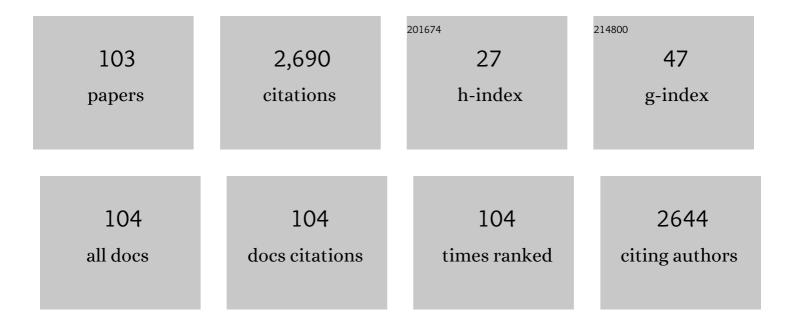
List of Publications by Year in descending order

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ΕΛΒΙΟ ΤΑΝΕΛΝΙ

#	Article	IF	CITATIONS
1	N-(carboxymethylidene)chitosans and N-(carboxymethyl)chitosans: Novel chelating polyampholytes obtained from chitosan glyoxylate. Carbohydrate Research, 1982, 107, 199-214.	2.3	327
2	The N-permethylation of chitosan and the preparation of N-trimethyl chitosan iodide. Carbohydrate Polymers, 1985, 5, 297-307.	10.2	152
3	Structure-Function Analysis of the Zinc Finger Region of the DnaJ Molecular Chaperone. Journal of Biological Chemistry, 1996, 271, 14840-14848.	3.4	136
4	Chelating, film-forming, and coagulating ability of the chitosan-glucan complex fromAspergillus niger industrial wastes. Biotechnology and Bioengineering, 1980, 22, 885-896.	3.3	114
5	Sulfated N-(carboxymethyl)chitosans: Novel blood anticoagulants. Carbohydrate Research, 1984, 126, 225-231.	2.3	111
6	Porcine odorant-binding protein: structural stability and ligand affinities measured by Fourier-transform infrared spectroscopy and fluorescence spectroscopy. BBA - Proteins and Proteomics, 1999, 1431, 179-188.	2.1	97
7	HtrA Heat Shock Protease Interacts with Phospholipid Membranes and Undergoes Conformational Changes. Journal of Biological Chemistry, 1997, 272, 8974-8982.	3.4	63
8	Effects of temperature and SDS on the structure of β-glycosidase from the thermophilic archaeon Sulfolobus solfataricus. Biochemical Journal, 1997, 323, 833-840.	3.7	60
9	A new fluorescence method to detect singlet oxygen inside phospholipid model membranes. Lipids and Lipid Metabolism, 1991, 1082, 94-100.	2.6	54
10	Thymoquinone, a potential therapeutic agent of Nigella sativa, binds to site I of human serum albumin. Phytomedicine, 2010, 17, 714-720.	5.3	52
11	The N-terminal region of HtrA heat shock protease from Escherichia coli is essential for stabilization of HtrA primary structure and maintaining of its oligomeric structure. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2003, 1649, 171-182.	2.3	51
12	N-(o-carboxybenzyl) chitosans: Novel chelating polyampholytes. Carbohydrate Polymers, 1982, 2, 145-157.	10.2	49
13	The degree of acetylation of chitins by gas chromatography and infrared spectroscopy. Journal of Proteomics, 1980, 2, 299-306.	2.4	47
14	The characterization of N-methyl, N-ethyl, N-propyl, N-butyl and N-hexyl chitosans, novel film-forming polymers. Journal of Membrane Science, 1983, 16, 295-308.	8.2	47
15	Comparison of the Structure of Wild-type HtrA Heat Shock Protease and Mutant HtrA Proteins. Journal of Biological Chemistry, 1995, 270, 11140-11146.	3.4	46
16	Reduced β-strand content in apoprotein B-100 in smaller and denser low-density lipoprotein subclasses as probed by Fourier-transform infrared spectroscopy. Biochemical Journal, 1997, 322, 765-769.	3.7	41
17	Preparation and characteristic properties of dithiocarbamate chitosan, a chelating polymer. Carbohydrate Research, 1982, 104, 235-243.	2.3	38
18	Structural and thermal stability analysis of Escherichia coli and Alicyclobacillus acidocaldarius thioredoxin revealed a molten globule-like state in thermal denaturation pathway of the proteins: an infrared spectroscopic study. Biochemical Journal, 2003, 373, 875-883.	3.7	37

ΓΑΒΙΟ ΤΑΝΓΑΝΙ

#	Article	IF	CITATIONS
19	Aspartate glucan, glycine glucan, and serine glucan for the removal of cobalt and copper from solutions and brines. Biotechnology and Bioengineering, 1985, 27, 1115-1121.	3.3	36
20	Structure-function studies on β-glycosidase from Sulfolobus solfataricus. Molecular bases of thermostability. Biochimie, 1998, 80, 949-957.	2.6	36
21	Thermal Stability and Aggregation of Sulfolobus solfataricus β-Glycosidase Are Dependent upon the N-â^-Methylation of Specific Lysyl Residues. Journal of Biological Chemistry, 2004, 279, 10185-10194.	3.4	36
