

# Xavier Deupi

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

75  
papers

5,714  
citations

37  
h-index

75  
g-index

85  
ext. papers

6,472  
ext. citations

9.9  
avg, IF

5.72  
L-index

#	Paper	IF	Citations
75	Structural Elements Directing G Proteins and Arrestin Interactions with the Human Melatonin Type 2 Receptor Revealed by Natural Variants. <i>ACS Pharmacology and Translational Science</i> , <b>2022</b> , 5, 89-101	5.9	1
74	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. <i>Science Advances</i> , <b>2021</b> , 7,	14.3	8
73	High-mass MALDI-MS unravels ligand-mediated G protein-coupling selectivity to GPCRs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2021</b> , 118,	11.5	2
72	Identification of Key Regions Mediating Human Melatonin Type 1 Receptor Functional Selectivity Revealed by Natural Variants. <i>ACS Pharmacology and Translational Science</i> , <b>2021</b> , 4, 1614-1627	5.9	2
71	Chimeric single helical domains as rigid fusion protein connections for protein nanotechnology and structural biology. <i>Structure</i> , <b>2021</b> ,	5.2	2
70	Unraveling binding mechanism and kinetics of macrocyclic G protein inhibitors. <i>Pharmacological Research</i> , <b>2021</b> , 173, 105880	10.2	1
69	An experimental strategy to probe Gq contribution to signal transduction in living cells. <i>Journal of Biological Chemistry</i> , <b>2021</b> , 296, 100472	5.4	6
68	Femtosecond-to-millisecond structural changes in a light-driven sodium pump. <i>Nature</i> , <b>2020</b> , 583, 314-318	50.4	48
67	Triazolo-Peptidomimetics: Novel Radiolabeled Minigastrin Analogs for Improved Tumor Targeting. <i>Journal of Medicinal Chemistry</i> , <b>2020</b> , 63, 4484-4495	8.3	10
66	Distance-Dependent Cellular Uptake of Oligoproline-Based Homobivalent Ligands Targeting GPCRs-An Experimental and Computational Analysis. <i>Bioconjugate Chemistry</i> , <b>2020</b> , 31, 2431-2438	6.3	0
65	GPCRmd uncovers the dynamics of the 3D-GPCRome. <i>Nature Methods</i> , <b>2020</b> , 17, 777-787	21.6	34
64	The counterion-retinylidene Schiff base interaction of an invertebrate rhodopsin rearranges upon light activation. <i>Communications Biology</i> , <b>2019</b> , 2, 180	6.7	14
63	An online resource for GPCR structure determination and analysis. <i>Nature Methods</i> , <b>2019</b> , 16, 151-162	21.6	71
62	Arrestin-1 engineering facilitates complex stabilization with native rhodopsin. <i>Scientific Reports</i> , <b>2019</b> , 9, 439	4.9	5
61	Distinct G protein-coupled receptor phosphorylation motifs modulate arrestin affinity and activation and global conformation. <i>Nature Communications</i> , <b>2019</b> , 10, 1261	17.4	52
60	The Two-Photon Reversible Reaction of the Bistable Jumping Spider Rhodopsin-1. <i>Biophysical Journal</i> , <b>2019</b> , 116, 1248-1258	2.9	11
59	Crystal structure of jumping spider rhodopsin-1 as a light sensitive GPCR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 14547-14556	11.5	20

