

Brian F Volkman

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.

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	Tumor Derived Extracellular Vesicles Drive T Cell Exhaustion in Tumor Microenvironment through Sphingosine Mediated Signaling and Impacting Immunotherapy Outcomes in Ovarian Cancer.. <i>Advanced Science</i> , 2022 , e2104452	13.6	0
207	The non-ELR CXC chemokine encoded by human cytomegalovirus UL146 genotype 5 contains a C-terminal hairpin and induces neutrophil migration as a selective CXCR2 agonist.. <i>PLoS Pathogens</i> , 2022 , 18, e1010355	7.6	0
206	Structural bioinformatics enhances the interpretation of somatic mutations in KDM6A found in human cancers. <i>Computational and Structural Biotechnology Journal</i> , 2022 , 20, 2200-2211	6.8	0
205	Design and discovery of metamorphic proteins.. <i>Current Opinion in Structural Biology</i> , 2022 , 74, 102380	8.1	0
204	Trisubstituted 1,3,5-Triazines: The First Ligands of the sY12-Binding Pocket on Chemokine CXCL12. <i>ACS Medicinal Chemistry Letters</i> , 2021 , 12, 1773-1782	4.3	1
203	Specific binding-induced modulation of the XCL1 metamorphic equilibrium. <i>Biopolymers</i> , 2021 , 112, e23402	4.0	0
202	Targeted biologic inhibition of both tumor cell-intrinsic and intercellular CLPTM1L/CRR9-mediated chemotherapeutic drug resistance. <i>Npj Precision Oncology</i> , 2021 , 5, 16	9.8	7
201	Targeting the CCR6/CCL20 Axis in Enteseal and Cutaneous Inflammation. <i>Arthritis and Rheumatology</i> , 2021 , 73, 2271-2281	9.5	4
200	Molecular mechanics and dynamic simulations of well-known Kabuki syndrome-associated KDM6A variants reveal putative mechanisms of dysfunction. <i>Orphanet Journal of Rare Diseases</i> , 2021 , 16, 66	4.2	3
199	Interactions between AMOT PPxY motifs and NEDD4L WW domains function in HIV-1 release. <i>Journal of Biological Chemistry</i> , 2021 , 297, 100975	5.4	2
198	The C-terminal peptide of CCL21 drastically augments CCL21 activity through the dendritic cell lymph node homing receptor CCR7 by interaction with the receptor N-terminus. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 6963-6978	10.3	2
197	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,	11.5	5
196	Age-associated changes in microRNAs affect the differentiation potential of human mesenchymal stem cells: Novel role of miR-29b-1-5p expression. <i>Bone</i> , 2021 , 153, 116154	4.7	2
195	Investigations on T cell transmigration in a human skin-on-chip (SoC) model. <i>Lab on A Chip</i> , 2021 , 21, 1527-1539	5.5	5
194	Evolution of fold switching in a metamorphic protein. <i>Science</i> , 2021 , 371, 86-90	33.3	17
193	Chemokine CCL28 Is a Potent Therapeutic Agent for Oropharyngeal Candidiasis. <i>Antimicrobial Agents and Chemotherapy</i> , 2020 , 64,	5.9	2
192	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> , 2020 , 12, 100270	2.6	12

