

Javier Gomez

List of Publications by Year in descending order

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45
papers

2,314
citations

361413

20
h-index

254184

43
g-index

45
all docs

45
docs citations

45
times ranked

2256
citing authors

#	ARTICLE	IF	CITATIONS
1	The heat capacity of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 22, 404-412.	2.6	421
2	Enzyme Kinetics Determined Using Calorimetry: A General Assay for Enzyme Activity?. <i>Analytical Biochemistry</i> , 2001, 296, 179-187.	2.4	313
3	Thermodynamic Mapping of the Inhibitor Site of the Aspartic Protease Endothiapepsin. <i>Journal of Molecular Biology</i> , 1995, 252, 337-350.	4.2	243
4	The magnitude of the backbone conformational entropy change in protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996, 25, 143-156.	2.6	222
5	The enthalpy change in protein folding and binding: Refinement of parameters for structure-based calculations. , 1996, 26, 123-133.		127
6	The magnitude of the backbone conformational entropy change in protein folding. , 1996, 25, 143-156.		116
7	Molecular Basis of Resistance to HIV-1 Protease Inhibition: A Plausible Hypothesis. <i>Biochemistry</i> , 1998, 37, 5791-5797.	2.5	82
8	Toward a solvent basicity scale: the calorimetry of the pyrrole probe. <i>Journal of the American Chemical Society</i> , 1990, 112, 1678-1681.	13.7	72
9	Acidity and Basicity of Indazole and its N-Methyl Derivatives in the Ground and in the Excited State. <i>The Journal of Physical Chemistry</i> , 1994, 98, 10606-10612.	2.9	68
10	The Isolated C-Terminal Domain of Ring1B Is a Dimer Made of Stable, Well-Structured Monomers. <i>Biochemistry</i> , 2007, 46, 12764-12776.	2.5	46
11	The dimerization domain of the HIV-1 capsid protein binds a capsid protein-derived peptide: A biophysical characterization. <i>Protein Science</i> , 2004, 13, 1512-1523.	7.6	44
12	Structure-based thermodynamic design of peptide ligands: Application to peptide inhibitors of the aspartic protease endothiapepsin. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 30, 74-85.	2.6	38
13	Effect of Chitosan Degradation on Its Interaction with β -Lactoglobulin. <i>Biomacromolecules</i> , 2011, 12, 1015-1023.	5.4	37
14	The Basic Helix-Loop-Helix Region of Human Neurogenin 1 Is a Monomeric Natively Unfolded Protein Which Forms a "Fuzzy" Complex upon DNA Binding. <i>Biochemistry</i> , 2010, 49, 1577-1589.	2.5	36
15	Effects of Conducting and Blocking Ions on the Structure and Stability of the Potassium Channel KcsA. <i>Journal of Biological Chemistry</i> , 2006, 281, 29905-29915.	3.4	30
16	Structure and Dynamics of Lysozyme Encapsulated in a Silica Sol-Gel Matrix. <i>Journal of Physical Chemistry B</i> , 2007, 111, 11603-11610.	2.6	30
17	Equilibrium Unfolding of the C-Terminal SAM Domain of p73. <i>Biochemistry</i> , 2002, 41, 5743-5753.	2.5	29
18	The Monomeric Species of the Regulatory Domain of Tyrosine Hydroxylase Has a Low Conformational Stability. <i>Biochemistry</i> , 2016, 55, 3418-3431.	2.5	29

