

Gerhard GrÃ¼ber

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5138944/publications.pdf>

Version: 2024-02-01

174
papers

4,047
citations

136950

32
h-index

168389

53
g-index

174
all docs

174
docs citations

174
times ranked

3598
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystal Structure of the NS3 Protease-Helicase from Dengue Virus. <i>Journal of Virology</i> , 2008, 82, 173-183.	3.4	241
2	Eukaryotic V-ATPase: Novel structural findings and functional insights. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 857-879.	1.0	150
3	Exploiting the synthetic lethality between terminal respiratory oxidases to kill <i>Mycobacterium tuberculosis</i> and clear host infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 7426-7431.	7.1	141
4	A WNK kinase binds and phosphorylates V-ATPase subunit C. <i>FEBS Letters</i> , 2006, 580, 932-939.	2.8	114
5	The C-terminal 50 Amino Acid Residues of Dengue NS3 Protein Are Important for NS3-NS5 Interaction and Viral Replication. <i>Journal of Biological Chemistry</i> , 2015, 290, 2379-2394.	3.4	105
6	The Structure of the V1-ATPase Determined by Three-Dimensional Electron Microscopy of Single Particles. <i>Journal of Structural Biology</i> , 2001, 135, 26-37.	2.8	102
7	ATP synthases from archaea: The beauty of a molecular motor. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 940-952.	1.0	98
8	New insights into structure-function relationships between archeal ATP synthase (A ₁ A ₀) and vacuolar type ATPase (V ₁ V ₀). <i>BioEssays</i> , 2008, 30, 1096-1109.	2.5	76
9	Three-Dimensional Structure and Subunit Topology of the V ₁ ATPase from <i>Manduca sexta</i> Midgut. <i>Biochemistry</i> , 2000, 39, 8609-8616.	2.5	71
10	Expression, purification, and characterization of subunit E, an essential subunit of the vacuolar ATPase. <i>Biochemical and Biophysical Research Communications</i> , 2002, 298, 383-391.	2.1	69
11	Pyrazinamide triggers degradation of its target aspartate decarboxylase. <i>Nature Communications</i> , 2020, 11, 1661.	12.8	66
12	The plasma membrane H ⁺ -V-ATPase from tobacco hornworm midgut. <i>Journal of Bioenergetics and Biomembranes</i> , 1999, 31, 67-74.	2.3	65
13	Structural changes in the $\hat{\nu}$ ³ and $\hat{\mu}$ subunits of the <i>Escherichia coli</i> F1F0-type ATPase during energy coupling. <i>Journal of Bioenergetics and Biomembranes</i> , 1996, 28, 397-401.	2.3	64
14	Variations of Subunit $\hat{\mu}$ of the <i>Mycobacterium tuberculosis</i> F ₁ F _o ATP Synthase and a Novel Model for Mechanism of Action of the Tuberculosis Drug TMC207. <i>Antimicrobial Agents and Chemotherapy</i> , 2013, 57, 168-176.	3.2	64
15	Targeting the <i>Mycobacterium ulcerans</i> cytochrome bc1:aa3 for the treatment of Buruli ulcer. <i>Nature Communications</i> , 2018, 9, 5370.	12.8	64
16	Crystal Structure of the Archaeal A1AO ATP Synthase Subunit B from <i>Methanosarcina mazei</i> GÅ1: Implications of Nucleotide-binding Differences in the Major A1AO Subunits A and B. <i>Journal of Molecular Biology</i> , 2006, 358, 725-740.	4.2	60
17	Structure and Subunit Arrangement of the A-type ATP Synthase Complex from the Archaeon <i>Methanococcus jannaschii</i> Visualized by Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2004, 279, 38644-38648.	3.4	59
18	Bedaquiline Targets the $\hat{\mu}$ Subunit of <i>Mycobacterial</i> F-ATP Synthase. <i>Antimicrobial Agents and Chemotherapy</i> , 2016, 60, 6977-6979.	3.2	58

