

Javier Gomez

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

45 papers	2,069 citations	21 h-index	45 g-index
45 ext. papers	2,182 ext. citations	4.3 avg, IF	4.27 L-index

#	Paper	IF	Citations
45	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	6	1
44	Human importin β and its N-terminal truncated form, without the importin- β binding domain, are oligomeric species with a low conformational stability in solution. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020 , 1864, 129609	4	8
43	The Monomeric Species of the Regulatory Domain of Tyrosine Hydroxylase Has a Low Conformational Stability. <i>Biochemistry</i> , 2016 , 55, 3418-31	3.2	19
42	Thermal stability of matrix protein from Newcastle disease virus. <i>International Journal of Biological Macromolecules</i> , 2013 , 61, 390-5	7.9	4
41	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, 253-68	3.5	13
40	Mutation of Ser-50 and Cys-66 in Snapin modulates protein structure and stability. <i>Biochemistry</i> , 2012 , 51, 3470-84	3.2	6
39	Contribution of ion binding affinity to ion selectivity and permeation in KcsA, a model potassium channel. <i>Biochemistry</i> , 2012 , 51, 3891-900	3.2	10
38	Complexation of WPI and microwave-assisted extracted agars with different physicochemical properties. <i>Carbohydrate Polymers</i> , 2012 , 89, 1073-80	10.3	7
37	Effect of chitosan degradation on its interaction with β -lactoglobulin. <i>Biomacromolecules</i> , 2011 , 12, 1015-23	10.3	32
36	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, 3252-64	6.9	4
35	Nucleotide-induced conformational transitions in the CBS domain protein MJ0729 of <i>Methanocaldococcus jannaschii</i> . <i>Protein Engineering, Design and Selection</i> , 2011 , 24, 161-9	1.9	3
34	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	3.7	5
33	Rationally designed interfacial peptides are efficient in vitro inhibitors of HIV-1 capsid assembly with antiviral activity. <i>PLoS ONE</i> , 2011 , 6, e23877	3.7	21
32	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, 729-42	1.9	6
31	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, 1577-89	3.2	32
30	Ion binding to KcsA: implications in ion selectivity and channel gating. <i>Biochemistry</i> , 2010 , 49, 9480-7	3.2	14
29	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, 2760-76	3.2	10

28	The family 52 beta-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, 1924-34	4	14
27	The isolated C-terminal domain of Ring1B is a dimer made of stable, well-structured monomers. <i>Biochemistry</i> , 2007 , 46, 12764-76	3.2	45
26	Structure and dynamics of lysozyme encapsulated in a silica sol-gel matrix. <i>Journal of Physical Chemistry B</i> , 2007 , 111, 11603-10	3.4	27
25	Folding and unfolding in the blue copper protein rusticyanin: role of the oxidation state. <i>Bioinorganic Chemistry and Applications</i> , 2007 , 2007, 54232	4.2	14
24	Effects of conducting and blocking ions on the structure and stability of the potassium channel KcsA. <i>Journal of Biological Chemistry</i> , 2006 , 281, 29905-15	5.4	24
23	Biophysical characterization of the enzyme I of the <i>Streptomyces coelicolor</i> phosphoenolpyruvate:sugar phosphotransferase system. <i>Biophysical Journal</i> , 2006 , 90, 4592-604	2.9	13
22	Characterization of the non-native trifluoroethanol-induced intermediate conformational state of the Shiga toxin B-subunit. <i>Biochimie</i> , 2006 , 88, 1199-207	4.6	6
21	Energetics of 5-bromo-4-chloro-3-indolyl-alpha-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, 326-31		12
20	The conformational stability of the <i>Streptomyces coelicolor</i> histidine-phosphocarrier protein. Characterization of cold denaturation and urea-protein interactions. <i>FEBS Journal</i> , 2004 , 271, 2165-81		15
19	The dimerization domain of the HIV-1 capsid protein binds a capsid protein-derived peptide: a biophysical characterization. <i>Protein Science</i> , 2004 , 13, 1512-23	6.3	40
18	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	2.3	22
17	The histidine-phosphocarrier protein of <i>Streptomyces coelicolor</i> folds by a partially folded species at low pH. <i>FEBS Journal</i> , 2003 , 270, 2254-67		14
16	Thermodynamic analysis of the structural stability of the shiga toxin B-subunit. <i>Biochemistry</i> , 2003 , 42, 9498-506	3.2	21
15	Equilibrium unfolding of the C-terminal SAM domain of p73. <i>Biochemistry</i> , 2002 , 41, 5743-53	3.2	27
14	Enzyme kinetics determined using calorimetry: a general assay for enzyme activity?. <i>Analytical Biochemistry</i> , 2001 , 296, 179-87	3.1	281
13	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	4.2	37
12	Molecular basis of resistance to HIV-1 protease inhibition: a plausible hypothesis. <i>Biochemistry</i> , 1998 , 37, 5791-7	3.2	77
11	Structural thermodynamic study of the binding of renin inhibitors to endothiapepsin. <i>Advances in Experimental Medicine and Biology</i> , 1998 , 436, 325-8	3.6	1

10	The magnitude of the backbone conformational entropy change in protein folding. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 143-56	4.2	98
9	The enthalpy change in protein folding and binding: refinement of parameters for structure-based calculations. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 26, 123-33	4.2	115
8	Docking enzyme-inhibitor complexes using a preference-based free-energy surface. <i>Proteins: Structure, Function and Bioinformatics</i> , 1996 , 25, 403-19	4.2	209
7	The heat capacity of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995 , 22, 404-12	4.2	371
6	Thermodynamic mapping of the inhibitor site of the aspartic protease endothiapepsin. <i>Journal of Molecular Biology</i> , 1995 , 252, 337-50	6.5	226
5	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		14
4	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		59
3	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		21
2	Toward a solvent basicity scale: the calorimetry of the pyrrole probe. <i>Journal of the American Chemical Society</i> , 1990 , 112, 1678-1681	16.4	62
1	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	2.1	9