Xavier Deupi

List of Publications by Year
in descending order

74 papers	7,015 citations	81900 39 h-index	74163 75 g-index
85 all docs	85 docs citations	85 times ranked	7210 citing authors

#	Article	IF	Citations
1	Molecular signatures of G-protein-coupled receptors. Nature, 2013, 494, 185-194.	27.8	1,298
2	Conformational complexity of G-protein-coupled receptors. Trends in Pharmacological Sciences, 2007, 28, 397-406.	8.7	646
3	Coupling ligand structure to specific conformational switches in the Î²2-adrenoceptor. , 2006, 2, 417-422.		318
4	Tracking G-protein-coupled receptor activation using genetically encoded infrared probes. Nature, 2010, 464, 1386-1389.	27.8	245
5	Diverse activation pathways in class A GPCRs converge near the G-protein-coupling region. Nature, 2016, 536, 484-487.	27.8	245
6	Probing the Î²2 Adrenoceptor Binding Site with Catechol Reveals Differences in Binding and Activation by Agonists and Partial Agonists. Journal of Biological Chemistry, 2005, 280, 22165-22171.	3.4	242
7	Energy Landscapes as a Tool to Integrate GPCR Structure, Dynamics, and Function. Physiology, 2010, 25, 293-303.	3.1	227
8	Stabilized G protein binding site in the structure of constitutively active metarhodopsin-II. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 119-124.	7.1	226
9	The effect of ligand efficacy on the formation and stability of a GPCR-G protein complex. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9501-9506.	7.1	218
10	Structural insights into agonist-induced activation of G-protein-coupled receptors. Current Opinion in Structural Biology, 2011, 21, 541-551.	5.7	212
11	Serine and Threonine Residues Bend Î±-Helices in the Ï‡1=gâˆ' Conformation. Biophysical Journal, 2000, 79, 2754-2760.	0.5	173
12	Structural insights into biased G protein-coupled receptor signaling revealed by fluorescence spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 6733-6738.	7.1	173
13	Ligand-regulated oligomerization of Î²2-adrenoceptors in a model lipid bilayer. EMBO Journal, 2009, 28, 3315-3328.	7.8	172
14	Backbone NMR reveals allosteric signal transduction networks in the Î²1-adrenergic receptor. Nature, 2016, 530, 237-241.	27.8	155
15	The TXP Motif in the Second Transmembrane Helix of CCR5. Journal of Biological Chemistry, 2001, 276, 13217-13225.	3.4	118
16	The Role of Internal Water Molecules in the Structure and Function of the Rhodopsin Family of G Protein-Coupled Receptors. ChemBioChem, 2007, 8, 19-24.	2.6	118
17	Femtosecond-to-millisecond structural changes in a light-driven sodium pump. Nature, 2020, 583, 314-318.	27.8	115
18	An online resource for GPCR structure determination and analysis. Nature Methods, 2019, 16, 151-162.	19.0	108

