Alvaro Ortega

List of Publications by Year
in descending order

63 papers	2,807 citations	201674 27 h-index	182427 51 g-index
66 all docs	66 docs citations	66 times ranked	3975 citing authors

#	Article	IF	Citations
1	Prediction of Hydrodynamic and Other Solution Properties of Rigid Proteins from Atomic- and Residue-Level Models. Biophysical Journal, 2011, 101, 892-898.	0.5	569
2	Hydrodynamic properties of rodlike and disklike particles in dilute solution. Journal of Chemical Physics, 2003, 119, 9914-9919.	3.0	279
3	Sensory Repertoire of Bacterial Chemoreceptors. Microbiology and Molecular Biology Reviews, 2017, 81, .	6.6	158
4	Improved Calculation of Rotational Diffusion and Intrinsic Viscosity of Bead Models for Macromolecules and Nanoparticles. Journal of Physical Chemistry B, 2007, 111, 955-961.	2.6	141
5	Rosmarinic acid is a homoserine lactone mimic produced by plants that activates a bacterial quorum-sensing regulator. Science Signaling, 2016, 9, ra1.	3.6	106
6	FAK dimerization controls its kinase-dependent functions at focal adhesions. EMBO Journal, 2014, 33, 356-370.	7.8	101
7	Paralogous chemoreceptors mediate chemotaxis towards protein amino acids and the non€protein amino acid gamma€aminobutyrate (<scp>GABA</scp>). Molecular Microbiology, 2013, 88, 1230-1243.	2.5	87
8	Equivalent Radii and Ratios of Radii from Solution Properties as Indicators of Macromolecular Conformation, Shape, and Flexibility. Biomacromolecules, 2007, 8, 2464-2475.	5.4	86
9	Molecular flexibility of citrus pectins by combined sedimentation and viscosity analysis. Food Hydrocolloids, 2008, 22, 1435-1442.	10.7	78
10	Calculation of hydrodynamic properties of small nucleic acids from their atomic structure. Nucleic Acids Research, 2002, 30, 1782-1788.	14.5	73
11	Two different mechanisms mediate chemotaxis to inorganic phosphate in Pseudomonas aeruginosa. Scientific Reports, 2016, 6, 28967.	3.3	62
12	Solution Conformation of Wild-Type and Mutant IgG3 and IgG4 Immunoglobulins Using Crystallohydrodynamics: Possible Implications for Complement Activation. Biophysical Journal, 2007, 93, 3733-3744.	0.5	59
13	How Bacterial Chemoreceptors Evolve Novel Ligand Specificities. MBio, 2020, 11, .	4.1	52
14	Global conformation analysis of irradiated xyloglucans. Carbohydrate Polymers, 2008, 74, 845-851.	10.2	49
15	Global hydrodynamic analysis of the molecular flexibility of galactomannans. Carbohydrate Polymers, 2008, 72, 356-360.	10.2	44
16	The Molecular Mechanism of Nitrate Chemotaxis via Direct Ligand Binding to the PilJ Domain of McpN. MBio, 2019, 10, .	4.1	40
17	<scp>McpQ</scp> is a specific citrate chemoreceptor that responds preferentially to citrate/metal ion complexes. Environmental Microbiology, 2016, 18, 3284-3295.	3.8	39
18	Hydrodynamic Properties of Wormlike Macromolecules: Monte Carlo Simulation and Global Analysis of Experimental Data. Macromolecules, 2011, 44, 5788-5797.	4.8	38

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19	Calculation of the solution properties of flexible macromolecules: methods and applications. European Biophysics Journal, 2003, 32, 477-486.	2.2	35
20	Identification of a Chemoreceptor in Pseudomonas aeruginosa That Specifically Mediates Chemotaxis Toward α-Ketoglutarate. Frontiers in Microbiology, 2016, 7, 1937.	3.5	35
21	The activity of the C4-dicarboxylic acid chemoreceptor of Pseudomonas aeruginosa is controlled by chemoattractants and antagonists. Scientific Reports, 2018, 8, 2102.	3.3	35
22	Metabolic Value Chemoattractants Are Preferentially Recognized at Broad Ligand Range Chemoreceptor of Pseudomonas putida KT2440. Frontiers in Microbiology, 2017, 8, 990.	3.5	34
23	The role of solute binding proteins in signal transduction. Computational and Structural Biotechnology Journal, 2021, 19, 1786-1805.	4.1	34
24	Molecular Flexibility of Methylcelluloses of Differing Degree of Substitution by Combined Sedimentation and Viscosity Analysis. Macromolecular Bioscience, 2008, 8, 1108-1115.	4.1	33
25	Structural Basis for Polyamine Binding at the dCACHE Domain of the McpU Chemoreceptor from Pseudomonas putida. Journal of Molecular Biology, 2018, 430, 1950-1963.	4.2	33
26	Analytical ultracentrifugation studies of oligomerization and DNA-binding of TtCarH, a Thermus thermophilus coenzyme B12-based photosensory regulator. European Biophysics Journal, 2013, 42, 463-476.	2.2	31
27	Inducer-Modulated Cooperative Binding of the Tetrameric CggR Repressor to Operator DNA. Biophysical Journal, 2007, 92, 3215-3227.	0.5	30
28	SIMUFLEX: Algorithms and Tools for Simulation of the Conformation and Dynamics of Flexible Molecules and Nanoparticles in Dilute Solution. Journal of Chemical Theory and Computation, 2009, 5, 2606-2618.	5.3	30
29	Influence of ionic strength on the flexibility of alginate studied by size exclusion chromatography. Carbohydrate Polymers, 2014, 102, 223-230.	10.2	28
30	MULTIHYDRO and MONTEHYDRO: Conformational search and Monte Carlo calculation of solution properties of rigid or flexible bead models. Biophysical Chemistry, 2005, 116, 121-128.	2.8	27
31	The HBM domain: Introducing bimodularity to bacterial sensing. Protein Science, 2014, 23, 332-336.	7.6	27
32	Efficient, Accurate Calculation of Rotational Diffusion and NMR Relaxation of Globular Proteins from Atomic-Level Structures and Approximate Hydrodynamic Calculations. Journal of the American Chemical Society, 2005, 127, 12764-12765.	13.7	26
33	Fructose-1,6-bisphosphate Acts Both as an Inducer and as a Structural Cofactor of the Central Glycolytic Genes Repressor (CggR). Biochemistry, 2007, 46, 14996-15008.	2.5	25
34	Prediction of Hydrodynamic and Other Solution Properties of Partially Disordered Proteins with a Simple, Coarse-Grained Model. Journal of Chemical Theory and Computation, 2013, 9, 1678-1685.	5.3	23
35	Intrinsic viscosity of bead models for macromolecules and nanoparticles. European Biophysics Journal, 2010, 39, 381-388.	2.2	20
36	High-Throughput Screening to Identify Chemoreceptor Ligands. Methods in Molecular Biology, 2018, 1729, 291-301.	0.9	20