#	ARTICLE	IF	CITATIONS
19	Quaternary Structure of V1 and F1 ATPase: Significance of Structural Homologies and Diversities. <i>Biochemistry</i> , 1998, 37, 17659-17663.	2.5	56
20	Pyrazinoic Acid Inhibits Mycobacterial Coenzyme A Biosynthesis by Binding to Aspartate Decarboxylase PanD. <i>ACS Infectious Diseases</i> , 2017, 3, 807-819.	3.8	52
21	Evidence for major structural changes in subunit C of the vacuolar ATPase due to nucleotide binding. <i>FEBS Letters</i> , 2005, 579, 1961-1967.	2.8	51
22	Structure, mechanism and ensemble formation of the alkylhydroperoxide reductase subunits AhpC and AhpF from <i>Escherichia coli</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 2848-2862.	2.5	47
23	Dual inhibition of the terminal oxidases eradicates antibiotic-tolerant <i>Mycobacterium tuberculosis</i> . <i>EMBO Molecular Medicine</i> , 2021, 13, e13207.	6.9	47
24	Structural analysis of the stalk subunit Vma5p of the yeast V-ATPase in solution. <i>FEBS Letters</i> , 2004, 570, 119-125.	2.8	44
25	Deletion of a unique loop in the mycobacterial F ₁ ATP synthase $\hat{\mu}$ subunit sheds light on its inhibitory role in H^{+} pumping. <i>FEBS Journal</i> , 2016, 283, 1947-1961.	4.7	43
26	Structural Insights into the A1 ATPase from the Archaeon, <i>Methanosarcina mazei</i> GÅ¶1. <i>Biochemistry</i> , 2001, 40, 1890-1896.	2.5	42
27	The N Termini of α -Subunit Isoforms Are Involved in Signaling between Vacuolar H ⁺ -ATPase (V-ATPase) and Cytohesin-2*. <i>Journal of Biological Chemistry</i> , 2013, 288, 5896-5913.	3.4	42
28	Transamidase subunit GAA1/GPAA1 is a M28 family metallo-peptide-synthetase that catalyzes the peptide bond formation between the substrate protein's omega-site and the GPI lipid anchor's phosphoethanolamine. <i>Cell Cycle</i> , 2014, 13, 1912-1917.	2.6	41
29	Crystal Structure of Subunits D and F in Complex Gives Insight into Energy Transmission of the Eukaryotic V-ATPase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2015, 290, 3183-3196.	3.4	38
30	The NMR solution structure of <i>Mycobacterium tuberculosis</i> F ₁ ATP synthase subunit $\hat{\mu}$ provides new insight into energy coupling inside the rotary engine. <i>FEBS Journal</i> , 2018, 285, 1111-1128.	4.7	37
31	TBAJ-876 Retains Bedaquiline's Activity against Subunits c and $\hat{\mu}$ of <i>Mycobacterium tuberculosis</i> F ₁ -ATP Synthase. <i>Antimicrobial Agents and Chemotherapy</i> , 2019, 63, .	3.2	37
32	Re-Understanding the Mechanisms of Action of the Anti-Mycobacterial Drug Bedaquiline. <i>Antibiotics</i> , 2019, 8, 261.	3.7	37
33	Pharmacological and Molecular Mechanisms Behind the Sterilizing Activity of Pyrazinamide. <i>Trends in Pharmacological Sciences</i> , 2019, 40, 930-940.	8.7	35
34	Structural insight and flexible features of NS5 proteins from all four serotypes of <i>Dengue virus</i> in solution. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2015, 71, 2309-2327.	2.5	34
35	Zika Virus NS5 Forms Supramolecular Nuclear Bodies That Sequester Importin- β and Modulate the Host Immune and Pro-Inflammatory Response in Neuronal Cells. <i>ACS Infectious Diseases</i> , 2019, 5, 932-948.	3.8	34
36	Three-dimensional Organization of the Archaeal A1-ATPase from <i>Methanosarcina mazei</i> GÅ¶1. <i>Journal of Biological Chemistry</i> , 2004, 279, 22759-22764.	3.4	33

