Anne Poupon

List of Publications by Year
in descending order

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	Deciphering protein sequence information through hydrophobic cluster analysis (HCA): current status and perspectives. Cellular and Molecular Life Sciences, 1997, 53, 621-645.	5.4	468
2	The immunoglobulin fold family: sequence analysis and 3D structure comparisons. Protein Engineering, Design and Selection, 1999, 12, 563-571.	2.1	219
3	Voronoi and Voronoi-related tessellations in studies of protein structure and interaction. Current Opinion in Structural Biology, 2004, 14, 233-241.	5.7	157
4	Community-Wide Assessment of Protein-Interface Modeling Suggests Improvements to Design Methodology. Journal of Molecular Biology, 2011, 414, 289-302.	4.2	131
5	Mapping the follicle-stimulating hormone-induced signaling networks. Frontiers in Endocrinology, 2011, 2, 45.	3.5	130
6	The Translation Regulatory Subunit eIF3f Controls the Kinase-Dependent mTOR Signaling Required for Muscle Differentiation and Hypertrophy in Mouse. PLoS ONE, 2010, 5, e8994.	2.5	86
7	DiMoVo: a Voronoi tessellation-based method for discriminating crystallographic and biological protein–protein interactions. Bioinformatics, 2008, 24, 652-658.	4.1	83
8	Structure of Protein Phosphatase Methyltransferase 1 (PPM1), a Leucine Carboxyl Methyltransferase Involved in the Regulation of Protein Phosphatase 2A Activity. Journal of Biological Chemistry, 2004, 279, 8351-8358.	3.4	82
9	Competing G protein–coupled receptor kinases balance G protein and β–arrestin signaling. Molecular Systems Biology, 2012, 8, 590.	7.2	77
10	Assessing Gonadotropin Receptor Function by Resonance Energy Transfer-Based Assays. Frontiers in Endocrinology, 2015, 6, 130.	3.5	75
11	Crystal Structure of the Yeast Phox Homology (PX) Domain Protein Grd19p Complexed to Phosphatidylinositol-3-phosphate. Journal of Biological Chemistry, 2003, 278, 50371-50376.	3.4	64
12	Novel pathways in gonadotropin receptor signaling and biased agonism. Reviews in Endocrine and Metabolic Disorders, 2011, 12, 259-274.	5.7	59
13	Sequence and structural features of the T-fold, an original tunnelling building unit. Proteins: Structure, Function and Bioinformatics, 2000, 39, 142-154.	2.6	55
14	Biased signalling in follicle stimulating hormone action. Molecular and Cellular Endocrinology, 2014, 382, 452-459.	3.2	54
15	A new protein protein docking scoring function based on interface residue properties. Bioinformatics, 2007, 23, 555-562.	4.1	53
16	Populations of hydrophobic amino acids within protein globular domains: Identification of conserved "topohydrophobic" positions. , 1998, 33, 329-342.		52
17	Unraveling the molecular architecture of a G protein-coupled receptor/β-arrestin/Erk module complex. Scientific Reports, 2015, 5, 10760.	3.3	50
18	Developmental regulation of p70 S6 kinase by a G protein-coupled receptor dynamically modelized in primary cells. Cellular and Molecular Life Sciences, 2009, 66, 3487-3503.	5.4	48

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19	Predicting the protein folding nucleus from a sequence. FEBS Letters, 1999, 452, 283-289.	2.8	44
20	Profiling of FSHR negative allosteric modulators on LH/CGR reveals biased antagonism with implications in steroidogenesis. Molecular and Cellular Endocrinology, 2016, 436, 10-22.	3.2	41
21	β-arrestin signalling and bias in hormone-responsive GPCRs. Molecular and Cellular Endocrinology, 2017, 449, 28-41.	3.2	40
22	Agonist anti-ChemR23 mAb reduces tissue neutrophil accumulation and triggers chronic inflammation resolution. Science Advances, 2021, 7, .	10.3	34
23	Crystal Structure of the YDR533c S. cerevisiae Protein, a Class II Member of the Hsp31 Family. Structure, 2004, 12, 839-847.	3.3	31
24	Crystal Structure of the Bifunctional Chorismate Synthase from Saccharomyces cerevisiae. Journal of Biological Chemistry, 2004, 279, 619-625.	3.4	29
25	The Uteroglobin Fold. Annals of the New York Academy of Sciences, 2000, 923, 90-112.	3.8	29
26	mRNA-Selective Translation Induced by FSH in Primary Sertoli Cells. Molecular Endocrinology, 2012, 26, 669-680.	3.7	29
27	A Comprehensive View of the β-Arrestinome. Frontiers in Endocrinology, 2017, 8, 32.	3.5	29
28	Characterization of New Monoclonal PF4-Specific Antibodies as Useful Tools for Studies on Typical and Autoimmune Heparin-Induced Thrombocytopenia. Thrombosis and Haemostasis, 2021, 121, 322-331.	3.4	29
29	Design of a data model for developing laboratory information management and analysis systems for protein production. Proteins: Structure, Function and Bioinformatics, 2004, 58, 278-284.	2.6	27
30	A Collaborative Filtering Approach for Protein-Protein Docking Scoring Functions. PLoS ONE, 2011, 6, e18541.	2.5	27
31	The VIZIER project: Preparedness against pathogenic RNA viruses. Antiviral Research, 2008, 78, 37-46.	4.1	26
32	MAbTope: A Method for Improved Epitope Mapping. Journal of Immunology, 2018, 201, 3096-3105.	0.8	26
33	Biased Signaling and Allosteric Modulation at the FSHR. Frontiers in Endocrinology, 2019, 10, 148.	3.5	26
34	5B9, a monoclonal antiplatelet factor 4/heparin IgG with a human Fc fragment that mimics heparin-induced thrombocytopenia antibodies. Journal of Thrombosis and Haemostasis, 2017, 15, 2065-2075.	3.8	25
35	G protein-dependent signaling triggers a β-arrestin-scaffolded p70S6K/ rpS6 module that controls 5'TOP mRNA translation. FASEB Journal, 2018, 32, 1154-1169.	0.5	24
36	HalX: an open-source LIMS (Laboratory Information Management System) for small- to large-scale laboratories. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 671-678.	2.5	23