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37	Functional Annotation of Bacterial Signal Transduction Systems: Progress and Challenges. International Journal of Molecular Sciences, 2018, 19, 3755.	4.1	19
38	Determination of Ligand Profiles for Pseudomonas aeruginosa Solute Binding Proteins. International Journal of Molecular Sciences, 2019, 20, 5156.	4.1	19
39	Crystallohydrodynamics of Protein Assemblies: Combining Sedimentation, Viscometry, and X-Ray Scattering. Biophysical Journal, 2006, 91, 1688-1697.	0.5	17
40	Characterization of the Control Catabolite Protein of Gluconeogenic Genes Repressor by Fluorescence Cross-Correlation Spectroscopy and Other Biophysical Approaches. Biophysical Journal, 2008, 95, 4403-4415.	0.5	15
41	Estimating domain orientation of two human antibody IgG4 chimeras by crystallohydrodynamics. European Biophysics Journal, 2003, 32, 503-510.	2.2	13
42	Multiple Linear Least-Squares Fits with a Common Intercept: Determination of the Intrinsic Viscosity of Macromolecules in Solution. Journal of Chemical Education, 2003, 80, 1036.	2.3	13
43	Multi-scale calculation and global-fit analysis of hydrodynamic properties of biological macromolecules: determination of the overall conformation of antibody IgG molecules. European Biophysics Journal, 2010, 39, 361-370.	2.2	12
44	Multiple signals modulate the activity of the complex sensor kinase <scp>T</scp>od<scp>S</scp>. Microbial Biotechnology, 2015, 8, 103-115.	4.2	12
45	Purification and characterization of Pseudomonas aeruginosa LasR expressed in acyl-homoserine lactone free Escherichia coli cultures. Protein Expression and Purification, 2017, 130, 107-114.	1.3	12
46	Analytical Ultracentrifugation Studies of Phage Ï•29 Protein p6 Binding to DNA. Journal of Molecular Biology, 2009, 385, 1616-1629.	4.2	11
47	Global fit and structure optimization of flexible and rigid macromolecules and nanoparticles from analytical ultracentrifugation and other dilute solution properties. Methods, 2011, 54, 115-123.	3.8	11
48	So different and still so similar: The plant compound rosmarinic acid mimics bacterial homoserine lactone quorum sensing signals. Communicative and Integrative Biology, 2016, 9, e1156832.	1.4	11
49	Brownian dynamics simulation of analytical ultracentrifugation experiments. BMC Biophysics, 2011, 4, 6.	4.4	10
50	Bacterial Sirtuins Overview: An Open Niche to Explore. Frontiers in Microbiology, 2021, 12, 744416.	3.5	10
51	Methods and Tools for the Prediction of Hydrodynamic Coefficients and Other Solution Properties of Flexible Macromolecules in Solution. A Tutorial Minireview. Macromolecular Bioscience, 2010, 10, 721-730.	4.1	9
52	Identification of ligands for bacterial sensor proteins. Current Genetics, 2016, 62, 143-147.	1.7	8
53	Studying Antibody Conformations by Ultracentrifugation and Hydrodynamic Modeling. , 2004, 248, 93-114.		7
54	Characterization of low molecular mass thermosensitive diblock copolymers and their self-assembly by means of analytical ultracentrifugation. Colloid and Polymer Science, 2012, 290, 297-306.	2.1	4

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55	Chemoreceptors with C-terminal pentapeptides for CheR and CheB binding are abundant in bacteria that maintain host interactions. Computational and Structural Biotechnology Journal, 2020, 18, 1947-1955.	4.1	4
56	Use of the sedimentation coefficient for modelling antibodies. Refinements to the crystallohydrodynamics approach. , 0, , 113-118.		1
57	Mechanisms of Site-Specific Functions of Focal Adhesion Kinase. Biophysical Journal, 2013, 104, 609a.	0.5	1
58	HYDRO Suite of Computer Programs for Solution Properties of Rigid Macromolecules. , 2013, , 1002-1006.		1
59	Methylation of Proteins: Biochemistry and Functional Consequences. , 2018, , 571-584.		0
60	Crystallohydrodynamics of IgG. , 2013, , 397-403.		0
61	HYDFIT and Related Packages for Linear Molecules. , 2013, , 998-1002.		0
62	Hydrophobic Modifications of Biomolecules: An Introduction. , 2017, , 1-10.		0
63	Crystallohydrodynamics of IgG. , 2018, , 1-8.		0