

# Hugues Bedouelle

## List of Publications by Year in descending order

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52  
papers

2,561  
citations

236925

25  
h-index

189892

50  
g-index

52  
all docs

52  
docs citations

52  
times ranked

1928  
citing authors

#	ARTICLE	IF	CITATIONS
1	Principles and equations for measuring and interpreting protein stability: From monomer to tetramer. <i>Biochimie</i> , 2016, 121, 29-37.	2.6	13
2	Direct and indirect interactions in the recognition between a cross-neutralizing antibody and the four serotypes of dengue virus. <i>Journal of Molecular Recognition</i> , 2014, 27, 205-214.	2.1	12
3	Cross-reactivities between human IgMs and the four serotypes of dengue virus as probed with artificial homodimers of domain-III from the envelope proteins. <i>BMC Infectious Diseases</i> , 2013, 13, 302.	2.9	13
4	Thermodynamic stability of domain III from the envelope protein of flaviviruses and its improvement by molecular design. <i>Protein Engineering, Design and Selection</i> , 2013, 26, 389-399.	2.1	13
5	The folded and disordered domains of human ribosomal protein SA have both idiosyncratic and shared functions as membrane receptors. <i>Bioscience Reports</i> , 2013, 33, 113-24.	2.4	21
6	Multiple Folding States and Disorder of Ribosomal Protein SA, a Membrane Receptor for Laminin, Anticarcinogens, and Pathogens. <i>Biochemistry</i> , 2012, 51, 4807-4821.	2.5	15
7	Mechanism of Dengue Virus Broad Cross-Neutralization by a Monoclonal Antibody. <i>Structure</i> , 2012, 20, 303-314.	3.3	121
8	Reagentless fluorescent biosensors from artificial families of antigen binding proteins. <i>Biosensors and Bioelectronics</i> , 2011, 26, 4184-4190.	10.1	29
9	Knowledge-based design of reagentless fluorescent biosensors from a designed ankyrin repeat protein. <i>Protein Engineering, Design and Selection</i> , 2010, 23, 229-241.	2.1	16
10	Recombinant antibodies specific for the <i>Plasmodium falciparum</i> histidine-rich protein 2. <i>MAbs</i> , 2010, 2, 416-427.	5.2	7
11	NKp44 Receptor Mediates Interaction of the Envelope Glycoproteins from the West Nile and Dengue Viruses with NK Cells. <i>Journal of Immunology</i> , 2009, 183, 2610-2621.	0.8	124
12	Improvement of an Antibody Neutralizing the Anthrax Toxin by Simultaneous Mutagenesis of Its Six Hypervariable Loops. <i>Journal of Molecular Biology</i> , 2008, 378, 1094-1103.	4.2	26
13	Germline Humanization of a Non-human Primate Antibody that Neutralizes the Anthrax Toxin, by in Vitro and in Silico Engineering. <i>Journal of Molecular Biology</i> , 2008, 384, 1400-1407.	4.2	104
14	Mapping to completeness and transplantation of a group-specific, discontinuous, neutralizing epitope in the envelope protein of dengue virus. <i>Journal of General Virology</i> , 2007, 88, 2387-2397.	2.9	56
15	Pediatric Measles Vaccine Expressing a Dengue Antigen Induces Durable Serotype-specific Neutralizing Antibodies to Dengue Virus. <i>PLoS Neglected Tropical Diseases</i> , 2007, 1, e96.	3.0	75
16	Improving the Stability of an Antibody Variable Fragment by a Combination of Knowledge-based Approaches: Validation and Mechanisms. <i>Journal of Molecular Biology</i> , 2006, 362, 580-593.	4.2	48
17	Diversity and junction residues as hotspots of binding energy in an antibody neutralizing the dengue virus. <i>FEBS Journal</i> , 2006, 273, 34-46.	4.7	19
18	Quantitative measurement of protein stability from unfolding equilibria monitored with the fluorescence maximum wavelength. <i>Protein Engineering, Design and Selection</i> , 2005, 18, 445-456.	2.1	48