191	Switchable Membrane Remodeling and Antifungal Defense by Metamorphic Chemokine XCL1. <i>ACS Infectious Diseases</i> , 2020 , 6, 1204-1213	5.5	5
190	Characterization of heteromeric complexes between chemokine (C-X-C motif) receptor 4 and β -adrenergic receptors utilizing intermolecular bioluminescence resonance energy transfer assays. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 528, 368-375	3.4	5
189	A negative-feedback loop maintains optimal chemokine concentrations for directional cell migration. <i>Nature Cell Biology</i> , 2020 , 22, 266-273	23.4	17
188	Structural Features of an Extended C-Terminal Tail Modulate the Function of the Chemokine CCL21. <i>Biochemistry</i> , 2020 , 59, 1338-1350	3.2	6
187	Comparative modeling and docking of chemokine-receptor interactions with Rosetta. <i>Biochemical and Biophysical Research Communications</i> , 2020 , 528, 389-397	3.4	1
186	Natural and engineered chemokine (C-X-C motif) receptor 4 agonists prevent acute respiratory distress syndrome after lung ischemia-reperfusion injury and hemorrhage. <i>Scientific Reports</i> , 2020 , 10, 11359	4.9	5
185	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	5.4	3
184	Dynamic control of plant water use using designed ABA receptor agonists. <i>Science</i> , 2019 , 366,	33.3	60
183	Structure-function guided modeling of chemokine-GPCR specificity for the chemokine XCL1 and its receptor XCR1. <i>Science Signaling</i> , 2019 , 12,	8.8	8
182	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 & Therapeutics</i> , 2019 , 198, 90-108	13.9	12
181	Solution NMR spectroscopy of GPCRs: Residue-specific labeling strategies with a focus on C-methyl methionine labeling of the atypical chemokine receptor ACKR3. <i>Methods in Cell Biology</i> , 2019 , 149, 259-288	1.8	5
180	Modeling the complete chemokine-receptor interaction. <i>Methods in Cell Biology</i> , 2019 , 149, 289-314	1.8	4
179	Asymmetrical ligand-induced cross-regulation of chemokine (C-X-C motif) receptor 4 by β -adrenergic receptors at the heteromeric receptor complex. <i>Scientific Reports</i> , 2018 , 8, 2730	4.9	7
178	Identification and functional characterization of arginine vasopressin receptor 1A : atypical chemokine receptor 3 heteromers in vascular smooth muscle. <i>Open Biology</i> , 2018 , 8,	7	15
177	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> , 2018 , 175, 1419-1438	8.6	30
176	Mutational analysis of CCL20 reveals flexibility of N-terminal amino acid composition and length. <i>Journal of Leukocyte Biology</i> , 2018 , 104, 423-434	6.5	5
175	Decoding the chemotactic signal. <i>Journal of Leukocyte Biology</i> , 2018 , 104, 359-374	6.5	12
174	Development of a Molecular Probe Targeting Mitochondrial Fission Protein Fis1. <i>FASEB Journal</i> , 2018 , 32, 530.17	0.9	

173	Development and Validation of 2D Difference Intensity Analysis for Chemical Library Screening by Protein-Detected NMR Spectroscopy. <i>ChemBioChem</i> , 2018 , 19, 448-458	3.8	3
172	Partial agonist activity of β -adrenergic receptor antagonists for chemokine (C-X-C motif) receptor 4 and atypical chemokine receptor 3. <i>PLoS ONE</i> , 2018 , 13, e0204041	3.7	5
171	Biased antagonism of CXCR4 avoids antagonist tolerance. <i>Science Signaling</i> , 2018 , 11,	8.8	27
170	Unfolding the Mysteries of Protein Metamorphosis. <i>ACS Chemical Biology</i> , 2018 , 13, 1438-1446	4.9	40
169	The Solution Structure of CCL28 Reveals Structural Lability that Does Not Constrain Antifungal Activity. <i>Journal of Molecular Biology</i> , 2018 , 430, 3266-3282	6.5	10
168	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	5.2	12
167	Functional and structural consequences of chemokine (C-X-C motif) receptor 4 activation with cognate and non-cognate agonists. <i>Molecular and Cellular Biochemistry</i> , 2017 , 434, 143-151	4.2	11
166	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	6.5	8
165	Structural basis for chemokine recognition by a G protein-coupled receptor and implications for receptor activation. <i>Science Signaling</i> , 2017 , 10,	8.8	56
164	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	4.9	35
163	Effects of cognate, non-cognate and synthetic CXCR4 and ACKR3 ligands on human lung endothelial cell barrier function. <i>PLoS ONE</i> , 2017 , 12, e0187949	3.7	11
162	β 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> , 2017 , 6,	6	21
161	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> , 2017 , 114, 12460-12465	11.5	35
160	Exploiting agonist biased signaling of chemokines to target cancer. <i>Molecular Carcinogenesis</i> , 2017 , 56, 804-813	5	11
159	CCR7 Sulfotyrosine Enhances CCL21 Binding. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	12
158	Differences in Sulfotyrosine Binding amongst CXCR1 and CXCR2 Chemokine Ligands. <i>International Journal of Molecular Sciences</i> , 2017 , 18,	6.3	4
157	Evolution of a Protein Interaction Domain Family by Tuning Conformational Flexibility. <i>Journal of the American Chemical Society</i> , 2016 , 138, 15150-15156	16.4	10
156	Tyrosine-sulfated V2 peptides inhibit HIV-1 infection via coreceptor mimicry. <i>EBioMedicine</i> , 2016 , 10, 45-54	8.8	13