#	ARTICLE	IF	CITATIONS
37	Structural and functional analysis of the coupling subunit F in solution and topological arrangement of the stalk domains of the methanogenic A1AO ATP synthase. <i>Journal of Bioenergetics and Biomembranes</i> , 2006, 38, 83-92.	2.3	33
38	Specific motifs of the V-ATPase α -subunit isoform interact with catalytic and regulatory domains of ARNO. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 1398-1409.	1.0	33
39	The uniqueness of subunit $\hat{\nu}$ of mycobacterial F-ATP synthases: An evolutionary variant for niche adaptation. <i>Journal of Biological Chemistry</i> , 2017, 292, 11262-11279.	3.4	33
40	Cross-talk in the A1-ATPase from <i>Methanosarcina mazei</i> GÅ¶1 Due to Nucleotide Binding. <i>Journal of Biological Chemistry</i> , 2002, 277, 17327-17333.	3.4	32
41	Solution Structure and Conformational Changes of the <i>Streptomyces</i> Chitin-Binding Protein (CHB1). <i>Biochemistry</i> , 2000, 39, 10677-10683.	2.5	31
42	Abundant neuroprotective chaperone Lipocalin-type prostaglandin D synthase (L-PGDS) disassembles the Amyloid- $\hat{\nu}$ fibrils. <i>Scientific Reports</i> , 2019, 9, 12579.	3.3	31
43	Differentiation of Catalytic Sites on <i>Escherichia coli</i> F1ATPase by Laser Photoactivated Labeling with [3H]-2-Azido-ATP Using the Mutant $\hat{\nu}^2$ Glu381Cys: $\hat{\nu}$ Ser108Cys To Identify Different $\hat{\nu}^2$ Subunits by Their Interactions with $\hat{\nu}^3$ and $\hat{\nu}$ Subunits. <i>Biochemistry</i> , 1996, 35, 3875-3879.	2.5	30
44	Nucleotide Binding States of Subunit A of the A-ATP Synthase and the Implication of P-Loop Switch in Evolution. <i>Journal of Molecular Biology</i> , 2010, 396, 301-320.	4.2	30
45	The Trapping of Different Conformations of the <i>Escherichia coli</i> F1 ATPase by Disulfide Bond Formation. <i>Journal of Biological Chemistry</i> , 1996, 271, 32623-32628.	3.4	29
46	Resolution of the V1 ATPase from <i>Manduca sexta</i> into Subcomplexes and Visualization of an ATPase-active A3B3EG Complex by Electron Microscopy. <i>Journal of Biological Chemistry</i> , 2003, 278, 270-275.	3.4	29
47	The Molecular Motor F-ATP Synthase Is Targeted by the Tumoricidal Protein HAMLET. <i>Journal of Molecular Biology</i> , 2015, 427, 1866-1874.	4.2	29
48	Disrupting coupling within mycobacterial F-ATP synthases subunit $\hat{\nu}$ causes dysregulated energy production and cell wall biosynthesis. <i>Scientific Reports</i> , 2019, 9, 16759.	3.3	29
49	Discovery of a Novel Mycobacterial F-ATP Synthase Inhibitor and its Potency in Combination with Diarylquinolines. <i>Angewandte Chemie - International Edition</i> , 2020, 59, 13295-13304.	13.8	28
50	Molecular architecture of <i>Manduca sexta</i> midgut V ₁ ATPase visualized by electron microscopy. <i>FEBS Letters</i> , 1999, 453, 383-386.	2.8	27
51	Crystallographic and solution structure of the N-terminal domain of the Rel protein from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2017, 591, 2323-2337.	2.8	27
52	NMR Solution Structure of Subunit F of the Methanogenic A1AO Adenosine Triphosphate Synthase and Its Interaction with the Nucleotide-Binding Subunit B. <i>Biochemistry</i> , 2007, 46, 11684-11694.	2.5	26
53	Identification and characterization of a unique, zinc-containing transport ATPase essential for natural transformation in <i>Thermus thermophilus</i> HB27. <i>Extremophiles</i> , 2011, 15, 191-202.	2.3	26
54	Low Resolution Solution Structure of HAMLET and the Importance of Its Alpha-Domains in Tumoricidal Activity. <i>PLoS ONE</i> , 2012, 7, e53051.	2.5	25

#	ARTICLE	IF	CITATIONS
55	Power Stroke Angular Velocity Profiles of Archaeal A-ATP Synthase Versus Thermophilic and Mesophilic F-ATP Synthase Molecular Motors. <i>Journal of Biological Chemistry</i> , 2016, 291, 25351-25363.	3.4	25
56	The boxing glove shape of subunit d of the yeast V-ATPase in solution and the importance of disulfide formation for folding of this protein. <i>Journal of Bioenergetics and Biomembranes</i> , 2007, 39, 275-289.	2.3	24
57	Structural features of Zika virus non-structural proteins 3 and -5 and its individual domains in solution as well as insights into NS3 inhibition. <i>Antiviral Research</i> , 2017, 141, 73-90.	4.1	24
58	Spectroscopic and crystallographic studies of the mutant R416W give insight into the nucleotide binding traits of subunit B of the A ₁ A ₀ ATP synthase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 807-819.	2.6	22
59	Structure and subunit arrangement of Mycobacterial F1FO ATP synthase and novel features of the unique mycobacterial subunit f'. <i>Journal of Structural Biology</i> , 2019, 207, 199-208.	2.8	22
60	Unique structural and mechanistic properties of mycobacterial F-ATP synthases: Implications for drug design. <i>Progress in Biophysics and Molecular Biology</i> , 2020, 152, 64-73.	2.9	22
61	TBAJ-876 Displays Bedaquiline-Like Mycobactericidal Potency without Retaining the Parental Drug's Uncoupler Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	22
62	Structure of <i>Arabidopsis</i> CESA3 catalytic domain with its substrate UDP-glucose provides insight into the mechanism of cellulose synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	22
63	Small-Angle X-ray Scattering Reveals the Solution Structure of the Peripheral Stalk Subunit H of the A1A0 ATP Synthase from <i>Methanocaldococcus jannaschii</i> and Its Binding to the Catalytic A Subunit. <i>Biochemistry</i> , 2007, 46, 2070-2078.	2.5	21
64	Key roles of the <i>Escherichia coli</i> AhpC C-terminus in assembly and catalysis of alkylhydroperoxide reductase, an enzyme essential for the alleviation of oxidative stress. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2014, 1837, 1932-1943.	1.0	21
65	Transition steps in peroxide reduction and a molecular switch for peroxide robustness of prokaryotic peroxiredoxins. <i>Scientific Reports</i> , 2016, 6, 37610.	3.3	20
66	AhpC of the mycobacterial antioxidant defense system and its interaction with its reducing partner Thioredoxin-C. <i>Scientific Reports</i> , 2017, 7, 5159.	3.3	20
67	Cloning, purification, and nucleotide-binding traits of the catalytic subunit A of the V1VO ATPase from <i>Aedes albopictus</i> . <i>Protein Expression and Purification</i> , 2007, 53, 378-383.	1.3	19
68	Redox chemistry of <i>Mycobacterium tuberculosis</i> alkylhydroperoxide reductase E (AhpE): Structural and mechanistic insight into a mycoredoxin-1 independent reductive pathway of AhpE via mycothiol. <i>Free Radical Biology and Medicine</i> , 2016, 97, 588-601.	2.9	19
69	Partial Intrinsic Disorder Governs the Dengue Capsid Protein Conformational Ensemble. <i>ACS Chemical Biology</i> , 2018, 13, 1621-1630.	3.4	18
70	8-N ₃ -Biotinyl-ATP, a Novel Monofunctional Reagent: Differences in the F1- and V1-ATPases by Means of the ATP Analogue. <i>Biochemical and Biophysical Research Communications</i> , 2001, 286, 1218-1227.	2.1	17
71	Defined subcomplexes of the A ₁ ATPase from the archaeon <i>Methanosarcina mazei</i> CA1: biochemical properties and redox regulation. <i>FEBS Letters</i> , 2003, 544, 206-209.	2.8	17
72	Dimer formation of subunit G of the yeast V-ATPase. <i>FEBS Letters</i> , 2003, 546, 395-400.	2.8	17

