

Modesto Orozco Lopez

List of Publications by Citations

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395
papers

23,822
citations

78
h-index

138
g-index

412
ext. papers

26,470
ext. citations

9
avg, IF

6.78
L-index

#	Paper	IF	Citations
395	Refinement of the AMBER force field for nucleic acids: improving the description of alpha/gamma conformers. <i>Biophysical Journal</i> , 2007 , 92, 3817-29	2.9	1705
394	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2011 , 475, 101-5	50.4	1206
393	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2011 , 44, 47-52	36.3	752
392	Perspective on Electrostatic interactions of a solute with a continuum. A direct utilization of ab initio molecular potentials for the prevision of solvent effects <i>Theoretical Chemistry Accounts</i> , 2000 , 103, 343-345	1.9	592
391	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015 , 526, 519-24	50.4	565
390	Theoretical Methods for the Description of the Solvent Effect in Biomolecular Systems. <i>Chemical Reviews</i> , 2000 , 100, 4187-4226	68.1	538
389	Parmsc1: a refined force field for DNA simulations. <i>Nature Methods</i> , 2016 , 13, 55-8	21.6	483
388	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012 , 44, 1236-42	36.3	422
387	PMUT: a web-based tool for the annotation of pathological mutations on proteins. <i>Bioinformatics</i> , 2005 , 21, 3176-8	7.2	404
386	A systematic molecular dynamics study of nearest-neighbor effects on base pair and base pair step conformations and fluctuations in B-DNA. <i>Nucleic Acids Research</i> , 2010 , 38, 299-313	20.1	299
385	Tautomerism and Protonation of Guanine and Cytosine. Implications in the Formation of Hydrogen-Bonded Complexes. <i>Journal of the American Chemical Society</i> , 1996 , 118, 6811-6821	16.4	292
384	Performance of Molecular Mechanics Force Fields for RNA Simulations: Stability of UUCG and GNRA Hairpins.. <i>Journal of Chemical Theory and Computation</i> , 2010 , 6, 3836-3849	6.4	261
383	Target flexibility: an emerging consideration in drug discovery and design. <i>Journal of Medicinal Chemistry</i> , 2008 , 51, 6237-55	8.3	244
382	Molecular dynamics simulations: advances and applications. <i>Advances and Applications in Bioinformatics and Chemistry</i> , 2015 , 8, 37-47	1.5	229
381	Dynamics of B-DNA on the microsecond time scale. <i>Journal of the American Chemical Society</i> , 2007 , 129, 14739-45	16.4	224
380	Nature of base stacking: reference quantum-chemical stacking energies in ten unique B-DNA base-pair steps. <i>Chemistry - A European Journal</i> , 2006 , 12, 2854-65	4.8	204
379	A consensus view of protein dynamics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 796-801	11.5	194