155	New paradigms in chemokine receptor signal transduction: Moving beyond the two-site model. <i>Biochemical Pharmacology</i> , 2016 , 114, 53-68	6	66
154	Polysialylation controls dendritic cell trafficking by regulating chemokine recognition. <i>Science</i> , 2016 , 351, 186-90	33.3	97
153	Examination of Glycosaminoglycan Binding Sites on the XCL1 Dimer. <i>Biochemistry</i> , 2016 , 55, 1214-25	3.2	14
152	Binding of Crumbs to the Par-6 CRIB-PDZ Module Is Regulated by Cdc42. <i>Biochemistry</i> , 2016 , 55, 1455-61	3.2	20
151	The association and aggregation of the metamorphic chemokine lymphotactin with fondaparinux: from nm molecular complexes to μ m molecular assemblies. <i>Chemical Communications</i> , 2016 , 52, 394-7	5.8	3
150	The dependence of chemokine-glycosaminoglycan interactions on chemokine oligomerization. <i>Glycobiology</i> , 2016 , 26, 312-26	5.8	59
149	Evolution of an ancient protein function involved in organized multicellularity in animals. <i>ELife</i> , 2016 , 5, e10147	8.9	37
148	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> , 2016 , 17,	6.3	26
147	A Requirement for Metamorphic Interconversion in the Antimicrobial Activity of Chemokine XCL1. <i>Biochemistry</i> , 2016 , 55, 3784-93	3.2	14
146	Production of Recombinant Chemokines and Validation of Refolding. <i>Methods in Enzymology</i> , 2016 , 570, 539-65	1.7	16
145	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, 4342-51	8.3	24
144	Crystallographic Structure of Truncated CCL21 and the Putative Sulfotyrosine-Binding Site. <i>Biochemistry</i> , 2016 , 55, 5746-5753	3.2	6
143	Some (dis)assembly required: partial unfolding in the Par-6 allosteric switch. <i>Biophysical Reviews</i> , 2015 , 7, 183-190	3.7	1
142	Structure-function analysis of CCL28 in the development of post-viral asthma. <i>Journal of Biological Chemistry</i> , 2015 , 290, 4528-36	5.4	15
141	Interplay of Electrostatics and Hydrophobic Effects in the Metamorphic Protein Human Lymphotactin. <i>Journal of Physical Chemistry B</i> , 2015 , 119, 9547-58	3.4	1
140	The aspartate-less receiver (ALR) domains: distribution, structure and function. <i>PLoS Pathogens</i> , 2015 , 11, e1004795	7.6	19
139	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, 91-7	2	1
138	Expression platforms for producing eukaryotic proteins: a comparison of E. coli cell-based and wheat germ cell-free synthesis, affinity and solubility tags, and cloning strategies. <i>Journal of Structural and Functional Genomics</i> , 2015 , 16, 67-80		10

