Wim F Vranken

List of Publications by Year
in descending order

104	10,199	87723	37111
papers	citations	38 h-index	96 g-index

119	119	119	13831
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	The CCPN data model for NMR spectroscopy: Development of a software pipeline. Proteins: Structure, Function and Bioinformatics, 2005, 59, 687-696.	1.5	2,805
2	ACPYPE - AnteChamber PYthon Parser interfacE. BMC Research Notes, 2012, 5, 367.	0.6	1,864
3	RECOORD: A recalculated coordinate database of 500+ proteins from the PDB using restraints from the BioMagResBank. Proteins: Structure, Function and Bioinformatics, 2005, 59, 662-672.	1.5	323
4	Determination of Secondary Structure Populations in Disordered States of Proteins Using Nuclear Magnetic Resonance Chemical Shifts. Biochemistry, 2012, 51, 2224-2231.	1.2	316
5	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	6.5	242
6	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	6.5	190
7	MobiDB: intrinsically disordered proteins in 2021. Nucleic Acids Research, 2021, 49, D361-D367.	6.5	183
8	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	2.5	170
9	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2012, 40, D445-D452.	6.5	166
10	Determination of the three-dimensional solution structure of Raphanus sativus Antifungal Protein 1 by 1 H NMR 1 1Edited by P. E. Wright. Journal of Molecular Biology, 1998, 279, 257-270.	2.0	153
11	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-1570.	1.6	151
12	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	6.5	141
13	From protein sequence to dynamics and disorder with DynaMine. Nature Communications, 2013, 4, 2741.	5.8	139
14	Remediation of the protein data bank archive. Nucleic Acids Research, 2007, 36, D426-D433.	6.5	136
15	The DynaMine webserver: predicting protein dynamics from sequence. Nucleic Acids Research, 2014, 42, W264-W270.	6.5	125
16	EUROCarbDB: An open-access platform for glycoinformatics. Glycobiology, 2011, 21, 493-502.	1.3	116
17	DEOGEN2: prediction and interactive visualization of single amino acid variant deleteriousness in human proteins. Nucleic Acids Research, 2017, 45, W201-W206.	6.5	114
18	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2010, 38, D308-D317.	6.5	108

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19	CING: an integrated residue-based structure validation program suite. Journal of Biomolecular NMR, 2012, 54, 267-283.	1.6	106
20	E-MSD: the European Bioinformatics Institute Macromolecular Structure Database. Nucleic Acids Research, 2003, 31, 458-462.	6.5	93
21	DRESS: a database of REfined solution NMR structures. Proteins: Structure, Function and Bioinformatics, 2004, 55, 483-486.	1.5	91
22	E-MSD: an integrated data resource for bioinformatics. Nucleic Acids Research, 2004, 32, 211D-216.	6.5	90
23	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	6.5	87
24	Accurate Random Coil Chemical Shifts from an Analysis of Loop Regions in Native States of Proteins. Journal of the American Chemical Society, 2009, 131, 16332-16333.	6.6	85
25	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	9.0	80
26	Megabodies expand the nanobody toolkit for protein structure determination by single-particle cryo-EM. Nature Methods, 2021, 18, 60-68.	9.0	79
27	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	1.6	75
28	Seeing the trees through the forest: sequence-based homo- and heteromeric protein-protein interaction sites prediction using random forest. Bioinformatics, 2017, 33, 1479-1487.	1.8	66
29	Structure-based prediction of methyl chemical shifts in proteins. Journal of Biomolecular NMR, 2011, 50, 331-346.	1.6	65
30	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2011, 39, D402-D410.	6.5	64
31	The three-dimensional solution structure ofAesculus hippocastanum antimicrobial protein 1 determined by1H nuclear magnetic resonance. , 1999, 37, 388-403.		62
32	Small-Angle X-Ray Scattering- and Nuclear Magnetic Resonance-Derived Conformational Ensemble of the Highly Flexible Antitoxin PaaA2. Structure, 2014, 22, 854-865.	1.6	61
33	AmyPro: a database of proteins with validated amyloidogenic regions. Nucleic Acids Research, 2018, 46, D387-D392.	6.5	59
34	The complete Consensus V3 loop peptide of the envelope protein gp120 of HIV-1 shows pronounced helical character in solution. FEBS Letters, 1995, 374, 117-121.	1.3	56
35	BioMagResBank databases DOCR and FRED containing converted and filtered sets of experimental NMR restraints and coordinates from over 500 protein PDB structures. Journal of Biomolecular NMR, 2005, 32, 1-12.	1.6	50
36	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	6.5	46