58	Cryo-EM structure of the rhodopsin-Gβγ complex reveals binding of the rhodopsin C-terminal tail to the Gβγ subunit. <i>ELife</i> , <b>2019</b> , 8,	8.9	29
57	Elucidating the Structure-Activity Relationship of the Pentaglutamic Acid Sequence of Minigastrin with Cholecystokinin Receptor Subtype 2. <i>Bioconjugate Chemistry</i> , <b>2019</b> , 30, 657-666	6.3	8
56	GPCR-SAS: A web application for statistical analyses on G protein-coupled receptors sequences. <i>PLoS ONE</i> , <b>2018</b> , 13, e0199843	3.7	6
55	Crystal structure of rhodopsin in complex with a mini-G sheds light on the principles of G protein selectivity. <i>Science Advances</i> , <b>2018</b> , 4, eaat7052	14.3	37
54	Convergent evolution of tertiary structure in rhodopsin visual proteins from vertebrates and box jellyfish. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 6201-6206	11.5	10
53	The DRF motif of CXCR6 as chemokine receptor adaptation to adhesion. <i>PLoS ONE</i> , <b>2017</b> , 12, e0173486	3.7	11
52	Diverse activation pathways in class A GPCRs converge near the G-protein-coupling region. <i>Nature</i> , <b>2016</b> , 536, 484-7	50.4	184
51	Structural role of the T94I rhodopsin mutation in congenital stationary night blindness. <i>EMBO Reports</i> , <b>2016</b> , 17, 1431-1440	6.5	25
50	SAS-6 engineering reveals interdependence between cartwheel and microtubules in determining centriole architecture. <i>Nature Cell Biology</i> , <b>2016</b> , 18, 393-403	23.4	55
49	Backbone NMR reveals allosteric signal transduction networks in the β <sub>1</sub> -adrenergic receptor. <i>Nature</i> , <b>2016</b> , 530, 237-41	50.4	110
48	A Molecular Pharmacologist's Guide to G Protein-Coupled Receptor Crystallography. <i>Molecular Pharmacology</i> , <b>2015</b> , 88, 536-51	4.3	45
47	Conformational activation of visual rhodopsin in native disc membranes. <i>Science Signaling</i> , <b>2015</b> , 8, ra26	8.8	29
46	TMalphaDB and TMbetaDB: web servers to study the structural role of sequence motifs in Ehelix and Ebarrel domains of membrane proteins. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 266	3.6	4
45	Probing Gβγ protein activation at single-amino acid resolution. <i>Nature Structural and Molecular Biology</i> , <b>2015</b> , 22, 686-694	17.6	42
44	Batch crystallization of rhodopsin for structural dynamics using an X-ray free-electron laser. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , <b>2015</b> , 71, 856-60	1.1	11
43	Molecular dynamics: A stitch in time. <i>Nature Chemistry</i> , <b>2014</b> , 6, 7-8	17.6	10
42	Relevance of rhodopsin studies for GPCR activation. <i>Biochimica Et Biophysica Acta - Bioenergetics</i> , <b>2014</b> , 1837, 674-82	4.6	41
41	Structural and functional characterization of alternative transmembrane domain conformations in VEGF receptor 2 activation. <i>Structure</i> , <b>2014</b> , 22, 1077-1089	5.2	38

40	Functional map of arrestin-1 at single amino acid resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 1825-30	11.5	48
39	Coronin 1 regulates cognition and behavior through modulation of cAMP/protein kinase A signaling. <i>PLoS Biology</i> , <b>2014</b> , 12, e1001820	9.7	52
38	Relation between sequence and structure in membrane proteins. <i>Bioinformatics</i> , <b>2013</b> , 29, 1589-92	7.2	59
37	Molecular signatures of G-protein-coupled receptors. <i>Nature</i> , <b>2013</b> , 494, 185-94	50.4	1071
36	Structure of $\beta$ adrenergic receptors. <i>Methods in Enzymology</i> , <b>2013</b> , 520, 117-51	1.7	7
35	Insights into congenital stationary night blindness based on the structure of G90D rhodopsin. <i>EMBO Reports</i> , <b>2013</b> , 14, 520-6	6.5	72
34	Ligands stabilize specific GPCR conformations: but how?. <i>Structure</i> , <b>2012</b> , 20, 1289-90	5.2	5
33	Quantification of structural distortions in the transmembrane helices of GPCRs. <i>Methods in Molecular Biology</i> , <b>2012</b> , 914, 219-35	1.4	8
32	Structural insights into biased G protein-coupled receptor signaling revealed by fluorescence spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 6733-8	11.5	151
31	Conserved activation pathways in G-protein-coupled receptors. <i>Biochemical Society Transactions</i> , <b>2012</b> , 40, 383-8	5.1	40
30	Stabilized G protein binding site in the structure of constitutively active metarhodopsin-II. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 119-24	11.5	193
29	Molecular basis of ligand dissociation in $\beta$ adrenergic receptors. <i>PLoS ONE</i> , <b>2011</b> , 6, e23815	3.7	70
28	Structural insights into agonist-induced activation of G-protein-coupled receptors. <i>Current Opinion in Structural Biology</i> , <b>2011</b> , 21, 541-51	8.1	180
27	A structural insight into the reorientation of transmembrane domains 3 and 5 during family A G protein-coupled receptor activation. <i>Molecular Pharmacology</i> , <b>2011</b> , 79, 262-9	4.3	53
26	Structural Insights for Homology Modeling of Chemokine Receptors. <i>Methods and Principles in Medicinal Chemistry</i> , <b>2011</b> , 33-50	0.4	
25	Tracking G-protein-coupled receptor activation using genetically encoded infrared probes. <i>Nature</i> , <b>2010</b> , 464, 1386-9	50.4	220
24	Influence of the g- conformation of Ser and Thr on the structure of transmembrane helices. <i>Journal of Structural Biology</i> , <b>2010</b> , 169, 116-23	3.4	24
23	Energy landscapes as a tool to integrate GPCR structure, dynamics, and function. <i>Physiology</i> , <b>2010</b> , 25, 293-303	9.8	194