378	PupasView: a visual tool for selecting suitable SNPs, with putative pathological effect in genes, for genotyping purposes. <i>Nucleic Acids Research</i> , 2005 , 33, W501-5	20.1	192
377	Design, synthesis, and biological evaluation of dual binding site acetylcholinesterase inhibitors: new disease-modifying agents for Alzheimer's disease. <i>Journal of Medicinal Chemistry</i> , 2005 , 48, 7223-33	8.3	179
376	Correlated ab initio study of nucleic acid bases and their tautomers in the gas phase, in a microhydrated environment and in aqueous solution. <i>Physical Chemistry Chemical Physics</i> , 2002 , 4, 4192-4203	2.6	175
375	Frontiers in molecular dynamics simulations of DNA. <i>Accounts of Chemical Research</i> , 2012 , 45, 196-205	24.3	171
374	Characterization of disease-associated single amino acid polymorphisms in terms of sequence and structure properties. <i>Journal of Molecular Biology</i> , 2002 , 315, 771-86	6.5	171
373	Molecular dynamics simulations of the unfolding of barnase in water and 8 M aqueous urea. <i>Biochemistry</i> , 1997 , 36, 7313-29	3.2	162
372	New tacrine-huperzine A hybrids (huprines): highly potent tight-binding acetylcholinesterase inhibitors of interest for the treatment of Alzheimer's disease. <i>Journal of Medicinal Chemistry</i> , 2000 , 43, 4657-66	8.3	160
371	Molecular Dynamics Simulations of the d(TA _n) Triple Helix. <i>Journal of the American Chemical Society</i> , 1997 , 119, 7463-7469	16.4	156
370	On the performance of continuum solvation methods. A comment on "Universal approaches to solvation modeling". <i>Accounts of Chemical Research</i> , 2009 , 42, 489-92; discussion 493-7	24.3	152
369	Accuracy of free energies of hydration for organic molecules from 6-31g*-derived partial charges. <i>Journal of Computational Chemistry</i> , 1993 , 14, 1240-1249	3.5	142
368	Epigenomic analysis detects aberrant super-enhancer DNA methylation in human cancer. <i>Genome Biology</i> , 2016 , 17, 11	18.3	141
367	Theoretical methods for the simulation of nucleic acids. <i>Chemical Society Reviews</i> , 2003 , 32, 350-64	58.5	141
366	ABC: a systematic microsecond molecular dynamics study of tetranucleotide sequence effects in B-DNA. <i>Nucleic Acids Research</i> , 2014 , 42, 12272-83	20.1	138
365	Cooperativity in drug-DNA recognition: a molecular dynamics study. <i>Journal of the American Chemical Society</i> , 2001 , 123, 12658-63	16.4	133
364	Optimization of solute cavities and van der Waals parameters in ab initio MST-SCRF calculations of neutral molecules. <i>Journal of Computational Chemistry</i> , 1994 , 15, 446-454	3.5	131
363	Thorough validation of protein normal mode analysis: a comparative study with essential dynamics. <i>Structure</i> , 2007 , 15, 565-75	5.2	130
362	Towards a molecular dynamics consensus view of B-DNA flexibility. <i>Nucleic Acids Research</i> , 2008 , 36, 2379-94	2.4	128
361	Triplex-forming oligonucleotide target sequences in the human genome. <i>Nucleic Acids Research</i> , 2004 , 32, 354-60	20.1	127

360	Synthesis of enantiopure trans-3,4-disubstituted piperidines. An enantiodivergent synthesis of (+)- and (-)-paroxetine. <i>Journal of Organic Chemistry</i> , 2000 , 65, 3074-84	4.2	122
359	MDWeb and MDMoby: an integrated web-based platform for molecular dynamics simulations. <i>Bioinformatics</i> , 2012 , 28, 1278-9	7.2	120
358	Functional and structural conservation of CBS domains from CLC chloride channels. <i>Journal of Physiology</i> , 2004 , 557, 363-78	3.9	120
357	Direct measurement of the dielectric polarization properties of DNA. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E3624-30	11.5	119
356	CH π and CD Contacts in the Adenine-Uracil Watson-Crick and Uracil-Uracil Nucleic Acid Base Pairs: Nonempirical ab Initio Study with Inclusion of Electron Correlation Effects. <i>Journal of Physical Chemistry B</i> , 2000 , 104, 6286-6292	3.4	118
355	X-Pol Potential: An Electronic Structure-Based Force Field for Molecular Dynamics Simulation of a Solvated Protein in Water. <i>Journal of Chemical Theory and Computation</i> , 2009 , 5, 459-467	6.4	114
354	Induced dipole moment and atomic charges based on average electrostatic potentials in aqueous solution. <i>Journal of Chemical Physics</i> , 1993 , 98, 2975-2982	3.9	113
353	Single Stranded Loops of Quadruplex DNA As Key Benchmark for Testing Nucleic Acids Force Fields. <i>Journal of Chemical Theory and Computation</i> , 2009 , 5, 2514-30	6.4	112
352	Solvation in octanol: parametrization of the continuum MST model. <i>Journal of Computational Chemistry</i> , 2001 , 22, 1180-1193	3.5	112
351	Molecular basis of substrate-induced permeation by an amino acid antiporter. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 3935-40	11.5	111
350	The structure and dynamics of DNA in the gas phase. <i>Journal of the American Chemical Society</i> , 2003 , 125, 8007-14	16.4	111
349	Glutaryl-CoA dehydrogenase deficiency in Spain: evidence of two groups of patients, genetically, and biochemically distinct. <i>Pediatric Research</i> , 2000 , 48, 315-22	3.2	111
348	Recent advances in the study of nucleic acid flexibility by molecular dynamics. <i>Current Opinion in Structural Biology</i> , 2008 , 18, 185-93	8.1	105
347	The relative flexibility of B-DNA and A-RNA duplexes: database analysis. <i>Nucleic Acids Research</i> , 2004 , 32, 6144-51	20.1	105
346	On the potential role of the amino nitrogen atom as a hydrogen bond acceptor in macromolecules. <i>Journal of Molecular Biology</i> , 1998 , 279, 1123-36	6.5	105
345	Extension of MST/SCRF method to organic solvents: Ab initio and semiempirical parametrization for neutral solutes in CCl ₄ . <i>Journal of Computational Chemistry</i> , 1996 , 17, 806-820	3.5	104
344	Theoretical study of the truncated hemoglobin HbN: exploring the molecular basis of the NO detoxification mechanism. <i>Journal of the American Chemical Society</i> , 2005 , 127, 4433-44	16.4	102
343	Theoretical study of alkyl- π and aryl- π interactions. Reconciling theory and experiment. <i>Journal of Organic Chemistry</i> , 2002 , 67, 7057-65	4.2	101