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19	Improving the Sensitivity and Dynamic Range of Reagentless Fluorescent Immunosensors by Knowledge-Based Design. <i>Biochemistry</i> , 2004, 43, 15453-15462.	2.5	19
20	Deriving Topological Constraints from Functional Data for the Design of Reagentless Fluorescent Immunosensors. <i>Journal of Molecular Biology</i> , 2003, 326, 167-175.	4.2	26
21	Knowledge-based Design of Reagentless Fluorescent Biosensors from Recombinant Antibodies. <i>Journal of Molecular Biology</i> , 2002, 318, 429-442.	4.2	71
22	Harnessing MalE for the study of antigen/antibody recognitions. <i>Research in Microbiology</i> , 2002, 153, 395-398.	2.1	1
23	Structure and Dynamics of the Anticodon Arm Binding Domain of <i>Bacillus stearothermophilus</i> Tyrosyl-tRNA Synthetase. <i>Structure</i> , 2002, 10, 311-317.	3.3	16
24	An Essential Residue in the Flexible Peptide Linking the Two Idiosyncratic Domains of Bacterial Tyrosyl-tRNA Synthetases. <i>Biochemistry</i> , 2001, 40, 7192-7199.	2.5	5
25	Mapping of a dengue virus neutralizing epitope critical for the infectivity of all serotypes: insight into the neutralization mechanism. <i>Journal of General Virology</i> , 2001, 82, 1885-1892.	2.9	114
26	Mutational Scanning of a Hairpin Loop in the Tryptophan Synthase $\beta^2$ -Subunit Implicated in Allostery and Substrate Channeling. <i>Biological Chemistry</i> , 2000, 381, 1185-93.	2.5	2
27	The Anticodon-binding Domain of Tyrosyl-tRNA Synthetase: A State of Folding and Origin of the Crystallographic Disorder. <i>Biochemistry</i> , 2000, 39, 1739-1747.	2.5	13
28	Disordered C-terminal domain of tyrosyl-tRNA synthetase: Secondary structure prediction. <i>Biochimie</i> , 1999, 81, 235-244.	2.6	3
29	Secondary structure of the C-terminal domain of the tyrosyl-transfer RNA synthetase from <i>Bacillus stearothermophilus</i> : a novel type of anticodon binding domain?. <i>FEBS Letters</i> , 1999, 446, 81-85.	2.8	7
30	Experimental evolution of a dense cluster of residues in tyrosyl-tRNA synthetase: quantitative effects on activity, stability and dimerization 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1999, 286, 563-577.	4.2	4
31	Dimeric Tyrosyl-tRNA Synthetase from <i>Bacillus stearothermophilus</i> Unfolds through a Monomeric Intermediate. <i>Journal of Biological Chemistry</i> , 1998, 273, 18052-18059.	3.4	35
32	A Mutational Approach Shows Similar Mechanisms of Recognition for the Isolated and Integrated Versions of a Protein Epitope. <i>Journal of Biological Chemistry</i> , 1998, 273, 34753-34759.	3.4	6
33	Conformational and Functional Properties of an Undecapeptide Epitope Fused with the C-Terminal End of the Maltose Binding Protein. <i>Biochemistry</i> , 1997, 36, 8954-8961.	2.5	4
34	Mutational Analysis of an Antigenic Peptide Shows Recognition in a Loop Conformation. <i>Biochemistry</i> , 1997, 36, 8962-8968.	2.5	10
35	Energetic and Kinetic Contributions of Contact Residues of Antibody D1.3 in the Interaction with Lysozyme. <i>Biochemistry</i> , 1997, 36, 164-172.	2.5	58
36	Recognition of <i>E. coli</i> tryptophan synthase by single-chain Fv fragments: comparison of PCR-cloning variants with the parental antibodies. , 1997, 10, 169-181.		12

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37	Disordered C-terminal Domain of Tyrosyl Transfer-RNA Synthetase: Evidence for a Folded State. <i>Journal of Molecular Biology</i> , 1996, 255, 110-120.	4.2	9
38	Destabilizing interactions between the partners of a bifunctional fusion protein. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 231-238.	2.1	15
39	Mapping the Stability Determinants of Bacterial Tyrosyl Transfer RNA Synthetases by an Experimental Evolutionary Approach. <i>Journal of Molecular Biology</i> , 1993, 234, 209-221.	4.2	20
40	Role of residue Glu152 in the discrimination between transfer RNAs by Tyrosyl-tRNA synthetase from <i>Bacillus stearothermophilus</i> . <i>Journal of Molecular Biology</i> , 1992, 223, 801-810.	4.2	30
41	Engineering the quaternary structure of an exported protein with a leucine zipper. <i>Protein Engineering, Design and Selection</i> , 1991, 4, 457-461.	2.1	39
42	Export and purification of a cytoplasmic dimeric protein by fusion to the maltose-binding protein of <i>Escherichia coli</i> . <i>FEBS Journal</i> , 1990, 193, 325-330.	0.2	26
43	Structural and kinetic bases for the recognition of tRNA <sup>tyr</sup> by tyrosyl-tRNA synthetase. <i>Journal of Molecular Biology</i> , 1989, 205, 729-735.	4.2	45
44	Production in <i>Escherichia coli</i> and one-step purification of bifunctional hybrid proteins which bind maltose. Export of the Klenow polymerase into the periplasmic space. <i>FEBS Journal</i> , 1988, 171, 541-549.	0.2	124
45	Reconstruction by site-directed mutagenesis of the transition state for the activation of tyrosine by the tyrosyl-tRNA synthetase: a mobile loop envelopes the transition state in an induced-fit mechanism. <i>Biochemistry</i> , 1988, 27, 1581-1587.	2.5	171
46	Silent and functional changes in the periplasmic maltose-binding protein of <i>Escherichia coli</i> K12. <i>Journal of Molecular Biology</i> , 1987, 194, 663-673.	4.2	104
47	A model of synthetase/transfer RNA interaction as deduced by protein engineering. <i>Nature</i> , 1986, 320, 371-373.	27.8	127
48	Improved oligonucleotide site-directed mutagenesis using M13 vectors. <i>Nucleic Acids Research</i> , 1985, 13, 4431-4443.	14.5	566
49	Engineering of tyrosyl tRNA synthetase. <i>Biochimie</i> , 1985, 67, 737-743.	2.6	2
50	Mutations in the promoter regions of the malEFG and malK-lamB operons of <i>Escherichia coli</i> K12. <i>Journal of Molecular Biology</i> , 1983, 170, 861-882.	4.2	38
51	Promoters of the malEFG and malK-lamB operons in <i>Escherichia coli</i> K12. <i>Journal of Molecular Biology</i> , 1982, 161, 519-531.	4.2	45
52	A DNA sequence containing the control regions of the malEFG and malK-lamB operons in <i>Escherichia coli</i> K12. <i>Molecular Genetics and Genomics</i> , 1982, 185, 82-87.	2.4	34