

Anne Poupon

List of Publications by Year in descending order

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Version: 2024-02-01

66
papers

2,826
citations

236925

25
h-index

182427

51
g-index

67
all docs

67
docs citations

67
times ranked

3657
citing authors

#	ARTICLE	IF	CITATIONS
1	Transducer Cascades for Biological Literature-Based Discovery. <i>Information (Switzerland)</i> , 2022, 13, 262.	2.9	0
2	Characterization of New Monoclonal PF4-Specific Antibodies as Useful Tools for Studies on Typical and Autoimmune Heparin-Induced Thrombocytopenia. <i>Thrombosis and Haemostasis</i> , 2021, 121, 322-331.	3.4	29
3	Accurate determination of epitope for antibodies with unknown 3D structures. <i>MAbs</i> , 2021, 13, 1961349.	5.2	8
4	The RanBP2/RanGAP1-SUMO complex gates β -arrestin2 nuclear entry to regulate the Mdm2-p53 signaling axis. <i>Oncogene</i> , 2021, 40, 2243-2257.	5.9	13
5	Agonist anti-ChemR23 mAb reduces tissue neutrophil accumulation and triggers chronic inflammation resolution. <i>Science Advances</i> , 2021, 7, .	10.3	34
6	4C3 Human Monoclonal Antibody: A Proof of Concept for Non-pathogenic Proteinase 3 Anti-neutrophil Cytoplasmic Antibodies in Granulomatosis With Polyangiitis. <i>Frontiers in Immunology</i> , 2020, 11, 573040.	4.8	6
7	Biased Signaling and Allosteric Modulation at the FSHR. <i>Frontiers in Endocrinology</i> , 2019, 10, 148.	3.5	26
8	Methods to Determine Interaction Interfaces Between β -Arrestins and Their Protein Partners. <i>Methods in Molecular Biology</i> , 2019, 1957, 177-194.	0.9	0
9	A recycling anti-transferrin receptor-1 monoclonal antibody as an efficient therapy for erythroleukemia through target up-regulation and antibody-dependent cytotoxic effector functions. <i>MAbs</i> , 2019, 11, 593-605.	5.2	17
10	G protein-dependent signaling triggers a β -arrestin-scaffolded p70S6K/ rpS6 module that controls 5'TOP mRNA translation. <i>FASEB Journal</i> , 2018, 32, 1154-1169.	0.5	24
11	MABtope: A Method for Improved Epitope Mapping. <i>Journal of Immunology</i> , 2018, 201, 3096-3105.	0.8	26
12	A logic-based method to build signaling networks and propose experimental plans. <i>Scientific Reports</i> , 2018, 8, 7830.	3.3	4
13	Follicle-Stimulating Hormone Receptor: Advances and Remaining Challenges. <i>International Review of Cell and Molecular Biology</i> , 2018, 338, 1-58.	3.2	23
14	Advances in computational modeling approaches of pituitary gonadotropin signaling. <i>Expert Opinion on Drug Discovery</i> , 2018, 13, 799-813.	5.0	4
15	Postembryonic Fish Brain Proliferation Zones Exhibit Neuroepithelial-Type Gene Expression Profile. <i>Stem Cells</i> , 2017, 35, 1505-1518.	3.2	15
16	β -arrestin signalling and bias in hormone-responsive GPCRs. <i>Molecular and Cellular Endocrinology</i> , 2017, 449, 28-41.	3.2	40
17	Antibodies targeting G protein-coupled receptors: Recent advances and therapeutic challenges. <i>MAbs</i> , 2017, 9, 735-741.	5.2	19
18	5B9, a monoclonal antiplatelet factor 4/heparin IgG with a human Fc fragment that mimics heparin-induced thrombocytopenia antibodies. <i>Journal of Thrombosis and Haemostasis</i> , 2017, 15, 2065-2075.	3.8	25