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37	Computational identification of prion-like RNA-binding proteins that form liquid phase-separated condensates. Bioinformatics, 2019, 35, 4617-4623.	1.8	45
38	Study of the Structural and Dynamic Effects in the FimH Adhesin upon Î±-<scp>d</scp>-Heptyl Mannose Binding. Journal of Medicinal Chemistry, 2014, 57, 1416-1427.	2.9	43
39	A framework for scientific data modeling and automated software development. Bioinformatics, 2005, 21, 1678-1684.	1.8	42
40	Solution Structure of a Llama Single-Domain Antibody with Hydrophobic Residues Typical of the VH/VL Interface. Biochemistry, 2002, 41, 8570-8579.	1.2	41
41	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. Nature Structural and Molecular Biology, 2015, 22, 433-434.	3.6	40
42	Computational resources for identifying and describing proteins driving liquidâ€“liquid phase separation. Briefings in Bioinformatics, 2021, 22, .	3.2	40
43	Exploring the Sequence-based Prediction of Folding Initiation Sites in Proteins. Scientific Reports, 2017, 7, 8826.	1.6	39
44	Conformational Features of a Synthetic Cyclic Peptide Corresponding to the Complete V3 Loop of the RF HIV-1 Strain in Water and Water/Trifluoroethanol Solutions. FEBS Journal, 1996, 236, 100-108.	0.2	38
45	E-MSD: improving data deposition and structure quality. Nucleic Acids Research, 2006, 34, D287-D290.	6.5	38
46	Computational approaches for inferring the functions of intrinsically disordered proteins. Frontiers in Molecular Biosciences, 2015, 2, 45.	1.6	37
47	Design and Solution Structure of a Well-Folded Stack of Two Î²-Hairpins Based on the Amino-Terminal Fragment of Human Granulin Aâ€. Biochemistry, 2000, 39, 2878-2886.	1.2	34
48	NRG-CING: integrated validation reports of remediated experimental biomolecular NMR data and coordinates in wwPDB. Nucleic Acids Research, 2012, 40, D519-D524.	6.5	34
49	Multilevel biological characterization of exomic variants at the protein level significantly improves the identification of their deleterious effects. Bioinformatics, 2016, 32, 1797-1804.	1.8	32
50	Validation of archived chemical shifts through atomic coordinates. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2482-2489.	1.5	31
51	Solution Structure and Backbone Dynamics of the Functional Cytoplasmic Subdomain of Human Ephrin B2, a Cell-Surface Ligand with Bidirectional Signaling Propertiesâ€. Biochemistry, 2002, 41, 10942-10949.	1.2	28
52	Start2Fold: a database of hydrogen/deuterium exchange data on protein folding and stability. Nucleic Acids Research, 2016, 44, D429-D434.	6.5	28
53	Design of a data model for developing laboratory information management and analysis systems for protein production. Proteins: Structure, Function and Bioinformatics, 2004, 58, 278-284.	1.5	27
54	The second round of Critical Assessment of Automated Structure Determination of Proteins by NMR: CASD-NMR-2013. Journal of Biomolecular NMR, 2015, 62, 413-424.	1.6	27

