

# Brian F Volkman

## List of Publications by Citations

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208  
papers

9,596  
citations

46  
h-index

92  
g-index

239  
ext. papers

11,101  
ext. citations

7.2  
avg, IF

5.75  
L-index

#	Paper	IF	Citations
208	Abscisic acid inhibits type 2C protein phosphatases via the PYR/PYL family of START proteins. <i>Science</i> , <b>2009</b> , 324, 1068-71	33.3	1782
207	Two-state allosteric behavior in a single-domain signaling protein. <i>Science</i> , <b>2001</b> , 291, 2429-33	33.3	529
206	A gate-latch-lock mechanism for hormone signalling by abscisic acid receptors. <i>Nature</i> , <b>2009</b> , 462, 602-8	50.4	498
205	Structural basis of CXCR4 sulfotyrosine recognition by the chemokine SDF-1/CXCL12. <i>Science Signaling</i> , <b>2008</b> , 1, ra4	8.8	215
204	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> , <b>2008</b> , 105, 5057-62	11.5	209
203	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> , <b>2013</b> , 110, 12132-7	11.5	196
202	Structure of a transiently phosphorylated switch in bacterial signal transduction. <i>Nature</i> , <b>1999</b> , 402, 894-8	50.4	183
201	Structural and functional insights into core ABA signaling. <i>Current Opinion in Plant Biology</i> , <b>2010</b> , 13, 495-502	9.9	178
200	Microscopic pKa values of Escherichia coli thioredoxin. <i>Biochemistry</i> , <b>1997</b> , 36, 14985-91	3.2	158
199	Agrochemical control of plant water use using engineered abscisic acid receptors. <i>Nature</i> , <b>2015</b> , 520, 545-8	50.4	157
198	Monomeric and dimeric CXCL12 inhibit metastasis through distinct CXCR4 interactions and signaling pathways. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 17655-60	11.5	151
197	Structure of the N-WASP EVH1 domain-WIP complex: insight into the molecular basis of Wiskott-Aldrich Syndrome. <i>Cell</i> , <b>2002</b> , 111, 565-76	56.2	145
196	The monomer-dimer equilibrium of stromal cell-derived factor-1 (CXCL 12) is altered by pH, phosphate, sulfate, and heparin. <i>Protein Science</i> , <b>2005</b> , 14, 1071-81	6.3	143
195	Structure-based ligand discovery for the protein-protein interface of chemokine receptor CXCR4. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2012</b> , 109, 5517-22	11.5	123
194	Cell-free protein production and labeling protocol for NMR-based structural proteomics. <i>Nature Methods</i> , <b>2004</b> , 1, 149-53	21.6	123
193	Cdc42 regulates the Par-6 PDZ domain through an allosteric CRIB-PDZ transition. <i>Molecular Cell</i> , <b>2004</b> , 13, 665-76	17.6	122
192	Three-dimensional solution structure of the N-terminal receiver domain of NTRC. <i>Biochemistry</i> , <b>1995</b> , 34, 1413-24	3.2	102