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19	A Comprehensive View of the β -Arrestinome. <i>Frontiers in Endocrinology</i> , 2017, 8, 32.	3.5	29
20	Eculizumab epitope on complement C5: Progress towards a better understanding of the mechanism of action. <i>Molecular Immunology</i> , 2016, 77, 126-131.	2.2	21
21	Profiling of FSHR negative allosteric modulators on LH/CGR reveals biased antagonism with implications in steroidogenesis. <i>Molecular and Cellular Endocrinology</i> , 2016, 436, 10-22.	3.2	41
22	Computational modeling approaches in gonadotropin signaling. <i>Theriogenology</i> , 2016, 86, 22-31.	2.1	5
23	Unraveling the molecular architecture of a G protein-coupled receptor/ β -arrestin/Erk module complex. <i>Scientific Reports</i> , 2015, 5, 10760.	3.3	50
24	Assessing Gonadotropin Receptor Function by Resonance Energy Transfer-Based Assays. <i>Frontiers in Endocrinology</i> , 2015, 6, 130.	3.5	75
25	Biased signalling in follicle stimulating hormone action. <i>Molecular and Cellular Endocrinology</i> , 2014, 382, 452-459.	3.2	54
26	Integrating microRNAs into the complexity of gonadotropin signaling networks. <i>Frontiers in Cell and Developmental Biology</i> , 2013, 1, 3.	3.7	9
27	mRNA-Selective Translation Induced by FSH in Primary Sertoli Cells. <i>Molecular Endocrinology</i> , 2012, 26, 669-680.	3.7	29
28	Competing G protein-coupled receptor kinases balance G protein and β -arrestin signaling. <i>Molecular Systems Biology</i> , 2012, 8, 590.	7.2	77
29	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. <i>Journal of Molecular Biology</i> , 2011, 414, 289-302.	4.2	131
30	Mapping the follicle-stimulating hormone-induced signaling networks. <i>Frontiers in Endocrinology</i> , 2011, 2, 45.	3.5	130
31	A Collaborative Filtering Approach for Protein-Protein Docking Scoring Functions. <i>PLoS ONE</i> , 2011, 6, e18541.	2.5	27
32	Novel pathways in gonadotropin receptor signaling and biased agonism. <i>Reviews in Endocrine and Metabolic Disorders</i> , 2011, 12, 259-274.	5.7	59
33	Using Kendall- τ , Meta-Bagging to Improve Protein-Protein Docking Predictions. <i>Lecture Notes in Computer Science</i> , 2011, , 284-295.	1.3	4
34	The Translation Regulatory Subunit eIF3f Controls the Kinase-Dependent mTOR Signaling Required for Muscle Differentiation and Hypertrophy in Mouse. <i>PLoS ONE</i> , 2010, 5, e8994.	2.5	86
35	Comparing Voronoi and Laguerre Tessellations in the Protein-Protein Docking Context. , 2009, , .		3
36	Developmental regulation of p70 S6 kinase by a G protein-coupled receptor dynamically modeled in primary cells. <i>Cellular and Molecular Life Sciences</i> , 2009, 66, 3487-3503.	5.4	48

