Michel A Cuendet

List of Publications by Year
in descending order

49 papers	3,646 citations	377584 21 h-index	355658 38 g-index
53 all docs	53 docs citations	53 times ranked	6196 citing authors

#	Article	IF	Citations
1	Safety and Efficacy of Ipilimumab plus Nivolumab and Sequential Selective Internal Radiation Therapy in Hepatic and Extrahepatic Metastatic Uveal Melanoma. Cancers, 2022, 14, 1162.	1.7	9
2	A Graphic Encoding Method for Quantitative Classification of Protein Structure and Representation of Conformational Changes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1336-1349.	1.9	4
3	A lightweight method for evaluating in situ workflow efficiency. Journal of Computational Science, 2021, 48, 101259.	1.5	7
4	Digitalization is Fueling a Revolution in Precision Oncology. , 2021, , 342-346.		1
5	A Process Mining Approach to Statistical Analysis: Application to a Real-World Advanced Melanoma Dataset. Lecture Notes in Business Information Processing, 2021, , 291-304.	0.8	4
6	Probing the Conformational Dynamics of Affinity-Enhanced T Cell Receptor Variants upon Binding the Peptide-Bound Major Histocompatibility Complex by Hydrogen/Deuterium Exchange Mass Spectrometry. Biochemistry, 2021, 60, 859-872.	1.2	3
7	Unusual mode of dimerization of retinitis pigmentosa-associated F220C rhodopsin. Scientific Reports, 2021, 11, 10536.	1.6	7
8	Turning tumors from cold to inflamed to improve immunotherapy response. Cancer Treatment Reviews, 2021, 101, 102227.	3.4	42
9	Acquired resistance to anti-MAPK targeted therapy confers an immune-evasive tumor microenvironment and cross-resistance to immunotherapy in melanoma. Nature Cancer, 2021, 2, 693-708.	5.7	102
10	Truly privacy-preserving federated analytics for precision medicine with multiparty homomorphic encryption. Nature Communications, 2021, 12, 5910.	5.8	64
11	The combination of stereotactic radiosurgery with immune checkpoint inhibition or targeted therapy in melanoma patients with brain metastases: a retrospective study. Journal of Neuro-Oncology, 2020, 146, 181-193.	1.4	18
12	What Role Can Process Mining Play in Recurrent Clinical Guidelines Issues? A Position Paper. International Journal of Environmental Research and Public Health, 2020, 17, 6616.	1.2	12
13	Long-lasting, irreversible and late-onset immune-related adverse events (irAEs) from immune checkpoint inhibitors (ICIs): A real-world data analysis.. Journal of Clinical Oncology, 2020, 38, e15095-e15095.	0.8	3
14	A process mining approach to real-world advanced melanoma treatments.. Journal of Clinical Oncology, 2020, 38, e22040-e22040.	0.8	1
15	A Novel Metric to Evaluate In Situ Workflows. Lecture Notes in Computer Science, 2020, , 538-553.	1.0	2
16	CD8 Binding of MHC-Peptide Complexes in cis or trans Regulates CD8+ T-cell Responses. Journal of Molecular Biology, 2019, 431, 4941-4958.	2.0	7
17	Characterizing In Situ and In Transit Analytics of Molecular Dynamics Simulations for Next-Generation Supercomputers. , 2019, , .		4
18	Thermodynamic Coupling Function Analysis of Allosteric Mechanisms in the Human Dopamine Transporter. Biophysical Journal, 2018, 114, 10-14.	0.2	18