191	Recognition of a CXCR4 sulfotyrosine by the chemokine stromal cell-derived factor-1alpha (SDF-1alpha/CXCL12). <i>Journal of Molecular Biology</i> , <b>2006</b> , 359, 1400-9	6.5	99
190	Polysialylation controls dendritic cell trafficking by regulating chemokine recognition. <i>Science</i> , <b>2016</b> , 351, 186-90	33.3	97
189	Structural basis for selective activation of ABA receptors. <i>Nature Structural and Molecular Biology</i> , <b>2010</b> , 17, 1109-13	17.6	88
188	Altered dimer interface decreases stability in an amyloidogenic protein. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 15853-60	5.4	87
187	Short peptide fragments derived from HMG-I/Y proteins bind specifically to the minor groove of DNA. <i>Biochemistry</i> , <b>1994</b> , 33, 5347-55	3.2	82
186	Project management system for structural and functional proteomics: Sesame. <i>Journal of Structural and Functional Genomics</i> , <b>2003</b> , 4, 11-23		80
185	Tyrosine residues mediate fibril formation in a dynamic light chain dimer interface.. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 35541	5.4	78
184	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> , <b>2011</b> , 108, 20838-43	11.5	74
183	Solution structure of a type I dockerin domain, a novel prokaryotic, extracellular calcium-binding domain. <i>Journal of Molecular Biology</i> , <b>2001</b> , 307, 745-53	6.5	74
182	The CXC chemokine receptor 4 ligands ubiquitin and stromal cell-derived factor-1 function through distinct receptor interactions. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 33466-77	5.4	71
181	New paradigms in chemokine receptor signal transduction: Moving beyond the two-site model. <i>Biochemical Pharmacology</i> , <b>2016</b> , 114, 53-68	6	66
180	Heparin oligosaccharides inhibit chemokine (CXC motif) ligand 12 (CXCL12) cardioprotection by binding orthogonal to the dimerization interface, promoting oligomerization, and competing with the chemokine (CXC motif) receptor 4 (CXCR4) N terminus. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 737-44	5.4	65
179	Refined structure and metal binding site of the kalata B1 peptide. <i>Archives of Biochemistry and Biophysics</i> , <b>2002</b> , 399, 142-8	4.1	65
178	Sequential tyrosine sulfation of CXCR4 by tyrosylprotein sulfotransferases. <i>Biochemistry</i> , <b>2008</b> , 47, 11251-62	3.62	62
177	Identification and characterization of a glycosaminoglycan recognition element of the C chemokine lymphotactin. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 12598-604	5.4	62
176	Monomeric structure of the cardioprotective chemokine SDF-1/CXCL12. <i>Protein Science</i> , <b>2009</b> , 18, 1359-69	6.9	61
175	Site-specific isotopic labeling of proteins for NMR studies. <i>Journal of the American Chemical Society</i> , <b>1992</b> , 114, 7959-7961	16.4	61
174	Dynamic control of plant water use using designed ABA receptor agonists. <i>Science</i> , <b>2019</b> , 366,	33.3	60

173	Structural rearrangement of human lymphotactin, a C chemokine, under physiological solution conditions. <i>Journal of Biological Chemistry</i> , <b>2002</b> , 277, 17863-70	5.4	60
172	The dependence of chemokine-glycosaminoglycan interactions on chemokine oligomerization. <i>Glycobiology</i> , <b>2016</b> , 26, 312-26	5.8	59
171	Orphan macrodomain protein (human C6orf130) is an O-acyl-ADP-ribose deacylase: solution structure and catalytic properties. <i>Journal of Biological Chemistry</i> , <b>2011</b> , 286, 35955-35965	5.4	59
170	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> , <b>2010</b> , 132, 7242-3	16.4	58
169	Structural basis for chemokine recognition by a G protein-coupled receptor and implications for receptor activation. <i>Science Signaling</i> , <b>2017</b> , 10,	8.8	56
168	Secondary structure and calcium-induced folding of the Clostridium thermocellum dockerin domain determined by NMR spectroscopy. <i>Archives of Biochemistry and Biophysics</i> , <b>2000</b> , 379, 237-44	4.1	56
167	Structures of two Arabidopsis thaliana major latex proteins represent novel helix-grip folds. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2009</b> , 76, 237-43	4.2	52
166	Comparison of cell-based and cell-free protocols for producing target proteins from the Arabidopsis thaliana genome for structural studies. <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2005</b> , 59, 633-43	4.2	52
165	Protonation behavior of histidine 24 and histidine 119 in forming the pH 4 folding intermediate of apomyoglobin. <i>Biochemistry</i> , <b>1998</b> , 37, 4254-65	3.2	51
164	Binding site identification and structure determination of protein-ligand complexes by NMR a semiautomated approach. <i>Methods in Enzymology</i> , <b>2011</b> , 493, 241-75	1.7	49
163	Monomeric solution structure of the prototypical C chemokine lymphotactin. <i>Biochemistry</i> , <b>2001</b> , 40, 12486-96	3.2	47
162	Structure of the B3 domain from Arabidopsis thaliana protein At1g16640. <i>Protein Science</i> , <b>2005</b> , 14, 2478-83	6.3	46
161	Distal interactions within the par3-VE-cadherin complex. <i>Biochemistry</i> , <b>2010</b> , 49, 951-7	3.2	45
160	Heteromerization of chemokine (C-X-C motif) receptor 4 with $\alpha$ A/B-adrenergic receptors controls $\alpha$ A/B-adrenergic receptor function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, E1659-68	11.5	44
159	A locked, dimeric CXCL12 variant effectively inhibits pulmonary metastasis of CXCR4-expressing melanoma cells due to enhanced serum stability. <i>Molecular Cancer Therapeutics</i> , <b>2012</b> , 11, 2516-25	6.1	44
158	Chemical shift mapping of the RNA-binding interface of the multiple-RBD protein sex-lethal. <i>Biochemistry</i> , <b>1997</b> , 36, 14306-17	3.2	44
157	Combine and conquer: surfactants, solvents, and chaotropes for robust mass spectrometry based analyses of membrane proteins. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 1551-9	7.8	42
156	An engineered second disulfide bond restricts lymphotactin/XCL1 to a chemokine-like conformation with XCR1 agonist activity. <i>Biochemistry</i> , <b>2007</b> , 46, 2564-73	3.2	42