137	Heteromerization of chemokine (C-X-C motif) receptor 4 with α A/B-adrenergic receptors controls α -adrenergic receptor function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E1659-68	11.5	44
136	Pancreatic Cancer Cell Migration and Metastasis Is Regulated by Chemokine-Biased Agonism and Bioenergetic Signaling. <i>Cancer Research</i> , 2015 , 75, 3529-42	10.1	38
135	Engineering Metamorphic Chemokine Lymphotactin/XCL1 into the GAG-Binding, HIV-Inhibitory Dimer Conformation. <i>ACS Chemical Biology</i> , 2015 , 10, 2580-8	4.9	20
134	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	3	8
133	Structural and agonist properties of XCL2, the other member of the C-chemokine subfamily. <i>Cytokine</i> , 2015 , 71, 302-11	4	29
132	Cytokines and growth factors cross-link heparan sulfate. <i>Open Biology</i> , 2015 , 5,	7	39
131	Structural Determinants for the Selective Anti-HIV-1 Activity of the All- β -Alternative Conformer of XCL1. <i>Journal of Virology</i> , 2015 , 89, 9061-7	6.6	11
130	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> , 2015 , 17, 10538-50	3.6	12
129	Agrochemical control of plant water use using engineered abscisic acid receptors. <i>Nature</i> , 2015 , 520, 545-8	50.4	157
128	Dissecting the dynamic conformations of the metamorphic protein lymphotactin. <i>Journal of Physical Chemistry B</i> , 2014 , 118, 12348-59	3.4	28
127	Chemokines in colitis: microRNA control. <i>Gut</i> , 2014 , 63, 1202-4	19.2	5
126	CXC chemokine receptor 4 signaling upon co-activation with stromal cell-derived factor-1 and ubiquitin. <i>Cytokine</i> , 2014 , 65, 121-5	4	25
125	Combine and conquer: surfactants, solvents, and chaotropes for robust mass spectrometry based analyses of membrane proteins. <i>Analytical Chemistry</i> , 2014 , 86, 1551-9	7.8	42
124	P-D4 Inhibition of HIV-1 by the C-chemokine XCL1/Lymphotactin is dependent on high affinity binding to glycosaminoglycans (GAG). <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014 , 67, 88	3.1	1
123	P-D6 Structure-Function Relationships in the Second Variable Domain (V2) of HIV-1 gp120. <i>Journal of Acquired Immune Deficiency Syndromes (1999)</i> , 2014 , 67, 89	3.1	
122	Chemokine (C-X-C motif) receptor 4 and atypical chemokine receptor 3 regulate vascular β -adrenergic receptor function. <i>Molecular Medicine</i> , 2014 , 20, 435-47	6.2	29
121	Chemokine cooperativity is caused by competitive glycosaminoglycan binding. <i>Journal of Immunology</i> , 2014 , 192, 3908-3914	5.3	26
120	Structural analysis of a novel small molecule ligand bound to the CXCL12 chemokine. <i>Journal of Medicinal Chemistry</i> , 2014 , 57, 9693-9	8.3	18

119	Identification of the major ubiquitin-binding domain of the <i>Pseudomonas aeruginosa</i> ExoU A2 phospholipase. <i>Journal of Biological Chemistry</i> , 2013 , 288, 26741-52	5.4	23
118	Sulfopeptide probes of the CXCR4/CXCL12 interface reveal oligomer-specific contacts and chemokine allostery. <i>ACS Chemical Biology</i> , 2013 , 8, 1955-63	4.9	41
117	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> , 2013 , 288, 737-46	5.4	65
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> , 2013 , 425, 19-31	6.5	24
115	Modulation of the CXC chemokine receptor 4 agonist activity of ubiquitin through C-terminal protein modification. <i>Biochemistry</i> , 2013 , 52, 4184-92	3.2	19
114	Allosteric activation of the Par-6 PDZ via a partial unfolding transition. <i>Journal of the American Chemical Society</i> , 2013 , 135, 9377-83	16.4	7
113	The CD8-derived chemokine XCL1/lymphotactin is a conformation-dependent, broad-spectrum inhibitor of HIV-1. <i>PLoS Pathogens</i> , 2013 , 9, e1003852	7.6	24
112	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, 12132-7	11.5	196
111	NMR in the Analysis of Functional Chemokine Interactions and Drug Discovery. <i>Drug Discovery Today: Technologies</i> , 2012 , 9, e293-e299	7.1	2
110	Electrostatic optimization of the conformational energy landscape in a metamorphic protein. <i>Biochemistry</i> , 2012 , 51, 9067-75	3.2	14
109	E2-binding surface on Uba3 β grasp domain undergoes a conformational transition. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012 , 80, 2482-7	4.2	3
108	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> , 2012 , 109, 5517-22	11.5	123
107	Tyrosine residues mediate fibril formation in a dynamic light chain dimer interface. <i>Journal of Biological Chemistry</i> , 2012 , 287, 27997-8006	5.4	18
106	A locked, dimeric CXCL12 variant effectively inhibits pulmonary metastasis of CXCR4-expressing melanoma cells due to enhanced serum stability. <i>Molecular Cancer Therapeutics</i> , 2012 , 11, 2516-25	6.1	44
105	Tyrosine residues mediate fibril formation in a dynamic light chain dimer interface.. <i>Journal of Biological Chemistry</i> , 2012 , 287, 35541	5.4	78
104	Fragment-based optimization of small molecule CXCL12 inhibitors for antagonizing the CXCL12/CXCR4 interaction. <i>Current Topics in Medicinal Chemistry</i> , 2012 , 12, 2727-40	3	18
103	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> , 2011 , 108, 17655-60	11.5	151
102	Binding site identification and structure determination of protein-ligand complexes by NMR a semiautomated approach. <i>Methods in Enzymology</i> , 2011 , 493, 241-75	1.7	49

