATP synthase from <i>Mycobacterium smegmatis</i> provides targets for treating tuberculosis. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	27
4	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
5	Structure of the dimeric ATP synthase from bovine mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 23519-23526.	7.1	136
6	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
7	Comment on "Protein assemblies ejected directly from native membranes yield complexes for mass spectrometry". Science, 2019, 366, .	12.6	10
8	The structure of the catalytic domain of the ATP synthase from <i>Mycobacterium smegmatis</i> is a target for developing antitubercular drugs. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 4206-4211.	7.1	38
9	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
10	Structure of F ₁ -ATPase from the obligate anaerobe <i>Fusobacterium nucleatum</i> . Open Biology, 2019, 9, 190066.	3.6	3
11	Extrinsic conditions influence the self-association and structure of IF ₁ , the regulatory protein of mitochondrial ATP synthase. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 10354-10359.	7.1	25
12	Modular Assembly of ATP Synthase. , 2019, , 119-134.		2
13	ATP synthase from <i>Trypanosoma brucei</i> has an elaborated canonical F ₁ -domain and conventional catalytic sites. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2102-2107.	7.1	27
14	Assembly of the membrane domain of ATP synthase in human mitochondria. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2988-2993.	7.1	152
15	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
16	Regulation, functional analysis and assembly of dimeric ATP synthases in mitochondria. Biochimica Et Biophysica Acta - Bioenergetics, 2018, 1859, e2-e3.	1.0	0
17	Deletion of subunits of human ATP synthase and impact on the mitochondrial permeability transition. Biochimica Et Biophysica Acta - Bioenergetics, 2018, 1859, e111.	1.0	0
18	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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19	Human METTL12 is a mitochondrial methyltransferase that modifies citrate synthase. <i>FEBS Letters</i> , 2017, 591, 1641-1652.	2.8	32
20	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
21	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
22	Structure, Mechanism and Regulation of ATP Synthases. <i>Chemical Biology</i> , 2017, , 338-373.	0.2	15
23	Cardiolipin binds selectively but transiently to conserved lysine residues in the rotor of metazoan ATP synthases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 8687-8692.	7.1	116
24	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
25	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
26	NDUFAF5 Hydroxylates NDUF57 at an Early Stage in the Assembly of Human Complex I. <i>Journal of Biological Chemistry</i> , 2016, 291, 14851-14860.	3.4	43
27	Purification, characterization and crystallization of the F-ATPase from <i>Paracoccus denitrificans</i> . <i>Open Biology</i> , 2015, 5, 150119.	3.6	13
28	Structure of a catalytic dimer of the $\hat{1}\pm$ - and $\hat{1}^2$ -subunits of the F-ATPase from <i>Paracoccus denitrificans</i> at 2.3 Å resolution. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2015, 71, 1309-1317.	0.8	9
29	Structure and conformational states of the bovine mitochondrial ATP synthase by cryo-EM. <i>ELife</i> , 2015, 4, e10180.	6.0	264
30	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
31	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
32	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
33	The purification and characterization of ATP synthase complexes from the mitochondria of four fungal species. <i>Biochemical Journal</i> , 2015, 468, 167-175.	3.7	23
34	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
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	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

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37	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
38	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
39	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
40	PINK1 rendered temperature sensitive by disease-associated and engineered mutations. <i>Human Molecular Genetics</i> , 2013, 22, 2572-2589.	2.9	23
41	The ATP synthase: the understood, the uncertain and the unknown. <i>Biochemical Society Transactions</i> , 2013, 41, 1-16.	3.4	499
42	The affinity purification and characterization of ATP synthase complexes from mitochondria. <i>Open Biology</i> , 2013, 3, 120160.	3.6	50
43	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
44	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
45	Structural evidence of a new catalytic intermediate in the pathway of ATP hydrolysis by F ₁ -ATPase from bovine heart mitochondria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11139-11143.	7.1	80
46	Arrangement of subunits in intact mammalian mitochondrial ATP synthase determined by cryo-EM. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 11675-11680.	7.1	112
47	Binding of the Inhibitor Protein IF ₁ to Bovine F ₁ -ATPase. <i>Journal of Molecular Biology</i> , 2011, 406, 443-453.	4.2	59
48	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
49	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
50	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
51	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
52	Ground State Structure of F ₁ -ATPase from Bovine Heart Mitochondria at 1.9 Å Resolution. <i>Journal of Biological Chemistry</i> , 2007, 282, 14238-14242.	3.4	176
53	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
54	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