#	ARTICLE	IF	CITATIONS
73	Targeting the menaquinol binding loop of mycobacterial cytochrome bd oxidase. <i>Molecular Diversity</i> , 2021, 25, 517-524.	3.9	17
74	Structural and functional features of the <i>Escherichia coli</i> F1-ATPase. , 2000, 32, 341-346.		16
75	Solution Structure, Determined by Nuclear Magnetic Resonance, of the b30-82 Domain of Subunit b of <i>Escherichia coli</i> F1Fo ATP Synthase. <i>Journal of Bacteriology</i> , 2009, 191, 7538-7544.	2.2	16
76	Solution structure of subunit \hat{b} (\hat{b} 1-204) of the <i>Mycobacterium tuberculosis</i> F-ATP synthase and the unique loop of \hat{b} 165-178, representing a novel TB drug target. <i>Journal of Bioenergetics and Biomembranes</i> , 2013, 45, 121-129.	2.3	16
77	Assembly of subunit d (Vma6p) and G (Vma10p) and the NMR solution structure of subunit G (G1 \hat{a} 59) of the <i>Saccharomyces cerevisiae</i> V1VO ATPase. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2009, 1787, 242-251.	1.0	14
78	The Structure of Subunit E of the <i>Pyrococcus horikoshii</i> OT3 A-ATP Synthase Gives Insight into the Elasticity of the Peripheral Stalk. <i>Journal of Molecular Biology</i> , 2012, 420, 155-163.	4.2	14
79	Identification of the critical linker residues conferring differences in the compactness of NS5 from <i>Dengue virus</i> serotype 4 and NS5 from <i>Dengue virus</i> serotypes 1 \hat{a} 3. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 795-807.	2.3	14
80	Introduction: Novel insights into TB research and drug discovery. <i>Progress in Biophysics and Molecular Biology</i> , 2020, 152, 2-5.	2.9	14
81	Ligand-Dependent Structural Changes in the V1ATPase from <i>Manduca sexta</i> . <i>Journal of Bioenergetics and Biomembranes</i> , 2004, 36, 249-256.	2.3	12
82	ATP/ADP Binding to a Novel Nucleotide Binding Domain of the Reticulocyte-binding Protein Py235 of <i>Plasmodium yoelii</i> . <i>Journal of Biological Chemistry</i> , 2008, 283, 36386-36396.	3.4	12
83	Structural insight into the glycosylphosphatidylinositol transamidase subunits PIG-K and PIG-S from yeast. <i>Journal of Structural Biology</i> , 2011, 173, 271-281.	2.8	12
84	Solution structure of subunit a, a 104-363, of the <i>Saccharomyces cerevisiae</i> V-ATPase and the importance of its C-terminus in structure formation. <i>Journal of Bioenergetics and Biomembranes</i> , 2012, 44, 341-350.	2.3	12
85	Crystallographic and solution studies of NAD $\hat{+}$ - and NADH-bound alkylhydroperoxide reductase subunit F (AhpF) from <i>Escherichia coli</i> provide insight into sequential enzymatic steps. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2015, 1847, 1139-1152.	1.0	12
86	Disk-like nanojets with steerable trajectory using platinum nozzle nanoengines. <i>RSC Advances</i> , 2016, 6, 3399-3405.	3.6	12
87	Structural features of NS3 of <i>Dengue virus</i> serotypes 2 and 4 in solution and insight into RNA binding and the inhibitory role of quercetin. <i>Acta Crystallographica Section D: Structural Biology</i> , 2017, 73, 402-419.	2.3	12
88	Temperature effects on disk-like gold-nickel-platinum nanoswimmer \hat{a} ™s propulsion fuelled by hydrogen peroxide. <i>Sensors and Actuators B: Chemical</i> , 2017, 239, 586-596.	7.8	12
89	The Unique C-Terminal Extension of Mycobacterial F-ATP Synthase Subunit \hat{b} Is the Major Contributor to Its Latent ATP Hydrolysis Activity. <i>Antimicrobial Agents and Chemotherapy</i> , 2020, 64, .	3.2	12
90	ATP synthesis and hydrolysis of the ATP-synthase from <i>Micrococcus luteus</i> regulated by an inhibitor subunit and membrane energization. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 1994, 1186, 43-51.	1.0	11