155	Multiple WASP-interacting protein recognition motifs are required for a functional interaction with N-WASP. <i>Journal of Biological Chemistry</i> , <b>2007</b> , 282, 8446-53	5.4	42
154	Sulfopeptide probes of the CXCR4/CXCL12 interface reveal oligomer-specific contacts and chemokine allostery. <i>ACS Chemical Biology</i> , <b>2013</b> , 8, 1955-63	4.9	41
153	Determination of internuclear angles of DNA using paramagnetic-assisted magnetic alignment. <i>Journal of Magnetic Resonance</i> , <b>1998</b> , 135, 256-9	3	40
152	Unfolding the Mysteries of Protein Metamorphosis. <i>ACS Chemical Biology</i> , <b>2018</b> , 13, 1438-1446	4.9	40
151	Cytokines and growth factors cross-link heparan sulfate. <i>Open Biology</i> , <b>2015</b> , 5,	7	39
150	Pancreatic Cancer Cell Migration and Metastasis Is Regulated by Chemokine-Biased Agonism and Bioenergetic Signaling. <i>Cancer Research</i> , <b>2015</b> , 75, 3529-42	10.1	38
149	Evolution of an ancient protein function involved in organized multicellularity in animals. <i>ELife</i> , <b>2016</b> , 5, e10147	8.9	37
148	Residues within a lipid-associated segment of the PECAM-1 cytoplasmic domain are susceptible to inducible, sequential phosphorylation. <i>Blood</i> , <b>2011</b> , 117, 6012-23	2.2	36
147	Biosynthesis of d-Alanyl-Lipoteichoic Acid: The Tertiary Structure of apo-d-Alanyl Carrier Protein,. <i>Biochemistry</i> , <b>2001</b> , 40, 7964-7972	3.2	36
146	Contribution of Backbone Dynamics to Entropy Changes Occurring on Oxidation of Cytochrome b5. Can Redox Linked Changes in Hydrogen Bond Networks Modulate Reduction Potentials?. <i>Journal of Physical Chemistry B</i> , <b>1998</b> , 102, 8201-8208	3.4	36
145	A Rationally Designed Agonist Defines Subfamily IIIA Abscisic Acid Receptors As Critical Targets for Manipulating Transpiration. <i>ACS Chemical Biology</i> , <b>2017</b> , 12, 2842-2848	4.9	35
144	Protein engineering of the chemokine CCL20 prevents psoriasiform dermatitis in an IL-23-dependent murine model. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 12460-12465	11.5	35
143	Structural basis for recognition of phosphodiester-containing lysosomal enzymes by the cation-independent mannose 6-phosphate receptor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2010</b> , 107, 12493-8	11.5	35
142	A single mutation promotes amyloidogenicity through a highly promiscuous dimer interface. <i>Structure</i> , <b>2010</b> , 18, 563-70	5.2	35
141	Diversity of polyproline recognition by EVH1 domains. <i>Frontiers in Bioscience - Landmark</i> , <b>2009</b> , 14, 833-46.8		34
140	The NMR solution structure of BeF <sub>3</sub> (-)-activated Spo0F reveals the conformational switch in a phosphorelay system. <i>Journal of Molecular Biology</i> , <b>2003</b> , 331, 245-54	6.5	34
139	Native-state interconversion of a metamorphic protein requires global unfolding. <i>Biochemistry</i> , <b>2011</b> , 50, 7077-9	3.2	33
138	Structure of the insect cytokine peptide plasmacyte-spreading peptide 1 from <i>Pseudoplusia includens</i> . <i>Journal of Biological Chemistry</i> , <b>1999</b> , 274, 4493-6	5.4	33