22	Steady-state fluorescence anisotropy and multifrequency phase fluorometry on oxidized phosphatidylcholine vesicles. Chemistry and Physics of Lipids, 1989, 50, 1-9.	3.2	34
23	N-Acylethanolamines as membrane topological stress compromising agents. Biochimica Et Biophysica Acta - Biomembranes, 1993, 1148, 351-355.	2.6	33
24	Indolinonic and quinolinic aminoxyls as protectants against oxidative stress. Free Radical Biology and Medicine, 1993, 15, 203-208.	2.9	32
25	Temperature-Induced Molten Globule-like State in Human α1-Acid Glycoprotein: An Infrared Spectroscopic Studyâ€. Biochemistry, 2005, 44, 15997-16006.	2.5	31
26	Binding of glutamine to glutamine-binding protein from Escherichia coli induces changes in protein structure and increases protein stability. Proteins: Structure, Function and Bioinformatics, 2004, 58, 80-87.	2.6	30
27	Stability and conformational dynamics of metallothioneins from the antarctic fishNotothenia coriiceps and mouse. Proteins: Structure, Function and Bioinformatics, 2002, 46, 259-267.	2.6	27
28	The esterase from the thermophilic eubacteriumBacillus acidocaldarius: Structural-functional relationship and comparison with the esterase from the hyperthermophilic archaeonArchaeoglobus fulgidus. Proteins: Structure, Function and Bioinformatics, 2000, 40, 473-481.	2.6	26
29	Structure–activity relationship on fungal laccase from Rigidoporus lignosus: a Fourier-transform infrared spectroscopic study. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2002, 1601, 155-162.	2.3	26
30	Characterization of Thymoquinone Binding to Human Î ± 1 -Acid Glycoprotein. Journal of Pharmaceutical Sciences, 2012, 101, 2564-2573.	3.3	26
31	Binding of Glucose to the d-Galactose/d-Glucose–Binding Protein from Escherichia coli Restores the Native Protein Secondary Structure and Thermostability That Are Lost upon Calcium Depletion. Journal of Biochemistry, 2006, 139, 213-221.	1.7	25
32	Two-dimensional IR correlation spectroscopy of mutants of the Î ² -glycosidase from the hyperthermophilic archaeon Sulfolobus solfataricus identifies the mechanism of quaternary structure stabilization and unravels the sequence of thermal unfolding events. Biochemical Journal, 2004, 384, 69-78.	3.7	24
33	Structural and Thermal Stability Characterization of Escherichia colid-Galactose/d-Glucose-Binding Protein. Biotechnology Progress, 2008, 20, 330-337.	2.6	24
34	Specific interaction of cytosolic and mitochondrial glyoxalase II with acidic phospholipids in form of liposomes results in the inhibition of the cytosolic enzyme only. Proteins: Structure, Function and Bioinformatics, 2000, 41, 33-39.	2.6	22
35	Nitroxides are more efficient inhibitors of oxidative damage to calf skin collagen than antioxidant vitamins. Biochimica Et Biophysica Acta - General Subjects, 2008, 1780, 58-68.	2.4	21
36	Quinolinic Aminoxyl Protects Albumin Against Peroxyl Radical Mediated Damage. Free Radical Research, 1994, 21, 309-315.	3.3	20

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37	D-Trehalose/D-maltose-binding protein from the hyperthermophilic archaeon Thermococcus litoralis: The binding of trehalose and maltose results in different protein conformational states. Proteins: Structure, Function and Bioinformatics, 2006, 63, 754-767.	2.6	20
38	Amino acid transport in thermophiles: characterization of an arginine-binding protein in Thermotoga maritima. 2. Molecular organization and structural stability. Molecular BioSystems, 2010, 6, 687.	2.9	20
39	The thermophilic esterase fromArchaeoglobus fulgidus: Structure and conformational dynamics at high temperature. , 2000, 38, 351-360.		19
40	A comparative infrared spectroscopic study of glycoside hydrolases from extremophilic archaea revealed different molecular mechanisms of adaptation to high temperatures. Proteins: Structure, Function and Bioinformatics, 2007, 67, 991-1001.	2.6	19
