Francis C Peterson

List of Publications by Year
in descending order

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64 papers	3,851 citations	201674 27 h-index	133252 59 g-index
66 all docs	66 docs citations	66 times ranked	4580 citing authors

#	Article	IF	Citations
1	The Synthesis and Anti-Cytomegalovirus Activity of Piperidine-4-Carboxamides. Viruses, 2022, 14, 234.	3.3	1
2	Selective Boosting of CCR7-Acting Chemokines; Short Peptides Boost Chemokines with Short Basic Tails, Longer Peptides Boost Chemokines with Long Basic Tails. International Journal of Molecular Sciences, 2022, 23, 1397.	4.1	3
3	Structural Insights into Molecular Recognition by Human Chemokine CCL19. Biochemistry, 2022, 61, 311-318.	2.5	4
4	The non-ELR CXC chemokine encoded by human cytomegalovirus UL146 genotype 5 contains a C-terminal Î²-hairpin and induces neutrophil migration as a selective CXCR2 agonist. PLoS Pathogens, 2022, 18, e1010355.	4.7	4
5	Structural Basis of Nanobody Induced ACKR3 Inhibition. FASEB Journal, 2022, 36, .	0.5	0
6	Rapid biosensor development using plant hormone receptors as reprogrammable scaffolds. Nature Biotechnology, 2022, 40, 1855-1861.	17.5	34
7	Conformational selection guides Î²-arrestin recruitment at a biased G proteinâ€“coupled receptor. Science, 2022, 377, 222-228.	12.6	16
8	The dimeric form of CXCL12 binds to atypical chemokine receptor 1. Science Signaling, 2021, 14, .	3.6	19
9	Interactions between AMOT PPxY motifs and NEDD4L WW domains function in HIV-1 release. Journal of Biological Chemistry, 2021, 297, 100975.	3.4	8
10	Click-to-lead design of a picomolar ABA receptor antagonist with potent activity in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	20
11	Evolution of fold switching in a metamorphic protein. Science, 2021, 371, 86-90.	12.6	59
12	Specific bindingâ€induced modulation of the XCL1 metamorphic equilibrium. Biopolymers, 2020, 112, e23402.	2.4	1
13	The chemokine X-factor: Structure-function analysis of the CXC motif at CXCR4 and ACKR3. Journal of Biological Chemistry, 2020, 295, 13927-13939.	3.4	7
14	A negative-feedback loop maintains optimal chemokine concentrations for directional cell migration. Nature Cell Biology, 2020, 22, 266-273.	10.3	40
15	Structural Features of an Extended C-Terminal Tail Modulate the Function of the Chemokine CCL21. Biochemistry, 2020, 59, 1338-1350.	2.5	11
16	Dynamic control of plant water use using designed ABA receptor agonists. Science, 2019, 366, .	12.6	107
17	Solution NMR spectroscopy of GPCRs: Residue-specific labeling strategies with a focus on 13C-methyl methionine labeling of the atypical chemokine receptor ACKR3. Methods in Cell Biology, 2019, 149, 259-288.	1.1	9
18	Development and Validation of 2D Difference Intensity Analysis for Chemical Library Screening by Proteinâ€Detected NMR Spectroscopy. ChemBioChem, 2018, 19, 448-458.	2.6	13

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19	The Solution Structure of CCL28 Reveals Structural Lability that Does Not Constrain Antifungal Activity. Journal of Molecular Biology, 2018, 430, 3266-3282.	4.2	14
20	Development of a Molecular Probe Targeting Mitochondrial Fission Protein Fis1. FASEB Journal, 2018, 32, 530.17.	0.5	0
21	NMR Structure of the C-Terminal Transmembrane Domain of the HDL Receptor, SR-BI, and a Functionally Relevant Leucine Zipper Motif. Structure, 2017, 25, 446-457.	3.3	19
22	Structure and Dimerization of IreB, a Negative Regulator of Cephalosporin Resistance in Enterococcus faecalis. Journal of Molecular Biology, 2017, 429, 2324-2336.	4.2	15
23	Structural basis for chemokine recognition by a G proteinâ€“coupled receptor and implications for receptor activation. Science Signaling, 2017, 10, .	3.6	74
24	A Rationally Designed Agonist Defines Subfamily IIIA Abscisic Acid Receptors As Critical Targets for Manipulating Transpiration. ACS Chemical Biology, 2017, 12, 2842-2848.	3.4	57
25	CCR7 Sulfotyrosine Enhances CCL21 Binding. International Journal of Molecular Sciences, 2017, 18, 1857.	4.1	21
26	Production of Recombinant Chemokines and Validation of Refolding. Methods in Enzymology, 2016, 570, 539-565.	1.0	30
27	Structure-Based Identification of Novel Ligands Targeting Multiple Sites within a Chemokineâ€“G-Protein-Coupled-Receptor Interface. Journal of Medicinal Chemistry, 2016, 59, 4342-4351.	6.4	29
28	Tyrosine-sulfated V2 peptides inhibit HIV-1 infection via coreceptor mimicry. EBioMedicine, 2016, 10, 45-54.	6.1	13
29	Examination of Glycosaminoglycan Binding Sites on the XCL1 Dimer. Biochemistry, 2016, 55, 1214-1225.	2.5	15
30	Binding of Crumbs to the Par-6 CRIB-PDZ Module Is Regulated by Cdc42. Biochemistry, 2016, 55, 1455-1461.	2.5	29
31	Identification of a fourth mannose 6-phosphate binding site in the cation-independent mannose 6-phosphate receptor. Glycobiology, 2015, 25, 591-606.	2.5	29
32	Agrochemical control of plant water use using engineered abscisic acid receptors. Nature, 2015, 520, 545-548.	27.8	217
33	Structure-Function Analysis of CCL28 in the Development of Post-viral Asthma. Journal of Biological Chemistry, 2015, 290, 4528-4536.	3.4	19
34	Solution Structure of CCL19 and Identification of Overlapping CCR7 and PSGL-1 Binding Sites. Biochemistry, 2015, 54, 4163-4166.	2.5	37
35	Crystal Structure and Functional Analyses of the Lectin Domain of Glucosidase II: Insights into Oligomannose Recognition. Biochemistry, 2015, 54, 4097-4111.	2.5	15
36	The Aspartate-Less Receiver (ALR) Domains: Distribution, Structure and Function. PLoS Pathogens, 2015, 11, e1004795.	4.7	25