342	PMut: a web-based tool for the annotation of pathological variants on proteins, 2017 update. <i>Nucleic Acids Research</i> , 2017 , 45, W222-W228	20.1	100
341	MoDEL (Molecular Dynamics Extended Library): a database of atomistic molecular dynamics trajectories. <i>Structure</i> , 2010 , 18, 1399-409	5.2	100
340	Determining promoter location based on DNA structure first-principles calculations. <i>Genome Biology</i> , 2007 , 8, R263	18.3	98
339	Chromatin Unfolding by Epigenetic Modifications Explained by Dramatic Impairment of Internucleosome Interactions: A Multiscale Computational Study. <i>Journal of the American Chemical Society</i> , 2015 , 137, 10205-15	16.4	96
338	Molecular Dynamics Studies of DNA A-Tract Structure and Flexibility. <i>Journal of the American Chemical Society</i> , 1999 , 121, 5981-5991	16.4	96
337	Molecular Dynamics Simulation of a PNA-DNA-PNA Triple Helix in Aqueous Solution. <i>Journal of the American Chemical Society</i> , 1998 , 120, 5895-5904	16.4	94
336	Essential Dynamics: A Tool for Efficient Trajectory Compression and Management. <i>Journal of Chemical Theory and Computation</i> , 2006 , 2, 251-8	6.4	90
335	Synthesis, in vitro pharmacology, and molecular modeling of very potent tacrine-huperzine A hybrids as acetylcholinesterase inhibitors of potential interest for the treatment of Alzheimer's disease. <i>Journal of Medicinal Chemistry</i> , 1999 , 42, 3227-42	8.3	90
334	Impact of methylation on the physical properties of DNA. <i>Biophysical Journal</i> , 2012 , 102, 2140-8	2.9	89
333	Ligand-induced dynamical regulation of NO conversion in Mycobacterium tuberculosis truncated hemoglobin-N. <i>Proteins: Structure, Function and Bioinformatics</i> , 2006 , 64, 457-64	4.2	89
332	Interactions of Hydrated Mg ²⁺ Cation with Bases, Base Pairs, and Nucleotides. Electron Topology, Natural Bond Orbital, Electrostatic, and Vibrational Study. <i>Journal of Physical Chemistry B</i> , 2001 , 105, 6051-6060	3.4	89
331	An AM1-SCRF approach to the study of changes in molecular properties induced by solvent. <i>The Journal of Physical Chemistry</i> , 1993 , 97, 4386-4391		88
330	Exploring the counterion atmosphere around DNA: what can be learned from molecular dynamics simulations?. <i>Biophysical Journal</i> , 2004 , 87, 800-11	2.9	86
329	Development of optimized MST/SCRF methods for semiempirical calculations: The MNDO and PM3 Hamiltonians. <i>Journal of Computational Chemistry</i> , 1995 , 16, 563-575	3.5	86
328	Multiscale simulation of DNA. <i>Current Opinion in Structural Biology</i> , 2016 , 37, 29-45	8.1	85
327	A theoretical view of protein dynamics. <i>Chemical Society Reviews</i> , 2014 , 43, 5051-66	58.5	83
326	G-quadruplexes can maintain their structure in the gas phase. <i>Journal of the American Chemical Society</i> , 2006 , 128, 3608-19	16.4	82
325	Electrostatic component of solvation: comparison of SCRF continuum models. <i>Journal of Computational Chemistry</i> , 2003 , 24, 284-97	3.5	82