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55	The NMR restraints grid at BMRB for 5,266 protein and nucleic acid PDB entries. Journal of Biomolecular NMR, 2009, 45, 389-396.	1.6	26
56	Relationship between chemical shift value and accessible surface area for all amino acid atoms. BMC Structural Biology, 2009, 9, 20.	2.3	26
57	Improving 3D structure prediction from chemical shift data. Journal of Biomolecular NMR, 2013, 57, 27-35.	1.6	25
58	Structural Basis of the Subcellular Topology Landscape of Escherichia coli. Frontiers in Microbiology, 2019, 10, 1670.	1.5	25
59	Conformational model for the consensus V3 loop of the envelope protein gp120 of HIV-1 in a 20% trifluoroethanol/water solution. FEBS Journal, 2001, 268, 2620-2628.	0.2	23
60	Bayesian estimation of NMR restraint potential and weight: A validation on a representative set of protein structures. Proteins: Structure, Function and Bioinformatics, 2011, 79, 1525-1537.	1.5	23
61	Early Folding Events, Local Interactions, and Conservation of Protein Backbone Rigidity. Biophysical Journal, 2016, 110, 572-583.	0.2	23
62	RINspector: a Cytoscape app for centrality analyses and DynaMine flexibility prediction. Bioinformatics, 2018, 34, 294-296.	1.8	23
63	Prediction of Disordered Regions in Proteins with Recurrent Neural Networks and Protein Dynamics. Journal of Molecular Biology, 2022, 434, 167579.	2.0	22
64	Conformation of a Cdc42/Rac Interactive Binding Peptide in Complex with Cdc42 and Analysis of the Binding Interfaceâ€. Biochemistry, 1999, 38, 5968-5975.	1.2	21
65	A 30-residue fragment of the carp granulin-1 protein folds into a stack of two Î²-hairpins similar to that found in the native protein. Chemical Biology and Drug Design, 1999, 53, 590-597.	1.2	20
66	Using Sideâ€€Chain Aromatic Proton Chemical Shifts for a Quantitative Analysis of Protein Structures. Angewandte Chemie - International Edition, 2011, 50, 9620-9623.	7.2	20
67	Observation selection bias in contact prediction and its implications for structural bioinformatics. Scientific Reports, 2016, 6, 36679.	1.6	20
68	Accurate prediction of protein beta-aggregation with generalized statistical potentials. Bioinformatics, 2020, 36, 2076-2081.	1.8	20
69	SPINE bioinformatics and data-management aspects of high-throughput structural biology. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1184-1195.	2.5	19
70	Exploring the limitations of biophysical propensity scales coupled with machine learning for protein sequence analysis. Scientific Reports, 2019, 9, 16932.	1.6	19
71	Scop3P: A Comprehensive Resource of Human Phosphosites within Their Full Context. Journal of Proteome Research, 2020, 19, 3478-3486.	1.8	19
72	The three-dimensional solution structure of Aesculus hippocastanum antimicrobial protein 1 determined by 1H nuclear magnetic resonance. Proteins: Structure, Function and Bioinformatics, 1999, 37, 388-403.	1.5	18

