## Serge Bouaziz

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structure of the Human Telomere in K <sup>+</sup> Solution: A Stable Basket-Type G-Quadruplex with Only Two G-Tetrad Layers. Journal of the American Chemical Society, 2009, 131, 4301-4309.	13.7	439
2	APOBEC3A Is a Specific Inhibitor of the Early Phases of HIV-1 Infection in Myeloid Cells. PLoS Pathogens, 2011, 7, e1002221.	4.7	171
3	NMR Structure of the HIV-1 Regulatory Protein VPR. Journal of Molecular Biology, 2003, 327, 215-227.	4.2	155
4	Solution structure of a Na cation stabilized DNA quadruplex containing G·G·G·G and G·C·G·C tetrads formed by G-G-G-C repeats observed in adeno-associated viral DNA 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1998, 282, 619-636.	4.2	116
5	A K cation-induced conformational switch within a loop spanning segment of a DNA quadruplex containing G-G-G-C repeats 1 1Edited by I. Tinoco. Journal of Molecular Biology, 1998, 282, 637-652.	4.2	106
6	How the HIV-1 Nucleocapsid Protein Binds and Destabilises the (â^')Primer Binding Site During Reverse Transcription. Journal of Molecular Biology, 2008, 383, 1112-1128.	4.2	87
7	Helical structure determined by NMR of the HIV-1 (345-392)Gag sequence, surrounding p2: Implications for particle assembly and RNA packaging. Protein Science, 2005, 14, 375-386.	7.6	82
8	Localization of HIV-1 Vpr to the nuclear envelope: Impact on Vpr functions and virus replication in macrophages. Retrovirology, 2007, 4, 84.	2.0	73
9	Infectious Bursal Disease Virus, a Non-enveloped Virus, Possesses a Capsid-associated Peptide That Deforms and Perforates Biological Membranes. Journal of Biological Chemistry, 2007, 282, 20774-20784.	3.4	63
10	<i>Giardia</i> Telomeric Sequence d(TAGGG) <sub>4</sub> Forms Two Intramolecular G-Quadruplexes in K <sup>+</sup> Solution: Effect of Loop Length and Sequence on the Folding Topology. Journal of the American Chemical Society, 2009, 131, 16824-16831.	13.7	61
11	Bombyx mori single repeat telomeric DMA sequence forms a G-quadruplex capped by base triads. Nature Structural and Molecular Biology, 1997, 4, 382-389.	8.2	58
12	Determination of the p K a of the four Zn 2+ -coordinating residues of the distal finger motif of the HIV-1 nucleocapsid protein: Consequences on the binding of Zn 2+ 1 1Edited by M. F. Summers. Journal of Molecular Biology, 2001, 310, 659-672.	4.2	58
13	NMR structure of the HIV-1 regulatory protein Vpr in H2O/trifluoroethanol. FEBS Journal, 2002, 269, 3779-3788.	0.2	55
14	Putative Functional Domains of Human Cytomegalovirus pUL56 Involved in Dimerization and Benzimidazole D-Ribonucleoside Activity. Antiviral Therapy, 2008, 13, 643-654.	1.0	45
15	The C-terminal domain of the HIV-1 regulatory protein Vpr adopts an antiparallel dimeric structure in solution via its leucine-zipper-like domain. Biochemical Journal, 2005, 387, 333-341.	3.7	42
16	Direct Vpr-Vpr Interaction in Cells monitored by two Photon Fluorescence Correlation Spectroscopy and Fluorescence Lifetime Imaging. Retrovirology, 2008, 5, 87.	2.0	42
17	Synthesis and biological evaluation of a new derivative of bevirimat that targets the Gag CA-SP1 cleavage site. European Journal of Medicinal Chemistry, 2013, 62, 453-465.	5.5	42
18	Interlocked mismatch-aligned arrowhead DNA motifs. Structure, 1999, 7, 803-S4.	3.3	41