324	The structure of human 4F2hc ectodomain provides a model for homodimerization and electrostatic interaction with plasma membrane. <i>Journal of Biological Chemistry</i> , 2007 , 282, 31444-52	5.4	81
323	Continuum solvation models: Dissecting the free energy of solvation. <i>Physical Chemistry Chemical Physics</i> , 2003 , 5, 3827-3836	3.6	81
322	The structural impact of DNA mismatches. <i>Nucleic Acids Research</i> , 2015 , 43, 4309-21	20.1	80
321	How accurate are accurate force-fields for B-DNA?. <i>Nucleic Acids Research</i> , 2017 , 45, 4217-4230	20.1	79
320	Ab Initio Study of Stacking Interactions in A- and B-DNA. <i>Journal of Physical Chemistry B</i> , 1997 , 101, 3846-3853	3.4	79
319	Relative flexibility of DNA and RNA: a molecular dynamics study. <i>Journal of Molecular Biology</i> , 2004 , 343, 627-38	6.5	79
318	Classical molecular interaction potentials: improved setup procedure in molecular dynamics simulations of proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001 , 45, 428-37	4.2	79
317	Polarization effects in generalized molecular interaction potential: New Hamiltonian for reactivity studies and mixed QM/MM calculations. <i>Journal of Computational Chemistry</i> , 1998 , 19, 866-881	3.5	78
316	Dimerization of Carboxylic Acids: Reliability of Theoretical Calculations and the Effect of Solvent. <i>Journal of Physical Chemistry B</i> , 1998 , 102, 2269-2276	3.4	77
315	Colibactin DNA-damage signature indicates mutational impact in colorectal cancer. <i>Nature Medicine</i> , 2020 , 26, 1063-1069	50.5	76
314	Extension of the MST model to the IEF formalism: HF and B3LYP parametrizations. <i>Computational and Theoretical Chemistry</i> , 2005 , 727, 29-40		74
313	. <i>Journal of Physical Chemistry A</i> , 1999 , 103, 4525-4532	2.8	74
312	Induction effects in metal cation-benzene complexes. <i>Physical Chemistry Chemical Physics</i> , 2008 , 10, 2616-24	5.84	73
311	Interoperability with Moby 1.0--it's better than sharing your toothbrush!. <i>Briefings in Bioinformatics</i> , 2008 , 9, 220-31	13.4	73
310	Structure, Stiffness and Substates of the Dickerson-Drew Dodecamer. <i>Journal of Chemical Theory and Computation</i> , 2013 , 9, 707-721	6.4	72
309	Tautomerism of 1-Methyl Derivatives of Uracil, Thymine, and 5-Bromouracil. Is Tautomerism the Basis for the Mutagenicity of 5-Bromouridine?. <i>Journal of Physical Chemistry B</i> , 1998 , 102, 5228-5233	3.4	71
308	SDS-PAGE analysis of Aβ oligomers is disserving research into Alzheimer's disease: appealing for ESI-IM-MS. <i>Scientific Reports</i> , 2015 , 5, 14809	4.9	70
307	Exploring polymorphisms in B-DNA helical conformations. <i>Nucleic Acids Research</i> , 2012 , 40, 10668-78	20.1	68