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37	Follicle-Stimulating Hormone Receptor: Advances and Remaining Challenges. International Review of Cell and Molecular Biology, 2018, 338, 1-58.	3.2	23
38	Towards a systems biology approach of G protein-coupled receptor signalling: Challenges and expectations. Comptes Rendus - Biologies, 2009, 332, 947-957.	0.2	22
39	Eculizumab epitope on complement C5: Progress towards a better understanding of the mechanism of action. Molecular Immunology, 2016, 77, 126-131.	2.2	21
40	A structural genomics initiative on yeast proteins. Journal of Synchrotron Radiation, 2003, 10, 4-8.	2.4	20
41	Antibodies targeting G protein-coupled receptors: Recent advances and therapeutic challenges. MAbs, 2017, 9, 735-741.	5.2	19
42	The Paris-Sud yeast structural genomics pilot-project: from structure to function. Biochimie, 2004, 86, 617-623.	2.6	18
43	Crystal structure of the YGR205w protein from Saccharomyces cerevisiae : Close structural resemblance to E. coli pantothenate kinase. Proteins: Structure, Function and Bioinformatics, 2004, 54, 776-783.	2.6	17
44	A recycling anti-transferrin receptor-1 monoclonal antibody as an efficient therapy for erythroleukemia through target up-regulation and antibody-dependent cytotoxic effector functions. MAbs, 2019, 11, 593-605.	5.2	17
45	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. FEMS Microbiology Letters, 2003, 222, 59-68.	1.8	16
46	Postembryonic Fish Brain Proliferation Zones Exhibit Neuroepithelial-Type Gene Expression Profile. Stem Cells, 2017, 35, 1505-1518.	3.2	15
47	"Topohydrophobic positions" as key markers of globular protein folds. Theoretical Chemistry Accounts, 1999, 101, 2-8.	1.4	14
48	High-throughput crystal-optimization strategies in the South Paris Yeast Structural Genomics Project: one size fits all?. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 664-670.	2.5	14
49	A docking analysis of the statistical physics of protein–protein recognition. Physical Biology, 2005, 2, S17-S23.	1.8	14
50	Structure modelling and site-directed mutagenesis of the rat aromatic L-amino acid pyridoxal 5´-phosphate-dependent decarboxylase: A functional study. , 1999, 37, 191-203.		13
51	Crystal structure of the YML079w protein from Saccharomyces cerevisiae reveals a new sequence family of the jelly-roll fold. Protein Science, 2009, 14, 209-215.	7.6	13
52	The RanBP2/RanGAP1-SUMO complex gates β-arrestin2 nuclear entry to regulate the Mdm2-p53 signaling axis. Oncogene, 2021, 40, 2243-2257.	5.9	13
53	Crystal structure and confirmation of the alanine:glyoxylate aminotransferase activity of the YFL030w yeast protein. Biochimie, 2005, 87, 1041-1047.	2.6	12
54	Integrating microRNAs into the complexity of gonadotropin signaling networks. Frontiers in Cell and Developmental Biology, 2013, 1, 3.	3.7	9

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55	Production and Crystallization of Protein Domains: How Useful are Disorder Predictions ?. Current Protein and Peptide Science, 2007, 8, 151-160.	1.4	8
56	Accurate determination of epitope for antibodies with unknown 3D structures. MAbs, 2021, 13, 1961349.	5.2	8
57	4C3 Human Monoclonal Antibody: A Proof of Concept for Non-pathogenic Proteinase 3 Anti-neutrophil Cytoplasmic Antibodies in Granulomatosis With Polyangiitis. Frontiers in Immunology, 2020, 11, 573040.	4.8	6
58	Computational modeling approaches in gonadotropin signaling. Theriogenology, 2016, 86, 22-31.	2.1	5
59	Functional specificity conferred by the unique plasticity of fully α-helical Ras and Rho GAPs. FEBS Letters, 2000, 477, 99-105.	2.8	4
60	A logic-based method to build signaling networks and propose experimental plans. Scientific Reports, 2018, 8, 7830.	3.3	4
61	Advances in computational modeling approaches of pituitary gonadotropin signaling. Expert Opinion on Drug Discovery, 2018, 13, 799-813.	5.0	4
62	Using Kendall-τ Meta-Bagging to Improve Protein-Protein Docking Predictions. Lecture Notes in Computer Science, 2011, , 284-295.	1.3	4
63	Deciphering globular protein sequence-structure relationships: from observation to prediction. Theoretical Chemistry Accounts, 2001, 106, 113-120.	1.4	3
64	Comparing Voronoi and Laguerre Tessellations in the Protein-Protein Docking Context. , 2009, , .		3
65	Methods to Determine Interaction Interfaces Between β-Arrestins and Their Protein Partners. Methods in Molecular Biology, 2019, 1957, 177-194.	0.9	0
66	Transducer Cascades for Biological Literature-Based Discovery. Information (Switzerland), 2022, 13, 262.	2.9	0