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19	On-resin cyclization of peptide ligands of the Vascular Endothelial Growth Factor Receptor 1 by copper(I)-catalyzed 1,3-dipolar azide–alkyne cycloaddition. Bioorganic and Medicinal Chemistry Letters, 2007, 17, 5590-5594.	2.2	41
20	Structure-Function Relationship of Vpr: Biological Implications. Current HIV Research, 2009, 7, 184-210.	0.5	41
21	Targeting the Proangiogenic VEGF-VEGFR Protein-Protein Interface with Drug-like Compounds by In Silico and InÂVitro Screening. Chemistry and Biology, 2011, 18, 1631-1639.	6.0	38
22	Accurate nanoscale flexibility measurement of DNA and DNA–protein complexes by atomic force microscopy in liquid. Nanoscale, 2017, 9, 11327-11337.	5.6	36
23	Rational Design, Structure, and Biological Evaluation of Cyclic Peptides Mimicking the Vascular Endothelial Growth Factor. Journal of Medicinal Chemistry, 2007, 50, 5135-5146.	6.4	33
24	Interaction between the HIV-1 Protein Vpr and the Adenine Nucleotide Translocator. Chemical Biology and Drug Design, 2006, 67, 145-154.	3.2	29
25	Threeâ€dimensional solution structure of β cryptogein, a β elicitin secreted by a phytopathogenic fungus <i>phytophthora cryptogea</i> . Protein Science, 1997, 6, 2279-2284.	7.6	29
26	Emerging From the Unknown: Structural and Functional Features of Agnoprotein of Polyomaviruses. Journal of Cellular Physiology, 2016, 231, 2115-2127.	4.1	28
27	New Functional Domains of Human Cytomegalovirus pUL89 predicted by Sequence Analysis and Three-Dimensional Modelling of the Catalytic Site DEXDc. Antiviral Therapy, 2007, 12, 217-232.	1.0	27
28	The Toll-Like Receptor Agonist Imiquimod Is Active against Prions. PLoS ONE, 2013, 8, e72112.	2.5	26
29	A protein ballet around the viral genome orchestrated by HIV-1 reverse transcriptase leads to an architectural switch: From nucleocapsid-condensed RNA to Vpr-bridged DNA. Virus Research, 2013, 171, 287-303.	2.2	25
30	Expression of novel proteins by polyomaviruses and recent advances in the structural and functional features of agnoprotein of JC virus, BK virus, and simian virus 40. Journal of Cellular Physiology, 2019, 234, 8295-8315.	4.1	25
31	Target Specificity of Human Immunodeficiency Virus Type 1 NCp7 Requires an Intact Conformation of Its CCHC N-Terminal Zinc Finger. Journal of Virology, 2004, 78, 6682-6687.	3.4	24
32	HIV-1 Vpr Induces the Degradation of ZIP and sZIP, Adaptors of the NuRD Chromatin Remodeling Complex, by Hijacking DCAF1/VprBP. PLoS ONE, 2013, 8, e77320.	2.5	23
33	Structural Studies of HIV-1 Gag p6ct and Its Interaction with Vpr Determined by Solution Nuclear Magnetic Resonance <sup>,</sup> . Biochemistry, 2009, 48, 2355-2367.	2.5	22
34	Nuclear Magnetic Resonance Structure Revealed that the Human Polyomavirus JC Virus Agnoprotein Contains an α-Helix Encompassing the Leu/Ile/Phe-Rich Domain. Journal of Virology, 2014, 88, 6556-6575.	3.4	21
35	The Role of Membranes in the Organization of HIV-1 Gag p6 and Vpr: p6 Shows High Affinity for Membrane Bilayers Which Substantially Increases the Interaction between p6 and Vpr Journal of Medicinal Chemistry, 2009, 52, 7157-7162.	6.4	19
36	Structure of the zinc finger domain encompassing residues 13–51 of the nucleocapsid protein from simian immunodeficiency virus. Biochemical Journal, 2006, 393, 725-732.	3.7	18

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37	The 3- <i>O</i> -(3',3'-dimethylsuccinyl) derivative of betulinic acid (DSB) inhibits the assembly of virus-like particles in HIV-1 Gag precursor-expressing cells. Antiviral Therapy, 2007, 12, 1185-1204.	1.0	18
38	Resonance assignment, cysteine-pairing elucidation and secondary-structure determination of capsicein, an alpha-elicitin, by three-dimensional 1H NMR. FEBS Journal, 1994, 220, 427-438.	0.2	17
39	1H and 15N Resonance Assignment and Secondary Structure of Capsicein, an .alphaElicitin, Determined by Three-Dimensional Heteronuclear NMR. Biochemistry, 1994, 33, 8188-8197.	2.5	17
40	Molecular mimicry in inducing DNA damage between HIV-1 Vpr and the anticancer agent, cisplatin. Oncogene, 2008, 27, 32-43.	5.9	17
41	An expeditious synthesis of 6-aminophenanthridines. Tetrahedron Letters, 2005, 46, 3725-3727.	1.4	16
42	Contribution of the visual perception and graphic production systems to the copying of complex geometrical drawings: A developmental study. Cognitive Development, 2007, 22, 5-15.	1.3	16
43	The 3-O-(3',3'-dimethylsuccinyl) derivative of betulinic acid (DSB) inhibits the assembly of virus-like particles in HIV-1 Gag precursor-expressing cells. Antiviral Therapy, 2007, 12, 1185-203.	1.0	16
44	Determination of and Coupling Constants in 13C-Labeled Nucleic Acids Using Constant-Time HMQC. Journal of Magnetic Resonance, 1999, 139, 181-185.	2.1	15
45	The inhibition of assembly of HIV-1 virus-like particles by 3-O-(3',3'-dimethylsuccinyl) betulinic acid (DSB) is counteracted by Vif and requires its Zinc-binding domain. Virology Journal, 2008, 5, 162.	3.4	15
46	NMR Structure of a Viral Peptide Inserted in Artificial Membranes. Journal of Biological Chemistry, 2010, 285, 19409-19421.	3.4	15
47	Human H4 tail stimulates HIV-1 integration through binding to the carboxy-terminal domain of integrase. Nucleic Acids Research, 2019, 47, 3607-3618.	14.5	15
48	Evaluation of the antiprion activity of 6-aminophenanthridines and related heterocycles. European Journal of Medicinal Chemistry, 2014, 82, 363-371.	5.5	13
49	Insight into the structure of the pUL89 Câ€ŧerminal domain of the human cytomegalovirus terminase complex. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1520-1530.	2.6	11
50	Synthesis and characterization of water-soluble macrocyclic peptides stabilizing protein α-turn. Organic and Biomolecular Chemistry, 2018, 16, 459-471.	2.8	11
51	Insight into the mechanism of action of EP-39, a bevirimat derivative that inhibits HIV-1 maturation. Antiviral Research, 2019, 164, 162-175.	4.1	11
52	Biophysical Studies of the Induced Dimerization of Human VEGF Receptor 1 Binding Domain by Divalent Metals Competing with VEGF-A. PLoS ONE, 2016, 11, e0167755.	2.5	10
53	Conserved domains and structure prediction of human cytomegalovirus UL27 protein. Antiviral Therapy, 2009, 14, 663-672.	1.0	10
54	Iminothiol/thiourea tautomeric equilibrium in thiourea lipids impacts DNA compaction by inducing a cationic nucleation for complex assembly. Biophysical Chemistry, 2009, 145, 7-16.	2.8	9

