

F Marty Ytreberg

List of Publications by Year in descending order

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Version: 2024-02-01

44
papers

963
citations

430874

18
h-index

477307

29
g-index

49
all docs

49
docs citations

49
times ranked

1271
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Paired Simulations and Experimental Investigations into the Calcium-Dependent Conformation of Albumin. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 1282-1293. | 5.4 | 7 |
| 2 | Searching for a mechanistic description of pairwise epistasis in protein systems. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 1474-1485. | 2.6 | 3 |
| 3 | Molecular Modeling Predicts Novel Antibody Escape Mutations in the Respiratory Syncytial Virus Fusion Glycoprotein. <i>Journal of Virology</i> , 2022, 96, . | 3.4 | 6 |
| 4 | Implementing and Assessing an Alchemical Method for Calculating Protein-Protein Binding Free Energy. <i>Journal of Chemical Theory and Computation</i> , 2021, 17, 2457-2464. | 5.3 | 16 |
| 5 | EfgA is a conserved formaldehyde sensor that leads to bacterial growth arrest in response to elevated formaldehyde. <i>PLoS Biology</i> , 2021, 19, e3001208. | 5.6 | 13 |
| 6 | Protein Stability in Titan's Subsurface Water Ocean. <i>Astrobiology</i> , 2020, 20, 190-198. | 3.0 | 1 |
| 7 | Predicting the viability of beta-lactamase: How folding and binding free energies correlate with beta-lactamase fitness. <i>PLoS ONE</i> , 2020, 15, e0233509. | 2.5 | 26 |
| 8 | Assessment of software methods for estimating protein-protein relative binding affinities. <i>PLoS ONE</i> , 2020, 15, e0240573. | 2.5 | 11 |
| 9 | Title is missing!. , 2020, 15, e0233509. | | 0 |
| 10 | Title is missing!. , 2020, 15, e0233509. | | 0 |
| 11 | Title is missing!. , 2020, 15, e0233509. | | 0 |
| 12 | Title is missing!. , 2020, 15, e0233509. | | 0 |
| 13 | Expanding the watch list for potential Ebola virus antibody escape mutations. <i>PLoS ONE</i> , 2019, 14, e0211093. | 2.5 | 25 |
| 14 | Fast Calculation of Protein-Protein Binding Free Energies Using Umbrella Sampling with a Coarse-Grained Model. <i>Journal of Chemical Theory and Computation</i> , 2018, 14, 991-997. | 5.3 | 38 |
| 15 | Predicting peak spectral sensitivities of vertebrate cone visual pigments using atomistic molecular simulations. <i>PLoS Computational Biology</i> , 2018, 14, e1005974. | 3.2 | 15 |
| 16 | Parallel Mutations Result in a Wide Range of Cooperation and Community Consequences in a Two-Species Bacterial Consortium. <i>PLoS ONE</i> , 2016, 11, e0161837. | 2.5 | 23 |
| 17 | New Perspectives on Ebola Virus Evolution. <i>PLoS ONE</i> , 2016, 11, e0160410. | 2.5 | 6 |
| 18 | Initiating a watch list for Ebola virus antibody escape mutations. <i>PeerJ</i> , 2016, 4, e1674. | 2.0 | 36 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 19 | The cis conformation of proline leads to weaker binding of a p53 peptide to MDM2 compared to trans. Archives of Biochemistry and Biophysics, 2015, 575, 22-29. | 3.0 | 10 |
| 20 | Using chemical shifts to generate structural ensembles for intrinsically disordered proteins with converged distributions of secondary structure. Intrinsically Disordered Proteins, 2015, 3, e984565. | 1.9 | 10 |
| 21 | Changing Folding and Binding Stability in a Viral Coat Protein: A Comparison between Substitutions Accessible through Mutation and Those Fixed by Natural Selection. PLoS ONE, 2014, 9, e112988. | 2.5 | 13 |