41	Temperature-induced conformational changes within the regulatory loops L1–L2–LA of the HtrA heat-shock protease from Escherichia coli. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2009, 1794, 1573-1582.	2.3	19
42	Effect of N-acylethanolamines with different acyl-chains on DPPC multilamellar liposomes. Chemistry and Physics of Lipids, 1993, 65, 165-169.	3.2	18
43	Conformational stability of human erythrocyte transglutaminase. Patterns of thermal unfolding at acid and alkaline pH. FEBS Journal, 1999, 266, 575-582.	0.2	18
44	Structure and Stability of a Rat Odorant-Binding Protein: Another Brick in the Wall. Journal of Proteome Research, 2009, 8, 4005-4013.	3.7	17
45	Structural investigation of transglutaminase by Fourier transform infrared spectroscopy. FEBS Journal, 1993, 218, 499-505.	0.2	16
46	Thermal denaturation pathway of starch phosphorylase from <i>Corynebacterium callunae</i> : Oxyanion binding provides the glue that efficiently stabilizes the dimer structure of the protein. Protein Science, 2000, 9, 1149-1161.	7.6	16
47	Temperature-, SDS-, and pH-Induced Conformational Changes in Protein Disulfide Oxidoreductase from the ArchaeonPyrococcusfuriosus:Â A Dynamic Simulation and Fourier Transform Infrared Spectroscopic Study. Journal of Proteome Research, 2005, 4, 1972-1980.	3.7	16
48	Structural basis ofÂtheÂdestabilization produced byÂanÂamino-terminal tag inÂtheÂl²-glycosidase from theÂhyperthermophilic archeon SulfolobusÂsolfataricus. Biochimie, 2006, 88, 807-817.	2.6	16
49	A Strategic Fluorescence Labeling ofd-Galactose/d-Glucose-Binding Protein fromEscherichiacoliHelps to Shed Light on the Protein Structural Stability and Dynamics. Journal of Proteome Research, 2007, 6, 4119-4126.	3.7	16
50	Wild-Type and Mutant Bovine Odorant-Binding Proteins To Probe the Role of the Quaternary Structure Organization in the Protein Thermal Stability. Journal of Proteome Research, 2008, 7, 5221-5229.	3.7	16
51	The belonging of gpMuc, a glycoprotein from Mucuna pruriens seeds, to the Kunitz-type trypsin inhibitor family explains its direct anti-snake venom activity. Phytomedicine, 2011, 18, 887-895.	5.3	16
52	The thermal unfolding of the ribosome-inactivating protein saporin-S6 characterized by infrared spectroscopy. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2015, 1854, 1357-1364.	2.3	16
53	Effect of the fungicides tributyltin acetate and tributyltin chloride on multilamellar liposomes: fluorescence studies. Chemistry and Physics of Lipids, 1991, 59, 189-197.	3.2	15
54	Structure/function of KRAB repression domains: Structural properties of KRAB modules inferred from hydrodynamic, circular dichroism, and FTIR spectroscopic analyses. Proteins: Structure, Function and Bioinformatics, 2005, 62, 604-616.	2.6	15

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55	Permeability of oxidized phosphatidylcholine liposomes. Biochemical and Biophysical Research Communications, 1989, 163, 241-246.	2.1	14
56	Interaction of the herbicide atrazine with model membranes I: physico-chemical studies on dipalmitoyl phosphatidylcholine liposomes. Chemistry and Physics of Lipids, 1990, 55, 179-189.	3.2	14
57	Structural and functional relationships in 5′-nucleotidase from bull seminal plasma. A Fourier transform infrared study. BBA - Proteins and Proteomics, 1992, 1118, 187-193.	2.1	14
58	Fibrillation properties of human α1-acid glycoprotein. Biochimie, 2013, 95, 158-166.	2.6	14
59	ESR characterization of chitins and chitosans. Biochemical and Biophysical Research Communications, 1979, 89, 706-712.	2.1	13
60	Importance of pH and disulfide bridges on the structural and binding properties of human α1-acid glycoprotein. Biochimie, 2011, 93, 1529-1536.	2.6	13
61	Ligand-Exchange Chromatography of Amino Acids on Copper-Loaded Chitosan. Separation Science and Technology, 1978, 13, 869-879.	2.5	12