306	Theoretical study of large conformational transitions in DNA: the BA conformational change in water and ethanol/water. <i>Nucleic Acids Research</i> , 2007 , 35, 3330-8	20.1	68
305	An optimized AM1/MST method for the MST-SCRF representation of solvated systems. <i>Journal of Computational Chemistry</i> , 1994 , 15, 847-857	3.5	68
304	Long-timescale dynamics of the Drew-Dickerson dodecamer. <i>Nucleic Acids Research</i> , 2016 , 44, 4052-66	20.1	68
303	FlexServ: an integrated tool for the analysis of protein flexibility. <i>Bioinformatics</i> , 2009 , 25, 1709-10	7.2	67
302	Compaction of Duplex Nucleic Acids upon Native Electrospray Mass Spectrometry. <i>ACS Central Science</i> , 2017 , 3, 454-461	16.8	65
301	Theoretical Study of Azido-Tetrazole Isomerism: Effect of Solvent and Substituents and Mechanism of Isomerization. <i>Journal of the American Chemical Society</i> , 1998 , 120, 4723-4731	16.4	65
300	Tautomerism of Xanthine Oxidase Substrates Hypoxanthine and Allopurinol. <i>Journal of Organic Chemistry</i> , 1996 , 61, 5964-5971	4.2	64
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298	Unraveling the sequence-dependent polymorphic behavior of d(CpG) steps in B-DNA. <i>Nucleic Acids Research</i> , 2014 , 42, 11304-20	20.1	63
297	Theoretical study of anion binding to calix[4]pyrrole: the effects of solvent, fluorine substitution, cosolute, and water traces. <i>Journal of the American Chemical Society</i> , 2002 , 124, 12796-805	16.4	63
296	Molecular Dynamics Simulations of PNA/DNA and PNA/RNA Duplexes in Aqueous Solution. <i>Journal of the American Chemical Society</i> , 2000 , 122, 5997-6008	16.4	63
295	Optimization of the cavity size for ab initio MST-SCRF calculations of monovalent ions. <i>Chemical Physics</i> , 1994 , 182, 237-248	2.3	63
294	Comprehensive characterization of complex structural variations in cancer by directly comparing genome sequence reads. <i>Nature Biotechnology</i> , 2014 , 32, 1106-12	44.5	62
293	Conformational dynamics of the human propeller telomeric DNA quadruplex on a microsecond time scale. <i>Nucleic Acids Research</i> , 2013 , 41, 2723-35	20.1	60
292	Structural characterization of protein-protein complexes by integrating computational docking with small-angle scattering data. <i>Journal of Molecular Biology</i> , 2010 , 403, 217-30	6.5	59
291	The impact of monovalent ion force field model in nucleic acids simulations. <i>Physical Chemistry Chemical Physics</i> , 2009 , 11, 10596-607	3.6	59
290	Comparison of 6-31G*-based MST/SCRF and FEP evaluations of the free energies of hydration for small neutral molecules. <i>Journal of Computational Chemistry</i> , 1993 , 14, 1498-1503	3.5	59
289	Nucleic Acid Triple Helices: Stability Effects of Nucleobase Modifications. <i>Current Organic Chemistry</i> , 2002 , 6, 1333-1368	1.7	59