101	Residues within a lipid-associated segment of the PECAM-1 cytoplasmic domain are susceptible to inducible, sequential phosphorylation. <i>Blood</i> , 2011 , 117, 6012-23	2.2	36
100	A conformational switch in the CRIB-PDZ module of Par-6. <i>Structure</i> , 2011 , 19, 1711-22	5.2	16
99	Dynamic interchanging native states of lymphotactin examined by SNAPP-MS. <i>Journal of the American Society for Mass Spectrometry</i> , 2011 , 22, 399-407	3.5	8
98	Native-state interconversion of a metamorphic protein requires global unfolding. <i>Biochemistry</i> , 2011 , 50, 7077-9	3.2	33
97	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, 20838-43	11.5	74
96	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> , 2011 , 108, E973-8	11.5	25
95	Orphan macrodomain protein (human C6orf130) is an O-acyl-ADP-ribose deacylase: solution structure and catalytic properties. <i>Journal of Biological Chemistry</i> , 2011 , 286, 35955-35965	5.4	59
94	The CXC chemokine receptor 4 ligands ubiquitin and stromal cell-derived factor-1 function through distinct receptor interactions. <i>Journal of Biological Chemistry</i> , 2011 , 286, 33466-77	5.4	71
93	Sulfotyrosine recognition as marker for druggable sites in the extracellular space. <i>International Journal of Molecular Sciences</i> , 2011 , 12, 3740-56	6.3	11
92	Structural basis for selective activation of ABA receptors. <i>Nature Structural and Molecular Biology</i> , 2010 , 17, 1109-13	17.6	88
91	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> , 2010 , 107, 12493-8	11.5	35
90	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, 7242-3	16.4	58
89	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> , 2010 , 49, 10616-22	3.2	13
88	Distal interactions within the par3-VE-cadherin complex. <i>Biochemistry</i> , 2010 , 49, 951-7	3.2	45
87	An NMR structural study of nickel-substituted rubredoxin. <i>Journal of Biological Inorganic Chemistry</i> , 2010 , 15, 409-20	3.7	13
86	Structural and functional insights into core ABA signaling. <i>Current Opinion in Plant Biology</i> , 2010 , 13, 495-502	9.9	178
85	A single mutation promotes amyloidogenicity through a highly promiscuous dimer interface. <i>Structure</i> , 2010 , 18, 563-70	5.2	35
84	Rapid, robotic, small-scale protein production for NMR screening and structure determination. <i>Protein Science</i> , 2010 , 19, 570-8	6.3	5