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19	Denaturation and Leaching Study of Horseradish Peroxidase Encapsulated in Sol-Gel Matrices. <i>Journal of Sol-Gel Science and Technology</i> , 2003, 26, 1169-1172.	2.4	28
20	Thermodynamic Analysis of the Structural Stability of the Shiga Toxin B-Subunit. <i>Biochemistry</i> , 2003, 42, 9498-9506.	2.5	24
21	Rationally Designed Interfacial Peptides Are Efficient In Vitro Inhibitors of HIV-1 Capsid Assembly with Antiviral Activity. <i>PLoS ONE</i> , 2011, 6, e23877.	2.5	24
22	Towards a solvent acidity scale: the calorimetry of the N-methyl imidazole probe. <i>Journal of the Chemical Society Perkin Transactions II</i> , 1992, , 1181-1185.	0.9	23
23	Ion Binding to KcsA: Implications in Ion Selectivity and Channel Gating. <i>Biochemistry</i> , 2010, 49, 9480-9487.	2.5	19
24	The family 52 β -xylosidase from <i>Geobacillus stearothermophilus</i> is a dimer: Structural and biophysical characterization of a glycoside hydrolase. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2008, 1784, 1924-1934.	2.3	17
25	The conformational stability of the <i>Streptomyces coelicolor</i> histidine-phosphocarrier protein. <i>FEBS Journal</i> , 2004, 271, 2165-2181.	0.2	16
26	Folding and Unfolding in the Blue Copper Protein Rusticyanin: Role of the Oxidation State. <i>Bioinorganic Chemistry and Applications</i> , 2007, 2007, 1-9.	4.1	16
27	Calorimetric quantification of the hydrogen-bond acidity of solvents and its relationship with solvent polarity. <i>Journal of the Chemical Society Perkin Transactions II</i> , 1995, , 2301-2305.	0.9	15
28	The histidine-phosphocarrier protein of <i>Streptomyces coelicolor</i> folds by a partially folded species at low pH. <i>FEBS Journal</i> , 2003, 270, 2254-2267.	0.2	15
29	Biophysical Characterization of the Enzyme I of the <i>Streptomyces coelicolor</i> Phosphoenolpyruvate: Sugar Phosphotransferase System. <i>Biophysical Journal</i> , 2006, 90, 4592-4604.	0.5	14
30	Synthesis and characterization of a novel thermoresponsive copolymer series and their application in cell and cell sheet regeneration. <i>Journal of Biomaterials Science, Polymer Edition</i> , 2013, 24, 253-268.	3.5	14
31	Energetics of 5-bromo-4-chloro-3-indolyl- β -D-mannose binding to the <i>Parkia platycephala</i> seed lectin and its use for MAD phasing. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2005, 61, 326-331.	0.7	13
32	Contribution of Ion Binding Affinity to Ion Selectivity and Permeation in KcsA, a Model Potassium Channel. <i>Biochemistry</i> , 2012, 51, 3891-3900.	2.5	12
33	Calorimetric study of the effect of N-methylation in azoles: Loss of an active centre of solvation. <i>Journal of Physical Organic Chemistry</i> , 1989, 2, 646-652.	1.9	11
34	Human importin β 3 and its N-terminal truncated form, without the importin β 2-binding domain, are oligomeric species with a low conformational stability in solution. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129609.	2.4	11
35	The CBS Domain Protein MJ0729 of <i>Methanocaldococcus jannaschii</i> Is a Thermostable Protein with a pH-Dependent Self-Oligomerization. <i>Biochemistry</i> , 2009, 48, 2760-2776.	2.5	10
36	Characterization of the non-native trifluoroethanol-induced intermediate conformational state of the Shiga toxin B-subunit. <i>Biochimie</i> , 2006, 88, 1199-1207.	2.6	7

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37	The N-terminal domain of the enzyme I is a monomeric well-folded protein with a low conformational stability and residual structure in the unfolded state. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 729-742.	2.1	7
38	Complexation of WPI and microwave-assisted extracted agars with different physicochemical properties. <i>Carbohydrate Polymers</i> , 2012, 89, 1073-1080.	10.2	7
39	Mutation of Ser-50 and Cys-66 in Snapin Modulates Protein Structure and Stability. <i>Biochemistry</i> , 2012, 51, 3470-3484.	2.5	6
40	The Conformational Stability and Biophysical Properties of the Eukaryotic Thioredoxins of <i>Pisum Sativum</i> Are Not Family-Conserved. <i>PLoS ONE</i> , 2011, 6, e17068.	2.5	6
41	Thermal stability of matrix protein from Newcastle disease virus. <i>International Journal of Biological Macromolecules</i> , 2013, 61, 390-395.	7.5	5
42	Larger Helical Populations in Peptides Derived from the Dimerization Helix of the Capsid Protein of HIV-1 Results in Peptide Binding toward Regions Other than the "Hotspot" Interface. <i>Biomacromolecules</i> , 2011, 12, 3252-3264.	5.4	4
43	Nucleotide-induced conformational transitions in the CBS domain protein MJ0729 of <i>Methanocaldococcus jannaschii</i> . <i>Protein Engineering, Design and Selection</i> , 2011, 24, 161-169.	2.1	3
44	Competitive inhibition of protein adsorption to silica surfaces by their coating with high density charge polyelectrolytes. <i>Colloids and Surfaces B: Biointerfaces</i> , 2020, 191, 110993.	5.0	3
45	Structural Thermodynamic Study of the Binding of Renin Inhibitors to Endothiapepsin. <i>Advances in Experimental Medicine and Biology</i> , 1998, 436, 325-328.	1.6	1