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19	An Activation Switch in the Rhodopsin Family of G Protein-coupled Receptors. Journal of Biological Chemistry, 2005, 280, 17135-17141.	3.4	106
20	GPCRmd uncovers the dynamics of the 3D-GPCRome. Nature Methods, 2020, 17, 777-787.	19.0	90
21	Ser and Thr Residues Modulate the Conformation of Pro-Kinked Transmembrane Î±-Helices. Biophysical Journal, 2004, 86, 105-115.	0.5	87
22	Distinct G protein-coupled receptor phosphorylation motifs modulate arrestin affinity and activation and global conformation. Nature Communications, 2019, 10, 1261.	12.8	86
23	Activation of CCR5 by Chemokines Involves an Aromatic Cluster between Transmembrane Helices 2 and 3. Journal of Biological Chemistry, 2003, 278, 1892-1903.	3.4	85
24	Activation of G Proteinâ€“Coupled Receptors. Advances in Protein Chemistry, 2007, 74, 137-166.	4.4	79
25	Molecular Basis of Ligand Dissociation in Î²-Adrenergic Receptors. PLoS ONE, 2011, 6, e23815.	2.5	79
26	Insights into congenital stationary night blindness based on the structure of G90D rhodopsin. EMBO Reports, 2013, 14, 520-526.	4.5	79
27	Relation between sequence and structure in membrane proteins. Bioinformatics, 2013, 29, 1589-1592.	4.1	76
28	SAS-6 engineering reveals interdependence between cartwheel and microtubules in determining centrioleÂarchitecture. Nature Cell Biology, 2016, 18, 393-403.	10.3	73
29	Crystal structure of rhodopsin in complex with a mini-G _o sheds light on the principles of G protein selectivity. Science Advances, 2018, 4, eaat7052.	10.3	65
30	Coronin 1 Regulates Cognition and Behavior through Modulation of cAMP/Protein Kinase A Signaling. PLoS Biology, 2014, 12, e1001820.	5.6	62
31	A Structural Insight into the Reorientation of Transmembrane Domains 3 and 5 during Family A G Protein-Coupled Receptor Activation. Molecular Pharmacology, 2011, 79, 262-269.	2.3	58
32	Probing GÎ±i1 protein activation at singleâ€“amino acid resolution. Nature Structural and Molecular Biology, 2015, 22, 686-694.	8.2	58
33	Functional map of arrestin-1 at single amino acid resolution. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 1825-1830.	7.1	56
34	Relevance of rhodopsin studies for GPCR activation. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 674-682.	1.0	53
35	Cryo-EM structure of the rhodopsin-GÎ±i-Î²Î³ complex reveals binding of the rhodopsin C-terminal tail to the gÎ² subunit. ELife, 2019, 8, .	6.0	52
36	A Molecular Pharmacologistâ€™s Guide to G Proteinâ€“Coupled Receptor Crystallography. Molecular Pharmacology, 2015, 88, 536-551.	2.3	50

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37	Design, Synthesis and Pharmacological Evaluation of 5-Hydroxytryptamine1aReceptor Ligands to Explore the Three-Dimensional Structure of the Receptor. Molecular Pharmacology, 2002, 62, 15-21.	2.3	49
38	Crystal structure of jumping spider rhodopsin-1 as a light sensitive GPCR. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 14547-14556.	7.1	48
39	Structural Models of Class A G Protein-Coupled Receptors as a Tool for Drug Design: Insights on Transmembrane Bundle Plasticity. Current Topics in Medicinal Chemistry, 2007, 7, 991-998.	2.1	45
40	Conserved activation pathways in G-protein-coupled receptors. Biochemical Society Transactions, 2012, 40, 383-388.	3.4	43
41	Structural and Functional Characterization of Alternative Transmembrane Domain Conformations in VEGF Receptor 2 Activation. Structure, 2014, 22, 1077-1089.	3.3	43
42	Conformational activation of visual rhodopsin in native disc membranes. Science Signaling, 2015, 8, ra26.	3.6	37
43	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. Science Advances, 2021, 7, .	10.3	36
44	Structural role of the T94I rhodopsin mutation in congenital stationary night blindness. EMBO Reports, 2016, 17, 1431-1440.	4.5	34
45	The counterionâ€"retinylidene Schiff base interaction of an invertebrate rhodopsin rearranges upon light activation. Communications Biology, 2019, 2, 180.	4.4	31
46	Influence of the Environment in the Conformation of Î±-Helices Studied by Protein Database Search and Molecular Dynamics Simulations. Biophysical Journal, 2002, 82, 3207-3213.	0.5	29
47	Influence of the gâˆ' conformation of Ser and Thr on the structure of transmembrane helices. Journal of Structural Biology, 2010, 169, 116-123.	2.8	27
48	The activation mechanism of chemokine receptor CCR5 involves common structural changes but a different network of interhelical interactions relative to rhodopsin. Cellular Signalling, 2007, 19, 1446-1456.	3.6	26
49	The DRF motif of CXCR6 as chemokine receptor adaptation to adhesion. PLoS ONE, 2017, 12, e0173486.	2.5	23
50	An experimental strategy to probe Gq contribution to signal transduction in living cells. Journal of Biological Chemistry, 2021, 296, 100472.	3.4	22
51	Triazolo-Peptidomimetics: Novel Radiolabeled Minigastrin Analogs for Improved Tumor Targeting. Journal of Medicinal Chemistry, 2020, 63, 4484-4495.	6.4	20
52	Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 6201-6206.	7.1	19
53	The Two-Photon Reversible Reaction of the Bistable Jumping Spider Rhodopsin-1. Biophysical Journal, 2019, 116, 1248-1258.	0.5	18
54	Batch crystallization of rhodopsin for structural dynamics using an X-ray free-electron laser. Acta Crystallographica Section F, Structural Biology Communications, 2015, 71, 856-860.	0.8	12