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55	How the N-terminal Domain of the OSCP Subunit of Bovine F1Fo-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
56	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
57	The peripheral stalk of the mitochondrial ATP synthase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2006, 1757, 286-296.	1.0	167
58	On the structure of the stator of the mitochondrial ATP synthase. <i>EMBO Journal</i> , 2006, 25, 2911-2918.	7.8	178
59	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
60	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
61	The structure of bovine F1-ATPase inhibited by ADP and beryllium fluoride. <i>EMBO Journal</i> , 2004, 23, 2734-2744.	7.8	160
62	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
63	Altered chromatographic behaviour of mitochondrial ADP/ATP translocase induced by stabilization of the protein by binding of 6â€²-O-fluorescein-atractyloside. <i>Biochemical Journal</i> , 2003, 376, 757-763.	3.7	8
64	Solution structure of a C-terminal coiled-coil domain from bovine IF1: the inhibitor protein of F1 ATPase1 1Edited by M. F. Summers. <i>Journal of Molecular Biology</i> , 2001, 308, 325-339.	4.2	46
65	The structure and nucleotide occupancy of bovine mitochondrial F1-ATPase are not influenced by crystallisation at high concentrations of nucleotide. <i>FEBS Letters</i> , 2001, 494, 11-14.	2.8	35
66	Structure of Bovine Mitochondrial F1-ATPase with Nucleotide Bound to All Three Catalytic Sites. <i>Cell</i> , 2001, 106, 331-341.	28.9	452
67	ROTARY MECHANISM OF ATP SYNTHESIS. <i>Biochemical Society Transactions</i> , 2000, 28, A97-A97.	3.4	0
68	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
69	Structure of bovine mitochondrial F1-ATPase inhibited by Mg ²⁺ +ADP and aluminium fluoride. <i>Structure</i> , 2000, 8, 567-573.	3.3	163
70	Dimerization of Bovine F1-ATPase by Binding the Inhibitor Protein, IF1. <i>Journal of Biological Chemistry</i> , 2000, 275, 28353-28355.	3.4	97
71	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
72	Molecular Architecture of the Rotary Motor in ATP Synthase. <i>Science</i> , 1999, 286, 1700-1705.	12.6	1,224

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73	Novel features in the structure of bovine ATP synthase. <i>Journal of Molecular Biology</i> , 1999, 290, 379-384.	4.2	109
74	Bovine F1-ATPase covalently inhibited with 4-chloro-7-nitrobenzofurazan: the structure provides further support for a rotary catalytic mechanism. <i>Structure</i> , 1998, 6, 831-837.	3.3	95
75	ATP Synthesis by Rotary Catalysis (Nobel lecture). <i>Angewandte Chemie - International Edition</i> , 1998, 37, 2308-2319.	13.8	278
76	ATP Synthesis by Rotary Catalysis (Nobel lecture). , 1998, 37, 2308.		1
77	ATP Synthesis by Rotary Catalysis (Nobel lecture). , 1998, 37, 2308.		2
78	Model of the c-subunit oligomer in the membrane domain of F-ATPases. <i>FEBS Letters</i> , 1997, 410, 117-123.	2.8	44
79	The crystal structure of the nucleotide-free \hat{c}_3 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
80	The F1Fo-ATPase Complex from Bovine Heart Mitochondria: The Molar Ratio of the Subunits in the Stalk Region Linking the F1 and Fo Domains. <i>Biochemistry</i> , 1996, 35, 12640-12646.	2.5	76
81	The ATPase Inhibitor Protein from Bovine Heart Mitochondria: The Minimal Inhibitory Sequence. <i>Biochemistry</i> , 1996, 35, 15618-15625.	2.5	79
82	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
83	Structure at 2.8 Å resolution of F1-ATPase from bovine heart mitochondria. <i>Nature</i> , 1994, 370, 621-628.	27.8	3,138
84	ATP Synthase from Bovine Heart Mitochondria. <i>Journal of Molecular Biology</i> , 1994, 242, 408-421.	4.2	52
85	The role of the stalk in the coupling mechanism of F1FO-ATPases. <i>FEBS Letters</i> , 1994, 346, 39-43.	2.8	72
86	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
87	Electrospray ionization mass spectrometric analysis of subunits of NADH:ubiquinone oxidoreductase (complex I) from bovine heart mitochondria. <i>Biochemical Society Transactions</i> , 1994, 22, 551-555.	3.4	13
88	Sequence and pattern of expression of a bovine homologue of a human mitochondrial transport protein associated with Grave's disease. <i>DNA Sequence</i> , 1992, 3, 71-78.	0.7	22
89	Sequences of the human and bovine genes for the mitochondrial 2-oxoglutarate carrier. <i>DNA Sequence</i> , 1992, 3, 79-88.	0.7	60
90	The NADH:ubiquinone oxidoreductase (complex I) of respiratory chains. <i>Quarterly Reviews of Biophysics</i> , 1992, 25, 253-324.	5.7	738

