

# Michelle A Sahai

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3783342/publications.pdf>

Version: 2024-02-01

32  
papers

739  
citations

687363

13  
h-index

552781

26  
g-index

32  
all docs

32  
docs citations

32  
times ranked

1036  
citing authors

#	ARTICLE	IF	CITATIONS
1	Case study: Biochemistry without borders: a case study utilising infographics. <i>Essays in Biochemistry</i> , 2022, 66, 65-73.	4.7	3
2	The fine art of preparing membrane transport proteins for biomolecular simulations: Concepts and practical considerations. <i>Methods</i> , 2021, 185, 3-14.	3.8	6
3	Molecular Mechanisms of Action of Stimulant Novel Psychoactive Substances (NPS) that target the High-affinity Transporter for Dopamine. <i>Neuronal Signaling</i> , 2021, 5, NS20210006.	3.2	3
4	The Role of Dopamine in the Stimulant Characteristics of Novel Psychoactive Substances (NPS) – Neurobiological and Computational Assessment Using the Case of Desoxypradol (2-DPMP). <i>Frontiers in Pharmacology</i> , 2020, 11, 806.	3.5	6
5	Mechanistic Insights into the Stimulant Properties of Novel Psychoactive Substances (NPS) and Their Discrimination by the Dopamine Transporter – In Silico and In Vitro Exploration of Dissociative Diarylethylamines. <i>Brain Sciences</i> , 2018, 8, 63.	2.3	15
6	Combined in vitro and in silico approaches to the assessment of stimulant properties of novel psychoactive substances – The case of the benzofuran 5-MAPB. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2017, 75, 1-9.	4.8	17
7	Identification of a nucleoside analog active against adenosine kinase – expressing plasma cell malignancies. <i>Journal of Clinical Investigation</i> , 2017, 127, 2066-2080.	8.2	7
8	Computational Modeling of the N-Terminus of the Human Dopamine Transporter (hDAT). <i>Biophysical Journal</i> , 2015, 108, 252a.	0.5	2
9	Computational modeling of the N-terminus of the human dopamine transporter and its interaction with PIP <sub>2</sub> -containing membranes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2015, 83, 952-969.	2.6	47
10	Spontaneous Inward Opening of the Dopamine Transporter Is Triggered by PIP <sub>2</sub> -Regulated Dynamics of the N-Terminus. <i>ACS Chemical Neuroscience</i> , 2015, 6, 1825-1837.	3.5	95
11	Abstract 4496: Genomics-based resistome analysis revealed endogenous adenosine kinase levels as a chief determinant of specificity for a novel nucleoside analog lymphoma inhibitor. , 2015, , .		0
12	ESCRT-II/Vps25 Constrains Digit Number by Endosome-Mediated Selective Modulation of FGF-SHH Signaling. <i>Cell Reports</i> , 2014, 9, 674-687.	6.4	12
13	Missense dopamine transporter mutations associate with adult parkinsonism and ADHD. <i>Journal of Clinical Investigation</i> , 2014, 124, 3107-3120.	8.2	129
14	De novo mutation in the dopamine transporter gene associates dopamine dysfunction with autism spectrum disorder. <i>Molecular Psychiatry</i> , 2013, 18, 1315-1323.	7.9	181
15	Path Searching Towards the Symmetric Inward Open Structure of LeuT. <i>Biophysical Journal</i> , 2013, 104, 57a.	0.5	0
16	<i>Drosophila melanogaster</i> : a novel animal model for the behavioral characterization of autism-associated mutations in the dopamine transporter gene. <i>Molecular Psychiatry</i> , 2013, 18, 1235-1235.	7.9	9
17	Quantifying Water-Mediated Protein – Ligand Interactions in a Glutamate Receptor: A DFT Study. <i>Journal of Physical Chemistry B</i> , 2011, 115, 7085-7096.	2.6	16
18	A comparative analysis of the role of water in the binding pockets of ionotropic glutamate receptors. <i>Physical Chemistry Chemical Physics</i> , 2010, 12, 14057.	2.8	15

#	ARTICLE	IF	CITATIONS
19	Transition State Infrared Spectra for the Trans $\leftrightarrow$ Cis Isomerization of a Simple Peptide Model. <i>Journal of Physical Chemistry A</i> , 2007, 111, 8384-8389.	2.5	6
20	Quantifying the Intrinsic Effects of Two Point Mutation Models of Pro-Pro-Pro Triamino Acid Diamide. A First-Principle Computational Study. <i>Journal of Physical Chemistry B</i> , 2007, 111, 13135-13142.	2.6	14
21	Quantifying the Intrinsic Effects of Two Point Mutation Models of Proline $\leftrightarrow$ Proline Diamino Acid Diamide: A First-Principle Computational Study. <i>Journal of Physical Chemistry B</i> , 2007, 111, 11592-11602.	2.6	15
22	First-Principle Computational Study on the Full Conformational Space of l-Threonine Diamide, the Energetic Stability of Cis and Trans Isomers. <i>Journal of Physical Chemistry A</i> , 2006, 110, 11527-11536.	2.5	14
23	Selenocysteine derivatives I. Sidechain conformational potential energy surface of N-acetyl-l-selenocysteine-N-methylamide (MeCO-l-Sec-NH-Me) in its $\beta$ backbone conformation. <i>Computational and Theoretical Chemistry</i> , 2005, 725, 111-125.	1.5	4
24	First Principle Computational Study on the Full Conformational Space of l-Proline Diamides. <i>Journal of Physical Chemistry A</i> , 2005, 109, 2660-2679.	2.5	29
25	A modular numbering system of selected oligopeptides for molecular computations: using pre-computed amino acid building blocks. <i>Computational and Theoretical Chemistry</i> , 2003, 666-667, 169-218.	1.5	11
26	An ab initio exploratory study of the full conformational space of MeCO-l-threonine-NH-Me. <i>Computational and Theoretical Chemistry</i> , 2003, 666-667, 251-267.	1.5	7
27	An ab initio exploratory study on the conformational features of the dipeptide MeCO-Ala-Ala-NH-Me in its four different configurations: determination of the behaviour of d-enantiomer amino acids within a peptide chain. <i>Computational and Theoretical Chemistry</i> , 2003, 666-667, 291-301.	1.5	8
28	A model study of the IgA hinge region: an exploratory study of selected backbone conformations of MeCO-l-Pro-l-Thr-NH-Me. <i>Computational and Theoretical Chemistry</i> , 2003, 666-667, 311-319.	1.5	5
29	An ab initio exploratory study on selected conformational features of MeCO-l-Ala-l-Ala-l-Ala-NH-Me as a XxxYyyZzz tripeptide motif within a protein structure. <i>Computational and Theoretical Chemistry</i> , 2003, 666-667, 327-336.	1.5	4
30	Toward a computed peptide structure database: The role of a universal atomic numbering system of amino acids in peptides and internal hierarchy of database. <i>International Journal of Quantum Chemistry</i> , 2002, 90, 933-968.	2.0	54
31	Ab initio quantum mechanical characterization of platinum, palladium, and nickel complexes of L-ascorbic acid. <i>International Journal of Quantum Chemistry</i> , 2002, 90, 882-887.	2.0	4
32	Albert Szent-Györgyi $\text{€}^{\text{™}}$ The Scientist Who Discovered Vitamin C. <i>Frontiers for Young Minds</i> , 0, 8, .	0.8	1