

Francis C Peterson

List of Publications by Year in descending order

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Version: 2024-02-01

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	The Synthesis and Anti-Cytomegalovirus Activity of Piperidine-4-Carboxamides. <i>Viruses</i> , 2022, 14, 234.	1.5	1
2	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
3	Structural Insights into Molecular Recognition by Human Chemokine CCL19. <i>Biochemistry</i> , 2022, 61, 311-318.	1.2	4
4	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
5	Structural Basis of Nanobody Induced ACKR3 Inhibition. <i>FASEB Journal</i> , 2022, 36, .	0.2	0
6	Rapid biosensor development using plant hormone receptors as reprogrammable scaffolds. <i>Nature Biotechnology</i> , 2022, 40, 1855-1861.	9.4	34
7	Conformational selection guides β -arrestin recruitment at a biased G protein-coupled receptor. <i>Science</i> , 2022, 377, 222-228.	6.0	16
8	The dimeric form of CXCL12 binds to atypical chemokine receptor 1. <i>Science Signaling</i> , 2021, 14, .	1.6	19
9	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
10	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
11	Evolution of fold switching in a metamorphic protein. <i>Science</i> , 2021, 371, 86-90.	6.0	59
12	Specific binding-induced modulation of the XCL1 metamorphic equilibrium. <i>Biopolymers</i> , 2020, 112, e23402.	1.2	1
13	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
14	A negative-feedback loop maintains optimal chemokine concentrations for directional cell migration. <i>Nature Cell Biology</i> , 2020, 22, 266-273.	4.6	40
15	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
16	Dynamic control of plant water use using designed ABA receptor agonists. <i>Science</i> , 2019, 366, .	6.0	107
17	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
18	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

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19	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
20	Development of a Molecular Probe Targeting Mitochondrial Fission Protein Fis1. <i>FASEB Journal</i> , 2018, 32, 530.17.	0.2	0
21	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
22	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
23	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
24	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
25	CCR7 Sulfotyrosine Enhances CCL21 Binding. <i>International Journal of Molecular Sciences</i> , 2017, 18, 1857.	1.8	21
26	Production of Recombinant Chemokines and Validation of Refolding. <i>Methods in Enzymology</i> , 2016, 570, 539-565.	0.4	30
27	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
28	Tyrosine-sulfated V2 peptides inhibit HIV-1 infection via coreceptor mimicry. <i>EBioMedicine</i> , 2016, 10, 45-54.	2.7	13
29	Examination of Glycosaminoglycan Binding Sites on the XCL1 Dimer. <i>Biochemistry</i> , 2016, 55, 1214-1225.	1.2	15
30	Binding of Crumbs to the Par-6 CRIB-PDZ Module Is Regulated by Cdc42. <i>Biochemistry</i> , 2016, 55, 1455-1461.	1.2	29
31	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
32	Agrochemical control of plant water use using engineered abscisic acid receptors. <i>Nature</i> , 2015, 520, 545-548.	13.7	217
33	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
34	Solution Structure of CCL19 and Identification of Overlapping CCR7 and PSGL-1 Binding Sites. <i>Biochemistry</i> , 2015, 54, 4163-4166.	1.2	37
35	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
36	The Aspartate-Less Receiver (ALR) Domains: Distribution, Structure and Function. <i>PLoS Pathogens</i> , 2015, 11, e1004795.	2.1	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. <i>Protein Expression and Purification</i> , 2015, 111, 91-97.	0.6	1
38	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
39	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
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. <i>Journal of Biological Chemistry</i> , 2013, 288, 16460-16475.	1.6	26
41	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
42	Solution Structure of CCL21 and Identification of a Putative CCR7 Binding Site. <i>Biochemistry</i> , 2012, 51, 733-735.	1.2	39
43	Electrostatic Optimization of the Conformational Energy Landscape in a Metamorphic Protein. <i>Biochemistry</i> , 2012, 51, 9067-9075.	1.2	17
44	Structural and functional characterization of Glucosidase II N-glycan binding domain. <i>FASEB Journal</i> , 2012, 26, 796.1.	0.2	0
45	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
46	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
47	Structural and functional insights into core ABA signaling. <i>Current Opinion in Plant Biology</i> , 2010, 13, 495-502.	3.5	234
48	A Single Mutation Promotes Amyloidogenicity through a Highly Promiscuous Dimer Interface. <i>Structure</i> , 2010, 18, 563-570.	1.6	42
49	Structural basis for selective activation of ABA receptors. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1109-1113.	3.6	104
50	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
51	Monomeric structure of the cardioprotective chemokine SDF-1/CXCL12. <i>Protein Science</i> , 2009, 18, 1359-1369.	3.1	74
52	A gate-latch-lock mechanism for hormone signalling by abscisic acid receptors. <i>Nature</i> , 2009, 462, 602-608.	13.7	608
53	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
54	Structural Basis of CXCR4 Sulfotyrosine Recognition by the Chemokine SDF-1/CXCL12. <i>Science Signaling</i> , 2008, 1, ra4.	1.6	256

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55	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
56	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
57	Recognition of a CXCR4 Sulfotyrosine by the Chemokine Stromal Cell-derived Factor-1 β (SDF-1 β /CXCL12). <i>Journal of Molecular Biology</i> , 2006, 359, 1400-1409.	2.0	116
58	Structure of the SCAN Domain from the Tumor Suppressor protein MZF1. <i>Journal of Molecular Biology</i> , 2006, 363, 137-147.	2.0	23
59	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
60	Structural Determination of a SCAN Domain Homodimer and Heterodimer. <i>FASEB Journal</i> , 2006, 20, A95.	0.2	0
61	Solution structure of thioredoxin h1 from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , 2005, 14, 2195-2200.	3.1	27
62	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
63	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
64	Cdc42 Regulates the Par-6 PDZ Domain through an Allosteric CRIB-PDZ Transition. <i>Molecular Cell</i> , 2004, 13, 665-676.	4.5	142