

Francis C Peterson

List of Publications by Year in descending order

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64
papers

3,851
citations

201575

27
h-index

133188

59
g-index

66
all docs

66
docs citations

66
times ranked

4580
citing authors

#	ARTICLE	IF	CITATIONS
1	A gate-latch-lock mechanism for hormone signalling by abscisic acid receptors. <i>Nature</i> , 2009, 462, 602-608.	13.7	608
2	Activation of dimeric ABA receptors elicits guard cell closure, ABA-regulated gene expression, and drought tolerance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 12132-12137.	3.3	262
3	Structural Basis of CXCR4 Sulfotyrosine Recognition by the Chemokine SDF-1/CXCL12. <i>Science Signaling</i> , 2008, 1, ra4.	1.6	256
4	Interconversion between two unrelated protein folds in the lymphotactin native state. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 5057-5062.	3.3	248
5	Structural and functional insights into core ABA signaling. <i>Current Opinion in Plant Biology</i> , 2010, 13, 495-502.	3.5	234
6	Agrochemical control of plant water use using engineered abscisic acid receptors. <i>Nature</i> , 2015, 520, 545-548.	13.7	217
7	The monomer-dimer equilibrium of stromal cell-derived factor-1 (CXCL 12) is altered by pH, phosphate, sulfate, and heparin. <i>Protein Science</i> , 2005, 14, 1071-1081.	3.1	165
8	Cdc42 Regulates the Par-6 PDZ Domain through an Allosteric CRIB-PDZ Transition. <i>Molecular Cell</i> , 2004, 13, 665-676.	4.5	142
9	Recognition of a CXCR4 Sulfotyrosine by the Chemokine Stromal Cell-derived Factor-1 \pm (SDF-1 \pm /CXCL12). <i>Journal of Molecular Biology</i> , 2006, 359, 1400-1409.	2.0	116
10	Dynamic control of plant water use using designed ABA receptor agonists. <i>Science</i> , 2019, 366, .	6.0	107
11	Structural basis for selective activation of ABA receptors. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1109-1113.	3.6	104
12	Potent and selective activation of abscisic acid receptors in vivo by mutational stabilization of their agonist-bound conformation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 20838-20843.	3.3	89
13	Monomeric structure of the cardioprotective chemokine SDF-1/CXCL12. <i>Protein Science</i> , 2009, 18, 1359-1369.	3.1	74
14	Structural basis for chemokine recognition by a G protein-coupled receptor and implications for receptor activation. <i>Science Signaling</i> , 2017, 10, .	1.6	74
15	Identification and Characterization of a Glycosaminoglycan Recognition Element of the C Chemokine Lymphotactin. <i>Journal of Biological Chemistry</i> , 2004, 279, 12598-12604.	1.6	68
16	Targeting SDF-1/CXCL12 with a Ligand That Prevents Activation of CXCR4 through Structure-Based Drug Design. <i>Journal of the American Chemical Society</i> , 2010, 132, 7242-7243.	6.6	68
17	Orphan Macrodomein Protein (Human C6orf130) Is an O-Acyl-ADP-ribose Deacylase. <i>Journal of Biological Chemistry</i> , 2011, 286, 35955-35965.	1.6	65
18	Evolution of fold switching in a metamorphic protein. <i>Science</i> , 2021, 371, 86-90.	6.0	59