#	ARTICLE	IF	CITATIONS
91	An improved purification of ECF1 and ECF1F0 by using a cytochrome b ₅₅₉ -deficient strain of Escherichia coli facilitates crystallization of these complexes. FEBS Letters, 1997, 410, 165-168.	2.8	11
92	Structural Characterization of the Erythrocyte Binding Domain of the Reticulocyte Binding Protein Homologue Family of Plasmodium yoelii. Infection and Immunity, 2011, 79, 2880-2888.	2.2	11
93	Molecular mechanism of the Escherichia coli AhpC in the function of a chaperone under heat-shock conditions. Scientific Reports, 2018, 8, 14151.	3.3	11
94	Features and Functional Importance of Key Residues of the <i>Mycobacterium tuberculosis</i> Cytochrome b ₅₅₉ Oxidase. ACS Infectious Diseases, 2020, 6, 1697-1707.	3.8	11
95	A systematic assessment of mycobacterial F ₁ -ATPase subunit μ 's role in latent ATPase hydrolysis. FEBS Journal, 2021, 288, 818-836.	4.7	11
96	Structure of the nucleotide-binding subunit B of the energy producer A ₁ A ₀ ATP synthase in complex with adenosine diphosphate. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 1110-1115.	2.5	10
97	Identification of critical residues of subunit ϵ H in its interaction with subunit ϵ E of the A ₁ ATP synthase from <i>Methanocaldococcus jannaschii</i> . FEBS Journal, 2008, 275, 1803-1812.	4.7	10
98	Spectroscopical identification of residues of subunit G of the yeast V-ATPase in its connection with subunit E. Molecular Membrane Biology, 2008, 25, 400-410.	2.0	10
99	N-terminal domain of the V-ATPase a ₂ -subunit displays integral membrane protein properties. Protein Science, 2010, 19, 1850-1862.	7.6	10
100	Crystal and NMR Structures Give Insights into the Role and Dynamics of Subunit F of the Eukaryotic V-ATPase from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2013, 288, 11930-11939.	3.4	10
101	The stimulating role of subunit F in ATPase activity inside the A ₁ -complex of the Methanosarcina mazei γ 1 A ₁ A ₀ ATP synthase. Biochimica Et Biophysica Acta - Bioenergetics, 2016, 1857, 177-187.	1.0	10
102	Low resolution solution structure of an enzymatic active AhpC 10 :AhpF 2 ensemble of the Escherichia coli Alkyl hydroperoxide Reductase. Journal of Structural Biology, 2016, 193, 13-22.	2.8	10
103	Antituberculosis Activity of the Antimalaria Cytochrome b ₅₅₉ Oxidase Inhibitor SCR0911. ACS Infectious Diseases, 2020, 6, 725-737.	3.8	10
104	Low resolution structure of subunit b (b ₂₂ -156) of Escherichia coli F ₁ F ₀ ATP synthase in solution and the γ assembly. Journal of Bioenergetics and Biomembranes, 2008, 40, 245-55.	2.3	9
105	A second transient position of ATP on its trail to the nucleotide-binding site of subunit B of the motor protein A ₁ A ₀ ATP synthase. Journal of Structural Biology, 2009, 166, 38-45.	2.8	9
106	Structural Determination of Functional Units of the Nucleotide Binding Domain (NBD94) of the Reticulocyte Binding Protein Py235 of Plasmodium yoelii. PLoS ONE, 2010, 5, e9146.	2.5	9
107	The NMR solution structure of subunit G (G ₆₁ -101) of the eukaryotic V ₁ V ₀ ATPase from Saccharomyces cerevisiae. Biochimica Et Biophysica Acta - Biomembranes, 2010, 1798, 1961-1968.	2.6	9
108	Solution structure of subunit F (Vma7p) of the eukaryotic V ₁ V ₀ ATPase from Saccharomyces cerevisiae derived from SAXS and NMR spectroscopy. Biochimica Et Biophysica Acta - Biomembranes, 2011, 1808, 360-368.	2.6	9