| 22 | The effects of nanoscale geometry and spillover on room temperature storage of hydrogen on silica nanosprings. Journal Physics D: Applied Physics, 2013, 46, 505307. | 2.8 | 6 |
| 23 | Impact of the K24N mutation on the transactivation domain of p53 and its binding to murine double-minute clone 2. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1738-1747. | 2.6 | 20 |
| 24 | Understanding the structural ensembles of a highly extended disordered protein. Molecular BioSystems, 2012, 8, 308-319. | 2.9 | 37 |
| 25 | Effect of Gold Nanoparticle Conjugation on Peptide Dynamics and Structure. Entropy, 2012, 14, 630-641. | 2.2 | 24 |
| 26 | A Novel Mouse Dscam Mutation Inhibits Localization and Shedding of DSCAM. PLoS ONE, 2012, 7, e52652. | 2.5 | 27 |
| 27 | Effects of the binding of calcium ions on the structure and dynamics of the H1N1 virus investigated using molecular dynamics. Journal of Biological Physics, 2012, 38, 397-404. | 1.5 | 0 |
| 28 | Understanding Bernoulli's principle through simulations. American Journal of Physics, 2011, 79, 214-216. | 0.7 | 25 |
| 29 | Computational estimation of rainbow trout estrogen receptor binding affinities for environmental estrogens. Toxicology and Applied Pharmacology, 2011, 250, 322-326. | 2.8 | 18 |
| 30 | C5'-Functionalized DNA, LNA, and LNA: Positional Control of Polarity-Sensitive Fluorophores Leads to Improved SNP Typing. Chemistry - A European Journal, 2011, 17, 3157-3165. | 3.3 | 33 |
| 31 | First-Step Mutations for Adaptation at Elevated Temperature Increase Capsid Stability in a Virus. PLoS ONE, 2011, 6, e25640. | 2.5 | 24 |
| 32 | Computational Study of Small Molecule Binding for Both Tethered and Free Conditions. Journal of Physical Chemistry B, 2010, 114, 5431-5434. | 2.6 | 5 |
| 33 | Computational Study of Evolutionary Selection Pressure on Rainbow Trout Estrogen Receptors. PLoS ONE, 2010, 5, e9392. | 2.5 | 4 |
| 34 | Reducing the bias and uncertainty of free energy estimates by using regression to fit thermodynamic integration data. Journal of Computational Chemistry, 2009, 30, NA-NA. | 3.3 | 27 |
| 35 | Absolute FKBP binding affinities obtained via nonequilibrium unbinding simulations. Journal of Chemical Physics, 2009, 130, 164906. | 3.0 | 53 |
| 36 | A black-box re-weighting analysis can correct flawed simulation data. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7982-7987. | 7.1 | 10 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | Demonstrated Convergence of the Equilibrium Ensemble for a Fast United-Residue Protein Model. Journal of Chemical Theory and Computation, 2007, 3, 1860-1866. | 5.3 | 4 |
| 38 | Comparison of free energy methods for molecular systems. Journal of Chemical Physics, 2006, 125, 184114. | 3.0 | 129 |
| 39 | Simple estimation of absolute free energies for biomolecules. Journal of Chemical Physics, 2006, 124, 104105. | 3.0 | 33 |
| 40 | Peptide Conformational Equilibria Computed via a Single-Stage Shifting Protocol. Journal of Physical Chemistry B, 2005, 109, 9096-9103. | 2.6 | 16 |
| 41 | Single-ensemble nonequilibrium path-sampling estimates of free energy differences. Journal of Chemical Physics, 2004, 120, 10876-10879. | 3.0 | 99 |
| 42 | Efficient use of nonequilibrium measurement to estimate free energy differences for molecular systems. Journal of Computational Chemistry, 2004, 25, 1749-1759. | 3.3 | 74 |
| 43 | Calculated properties of field-induced aggregates in ferrofluids. Physical Review E, 2000, 61, 4107-4110. | 2.1 | 32 |
| 44 | Second mechanism for transitions in a reaction diffusion system. Physical Review E, 1999, 59, 3376-3381. | 2.1 | 3 |