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19	A Rationally Designed Agonist Defines Subfamily IIIA Abscisic Acid Receptors As Critical Targets for Manipulating Transpiration. <i>ACS Chemical Biology</i> , 2017, 12, 2842-2848.	1.6	57
20	An Engineered Second Disulfide Bond Restricts Lymphotactin/XCL1 to a Chemokine-like Conformation with XCR1 Agonist Activity. <i>Biochemistry</i> , 2007, 46, 2564-2573.	1.2	52
21	Multiple WASP-interacting Protein Recognition Motifs Are Required for a Functional Interaction with N-WASP. <i>Journal of Biological Chemistry</i> , 2007, 282, 8446-8453.	1.6	44
22	A Single Mutation Promotes Amyloidogenicity through a Highly Promiscuous Dimer Interface. <i>Structure</i> , 2010, 18, 563-570.	1.6	42
23	A negative-feedback loop maintains optimal chemokine concentrations for directional cell migration. <i>Nature Cell Biology</i> , 2020, 22, 266-273.	4.6	40
24	Solution Structure of CCL21 and Identification of a Putative CCR7 Binding Site. <i>Biochemistry</i> , 2012, 51, 733-735.	1.2	39
25	Solution Structure of CCL19 and Identification of Overlapping CCR7 and PSGL-1 Binding Sites. <i>Biochemistry</i> , 2015, 54, 4163-4166.	1.2	37
26	Structural Determinants Involved in the Regulation of CXCL14/BRAK Expression by the 26 S Proteasome. <i>Journal of Molecular Biology</i> , 2006, 363, 813-822.	2.0	34
27	Rapid biosensor development using plant hormone receptors as reprogrammable scaffolds. <i>Nature Biotechnology</i> , 2022, 40, 1855-1861.	9.4	34
28	Production of Recombinant Chemokines and Validation of Refolding. <i>Methods in Enzymology</i> , 2016, 570, 539-565.	0.4	30
29	Identification of a fourth mannose 6-phosphate binding site in the cation-independent mannose 6-phosphate receptor. <i>Glycobiology</i> , 2015, 25, 591-606.	1.3	29
30	Structure-Based Identification of Novel Ligands Targeting Multiple Sites within a Chemokine-G-Protein-Coupled-Receptor Interface. <i>Journal of Medicinal Chemistry</i> , 2016, 59, 4342-4351.	2.9	29
31	Binding of Crumbs to the Par-6 CRIB-PDZ Module Is Regulated by Cdc42. <i>Biochemistry</i> , 2016, 55, 1455-1461.	1.2	29
32	Solution structure of thioredoxin1 from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2005, 14, 2195-2200.	3.1	27
33	Structure of the Lectin Mannose 6-Phosphate Receptor Homology (MRH) Domain of Glucosidase II, an Enzyme That Regulates Glycoprotein Folding Quality Control in the Endoplasmic Reticulum. <i>Journal of Biological Chemistry</i> , 2013, 288, 16460-16475.	1.6	26
34	The Aspartate-Less Receiver (ALR) Domains: Distribution, Structure and Function. <i>PLoS Pathogens</i> , 2015, 11, e1004795.	2.1	25
35	Structure of the SCAN Domain from the Tumor Suppressor protein MZF1. <i>Journal of Molecular Biology</i> , 2006, 363, 137-147.	2.0	23
36	Engineering Metamorphic Chemokine Lymphotactin/XCL1 into the GAG-Binding, HIV-Inhibitory Dimer Conformation. <i>ACS Chemical Biology</i> , 2015, 10, 2580-2588.	1.6	23