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37	Bacterial expression of the phosphodiester-binding site of the cation-independent mannose 6-phosphate receptor for crystallographic and NMR studies. Protein Expression and Purification, 2015, 111, 91-97.	1.3	1
38	Engineering Metamorphic Chemokine Lymphotactin/XCL1 into the GAG-Binding, HIV-Inhibitory Dimer Conformation. ACS Chemical Biology, 2015, 10, 2580-2588.	3.4	23
39	Expression, purification and reconstitution of the C-terminal transmembrane domain of scavenger receptor BI into detergent micelles for NMR analysis. Protein Expression and Purification, 2015, 107, 35-42.	1.3	8
40	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. Journal of Biological Chemistry, 2013, 288, 16460-16475.	3.4	26
41	Activation of dimeric ABA receptors elicits guard cell closure, ABA-regulated gene expression, and drought tolerance. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 12132-12137.	7.1	262
42	Solution Structure of CCL21 and Identification of a Putative CCR7 Binding Site. Biochemistry, 2012, 51, 733-735.	2.5	39
43	Electrostatic Optimization of the Conformational Energy Landscape in a Metamorphic Protein. Biochemistry, 2012, 51, 9067-9075.	2.5	17
44	Structural and functional characterization of Glucosidase II Nâ€glycan binding domain. FASEB Journal, 2012, 26, 796.1.	0.5	0
45	Potent and selective activation of abscisic acid receptors in vivo by mutational stabilization of their agonist-bound conformation. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 20838-20843.	7.1	89
46	Orphan Macrodomain Protein (Human C6orf130) Is an O-Acyl-ADP-ribose Deacylase. Journal of Biological Chemistry, 2011, 286, 35955-35965.	3.4	65
47	Structural and functional insights into core ABA signaling. Current Opinion in Plant Biology, 2010, 13, 495-502.	7.1	234
48	A Single Mutation Promotes Amyloidogenicity through a Highly Promiscuous Dimer Interface. Structure, 2010, 18, 563-570.	3.3	42
49	Structural basis for selective activation of ABA receptors. Nature Structural and Molecular Biology, 2010, 17, 1109-1113.	8.2	104
50	Targeting SDF-1/CXCL12 with a Ligand That Prevents Activation of CXCR4 through Structure-Based Drug Design. Journal of the American Chemical Society, 2010, 132, 7242-7243.	13.7	68
51	Monomeric structure of the cardioprotective chemokine SDFâ€1/CXCL12. Protein Science, 2009, 18, 1359-1369.	7.6	74
52	A gateâ€“latchâ€“lock mechanism for hormone signalling by abscisic acid receptors. Nature, 2009, 462, 602-608.	27.8	608
53	Interconversion between two unrelated protein folds in the lymphotactin native state. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 5057-5062.	7.1	248
54	Structural Basis of CXCR4 Sulfotyrosine Recognition by the Chemokine SDF-1/CXCL12. Science Signaling, 2008, 1, ra4.	3.6	256

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55	Multiple WASP-interacting Protein Recognition Motifs Are Required for a Functional Interaction with N-WASP. Journal of Biological Chemistry, 2007, 282, 8446-8453.	3.4	44
56	An Engineered Second Disulfide Bond Restricts Lymphotactin/XCL1 to a Chemokine-like Conformation with XCR1 Agonist Activityâ€. Biochemistry, 2007, 46, 2564-2573.	2.5	52
57	Recognition of a CXCR4 Sulfotyrosine by the Chemokine Stromal Cell-derived Factor-1Î± (SDF-1Î±/CXCL12). Journal of Molecular Biology, 2006, 359, 1400-1409.	4.2	116
58	Structure of the SCAN Domain from the Tumor Suppressor protein MZF1. Journal of Molecular Biology, 2006, 363, 137-147.	4.2	23
59	Structural Determinants Involved in the Regulation of CXCL14/BRAK Expression by the 26 S Proteasome. Journal of Molecular Biology, 2006, 363, 813-822.	4.2	34
60	Structural Determination of a SCAN Domain Homodimer and Heterodimer. FASEB Journal, 2006, 20, A95.	0.5	0
61	Solution structure of thioredoxinh1 fromArabidopsis thaliana. Protein Science, 2005, 14, 2195-2200.	7.6	27
62	The monomer-dimer equilibrium of stromal cell-derived factor-1 (CXCL 12) is altered by pH, phosphate, sulfate, and heparin. Protein Science, 2005, 14, 1071-1081.	7.6	165
63	Identification and Characterization of a Glycosaminoglycan Recognition Element of the C Chemokine Lymphotactin. Journal of Biological Chemistry, 2004, 279, 12598-12604.	3.4	68
64	Cdc42 Regulates the Par-6 PDZ Domain through an Allosteric CRIB-PDZ Transition. Molecular Cell, 2004, 13, 665-676.	9.7	142