#	ARTICLE	IF	CITATIONS
109	The Transition-Like State and Pi Entrance into the Catalytic A Subunit of the Biological Engine A-ATP Synthase. <i>Journal of Molecular Biology</i> , 2011, 408, 736-754.	4.2	9
110	Structural elements of the C-terminal domain of subunit E (E133-222) from the <i>Saccharomyces cerevisiae</i> V1VO ATPase determined by solution NMR spectroscopy. <i>Journal of Bioenergetics and Biomembranes</i> , 2011, 43, 447-455.	2.3	9
111	Conformational Properties of Secondary Amino Acids: Replacement of Pipecolic Acid by <i>N</i> -Methyl-L-alanine in Efrapeptin C. <i>Chemistry and Biodiversity</i> , 2013, 10, 942-951.	2.1	9
112	Crystallographic structure of the turbine C-ring from spinach chloroplast F-ATP synthase. <i>Bioscience Reports</i> , 2014, 34, .	2.4	9
113	¹⁵ NMR studies reveal a novel grab and release mechanism for efficient catalysis of the bacterial Cys peroxiredoxin machinery. <i>FEBS Journal</i> , 2015, 282, 4620-4638.	4.7	9
114	Structural and mechanistic insights into Mycothiol Disulphide Reductase and the Mycoredoxin-1-alkylhydroperoxide reductase E assembly of <i>Mycobacterium tuberculosis</i> . <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 2354-2366.	2.4	9
115	Atomic structure and enzymatic insights into the vancomycin-resistant <i>Enterococcus faecalis</i> (V583) alkylhydroperoxide reductase subunit C. <i>Free Radical Biology and Medicine</i> , 2018, 115, 252-265.	2.9	9
116	Structure and function of <i>Mycobacterium</i> -specific components of F-ATP synthase subunits $\hat{\epsilon}$ and $\hat{\mu}$. <i>Journal of Structural Biology</i> , 2018, 204, 420-434.	2.8	9
117	<i>Mycobacterium tuberculosis</i> PanD Structure – Function Analysis and Identification of a Potent Pyrazinoic Acid-Derived Enzyme Inhibitor. <i>ACS Chemical Biology</i> , 2021, 16, 1030-1039.	3.4	9
118	Interaction between subunit C (Vma5p) of the yeast vacuolar ATPase and the stalk of the C-depleted V1 ATPase from <i>Manduca sexta</i> midgut. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2005, 1708, 196-200.	1.0	8
119	Hydrogen-peroxide-fuelled platinum-nickel-SU-8 microrocket with steerable propulsion using an eccentric nanoengine. <i>RSC Advances</i> , 2016, 6, 102513-102518.	3.6	8
120	Conformational dynamics of the rotary subunit F in the A ₃ B ₃ DF complex of <i>Methanosarcina mazei</i> $\hat{\Gamma}$ 1 A-ATP synthase monitored by single-molecule FRET. <i>FEBS Letters</i> , 2017, 591, 854-862.	2.8	8
121	Overexpression, purification, enzymatic and microscopic characterization of recombinant mycobacterial F-ATP synthase. <i>Biochemical and Biophysical Research Communications</i> , 2020, 522, 374-380.	2.1	8
122	Targeting Mycobacterial F-ATP Synthase C-Terminal $\hat{\epsilon}$ Subunit Interaction Motif on Rotary Subunit $\hat{\epsilon}$. <i>Antibiotics</i> , 2021, 10, 1456.	3.7	8
123	Association of the eukaryotic V ₁ V _O ATPase subunits <i>a</i> with <i>d</i> and <i>d</i> with A. <i>FEBS Letters</i> , 2009, 583, 1090-1095.	2.8	7
124	Crosstalk along the Stalk: Dynamics of the Interaction of Subunits B and F in the A ₁ A _O ATP Synthase of <i>Methanosarcina mazei</i> $\hat{\Gamma}$ 1. <i>Biochemistry</i> , 2010, 49, 4181-4190.	2.5	7
125	Conserved Glycine Residues in the P-Loop of ATP Synthases Form a Doorframe for Nucleotide Entrance. <i>Journal of Molecular Biology</i> , 2011, 413, 657-666.	4.2	7
126	NMR solution structure of subunit E (fragment E1-69) of the <i>Saccharomyces cerevisiae</i> V1VO ATPase. <i>Journal of Bioenergetics and Biomembranes</i> , 2011, 43, 187-193.	2.3	7