137	NMR solution structure of plastocyanin from the photosynthetic prokaryote, <i>Prochlorothrix hollandica</i> . <i>Biochemistry</i> , <b>1999</b> , 38, 4988-95	3.2	33
136	Redox-Dependent Magnetic Alignment of <i>Clostridium pasteurianum</i> Rubredoxin: Measurement of Magnetic Susceptibility Anisotropy and Prediction of Pseudocontact Shift Contributions. <i>Journal of the American Chemical Society</i> , <b>1999</b> , 121, 4677-4683	16.4	33
135	A novel zinc finger is required for Mcm10 homocomplex assembly. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 36051-8	5.4	31
134	Different contributions of chemokine N-terminal features attest to a different ligand binding mode and a bias towards activation of ACKR3/CXCR7 compared with CXCR4 and CXCR3. <i>British Journal of Pharmacology</i> , <b>2018</b> , 175, 1419-1438	8.6	30
133	Structural and agonist properties of XCL2, the other member of the C-chemokine subfamily. <i>Cytokine</i> , <b>2015</b> , 71, 302-11	4	29
132	Chemokine (C-X-C motif) receptor 4 and atypical chemokine receptor 3 regulate vascular adrenergic receptor function. <i>Molecular Medicine</i> , <b>2014</b> , 20, 435-47	6.2	29
131	Dissecting the dynamic conformations of the metamorphic protein lymphotactin. <i>Journal of Physical Chemistry B</i> , <b>2014</b> , 118, 12348-59	3.4	28
130	Structural determinants involved in the regulation of CXCL14/BRAK expression by the 26 S proteasome. <i>Journal of Molecular Biology</i> , <b>2006</b> , 363, 813-22	6.5	28
129	On-column refolding of recombinant chemokines for NMR studies and biological assays. <i>Protein Expression and Purification</i> , <b>2007</b> , 52, 202-9	2	27
128	Biased antagonism of CXCR4 avoids antagonist tolerance. <i>Science Signaling</i> , <b>2018</b> , 11,	8.8	27
127	Chemokine cooperativity is caused by competitive glycosaminoglycan binding. <i>Journal of Immunology</i> , <b>2014</b> , 192, 3908-3914	5.3	26
126	Evidence for oxidation-state-dependent conformational changes in human ferredoxin from multinuclear, multidimensional NMR spectroscopy. <i>Biochemistry</i> , <b>1998</b> , 37, 3965-73	3.2	26
125	Solution structure of a ubiquitin-like domain from tubulin-binding cofactor B. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 46787-93	5.4	26
124	Solution structure of thioredoxin h1 from <i>Arabidopsis thaliana</i> . <i>Protein Science</i> , <b>2005</b> , 14, 2195-200	6.3	26
123	Inadequacies of the Point-Dipole Approximation for Describing Electron-Nuclear Interactions in Paramagnetic Proteins: Hybrid Density Functional Calculations and the Analysis of NMR Relaxation of High-Spin Iron(III) Rubredoxin. <i>Journal of Physical Chemistry B</i> , <b>1998</b> , 102, 8300-8305	3.4	26
122	New Insights into Mechanisms and Functions of Chemokine (C-X-C Motif) Receptor 4 Heteromerization in Vascular Smooth Muscle. <i>International Journal of Molecular Sciences</i> , <b>2016</b> , 17,	6.3	26
121	CXC chemokine receptor 4 signaling upon co-activation with stromal cell-derived factor-1 and ubiquitin. <i>Cytokine</i> , <b>2014</b> , 65, 121-5	4	25
120	The Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , <b>2009</b> , 10, 165-79		25