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55	HIV-1 viral protein r: from structure to function. Future Virology, 2010, 5, 607-625.	1.8	9
56	Nuclear Magnetic Resonance Structure of the Human Polyoma JC Virus Agnoprotein. Journal of Cellular Biochemistry, 2017, 118, 3268-3280.	2.6	9
57	Mixed Polymeric Micelles for Rapamycin Skin Delivery. Pharmaceutics, 2022, 14, 569.	4.5	9
58	Characterization of a Novel Type of HIV-1 Particle Assembly Inhibitor Using a Quantitative Luciferase-Vpr Packaging-Based Assay. PLoS ONE, 2011, 6, e27234.	2.5	8
59	Structural studies of the binding of an antagonistic cyclic peptide to the VEGFR1 domain 2. European Journal of Medicinal Chemistry, 2019, 169, 65-75.	5.5	8
60	A peptide derived from the rotavirus outer capsid protein VP7 permeabilizes artificial membranes. Biochimica Et Biophysica Acta - Biomembranes, 2014, 1838, 2026-2035.	2.6	7
61	Guttiferone A Aggregates Modulate Silent Information Regulator 1 (SIRT1) Activity. Journal of Medicinal Chemistry, 2016, 59, 9560-9566.	6.4	6
62	The HIV-1 maturation inhibitor, EP39, interferes with the dynamic helix-coil equilibrium of the CA-SP1 junction of Gag. European Journal of Medicinal Chemistry, 2020, 204, 112634.	5.5	5
63	Reconciling NMR Structures of the HIV-1 Nucleocapsid Protein NCp7 Using Extensive Polarizable Force Field Free-Energy Simulations. Journal of Chemical Theory and Computation, 2020, 16, 2013-2020.	5.3	4
64	Synthesis of 6-Pyridylaminopurines. Heterocycles, 2008, 75, 1735.	0.7	4
65	Insight into protein nuclear magnetic resonance research. Biochimie, 1990, 72, 531-535.	2.6	3
66	Is Uracil-DNA Glycosylase UNG2 a New Cellular Weapon Against HIV-1?. Current HIV Research, 2019, 17, 148-160.	0.5	3
67	1H, 13C and 15N backbone resonance assignment of HIV-1 Gag (276–432) encompassing the C-terminal domain of the capsid protein, the spacer peptide 1 and the nucleocapsid protein. Biomolecular NMR Assignments, 2021, 15, 267-271.	0.8	2
68	Acetonitrile allows indirect replacement of nondeuterated lipid detergents by deuterated lipid detergents for the nuclear magnetic resonance study of detergentâ€soluble proteins. Protein Science, 2021, 30, 2324-2332.	7.6	2
69	Backbone resonance assignment of the human uracil DNA glycosylase-2. Biomolecular NMR Assignments, 2018, 12, 37-42.	0.8	1
70	An Expeditious Synthesis of 6-Aminophenanthridines ChemInform, 2005, 36, no.	0.0	0
71	Quantitative DNA Binding, Looping, and Compaction Properties of the HIV-1 Viral Protein R. Biophysical Journal, 2015, 108, 399a.	0.5	0
72	HIV-1 Pre-Integration Complexes. Structures, Functions and Drug Design. Biophysical Journal, 2020, 118, 500a.	0.5	0

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73	The three lives of Pierre Boulanger. Retrovirology, 2020, 17, 9.	2.0	0