#	ARTICLE	IF	CITATIONS
127	Active site CP-loop dynamics modulate substrate binding, catalysis, oligomerization, stability, over-oxidation and recycling of 2-Cys Peroxiredoxins. <i>Free Radical Biology and Medicine</i> , 2018, 118, 59-70.	2.9	7
128	Introduction: A close look at the vacuolar ATPase. <i>Journal of Bioenergetics and Biomembranes</i> , 2003, 35, 277-280.	2.3	6
129	Domain Features of the Peripheral Stalk Subunit H of the Methanogenic A1AO ATP Synthase and the NMR Solution Structure of H1-47. <i>Biophysical Journal</i> , 2009, 97, 286-294.	0.5	6
130	The DNA uptake ATPase PilF of <i>Thermus thermophilus</i> : a reexamination of the zinc content. <i>Extremophiles</i> , 2013, 17, 697-698.	2.3	6
131	Low-resolution structure of the soluble domain GPAA1 (yGPAA170â€“247) of the glycosylphosphatidylinositol transamidase subunit GPAA1 from <i>Saccharomyces cerevisiae</i> . <i>Bioscience Reports</i> , 2013, 33, e00033.	2.4	6
132	Zika virus nonstructural protein 5 residue R681 is critical for dimer formation and enzymatic activity. <i>FEBS Letters</i> , 2019, 593, 1272-1291.	2.8	6
133	Mutational Analysis of Mycobacterial F-ATP Synthase Subunit $\hat{\Gamma}$ Leads to a Potent $\hat{\Gamma}$ Enzyme Inhibitor. <i>ACS Chemical Biology</i> , 2022, 17, 529-535.	3.4	6
134	Trapping of conformations of the <i>Escherichia coli</i> F1ATPase by disulfide bond formation. <i>FEBS Letters</i> , 1998, 426, 37-40.	2.8	5
135	Structural Characterization of an ATPase Active F1-/V1 -ATPase ($\hat{\Gamma}$ 3 $\hat{\Gamma}$ 23EG) Hybrid Complex. <i>Journal of Biological Chemistry</i> , 2004, 279, 47866-47870.	3.4	5
136	NMR solution structure of the N-terminal domain of subunit E (E1â€“52) of A1AO ATP synthase from <i>Methanocaldococcus jannaschii</i> . <i>Journal of Bioenergetics and Biomembranes</i> , 2009, 41, 343-348.	2.3	5
137	Crystal and solution structure of the C-terminal part of the <i>Methanocaldococcus jannaschii</i> A1AO ATP synthase subunit E revealed by X-ray diffraction and small-angle X-ray scattering. <i>Journal of Bioenergetics and Biomembranes</i> , 2010, 42, 311-320.	2.3	5
138	Essential role of the flexible linker on the conformational equilibrium of bacterial peroxiredoxin reductase for effective regeneration of peroxiredoxin. <i>Journal of Biological Chemistry</i> , 2017, 292, 6667-6679.	3.4	5
139	Atomic solution structure of <i>Mycobacterium abscessus</i> $\langle scp \rangle$ Fâ€“ATP $\langle scp \rangle$ synthase subunit $\hat{\mu}$ and identification of $\langle scp \rangle$ Ep1 $\langle i \rangle$ Mab $\langle i \rangle$ F1 $\langle scp \rangle$ as a targeted inhibitor. <i>FEBS Journal</i> , 2022, 289, 6308-6323.	4.7	5
140	Purification and crystallization of the entire recombinant subunit E of the energy producer A1AoATP synthase. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 324-326.	0.7	4
141	The Critical Roles of Residues P235 and F236 of Subunit A of the Motor Protein A-ATP Synthase in P-Loop Formation and Nucleotide Binding. <i>Journal of Molecular Biology</i> , 2010, 401, 892-905.	4.2	4
142	Binding of subunit E into the Aâ€“B interface of the A1AO ATP synthase. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2011, 1808, 2111-2118.	2.6	4
143	Structural architecture and interplay of the nucleotide- and erythrocyte binding domain of the reticulocyte binding protein Py235 from <i>Plasmodium yoelii</i> . <i>International Journal for Parasitology</i> , 2012, 42, 1083-1089.	3.1	4
144	Substrateâ€“induced structural alterations of Mycobacterial mycothione reductase and critical residues involved. <i>FEBS Letters</i> , 2018, 592, 568-585.	2.8	4