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73	A nomenclature and data model to describe NMR experiments. Journal of Biomolecular NMR, 2006, 36, 147-155.	1.6	17
74	COCO: A simple tool to enrich the representation of conformational variability in NMR structures. Proteins: Structure, Function and Bioinformatics, 2009, 75, 206-216.	1.5	17
75	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. Biophysical Journal, 2020, 118, 2952-2965.	0.2	17
76	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping. Bioinformatics, 2018, 34, 3118-3125.	1.8	13
77	Solution structures of a 30-residue amino-terminal domain of the carp granulin-1 protein and its amino-terminally truncated 3-30 subfragment: Implications for the conformational stability of the stack of two Î²-hairpins. Proteins: Structure, Function and Bioinformatics, 2002, 47, 14-24.	1.5	12
78	NMR structure validation in relation to dynamics and structure determination. Progress in Nuclear Magnetic Resonance Spectroscopy, 2014, 82, 27-38.	3.9	12
79	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	0.8	12
80	An Evolutionary View on Disulfide Bond Connectivities Prediction Using Phylogenetic Trees and a Simple Cysteine Mutation Model. PLoS ONE, 2015, 10, e0131792.	1.1	11
81	A global analysis of NMR distance constraints from the PDB. Journal of Biomolecular NMR, 2007, 39, 303-314.	1.6	10
82	Clustering-based model of cysteine co-evolution improves disulfide bond connectivity prediction and reduces homologous sequence requirements. Bioinformatics, 2015, 31, 1219-1225.	1.8	10
83	An NMR-based identification of peptide fragments mimicking the interactions of the cathepsin B propeptide. FEBS Letters, 1998, 429, 9-16.	1.3	9
84	b2bTools: online predictions for protein biophysical features and their conservation. Nucleic Acids Research, 2021, 49, W52-W59.	6.5	9
85	SVM-dependent pairwise HMM: an application to protein pairwise alignments. Bioinformatics, 2017, 33, 3902-3908.	1.8	8
86	Straightforward and complete deposition of NMR data to the PDBe. Journal of Biomolecular NMR, 2010, 48, 85-92.	1.6	7
87	Large-scale in-silico statistical mutagenesis analysis sheds light on the deleteriousness landscape of the human proteome. Scientific Reports, 2018, 8, 16980.	1.6	7
88	Protein Structure Validation Using Side-Chain Chemical Shifts. Journal of Physical Chemistry B, 2012, 116, 4754-4759.	1.2	5
89	Auto-encoding NMR chemical shifts from their native vector space to a residue-level biophysical index. Nature Communications, 2019, 10, 2511.	5.8	5
90	Interpreting a black box predictor to gain insights into early folding mechanisms. Computational and Structural Biotechnology Journal, 2021, 19, 4919-4930.	1.9	5

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91	NMR-Based Modeling and Refinement of Protein 3D Structures. Methods in Molecular Biology, 2015, 1215, 351-380.	0.4	5
92	Massively parallel interrogation of protein fragment secretability using SECRiFY reveals features influencing secretory system transit. Nature Communications, 2021, 12, 6414.	5.8	5
93	Analysis of the structural quality of the CASD-NMR 2013 entries. Journal of Biomolecular NMR, 2015, 62, 527-540.	1.6	4
94	Investigating the Molecular Mechanisms Behind Uncharacterized Cysteine Losses from Prediction of Their Oxidation State. Human Mutation, 2017, 38, 86-94.	1.1	4
95	Conformational Features of a Synthetic Cyclic Peptide Corresponding to the Complete V3 Loop of the ELI HIV-1 Strain in Water. Collection of Czechoslovak Chemical Communications, 1996, 61, 742-750.	1.0	4
96	Solution structures of a 30-residue amino-terminal domain of the carp granulin-1 protein and its amino-terminally truncated 3-30 subfragment: implications for the conformational stability of the stack of two beta-hairpins. Proteins: Structure, Function and Bioinformatics, 2002, 47, 14-24.	1.5	4
97	Lexicon Visualization Library and JavaScript for Scientific Data Visualization. Computing in Science and Engineering, 2018, 20, 50-65.	1.2	3
98	Pescador: the PEptides in Solution ConformAtion Database: Online Resource. Journal of Biomolecular NMR, 2002, 23, 85-102.	1.6	2
99	MEMOPS: Data modelling and automatic code generation. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	2
100	MutaFrameâ€"an interpretative visualization framework for deleteriousness prediction of missense variants in the human exome. Bioinformatics, 2021, 38, 265-266.	1.8	2
101	MEMOPS: data modelling and automatic code generation. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	2
102	ShiftCrypt: a web server to understand and biophysically align proteins through their NMR chemical shift values. Nucleic Acids Research, 2020, 48, W36-W40.	6.5	1
103	Online biophysical predictions for SARS-CoV-2 proteins. BMC Molecular and Cell Biology, 2021, 22, 23.	1.0	1
104	Solution structures of a 30-residue amino-terminal domain of the carp granulin-1 protein and its amino-terminally truncated 3-30 subfragment: Implications for the conformational stability of the stack of two Î²-hairpins. , 2002, 47, 14.		1