119	Conversion of the enzyme guanylate kinase into a mitotic-spindle orienting protein by a single mutation that inhibits GMP-induced closing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, E973-8	11.5	25
118	Solution structure and backbone dynamics of component IV Glycera dibranchiata monomeric hemoglobin-CO. <i>Biochemistry</i> , <b>1998</b> , 37, 10906-19	3.2	25
117	The first structure from the SOUL/HBP family of heme-binding proteins, murine P22HBP. <i>Journal of Biological Chemistry</i> , <b>2006</b> , 281, 31553-61	5.4	25
116	Unfolding of the C-terminal domain of the J-protein Zuo1 releases autoinhibition and activates Pdr1-dependent transcription. <i>Journal of Molecular Biology</i> , <b>2013</b> , 425, 19-31	6.5	24
115	The CD8-derived chemokine XCL1/lymphotactin is a conformation-dependent, broad-spectrum inhibitor of HIV-1. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003852	7.6	24
114	N-terminal residues of plasmacyte-spreading peptide possess specific determinants required for biological activity. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 37431-5	5.4	24
113	Structure-Based Identification of Novel Ligands Targeting Multiple Sites within a Chemokine-G-Protein-Coupled-Receptor Interface. <i>Journal of Medicinal Chemistry</i> , <b>2016</b> , 59, 4342-51	8.3	24
112	Identification of the major ubiquitin-binding domain of the Pseudomonas aeruginosa ExoU A2 phospholipase. <i>Journal of Biological Chemistry</i> , <b>2013</b> , 288, 26741-52	5.4	23
111	Chapter 3. Lymphotactin structural dynamics. <i>Methods in Enzymology</i> , <b>2009</b> , 461, 51-70	1.7	23
110	Alanine-scanning mutagenesis of plasmacyte spreading peptide identifies critical residues for biological activity. <i>Journal of Biological Chemistry</i> , <b>2001</b> , 276, 18491-6	5.4	23
109	Gamma-glutamylcysteine synthetase-glutathione synthetase: domain structure and identification of residues important in substrate and glutathione binding. <i>Biochemistry</i> , <b>2006</b> , 45, 10461-73	3.2	22
108	Production in two-liter beverage bottles of proteins for NMR structure determination labeled with either <sup>15</sup> N- or <sup>13</sup> C- <sup>15</sup> N. <i>Journal of Structural and Functional Genomics</i> , <b>2004</b> , 5, 87-93		22
107	Adrenergic Receptors Function Within Hetero-Oligomeric Complexes With Atypical Chemokine Receptor 3 and Chemokine (C-X-C motif) Receptor 4 in Vascular Smooth Muscle Cells. <i>Journal of the American Heart Association</i> , <b>2017</b> , 6,	6	21
106	Engineering Metamorphic Chemokine Lymphotactin/XCL1 into the GAG-Binding, HIV-Inhibitory Dimer Conformation. <i>ACS Chemical Biology</i> , <b>2015</b> , 10, 2580-8	4.9	20
105	Binding of Crumbs to the Par-6 CRIB-PDZ Module Is Regulated by Cdc42. <i>Biochemistry</i> , <b>2016</b> , 55, 1455-61	3.2	20
104	Heterodimer formation of the myeloid zinc finger 1 SCAN domain and association with promyelocytic leukemia nuclear bodies. <i>Leukemia Research</i> , <b>2008</b> , 32, 1582-92	2.7	20
103	Macromolecular structure determination by NMR spectroscopy. <i>Methods of Biochemical Analysis</i> , <b>2003</b> , 44, 89-113		20
102	The aspartate-less receiver (ALR) domains: distribution, structure and function. <i>PLoS Pathogens</i> , <b>2015</b> , 11, e1004795	7.6	19