62	Structural properties and thermal stability of human liver and heart fatty acid binding proteins: A fourier transform IR spectroscopy study. Biopolymers, 1995, 36, 569-577.	2.4	12
63	Salts Induce Structural Changes in Elongation Factor 1α from the Hyperthermophilic ArchaeonSulfolobus solfataricus: A Fourier Transform Infrared Spectroscopic Studyâ€,‡. Biochemistry, 2001, 40, 13143-13148.	2.5	11
64	The Role of Tyr41 and His155 in the Functional Properties of Superoxide Dismutase from the ArchaeonSulfolobus solfataricusâ€. Biochemistry, 2004, 43, 2199-2208.	2.5	11
65	Influence of ADP, AMP-PNP and of depletion of nucleotides on the structural properties of F1ATPase: a Fourier transform infrared spectroscopic study. FEBS Letters, 1995, 373, 141-145.	2.8	10
66	Structure of yeast plasma membrane H+-ATPase: comparison of activated and basal-level enzyme forms. Biochimica Et Biophysica Acta - Biomembranes, 1998, 1369, 109-118.	2.6	10
67	Pressure Affects the Structure and the Dynamics of thed-Galactose/d-Glucose-Binding Protein fromEscherichia coliby Perturbing the C-Terminal Domain of the Proteinâ€. Biochemistry, 2006, 45, 11885-11894.	2.5	10
68	Analysis of the Link between the Redox State and Enzymatic Activity of the HtrA (DegP) Protein from Escherichia coli. PLoS ONE, 2015, 10, e0117413.	2.5	10
69	Structural analysis of ASCUT-1, a protein component of the cuticle of the parasitic nematode Ascaris lumbricoides. FEBS Journal, 1998, 255, 588-594.	0.2	9
70	Mink Growth Hormone Structural–Functional Relationships: Effects of Renaturing and Storage Conditions. Protein Journal, 2008, 27, 170-180.	1.6	9
71	High hydrostatic pressure-induced conformational changes in protein disulfide oxidoreductase from the hyperthermophilic archaeon Pyrococcus furiosus. A Fourier-transform infrared spectroscopic study. Molecular BioSystems, 2010, 6, 2015.	2.9	9
72	Insights into the structural properties of d-serine dehydratase from Saccharomyces cerevisiae: An FT-IR spectroscopic and in silico approach. Biochimie, 2011, 93, 542-548.	2.6	9

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#	Article	IF	CITATIONS
73	Interaction of the herbicide atrazine with model membranes. II: Effect of atrazine on fusion of phospholipid vesicles. Chemistry and Physics of Lipids, 1990, 56, 101-108.	3.2	8
74	The effect of N-acyl ethanolamines on phosphatidylethanolamine phase transitions studied by laurdan generalised polarisation. Chemistry and Physics of Lipids, 1994, 72, 127-134.	3.2	8
75	Structural–Functional Relationships in Pig Heart AMP-Deaminase in the Presence of ATP, Orthophosphate, and Phosphatidate Bilayers. Molecular Genetics and Metabolism, 1998, 65, 51-58.	1.1	8
76	Molecular strategies for protein stabilization: The case of a trehalose/maltoseâ€binding protein from <i>Thermus thermophilus</i> . Proteins: Structure, Function and Bioinformatics, 2008, 73, 839-850.	2.6	8
77	Bovine α1-acid glycoprotein, a thermostable version of its human counterpart: Insights from Fourier transform infrared spectroscopy and in silico modelling. Biochimie, 2014, 102, 19-28.	2.6	8
78	Boar Sperm Proacrosin Infrared Investigation: Secondary Structure Analysis after Autoactivation and Suramin Binding. Biochemical and Molecular Medicine, 1996, 58, 37-45.	1.4	7
79	Effect of acidic phospholipids on the structural properties of recombinant cytosolic human glyoxalase II. Proteins: Structure, Function and Bioinformatics, 2002, 48, 126-133.	2.6	7
80	Glycidyl acrylate plasma glow discharged polymers. Biomaterials, 1990, 11, 585-589.	11.4	6
81	Interaction of tributylin acetate and tributyltin chloride with dipalmitoyl phosphatidylcholine model membrane. Chemistry and Physics of Lipids, 1991, 58, 73-80.	3.2	6
82	Comparison of the structure of wild-type HtrA heat shock protease and mutant HtrA proteins. A Fourier transform infrared spectroscopic study Journal of Biological Chemistry, 1995, 270, 31413.	3.4	6