288	Differential stability of 2'F-ANA*RNA and ANA*RNA hybrid duplexes: roles of structure, pseudohydrogen bonding, hydration, ion uptake and flexibility. <i>Nucleic Acids Research</i> , 2010 , 38, 2498-5111	20.1	58
287	The (in)dependence of alternative splicing and gene duplication. <i>PLoS Computational Biology</i> , 2007 , 3, e33	5	57
286	Molecular Dynamics Simulations in Aqueous Solution of Triple Helices Containing d(GCC) Trios. <i>Journal of the American Chemical Society</i> , 1998 , 120, 11226-11233	16.4	57
285	Observation of Spontaneous Base Pair Breathing Events in the Molecular Dynamics Simulation of a Difluorotoluene-Containing DNA Oligonucleotide. <i>Journal of the American Chemical Society</i> , 1999 , 121, 8653-8654	16.4	57
284	Theoretical Methods for the Representation of Solvent. <i>Journal of Molecular Modeling</i> , 1996 , 2, 1-15	2	57
283	Exploring the Essential Dynamics of B-DNA. <i>Journal of Chemical Theory and Computation</i> , 2005 , 1, 790-800	4	56
282	Epigenetic loss of RNA-methyltransferase NSUN5 in glioma targets ribosomes to drive a stress adaptive translational program. <i>Acta Neuropathologica</i> , 2019 , 138, 1053-1074	14.3	55
281	Dramatic effect of furanose C2' substitution on structure and stability: directing the folding of the human telomeric quadruplex with a single fluorine atom. <i>Journal of the American Chemical Society</i> , 2013 , 135, 5344-7	16.4	55
280	Ensemble Docking from Homology Models. <i>Journal of Chemical Theory and Computation</i> , 2010 , 6, 2547-554	4	55
279	A comprehensive DNA methylation profile of epithelial-to-mesenchymal transition. <i>Cancer Research</i> , 2014 , 74, 5608-19	10.1	54
278	nucleR: a package for non-parametric nucleosome positioning. <i>Bioinformatics</i> , 2011 , 27, 2149-50	7.2	54
277	Structure, recognition properties, and flexibility of the DNA.RNA hybrid. <i>Journal of the American Chemical Society</i> , 2005 , 127, 4910-20	16.4	53
276	Theoretical study of N-methylacetamide in vacuum and aqueous solution: implications for the peptide bond isomerization. <i>Journal of Organic Chemistry</i> , 1993 , 58, 6397-6405	4.2	53
275	Correlated motions are a fundamental property of β -sheets. <i>Nature Communications</i> , 2014 , 5, 4070	17.4	52
274	Approaching Elastic Network Models to Molecular Dynamics Flexibility. <i>Journal of Chemical Theory and Computation</i> , 2010 , 6, 2910-23	6.4	52
273	Evidence for transcript networks composed of chimeric RNAs in human cells. <i>PLoS ONE</i> , 2012 , 7, e28213	3.7	51
272	Scoring by intermolecular pairwise propensities of exposed residues (SIPPER): a new efficient potential for protein-protein docking. <i>Journal of Chemical Information and Modeling</i> , 2011 , 51, 370-7	6.1	51
271	Local aromaticity in natural nucleobases and their size-expanded benzo-fused derivatives. <i>Journal of Physical Chemistry A</i> , 2006 , 110, 12249-58	2.8	51

270	Role of Intramolecular Hydrogen Bonds in the Intermolecular Hydrogen Bonding of Carbohydrates. <i>Journal of Physical Chemistry A</i> , 1998 , 102, 6690-6696	2.8	51
269	Geometrical and electronic structure variability of the sugar-phosphate backbone in nucleic acids. <i>Journal of Physical Chemistry B</i> , 2008 , 112, 8188-97	3.4	50
268	Structure of triplex DNA in the gas phase. <i>Journal of the American Chemical Society</i> , 2012 , 134, 6596-6061	6.4	49
267	4D Genome Rewiring during Oncogene-Induced and Replicative Senescence. <i>Molecular Cell</i> , 2020 , 78, 522-538.e9	17.6	48
266	The native ensemble and folding of a protein molten-globule: functional consequence of downhill folding. <i>Journal of the American Chemical Society</i> , 2011 , 133, 12154-61	16.4	48
265	Theoretical study of the guanine → 6-thioguanine substitution in duplexes, triplexes, and tetraplexes. <i>Journal of the American Chemical Society</i> , 2004 , 126, 14642-50	16.4	48
264	Quantification of Pathway Cross-talk Reveals Novel Synergistic Drug Combinations for Breast Cancer. <i>Cancer Research</i> , 2017 , 77, 459-469	10.1	47
263	Toward a consensus view of duplex RNA flexibility. <i>Biophysical Journal</i> , 2010 , 99, 1876-85	2.9	46
262	New strategies to incorporate the solvent polarization in self-consistent reaction field and free-energy perturbation simulations. <i>Journal of Chemical Physics</i> , 1995 , 103, 10183-10191	3.9	46
261	Theoretical studies on the inhibition mechanism of cyclooxygenase-2. Is there a unique recognition site?. <i>Journal of Medicinal Chemistry</i> , 2003 , 46, 1372-82	8.3	45
260	Ligand-induced changes in the binding sites of proteins. <i>Bioinformatics</i> , 2002 , 18, 939-48	7.2	45
259	Molecular interaction potential: A new tool for the theoretical study of molecular reactivity. <i>Journal of Computational Chemistry</i> , 1993 , 14, 587-602	3.5	45
258	Dispersion and repulsion contributions to the solvation free energy: comparison of quantum mechanical and classical approaches in the polarizable continuum model. <i>Journal of Computational Chemistry</i> , 2006 , 27, 1769-80	3.5	44
257	Unique tautomeric properties of isoguanine. <i>Journal of the American Chemical Society</i> , 2004 , 126, 154-64	6.4	44
256	Hog1 bypasses stress-mediated down-regulation of transcription by RNA polymerase II redistribution and chromatin remodeling. <i>Genome Biology</i> , 2012 , 13, R106	18.3	43
255	Toward an atomistic description of the urea-denatured state of proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 5933-8	11.5	42
254	Theoretical Study of the Tautomerism and Protonation of 7-Aminopyrazolopyrimidine in the Gas Phase and in Aqueous Solution. <i>Journal of the American Chemical Society</i> , 1995 , 117, 1378-1386	16.4	42
253	Mechanism for the rotamase activity of FK506 binding protein from molecular dynamics simulations. <i>Biochemistry</i> , 1993 , 32, 12864-74	3.2	42