#	ARTICLE	IF	CITATIONS
145	Crystallographic and enzymatic insights into the mechanisms of Mg-ADP inhibition in the A1 complex of the A1AO ATP synthase. <i>Journal of Structural Biology</i> , 2018, 201, 26-35.	2.8	4
146	The structural features of <i>Acetobacterium woodii</i> ATP synthase reveal the importance of the unique subunit ϵ in Na ⁺ translocation and ATP synthesis. <i>FEBS Journal</i> , 2019, 286, 1894-1907.	4.7	4
147	Structure and flexibility of non-structural proteins 3 and -5 of Dengue- and Zika viruses in solution. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 143, 67-77.	2.9	4
148	Discovery of a Novel Mycobacterial ATP Synthase Inhibitor and its Potency in Combination with Diarylquinolines. <i>Angewandte Chemie</i> , 2020, 132, 13397-13406.	2.0	4
149	Atomic structure of and valine binding to the regulatory ACT domain of the <i>Mycobacterium tuberculosis</i> Rel protein. <i>FEBS Journal</i> , 2021, 288, 2377-2397.	4.7	4
150	Structural model of α 2-subunit N-terminus and its binding interface for Arf-GEF CTH2: Implication for regulation of V-ATPase, CTH2 function and rational drug design. <i>Current Topics in Membranes</i> , 2019, 83, 77-106.	0.9	4
151	Anti- <i>Mycobacterium abscessus</i> Activity of Tuberculosis F-ATP Synthase Inhibitor GaMF1. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, e0001822.	3.2	4
152	Structural and Mechanistic Insights into <i>Mycobacterium abscessus</i> Aspartate Decarboxylase PanD and a Pyrazinoic Acid-Derived Inhibitor. <i>ACS Infectious Diseases</i> , 2022, 8, 1324-1335.	3.8	4
153	¹ H, ¹³ C, and ¹⁵ N resonance assignments of subunit F of the A1AO ATP synthase from <i>Methanosarcina mazei</i> GÅ1. <i>Biomolecular NMR Assignments</i> , 2007, 1, 23-25.	0.8	3
154	NMR solution structure of NBD94483-502 of the nucleotide-binding domain of the <i>Plasmodium yoelii</i> reticulocyte-binding protein Py235. <i>FEMS Microbiology Letters</i> , 2011, 318, 152-158.	1.8	3
155	Purification and crystallization of yeast glycosylphosphatidylinositol transamidase subunit PIG-S (PIG-S71Å467). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 896-899.	0.7	3
156	Crystallization and preliminary X-ray crystallographic analysis of subunit F (F1Å94), an essential coupling subunit of the eukaryotic V1VO-ATPase from <i>Saccharomyces cerevisiae</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 1055-1059.	0.7	3
157	Relevance of the conserved histidine and asparagine residues in the phosphate-binding loop of the nucleotide binding subunit B of A1AO ATP synthases. <i>Journal of Structural Biology</i> , 2012, 180, 509-518.	2.8	3
158	Subunit F modulates ATP binding and migration in the nucleotide-binding subunit B of the A1AO ATP synthase of <i>Methanosarcina mazei</i> GÅ1. <i>Journal of Bioenergetics and Biomembranes</i> , 2012, 44, 213-224.	2.3	3
159	Eukaryotic V-ATPase and Its Super-complexes: From Structure and Function to Disease and Drug Targeting. , 2016, , 301-335.		3
160	Atomic structure of the regulatory TGS domain of Rel protein from <i>Mycobacterium tuberculosis</i> and its interaction with deacylated tRNA. <i>FEBS Letters</i> , 2021, 595, 3006.	2.8	3
161	The effect of NBD-Cl in nucleotide-binding of the major subunit ϵ and B of the motor proteins F1FO ATP synthase and A1AO ATP synthase. <i>Journal of Bioenergetics and Biomembranes</i> , 2010, 42, 1-10.	2.3	2
162	Disulfide linkage in the coiled-coil domain of subunit H of A₁A_O ATP synthase from <i>Methanocaldococcus jannaschii</i> and the NMR structure of the C-terminal segment H₈₅Å104. <i>FEBS Letters</i> , 2010, 584, 713-718.	2.8	2

#	ARTICLE	IF	CITATIONS
163	Protein-protein interactions within the ensemble, eukaryotic V-ATPase, and its concerted interactions with cellular machineries. <i>Progress in Biophysics and Molecular Biology</i> , 2015, 119, 84-93.	2.9	2
164	Novel insights into the vancomycin-resistant <i>Enterococcus faecalis</i> (V583) alkylhydroperoxide reductase subunit F. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 3201-3214.	2.4	2
165	Self-association and conformational variation of NS5A domain 1 of hepatitis C virus. <i>Journal of General Virology</i> , 2018, 99, 194-208.	2.9	2
166	Effect of the additional cysteine 503 of vancomycin-resistant <i>Enterococcus faecalis</i> (V583) alkylhydroperoxide reductase subunit F (AhpF) and the mechanism of AhpF and subunit C assembling. <i>Free Radical Biology and Medicine</i> , 2019, 138, 10-22.	2.9	1
167	3D reconstruction and flexibility of the hybrid engine <i>Acetobacterium woodii</i> F-ATP synthase. <i>Biochemical and Biophysical Research Communications</i> , 2020, 527, 518-524.	2.1	1
168	Crystallographic insight into the catalytic mechanism of subunit A of the A-ATP synthase and the P-loop switch in evolution. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , 2010, 1797, 32-33.	1.0	0
169	Crystallographic studies of the coupling segment NBD94674-781 of the nucleotide-binding domain of the <i>Plasmodium yoelii</i> reticulocyte-binding protein Py235. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1631-1634.	0.7	0
170	Engineered tryptophan in the adenine-binding pocket of catalytic subunit A of A-ATP synthase demonstrates the importance of aromatic residues in adenine binding, forming a tool for steady-state and time-resolved fluorescence spectroscopy. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1485-1491.	0.7	0
171	Conformational states of Zika virus non-structural protein 3 determined by molecular dynamics simulations with small-angle X-Ray scattering data. <i>Progress in Biophysics and Molecular Biology</i> , 2019, 143, 13-19.	2.9	0
172	Residues of helix É2 are critical for catalytic efficiency of mycobacterial alkylhydroperoxide reductase subunit C. <i>FEBS Letters</i> , 2020, 594, 2829-2839.	2.8	0
173	Novel role of cytohesinÉ2 in regulation of macropinocytosis pathway and cell proliferation. <i>FASEB Journal</i> , 2013, 27, 591.8.	0.5	0
174	Analyzing conformational changes in single FRET-labeled A1 parts of archaeal A1AO-ATP synthase. , 2018, , .		0