101	Modulation of the CXC chemokine receptor 4 agonist activity of ubiquitin through C-terminal protein modification. <i>Biochemistry</i> , <b>2013</b> , 52, 4184-92	3.2	19
100	Structural analysis of a novel small molecule ligand bound to the CXCL12 chemokine. <i>Journal of Medicinal Chemistry</i> , <b>2014</b> , 57, 9693-9	8.3	18
99	Tyrosine residues mediate fibril formation in a dynamic light chain dimer interface. <i>Journal of Biological Chemistry</i> , <b>2012</b> , 287, 27997-8006	5.4	18
98	Practical model fitting approaches to the direct extraction of NMR parameters simultaneously from all dimensions of multidimensional NMR spectra. <i>Journal of Biomolecular NMR</i> , <b>1998</b> , 12, 277-97	3	18
97	Fragment-based optimization of small molecule CXCL12 inhibitors for antagonizing the CXCL12/CXCR4 interaction. <i>Current Topics in Medicinal Chemistry</i> , <b>2012</b> , 12, 2727-40	3	18
96	A negative-feedback loop maintains optimal chemokine concentrations for directional cell migration. <i>Nature Cell Biology</i> , <b>2020</b> , 22, 266-273	23.4	17
95	Structure of the SCAN domain from the tumor suppressor protein MZF1. <i>Journal of Molecular Biology</i> , <b>2006</b> , 363, 137-47	6.5	17
94	Evolution of fold switching in a metamorphic protein. <i>Science</i> , <b>2021</b> , 371, 86-90	33.3	17
93	A conformational switch in the CRIB-PDZ module of Par-6. <i>Structure</i> , <b>2011</b> , 19, 1711-22	5.2	16
92	Production of Recombinant Chemokines and Validation of Refolding. <i>Methods in Enzymology</i> , <b>2016</b> , 570, 539-65	1.7	16
91	Structure-function analysis of CCL28 in the development of post-viral asthma. <i>Journal of Biological Chemistry</i> , <b>2015</b> , 290, 4528-36	5.4	15
90	Identification and functional characterization of arginine vasopressin receptor 1A : atypical chemokine receptor 3 heteromers in vascular smooth muscle. <i>Open Biology</i> , <b>2018</b> , 8,	7	15
89	Examination of Glycosaminoglycan Binding Sites on the XCL1 Dimer. <i>Biochemistry</i> , <b>2016</b> , 55, 1214-25	3.2	14
88	Electrostatic optimization of the conformational energy landscape in a metamorphic protein. <i>Biochemistry</i> , <b>2012</b> , 51, 9067-75	3.2	14
87	Assignment of <sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N signals of reduced <i>Clostridium pasteurianum</i> rubredoxin: oxidation state-dependent changes in chemical shifts and relaxation rates. <i>Journal of Biomolecular NMR</i> , <b>1997</b> , 10, 411-2	3	14
86	The solution structure of ZNF593 from <i>Homo sapiens</i> reveals a zinc finger in a predominantly unstructured protein. <i>Protein Science</i> , <b>2008</b> , 17, 571-6	6.3	14
85	Crystal structure of At2g03760, a putative steroid sulfotransferase from <i>Arabidopsis thaliana</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , <b>2004</b> , 57, 854-7	4.2	14
84	A Requirement for Metamorphic Interconversion in the Antimicrobial Activity of Chemokine XCL1. <i>Biochemistry</i> , <b>2016</b> , 55, 3784-93	3.2	14



83	Tyrosine-sulfated V2 peptides inhibit HIV-1 infection via coreceptor mimicry. <i>EBioMedicine</i> , <b>2016</b> , 10, 45-54	8.8	13
82	Oxidation of histidine residues in copper-zinc superoxide dismutase by bicarbonate-stimulated peroxidase and thiol oxidase activities: pulse EPR and NMR studies. <i>Biochemistry</i> , <b>2010</b> , 49, 10616-22	3.2	13
81	An NMR structural study of nickel-substituted rubredoxin. <i>Journal of Biological Inorganic Chemistry</i> , <b>2010</b> , 15, 409-20	3.7	13
80	Assignment of <sup>1</sup> H, <sup>13</sup> C, and <sup>15</sup> N signals of oxidized <i>Clostridium pasteurianum</i> rubredoxin. <i>Journal of Biomolecular NMR</i> , <b>1997</b> , 10, 409-10	3	13
79	Staphylococcal superantigens induce lymphotactin production by human CD4+ and CD8+ T cells. <i>Cytokine</i> , <b>2001</b> , 16, 73-8	4	13
78	NMR Structure of the C-Terminal Transmembrane Domain of the HDL Receptor, SR-BI, and a Functionally Relevant Leucine Zipper Motif. <i>Structure</i> , <b>2017</b> , 25, 446-457	5.2	12
77	Age-related increase of kynurenine enhances miR29b-1-5p to decrease both CXCL12 signaling and the epigenetic enzyme Hdac3 in bone marrow stromal cells. <i>Bone Reports</i> , <b>2020</b> , 12, 100270	2.6	12
76	Decoding the chemotactic signal. <i>Journal of Leukocyte Biology</i> , <b>2018</b> , 104, 359-374	6.5	12
75	CCR7 Sulfotyrosine Enhances CCL21 Binding. <i>International Journal of Molecular Sciences</i> , <b>2017</b> , 18,	6.3	12
74	Electron capture dissociation and drift tube ion mobility-mass spectrometry coupled with site directed mutations provide insights into the conformational diversity of a metamorphic protein. <i>Physical Chemistry Chemical Physics</i> , <b>2015</b> , 17, 10538-50	3.6	12
73	What doesn't kill you makes you stranger: Dipeptidyl peptidase-4 (CD26) proteolysis differentially modulates the activity of many peptide hormones and cytokines generating novel cryptic bioactive ligands. <i>Pharmacology &amp; Therapeutics</i> , <b>2019</b> , 198, 90-108	13.9	12
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