252	Backbone FC-H ₂ O hydrogen bonds in 2'F-substituted nucleic acids. <i>Angewandte Chemie - International Edition</i> , 2013 , 52, 12065-8	16.4	41
251	Role of tautomerism of 2-azaadenine and 2-azahypoxanthine in substrate recognition by xanthine oxidase. <i>Journal of Computer-Aided Molecular Design</i> , 1997 , 11, 153-62	4.2	41
250	Characterization of compensated mutations in terms of structural and physico-chemical properties. <i>Journal of Molecular Biology</i> , 2007 , 365, 249-56	6.5	41
249	Theoretical study of the mechanisms of substrate recognition by catalase. <i>Journal of the American Chemical Society</i> , 2001 , 123, 9665-72	16.4	41
248	Residues Coevolution Guides the Systematic Identification of Alternative Functional Conformations in Proteins. <i>Structure</i> , 2016 , 24, 116-126	5.2	40
247	Prevalent Sequences in the Human Genome Can Form Mini i-Motif Structures at Physiological pH. <i>Journal of the American Chemical Society</i> , 2017 , 139, 13985-13988	16.4	40
246	Proteins in the gas phase. <i>Wiley Interdisciplinary Reviews: Computational Molecular Science</i> , 2013 , 3, 408-425	16.4	40
245	Understanding the connection between epigenetic DNA methylation and nucleosome positioning from computer simulations. <i>PLoS Computational Biology</i> , 2013 , 9, e1003354	5	40
244	Theoretical characterization of the dynamical behavior and transport properties of alpha,gamma-peptide nanotubes in solution. <i>Journal of the American Chemical Society</i> , 2009 , 131, 15678-86	16.4	40
243	Deciphering the deformation modes associated with function retention and specialization in members of the Ras superfamily. <i>Structure</i> , 2010 , 18, 402-14	5.2	40
242	Multiple routes to characterize the folding of a small DNA hairpin. <i>Angewandte Chemie - International Edition</i> , 2010 , 49, 7673-6	16.4	40
241	MST continuum study of the hydration free energies of monovalent ionic species. <i>Journal of Physical Chemistry B</i> , 2005 , 109, 3565-74	3.4	40
240	The polarization contribution to the free energy of hydration. <i>Journal of Chemical Physics</i> , 1995 , 102, 6145-6152	3.9	40
239	MD and NMR analyses of choline and TMA binding to duplex DNA: on the origins of aberrant sequence-dependent stability by alkyl cations in aqueous and water-free solvents. <i>Journal of the American Chemical Society</i> , 2014 , 136, 3075-86	16.4	39
238	Exploring the suitability of coarse-grained techniques for the representation of protein dynamics. <i>Biophysical Journal</i> , 2008 , 95, 2127-38	2.9	39
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