# Gustavo Pierdominici-Sottile

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/8996605/publications.pdf

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|---|---|---|---|
| 20 papers | 190 citations | 1162889 8 h-index | 1058333 14 g-index |
| 20 all docs | 20 docs citations | 20 times ranked | 212 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Free Energy Study of the Catalytic Mechanism of Trypanosoma cruzitrans-Sialidase. From the Michaelis Complex to the Covalent Intermediate. Biochemistry, 2011, 50, 10150-10158. | 1.2 | 40 |
| 2 | Proton Transfer Facilitated by Ligand Binding. An Energetic Analysis of the Catalytic Mechanism ofTrypanosoma cruziTrans-Sialidase. Biochemistry, 2011, 50, 836-842. | 1.2 | 33 |
| 3 | Consistent Principal Component Modes from Molecular Dynamics Simulations of Proteins. Journal of Chemical Information and Modeling, 2017, 57, 826-834. | 2.5 | 20 |
| 4 | Unraveling the Differences of the Hydrolytic Activity of Trypanosoma cruzi trans-Sialidase and Trypanosoma rangeli Sialidase: A Quantum Mechanicsâ€“Molecular Mechanics Modeling Study. Journal of Physical Chemistry B, 2014, 118, 5807-5816. | 1.2 | 13 |
| 5 | Freeâ€energy computations identify the mutations required to confer transâ€sialidase activity into Trypanosoma rangeli sialidase. Proteins: Structure, Function and Bioinformatics, 2014, 82, 424-435. | 1.5 | 10 |
| 6 | The Dynamic Behavior of the P2X4 Ion Channel in the Closed Conformation. Biophysical Journal, 2016, 111, 2642-2650. | 0.2 | 10 |
| 7 | Molecular Dynamics Study of the Active Site of Methylamine Dehydrogenase. Journal of Physical Chemistry B, 2006, 110, 11592-11599. | 1.2 | 9 |
| 8 | New insights into the meaning and usefulness of principal component analysis of concatenated trajectories. Journal of Computational Chemistry, 2015, 36, 424-432. | 1.5 | 9 |
| 9 | Quantum study of the structure of the active site of methylamine dehydrogenase. International Journal of Quantum Chemistry, 2005, 105, 937-945. | 1.0 | 8 |
| 10 | Applications of Mixed-Quantum/Classical Trajectories to the Study of Nuclear Quantum Effects in Chemical Reactions and Vibrational Relaxation Processes. Advances in Quantum Chemistry, 2010, , 247-282. | 0.4 | 7 |
| 11 | Evaluation of the kinetic isotope effect in methylamine dehydrogenase using the wave function propagation approach. Chemical Physics, 2009, 363, 59-64. | 0.9 | 6 |
| 12 | QM/MM Molecular Dynamics Study of the Galactopyranose â†' Galactofuranose Reaction Catalysed by Trypanosoma cruzi UDP-Galactopyranose Mutase. PLoS ONE, 2014, 9, e109559. | 1.1 | 6 |
| 13 | Molecular Dynamics Simulations of Substrate Release from Trypanosoma cruzi UDP-Galactopyranose Mutase. Journal of Chemical Information and Modeling, 2019, 59, 809-817. | 2.5 | 4 |
| 14 | Molecular Dynamics Simulations Unveil the Basis of the Sequential Binding of RsmE to the Noncoding RNA RsmZ. Journal of Physical Chemistry B, 2021, 125, 3045-3056. | 1.2 | 4 |
| 15 | Steric Control of the Rate-Limiting Step of UDP-Galactopyranose Mutase. Biochemistry, 2018, 57, 3713-3721. | 1.2 | 3 |
| 16 | The role of residue Thr122 of methylamine dehydrogenase on the proton transfer from the iminoquinone intermediate to residue Asp76. Chemical Physics Letters, 2008, 456, 243-246. | 1.2 | 2 |
| 17 | Charge Discrimination in P2X4 Receptors Occurs in Two Consecutive Stages. Journal of Physical Chemistry B, 2019, 123, 1017-1025. | 1.2 | 2 |
| 18 | Recognition and Binding of RsmE to an AGGAC Motif of RsmZ: Insights from Molecular Dynamics Simulations. Journal of Chemical Information and Modeling, 2022, 62, 6614-6627. | 2.5 | 2 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Positively Charged Residues in the Head Domain of P2X4 Receptors Assist the Binding of ATP. Journal of Chemical Information and Modeling, 2020, 60, 923-932. | 2.5 | 1 |
| 20 | Ion Selectivity in P2X Receptors: A Comparison between hP2X3 and zfP2X4. Journal of Physical Chemistry B, 2021, , . | 1.2 | 1 |