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55	Elucidating the Structureâ€"Activity Relationship of the Pentaglutamic Acid Sequence of Minigastrin with Cholecystokinin Receptor Subtype 2. Bioconjugate Chemistry, 2019, 30, 657-666.	3.6	12
56	Characterization of a conformationally sensitive TOAC spin-labeled substance P. Peptides, 2008, 29, 1919-1929.	2.4	10
57	A stitch in time. Nature Chemistry, 2014, 6, 7-8.	13.6	10
58	Unraveling binding mechanism and kinetics of macrocyclic GÎ±q protein inhibitors. Pharmacological Research, 2021, 173, 105880.	7.1	10
59	Structure of Î²-Adrenergic Receptors. Methods in Enzymology, 2013, 520, 117-151.	1.0	9
60	High-mass MALDI-MS unravels ligand-mediated G proteinâ€"coupling selectivity to GPCRs. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	9
61	Selective Hydrolysis of 2,4-Diaminopyrimidine Systems:â€‰ A Theoretical and Experimental Insight into an Old Rule. Journal of Organic Chemistry, 2001, 66, 192-199.	3.2	8
62	Charge-charge and cation-Ï€ interactions in ligand binding to G protein-coupled receptors. Theoretical Chemistry Accounts, 2007, 118, 579-588.	1.4	8
63	Quantification of Structural Distortions in the Transmembrane Helices of GPCRs. Methods in Molecular Biology, 2012, 914, 219-235.	0.9	8
64	Arrestin-1 engineering facilitates complex stabilization with native rhodopsin. Scientific Reports, 2019, 9, 439.	3.3	8
65	GPCR-SAS: A web application for statistical analyses on G protein-coupled receptors sequences. PLoS ONE, 2018, 13, e0199843.	2.5	7
66	Ligands Stabilize Specific GPCR Conformations: But How?. Structure, 2012, 20, 1289-1290.	3.3	6
67	Retinal proteins â€" You can teach an old dog new tricks. Biochimica Et Biophysica Acta - Bioenergetics, 2014, 1837, 531-532.	1.0	6
68	Distance-Dependent Cellular Uptake of Oligoproline-Based Homobivalent Ligands Targeting GPCRsâ€"An Experimental and Computational Analysis. Bioconjugate Chemistry, 2020, 31, 2431-2438.	3.6	5
69	Exploring the signaling space of a GPCR using bivalent ligands with a rigid oligoproline backbone. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	5
70	TMalphaDB and TMbetaDB: web servers to study the structural role of sequence motifs in Î±-helix and Î²-barrel domains of membrane proteins. BMC Bioinformatics, 2015, 16, 266.	2.6	4
71	Identification of Key Regions Mediating Human Melatonin Type 1 Receptor Functional Selectivity Revealed by Natural Variants. ACS Pharmacology and Translational Science, 2021, 4, 1614-1627.	4.9	4
72	Chimeric single Î±-helical domains as rigid fusion protein connections for protein nanotechnology and structural biology. Structure, 2022, 30, 95-106.e7.	3.3	4

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73	Structural Elements Directing G Proteins and Î²-Arrestin Interactions with the Human Melatonin Type 2 Receptor Revealed by Natural Variants. ACS Pharmacology and Translational Science, 2022, 5, 89-101.	4.9	2
74	Conformational Plasticity of GPCR Binding Sites. Contemporary Clinical Neuroscience, 2005, , 363-388.	0.3	1