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37	CCR7 Sulfotyrosine Enhances CCL21 Binding. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1857.	1.8	21
38	Click-to-lead design of a picomolar ABA receptor antagonist with potent activity in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	20
39	Structure-Function Analysis of CCL28 in the Development of Post-viral Asthma. <i>Journal of Biological Chemistry</i> , 2015, 290, 4528-4536.	1.6	19
40	NMR Structure of the C-Terminal Transmembrane Domain of the HDL Receptor, SR-BI, and a Functionally Relevant Leucine Zipper Motif. <i>Structure</i> , 2017, 25, 446-457.	1.6	19
41	The dimeric form of CXCL12 binds to atypical chemokine receptor 1. <i>Science Signaling</i> , 2021, 14, .	1.6	19
42	Electrostatic Optimization of the Conformational Energy Landscape in a Metamorphic Protein. <i>Biochemistry</i> , 2012, 51, 9067-9075.	1.2	17
43	Conformational selection guides β^2 -arrestin recruitment at a biased G protein-coupled receptor. <i>Science</i> , 2022, 377, 222-228.	6.0	16
44	Crystal Structure and Functional Analyses of the Lectin Domain of Glucosidase II: Insights into Oligomannose Recognition. <i>Biochemistry</i> , 2015, 54, 4097-4111.	1.2	15
45	Examination of Glycosaminoglycan Binding Sites on the XCL1 Dimer. <i>Biochemistry</i> , 2016, 55, 1214-1225.	1.2	15
46	Structure and Dimerization of IreB, a Negative Regulator of Cephalosporin Resistance in <i>Enterococcus faecalis</i> . <i>Journal of Molecular Biology</i> , 2017, 429, 2324-2336.	2.0	15
47	The Solution Structure of CCL28 Reveals Structural Lability that Does Not Constrain Antifungal Activity. <i>Journal of Molecular Biology</i> , 2018, 430, 3266-3282.	2.0	14
48	Tyrosine-sulfated V2 peptides inhibit HIV-1 infection via coreceptor mimicry. <i>EBioMedicine</i> , 2016, 10, 45-54.	2.7	13
49	Development and Validation of 2D Difference Intensity Analysis for Chemical Library Screening by Protein-detected NMR Spectroscopy. <i>ChemBioChem</i> , 2018, 19, 448-458.	1.3	13
50	Structural Features of an Extended C-Terminal Tail Modulate the Function of the Chemokine CCL21. <i>Biochemistry</i> , 2020, 59, 1338-1350.	1.2	11
51	Solution NMR spectroscopy of GPCRs: Residue-specific labeling strategies with a focus on ^{13}C -methyl methionine labeling of the atypical chemokine receptor ACKR3. <i>Methods in Cell Biology</i> , 2019, 149, 259-288.	0.5	9
52	Expression, purification and reconstitution of the C-terminal transmembrane domain of scavenger receptor BI into detergent micelles for NMR analysis. <i>Protein Expression and Purification</i> , 2015, 107, 35-42.	0.6	8
53	Interactions between AMOT PPxY motifs and NEDD4L WW domains function in HIV-1 release. <i>Journal of Biological Chemistry</i> , 2021, 297, 100975.	1.6	8
54	The chemokine X-factor: Structure-function analysis of the CXC motif at CXCR4 and ACKR3. <i>Journal of Biological Chemistry</i> , 2020, 295, 13927-13939.	1.6	7

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55	Structural Insights into Molecular Recognition by Human Chemokine CCL19. <i>Biochemistry</i> , 2022, 61, 311-318.	1.2	4
56	The non-ELR CXC chemokine encoded by human cytomegalovirus UL146 genotype 5 contains a C-terminal β -hairpin and induces neutrophil migration as a selective CXCR2 agonist. <i>PLoS Pathogens</i> , 2022, 18, e1010355.	2.1	4
57	Selective Boosting of CCR7-Acting Chemokines; Short Peptides Boost Chemokines with Short Basic Tails, Longer Peptides Boost Chemokines with Long Basic Tails. <i>International Journal of Molecular Sciences</i> , 2022, 23, 1397.	1.8	3
58	Bacterial expression of the phosphodiester-binding site of the cation-independent mannose 6-phosphate receptor for crystallographic and NMR studies. <i>Protein Expression and Purification</i> , 2015, 111, 91-97.	0.6	1
59	Specific binding-induced modulation of the XCL1 metamorphic equilibrium. <i>Biopolymers</i> , 2020, 112, e23402.	1.2	1
60	The Synthesis and Anti-Cytomegalovirus Activity of Piperidine-4-Carboxamides. <i>Viruses</i> , 2022, 14, 234.	1.5	1
61	Structural Determination of a SCAN Domain Homodimer and Heterodimer. <i>FASEB Journal</i> , 2006, 20, A95.	0.2	0
62	Structural and functional characterization of Glucosidase II N-glycan binding domain. <i>FASEB Journal</i> , 2012, 26, 796.1.	0.2	0
63	Development of a Molecular Probe Targeting Mitochondrial Fission Protein Fis1. <i>FASEB Journal</i> , 2018, 32, 530.17.	0.2	0
64	Structural Basis of Nanobody Induced ACKR3 Inhibition. <i>FASEB Journal</i> , 2022, 36, .	0.2	0