22	The effect of ligand efficacy on the formation and stability of a GPCR-G protein complex. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2009</b> , 106, 9501-6	11.5	186
21	Ligand-regulated oligomerization of beta(2)-adrenoceptors in a model lipid bilayer. <i>EMBO Journal</i> , <b>2009</b> , 28, 3315-28	13	157
20	Characterization of a conformationally sensitive TOAC spin-labeled substance P. <i>Peptides</i> , <b>2008</b> , 29, 1919-24	3.8	9
19	The role of internal water molecules in the structure and function of the rhodopsin family of G protein-coupled receptors. <i>ChemBioChem</i> , <b>2007</b> , 8, 19-24	3.8	111
18	The activation mechanism of chemokine receptor CCR5 involves common structural changes but a different network of interhelical interactions relative to rhodopsin. <i>Cellular Signalling</i> , <b>2007</b> , 19, 1446-56	4.9	26
17	Charge-charge and cation-π interactions in ligand binding to G protein-coupled receptors. <i>Theoretical Chemistry Accounts</i> , <b>2007</b> , 118, 579-588	1.9	7
16	Structural models of class a G protein-coupled receptors as a tool for drug design: insights on transmembrane bundle plasticity. <i>Current Topics in Medicinal Chemistry</i> , <b>2007</b> , 7, 991-8	3	41
15	Conformational complexity of G-protein-coupled receptors. <i>Trends in Pharmacological Sciences</i> , <b>2007</b> , 28, 397-406	13.2	578
14	Activation of G protein-coupled receptors. <i>Advances in Protein Chemistry</i> , <b>2007</b> , 74, 137-66		61
13	3-D Structure of G Protein-coupled Receptors. <i>Methods and Principles in Medicinal Chemistry</i> , <b>2006</b> , 183-203		1
12	Coupling ligand structure to specific conformational switches in the beta2-adrenoceptor <b>2006</b> , 2, 417-22		280
11	Probing the beta2 adrenoceptor binding site with catechol reveals differences in binding and activation by agonists and partial agonists. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 22165-71	5.4	216
10	An activation switch in the rhodopsin family of G protein-coupled receptors: the thyrotropin receptor. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 17135-41	5.4	88
9	Conformational Plasticity of GPCR Binding Sites <b>2005</b> , 363-388		1
8	Ser and Thr residues modulate the conformation of pro-kinked transmembrane alpha-helices. <i>Biophysical Journal</i> , <b>2004</b> , 86, 105-15	2.9	83
7	Activation of CCR5 by chemokines involves an aromatic cluster between transmembrane helices 2 and 3. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 1892-903	5.4	80
6	Design, synthesis and pharmacological evaluation of 5-hydroxytryptamine(1a) receptor ligands to explore the three-dimensional structure of the receptor. <i>Molecular Pharmacology</i> , <b>2002</b> , 62, 15-21	4.3	47
5	Influence of the environment in the conformation of alpha-helices studied by protein database search and molecular dynamics simulations. <i>Biophysical Journal</i> , <b>2002</b> , 82, 3207-13	2.9	29

4	The TXP motif in the second transmembrane helix of CCR5. A structural determinant of chemokine-induced activation. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 13217-25	5.4	111
3	Selective hydrolysis of 2,4-diaminopyrimidine systems: a theoretical and experimental insight into an old rule. <i>Journal of Organic Chemistry</i> , <b>2001</b> , 66, 192-9	4.2	8
2	Serine and threonine residues bend alpha-helices in the chi(1) = g(-) conformation. <i>Biophysical Journal</i> , <b>2000</b> , 79, 2754-60	2.9	157
1	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist		1