83	Mechanism of thermal denaturation of maltodextrin phosphorylase from Escherichia coli. Biochemical Journal, 2000, 346, 255-263.	3.7	6
84	Interaction of Î ³ -conglutin from Lupinus albus with model phospholipid membranes: Investigations on structure, thermal stability and oligomerization status. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2018, 1866, 1242-1248.	2.3	6
85	Effect of neutral and acidic phospholipids on mitochondrial ATP synthase secondary structure. FEBS Letters, 1993, 336, 477-480.	2.8	5
86	Mutagenesis of the Dimer Interface Region of Corynebacterium callunae Starch Phosphorylase Perturbs the Phosphate-Dependent Conformational Relay that Enhances Oligomeric Stability of the Enzyme. Journal of Biochemistry, 2003, 134, 599-606.	1.7	5
87	Effects induced by mono- and divalent cations on protein regions responsible for thermal adaptation in 2-glycosidase from Sulfolobus solfataricus. European Biophysics Journal, 2004, 33, 38-49.	2.2	5
88	The role of the L2 loop in the regulation and maintaining the proteolytic activity of HtrA (DegP) protein from Escherichia coli. Archives of Biochemistry and Biophysics, 2010, 500, 123-130.	3.0	5
89	A Spectroscopic Study on Secondary Structure and Thermal Unfolding of the Plant Toxin Gelonin Confirms Some Typical Structural Characteristics and Unravels the Sequence of Thermal Unfolding Events. Toxins, 2019, 11, 483.	3.4	5
90	Effects of fluorescent pseudo-ATP and ATP-metal analogs on secondary structure of Na+/K+-ATPase. Biochimica Et Biophysica Acta - Bioenergetics, 2000, 1457, 94-102.	1.0	4

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91	The allergen Mus m 1.0102: Cysteine residues and molecular allergology. Molecular Immunology, 2020, 120, 1-12.	2.2	4
92	Effect of inhibitor binding to β subunits of F1ATPase on enzyme thermostability: a kinetic and FT-IR spectroscopic analysis. FEBS Letters, 1998, 432, 128-132.	2.8	3
93	Effects of Fe(III) binding to the nucleotide-independent site of F1-ATPase: enzyme thermostability and response to activating anions. FEBS Letters, 2001, 506, 221-224.	2.8	3
94	Oxyanion-Mediated Protein Stabilization: Differential Roles of Phosphate for Preventing Inactivation of Bacterial α-Glucan Phosphorylases. Biocatalysis and Biotransformation, 2001, 19, 379-398.	2.0	3
95	Turning pyridoxal-5′-phosphate-dependent enzymes into thermostable binding proteins: d-Serine dehydratase from baker's yeast as a case study. Biochimie, 2012, 94, 479-486.	2.6	3
96	Detection of temperature-induced molten globule states in small, $\hat{1}^2$ -sheet-rich proteins by infrared spectroscopy. Biomedical Spectroscopy and Imaging, 2012, 1, 247-259.	1.2	3
97	Mechanism of thermal denaturation of maltodextrin phosphorylase from Escherichia coli. Biochemical Journal, 2000, 346, 255.	3.7	3
98	Differential scanning calorimetry characterization of oxidized egg phosphatidylcholine liposomes. Biochemical and Biophysical Research Communications, 1990, 168, 1268-1273.	2.1	2
99	Two-dimensional gel electrophoresis and FTIR spectroscopy reveal both forms of yeast plasma membrane H+-ATPase in activated and basal-level enzyme preparations. FEBS Letters, 2001, 505, 155-158.	2.8	2
100	Computational, spectroscopic, and resonant mirror biosensor analysis of the interaction of adrenodoxin with native and tryptophan-modified NADPH-adrenodoxin reductase. Proteins: Structure, Function and Bioinformatics, 2004, 57, 302-310.	2.6	2
101	Amyloid fibril formation by bovine $\hat{l}\pm 1$ -acid glycoprotein in a reducing environment: The role of disulfide bridges on the observed aggregation kinetics. Biochimie, 2015, 118, 244-252.	2.6	2
102	Thermal stability, ligand binding and allergenicity data of Mus m 1.0102 allergen and its cysteine mutants. Data in Brief, 2020, 29, 105355.	1.0	2
103	Synthesis, Structural Insights and Activity of Different Classes of Biomolecules. , 2020, , 463-482.		1