83	Why not high-throughput eukaryotic protein structures?. <i>FASEB Journal</i> , 2010 , 24, lb229	0.9	
82	Diversity of polyproline recognition by EVH1 domains. <i>Frontiers in Bioscience - Landmark</i> , 2009 , 14, 833-468	34	
81	Chapter 3. Lymphotactin structural dynamics. <i>Methods in Enzymology</i> , 2009 , 461, 51-70	1.7	23
80	The Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , 2009 , 10, 165-79		25
79	Structures of two Arabidopsis thaliana major latex proteins represent novel helix-grip folds. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009 , 76, 237-43	4.2	52
78	Monomeric structure of the cardioprotective chemokine SDF-1/CXCL12. <i>Protein Science</i> , 2009 , 18, 1359-69	61	
77	A gate-latch-lock mechanism for hormone signalling by abscisic acid receptors. <i>Nature</i> , 2009 , 462, 602-8	50.4	498
76	Abscisic acid inhibits type 2C protein phosphatases via the PYR/PYL family of START proteins. <i>Science</i> , 2009 , 324, 1068-71	33.3	1782
75	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, 5057-62	11.5	209
74	Sequential tyrosine sulfation of CXCR4 by tyrosylprotein sulfotransferases. <i>Biochemistry</i> , 2008 , 47, 11253-62	62	
73	Altered dimer interface decreases stability in an amyloidogenic protein. <i>Journal of Biological Chemistry</i> , 2008 , 283, 15853-60	5.4	87
72	Structural basis of CXCR4 sulfotyrosine recognition by the chemokine SDF-1/CXCL12. <i>Science Signaling</i> , 2008 , 1, ra4	8.8	215
71	Solution structure of At3g28950 from Arabidopsis thaliana. <i>Proteins: Structure, Function and Bioinformatics</i> , 2008 , 71, 546-51	4.2	2
70	Heterodimer formation of the myeloid zinc finger 1 SCAN domain and association with promyelocytic leukemia nuclear bodies. <i>Leukemia Research</i> , 2008 , 32, 1582-92	2.7	20
69	The solution structure of ZNF593 from Homo sapiens reveals a zinc finger in a predominantly unstructured protein. <i>Protein Science</i> , 2008 , 17, 571-6	6.3	14
68	An engineered second disulfide bond restricts lymphotactin/XCL1 to a chemokine-like conformation with XCR1 agonist activity. <i>Biochemistry</i> , 2007 , 46, 2564-73	3.2	42
67	Solution structure of a membrane-anchored ubiquitin-fold (MUB) protein from Homo sapiens. <i>Protein Science</i> , 2007 , 16, 1479-84	6.3	6
66	Structures of proteins of biomedical interest from the Center for Eukaryotic Structural Genomics. <i>Journal of Structural and Functional Genomics</i> , 2007 , 8, 73-84	9	

65	Multiple WASP-interacting protein recognition motifs are required for a functional interaction with N-WASP. <i>Journal of Biological Chemistry</i> , 2007 , 282, 8446-53	5.4	42
64	On-column refolding of recombinant chemokines for NMR studies and biological assays. <i>Protein Expression and Purification</i> , 2007 , 52, 202-9	2	27
63	The first structure from the SOUL/HBP family of heme-binding proteins, murine P22HBP. <i>Journal of Biological Chemistry</i> , 2006 , 281, 31553-61	5.4	25
62	Gamma-glutamylcysteine synthetase-glutathione synthetase: domain structure and identification of residues important in substrate and glutathione binding. <i>Biochemistry</i> , 2006 , 45, 10461-73	3.2	22
61	Recognition of a CXCR4 sulfotyrosine by the chemokine stromal cell-derived factor-1alpha (SDF-1alpha/CXCL12). <i>Journal of Molecular Biology</i> , 2006 , 359, 1400-9	6.5	99
60	Structure of the SCAN domain from the tumor suppressor protein MZF1. <i>Journal of Molecular Biology</i> , 2006 , 363, 137-47	6.5	17
59	Structural determinants involved in the regulation of CXCL14/BRAK expression by the 26 S proteasome. <i>Journal of Molecular Biology</i> , 2006 , 363, 813-22	6.5	28
58	Solution structure of Arabidopsis thaliana protein At5g39720.1, a member of the AIG2-like protein family. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006 , 62, 490-3		6
57	Structural Determination of a SCAN Domain Homodimer and Heterodimer. <i>FASEB Journal</i> , 2006 , 20, A950.9		
56	The first structure from the SOUL/HBP family of hemebinding proteins, murine P22HBP. VOLUME 281 (2006) PAGES 31553-31561. <i>Journal of Biological Chemistry</i> , 2006 , 281, 38966	5.4	2
55	The First Structure from the SOUL/HBP Family of Heme-binding Proteins, Murine P22HBP. <i>Journal of Biological Chemistry</i> , 2006 , 281, 31553-31561	5.4	7
54	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, 1071-81	6.3	143
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