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37	Towards a systems biology approach of G protein-coupled receptor signalling: Challenges and expectations. <i>Comptes Rendus - Biologies</i> , 2009, 332, 947-957.	0.2	22
38	Crystal structure of the YML079w protein from <i>Saccharomyces cerevisiae</i> reveals a new sequence family of the jelly-roll fold. <i>Protein Science</i> , 2009, 14, 209-215.	7.6	13
39	The VIZIER project: Preparedness against pathogenic RNA viruses. <i>Antiviral Research</i> , 2008, 78, 37-46.	4.1	26
40	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological protein-protein interactions. <i>Bioinformatics</i> , 2008, 24, 652-658.	4.1	83
41	Production and Crystallization of Protein Domains: How Useful are Disorder Predictions ?. <i>Current Protein and Peptide Science</i> , 2007, 8, 151-160.	1.4	8
42	A new protein protein docking scoring function based on interface residue properties. <i>Bioinformatics</i> , 2007, 23, 555-562.	4.1	53
43	High-throughput crystal-optimization strategies in the South Paris Yeast Structural Genomics Project: one size fits all?. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 664-670.	2.5	14
44	HalX: an open-source LIMS (Laboratory Information Management System) for small- to large-scale laboratories. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 671-678.	2.5	23
45	A docking analysis of the statistical physics of protein-protein recognition. <i>Physical Biology</i> , 2005, 2, S17-S23.	1.8	14
46	Crystal structure and confirmation of the alanine:glyoxylate aminotransferase activity of the YFL030w yeast protein. <i>Biochimie</i> , 2005, 87, 1041-1047.	2.6	12
47	Crystal Structure of the Bifunctional Chorismate Synthase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 619-625.	3.4	29
48	Structure of Protein Phosphatase Methyltransferase 1 (PPM1), a Leucine Carboxyl Methyltransferase Involved in the Regulation of Protein Phosphatase 2A Activity. <i>Journal of Biological Chemistry</i> , 2004, 279, 8351-8358.	3.4	82
49	Crystal Structure of the YDR533c <i>S. cerevisiae</i> Protein, a Class II Member of the Hsp31 Family. <i>Structure</i> , 2004, 12, 839-847.	3.3	31
50	Voronoi and Voronoi-related tessellations in studies of protein structure and interaction. <i>Current Opinion in Structural Biology</i> , 2004, 14, 233-241.	5.7	157
51	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 278-284.	2.6	27
52	Crystal structure of the YGR205w protein from <i>Saccharomyces cerevisiae</i> : Close structural resemblance to <i>E. coli</i> pantothenate kinase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 54, 776-783.	2.6	17
53	The Paris-Sud yeast structural genomics pilot-project: from structure to function. <i>Biochimie</i> , 2004, 86, 617-623.	2.6	18
54	Origin and evolution of transmembrane Chl-binding proteins: hydrophobic cluster analysis suggests a common one-helix ancestor for prokaryotic (Pcb) and eukaryotic (LHC) antenna protein superfamilies. <i>FEMS Microbiology Letters</i> , 2003, 222, 59-68.	1.8	16

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55	A structural genomics initiative on yeast proteins. <i>Journal of Synchrotron Radiation</i> , 2003, 10, 4-8.	2.4	20
56	Crystal Structure of the Yeast Phox Homology (PX) Domain Protein Grd19p Complexed to Phosphatidylinositol-3-phosphate. <i>Journal of Biological Chemistry</i> , 2003, 278, 50371-50376.	3.4	64
57	Deciphering globular protein sequence-structure relationships: from observation to prediction. <i>Theoretical Chemistry Accounts</i> , 2001, 106, 113-120.	1.4	3
58	Sequence and structural features of the T-fold, an original tunnelling building unit. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 39, 142-154.	2.6	55
59	Functional specificity conferred by the unique plasticity of fully α -helical Ras and Rho GAPs. <i>FEBS Letters</i> , 2000, 477, 99-105.	2.8	4
60	The Uteroglobin Fold. <i>Annals of the New York Academy of Sciences</i> , 2000, 923, 90-112.	3.8	29
61	"Topohydrophobic positions" as key markers of globular protein folds. <i>Theoretical Chemistry Accounts</i> , 1999, 101, 2-8.	1.4	14
62	Structure modelling and site-directed mutagenesis of the rat aromatic L-amino acid pyridoxal 5 α '-phosphate-dependent decarboxylase: A functional study. , 1999, 37, 191-203.		13
63	The immunoglobulin fold family: sequence analysis and 3D structure comparisons. <i>Protein Engineering, Design and Selection</i> , 1999, 12, 563-571.	2.1	219
64	Predicting the protein folding nucleus from a sequence. <i>FEBS Letters</i> , 1999, 452, 283-289.	2.8	44
65	Populations of hydrophobic amino acids within protein globular domains: Identification of conserved α -topohydrophobic positions. , 1998, 33, 329-342.		52
66	Deciphering protein sequence information through hydrophobic cluster analysis (HCA): current status and perspectives. <i>Cellular and Molecular Life Sciences</i> , 1997, 53, 621-645.	5.4	468