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19	Thermodynamic Coupling Function Analysis of Allosteric Coupling between Na+ Release and Inward-Opening in the Human Dopamine Transporter. Biophysical Journal, 2018, 114, 421a.	0.2	0
20	Graphic Encoding of Macromolecules for Efficient High-Throughput Analysis. , 2018, , .		4
21	Substrate-modulated unwinding of transmembrane helices in the NSS transporter LeuT. Science Advances, 2018, 4, eaar6179.	4.7	47
22	Endpoint-restricted adiabatic free energy dynamics approach for the exploration of biomolecular conformational equilibria. Journal of Chemical Physics, 2018, 149, 072316.	1.2	11
23	Serum protein predictors of long term survival from combined ipilimumab and nivolumab therapy in metastatic melanoma patients.. Journal of Clinical Oncology, 2018, 36, e21513-e21513.	0.8	0
24	Rigorous Representation of Transporters as Allosteric Machines Enables a Quantitative Understanding of their Functional Mechanisms. Biophysical Journal, 2017, 112, 308a.	0.2	0
25	The Allostery Landscape: Quantifying Thermodynamic Couplings in Biomolecular Systems. Biophysical Journal, 2017, 112, 354a.	0.2	0
26	Vectorial Cholesterol Transport by STARD4 is Mediated by Specific PIP 2 Membrane Composition. Biophysical Journal, 2017, 112, 87a.	0.2	0
27	Cholesterol Promotes Protein Binding by Affecting Membrane Electrostatics and Solvation Properties. Biophysical Journal, 2017, 113, 2004-2015.	0.2	38
28	The T-Cell Receptor Can Bind to the Peptide-Bound Major Histocompatibility Complex and Uncomplexed Î²₂-Microglobulin through Distinct Binding Sites. Biochemistry, 2017, 56, 3945-3961.	1.2	8
29	Exploratory analysis of multiprotein serum predictors at baseline of progression-free survival of ipilimumab or ipilimumab and nivolumab in the Checkmate-069 study.. Journal of Clinical Oncology, 2017, 35, 9571-9571.	0.8	0
30	The Allostery Landscape: Quantifying Thermodynamic Couplings in Biomolecular Systems. Journal of Chemical Theory and Computation, 2016, 12, 5758-5767.	2.3	33
31	Dissecting Functional Correlates of a Double Mutation Enhancing GltPh Transport Efficiency using Alchemical Free Energy Calculations. Biophysical Journal, 2016, 110, 627a.	0.2	0
32	From Physics to Phenotype: New Insights into Allosteric Transport Mechanisms in LeuT. Biophysical Journal, 2016, 110, 362a.	0.2	0
33	Allosteric Mechanisms of Molecular Machines at the Membrane: Transport by Sodium-Coupled Symporters. Chemical Reviews, 2016, 116, 6552-6587.	23.0	71
34	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
35	Transport domain unlocking sets the uptake rate of an aspartate transporter. Nature, 2015, 518, 68-73.	13.7	144
36	Molecular Dynamics Simulation Study of a Mutant Construct of the Archaeal Glutamate Transporter GltPh with Transport Rates as Fast as its Human Counterpart. Biophysical Journal, 2015, 108, 198a.	0.2	0

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37	Free Energy Reconstruction from Metadynamics or Adiabatic Free Energy Dynamics Simulations. Journal of Chemical Theory and Computation, 2014, 10, 2975-2986.	2.3	53
38	How Accurately Do Current Force Fields Predict Experimental Peptide Conformations? An Adiabatic Free Energy Dynamics Study. Journal of Physical Chemistry B, 2014, 118, 6539-6552.	1.2	33
39	Heating and flooding: A unified approach for rapid generation of free energy surfaces. Journal of Chemical Physics, 2012, 137, 024102.	1.2	66
40	Alchemical Free Energy Differences in Flexible Molecules from Thermodynamic Integration or Free Energy Perturbation Combined with Driven Adiabatic Dynamics. Journal of Chemical Theory and Computation, 2012, 8, 3504-3512.	2.3	17
41	How T cell receptors interact with peptideâ€MHCs: A multiple steered molecular dynamics study. Proteins: Structure, Function and Bioinformatics, 2011, 79, 3007-3024.	1.5	43
42	SwissParam: A fast force field generation tool for small organic molecules. Journal of Computational Chemistry, 2011, 32, 2359-2368.	1.5	1,485
43	Use of the FACTS solvation model for proteinâ€“ligand docking calculations. Application to EADock. Journal of Molecular Recognition, 2010, 23, 457-461.	1.1	28
44	Implementation of the CHARMM Force Field in GROMACS: Analysis of Protein Stability Effects from Correction Maps, Virtual Interaction Sites, and Water Models. Journal of Chemical Theory and Computation, 2010, 6, 459-466.	2.3	866
45	Protein-Protein Interaction Investigated by Steered Molecular Dynamics: The TCR-pMHC Complex. Biophysical Journal, 2008, 95, 3575-3590.	0.2	117
46	Optical Spectra of Cu(II)â˜Azurin by Hybrid TDDFT-Molecular Dynamics Simulations. Journal of Physical Chemistry B, 2007, 111, 10248-10252.	1.2	38
47	On the calculation of velocity-dependent properties in molecular dynamics simulations using the leapfrog integration algorithm. Journal of Chemical Physics, 2007, 127, 184102.	1.2	95
48	The Jarzynski identity derived from general Hamiltonian or non-Hamiltonian dynamics reproducing NVT or NPT ensembles. Journal of Chemical Physics, 2006, 125, 144109.	1.2	41
49	Statistical Mechanical Derivation of Jarzynskiâ€™s Identity for Thermostated Non-Hamiltonian Dynamics. Physical Review Letters, 2006, 96, 120602.	2.9	32