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91	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
92	Mitochondrial ATP synthase subunitc storage in the ceroid-lipofuscinoses (Batten disease). <i>American Journal of Medical Genetics Part A</i> , 1992, 42, 561-567.	2.4	334
93	Identification of the subunits of F1F0-ATPase from bovine heart mitochondria. <i>Biochemistry</i> , 1991, 30, 5369-5378.	2.5	185
94	Structure and genes of ATP synthase. <i>Biochemical Society Transactions</i> , 1987, 15, 104-106.	3.4	14
95	ATP synthase from bovine mitochondria: sequences of imported precursors of oligomycin sensitivity conferral protein, factor 6, and adenosine triphosphatase inhibitor protein. <i>Biochemistry</i> , 1987, 26, 8613-8619.	2.5	91
96	A sixth subunit of ATP synthase, an F ₀ component, is encoded in the pea chloroplast genome. <i>EMBO Journal</i> , 1986, 5, 217-222.	7.8	109
97	A gelsolin-like Ca ²⁺ -dependent actin-binding domain in villin. <i>Nature</i> , 1985, 315, 248-250.	27.8	65
98	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
99	Regulation of bovine kidney branched-chain 2-oxoacid dehydrogenase complex by reversible phosphorylation. <i>FEBS Journal</i> , 1984, 145, 587-591.	0.2	51
100	Isolation of a novel calcium-binding protein from streptomyces erythreus. <i>FEBS Letters</i> , 1984, 178, 157-160.	2.8	28
101	Genes for bacterial and mitochondrial ATP synthase. <i>Biochemical Society Transactions</i> , 1984, 12, 234-235.	3.4	2
102	Homology between human bladder carcinoma oncogene product and mitochondrial ATP-synthase. <i>Nature</i> , 1983, 301, 262-264.	27.8	153
103	Internal sequence repeats and the path of polypeptide in mitochondrial ADP/ATP translocase. <i>FEBS Letters</i> , 1982, 144, 250-254.	2.8	297
104	Subunit equivalence in Escherichia coli and bovine heart mitochondrial F1 F0 ATPases. <i>FEBS Letters</i> , 1982, 146, 393-396.	2.8	94
105	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. <i>FEBS Journal</i> , 1982, 123, 253-260.	0.2	83
106	E. coli F1-ATPase interacts with a membrane protein component of a proton channel. <i>Nature</i> , 1982, 298, 867-869.	27.8	121
107	Domain structure of bacteriophage fd adsorption protein. <i>FEBS Letters</i> , 1981, 135, 167-172.	2.8	91
108	D-Glyceraldehyde-3-Phosphate Dehydrogenase. The Purification and Characterisation of the Enzyme from the Thermophiles Bacillus stearothermophilus and Thermus aquaticus. <i>FEBS Journal</i> , 1980, 108, 535-547.	0.2	34

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109	D-Glyceraldehyde-3-Phosphate Dehydrogenase. Complete Amino-Acid Sequence of the Enzyme from <i>Bacillus stearothermophilus</i> . FEBS Journal, 1980, 108, 549-565.	0.2	76
110	Heat Stability of a Tetrameric Enzyme, D-Glyceraldehyde-3-Phosphate Dehydrogenase. FEBS Journal, 1980, 108, 581-586.	0.2	117
111	Structural Comparisons of Superoxide Dismutases. FEBS Journal, 1980, 106, 297-303.	0.2	76
112	The topography of the purple membrane. Nature, 1979, 278, 653-654.	27.8	43
113	Overlapping Genes in Bacteriophages ϕ X174 and G4. Biochemical Society Transactions, 1978, 6, 63-67.	3.4	7
114	Coupling capacity of solid phase sequencing supports. FEBS Letters, 1977, 81, 403-405.	2.8	15
115	Lysine residue 199 of human serum albumin is modified by acetylsalicylic acid. FEBS Letters, 1976, 66, 173-175.	2.8	116
116	Homoserine Kinase from <i>Escherichia coli</i> K12. FEBS Journal, 1976, 62, 519-526.	0.2	46
117	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