Wim F Vranken

List of Publications by Year
in descending order

104 papers	10,199 citations	100601 38 h-index	42259 96 g-index
119 all docs	119 docs citations	119 times ranked	15288 citing authors

#	Article	IF	Citations
1	PDBe-KB: collaboratively defining the biological context of structural data. Nucleic Acids Research, 2022, 50, D534-D542.	6.5	46
2	Prediction of Disordered Regions in Proteins with Recurrent Neural Networks and Protein Dynamics. Journal of Molecular Biology, 2022, 434, 167579.	2.0	22
3	MobiDB: intrinsically disordered proteins in 2021. Nucleic Acids Research, 2021, 49, D361-D367.	6.5	183
4	Interpreting a black box predictor to gain insights into early folding mechanisms. Computational and Structural Biotechnology Journal, 2021, 19, 4919-4930.	1.9	5
5	Computational resources for identifying and describing proteins driving liquidâ€“liquid phase separation. Briefings in Bioinformatics, 2021, 22, .	3.2	40
6	Online biophysical predictions for SARS-CoV-2 proteins. BMC Molecular and Cell Biology, 2021, 22, 23.	1.0	1
7	b2bTools: online predictions for protein biophysical features and their conservation. Nucleic Acids Research, 2021, 49, W52-W59.	6.5	9
8	MutaFrameâ€”an interpretative visualization framework for deleteriousness prediction of missense variants in the human exome. Bioinformatics, 2021, 38, 265-266.	1.8	2
9	Megabodies expand the nanobody toolkit for protein structure determination by single-particle cryo-EM. Nature Methods, 2021, 18, 60-68.	9.0	79
10	Massively parallel interrogation of protein fragment secretability using SECRiFY reveals features influencing secretory system transit. Nature Communications, 2021, 12, 6414.	5.8	5
11	DisProt: intrinsic protein disorder annotation in 2020. Nucleic Acids Research, 2020, 48, D269-D276.	6.5	141
12	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	6.5	87
13	Accurate prediction of protein beta-aggregation with generalized statistical potentials. Bioinformatics, 2020, 36, 2076-2081.	1.8	20
14	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
15	Scop3P: A Comprehensive Resource of Human Phosphosites within Their Full Context. Journal of Proteome Research, 2020, 19, 3478-3486.	1.8	19
16	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. Biophysical Journal, 2020, 118, 2952-2965.	0.2	17
17	Structural Basis of the Subcellular Topology Landscape of Escherichia coli. Frontiers in Microbiology, 2019, 10, 1670.	1.5	25
18	Auto-encoding NMR chemical shifts from their native vector space to a residue-level biophysical index. Nature Communications, 2019, 10, 2511.	5.8	5

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19	Computational identification of prion-like RNA-binding proteins that form liquid phase-separated condensates. Bioinformatics, 2019, 35, 4617-4623.	1.8	45
20	Exploring the limitations of biophysical propensity scales coupled with machine learning for protein sequence analysis. Scientific Reports, 2019, 9, 16932.	1.6	19
21	An intrinsically disordered proteins community for ELIXIR. F1000Research, 2019, 8, 1753.	0.8	12
22	Lexicon Visualization Library and JavaScript for Scientific Data Visualization. Computing in Science and Engineering, 2018, 20, 50-65.	1.2	3
23	RINspector: a Cytoscape app for centrality analyses and DynaMine flexibility prediction. Bioinformatics, 2018, 34, 294-296.	1.8	23
24	AmyPro: a database of proteins with validated amyloidogenic regions. Nucleic Acids Research, 2018, 46, D387-D392.	6.5	59
25	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
26	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping. Bioinformatics, 2018, 34, 3118-3125.	1.8	13
27	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. Nucleic Acids Research, 2018, 46, D471-D476.	6.5	190
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	DisProt 7.0: a major update of the database of disordered proteins. Nucleic Acids Research, 2017, 45, D219-D227.	6.5	242
30	Exploring the Sequence-based Prediction of Folding Initiation Sites in Proteins. Scientific Reports, 2017, 7, 8826.	1.6	39
31	SVM-dependent pairwise HMM: an application to protein pairwise alignments. Bioinformatics, 2017, 33, 3902-3908.	1.8	8
32	DEOGEN2: prediction and interactive visualization of single amino acid variant deleteriousness in human proteins. Nucleic Acids Research, 2017, 45, W201-W206.	6.5	114
33	Investigating the Molecular Mechanisms Behind Uncharacterized Cysteine Losses from Prediction of Their Oxidation State. Human Mutation, 2017, 38, 86-94.	1.1	4
34	Start2Fold: a database of hydrogen/deuterium exchange data on protein folding and stability. Nucleic Acids Research, 2016, 44, D429-D434.	6.5	28
35	Observation selection bias in contact prediction and its implications for structural bioinformatics. Scientific Reports, 2016, 6, 36679.	1.6	20
36	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

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37	Early Folding Events, Local Interactions, and Conservation of Protein Backbone Rigidity. Biophysical Journal, 2016, 110, 572-583.	0.2	23
38	Computational approaches for inferring the functions of intrinsically disordered proteins. Frontiers in Molecular Biosciences, 2015, 2, 45.	1.6	37
39	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
40	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
41	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
42	Analysis of the structural quality of the CASD-NMR 2013 entries. Journal of Biomolecular NMR, 2015, 62, 527-540.	1.6	4
43	NMR-Based Modeling and Refinement of Protein 3D Structures. Methods in Molecular Biology, 2015, 1215, 351-380.	0.4	5
44	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
45	The DynaMine webserver: predicting protein dynamics from sequence. Nucleic Acids Research, 2014, 42, W264-W270.	6.5	125
46	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
47	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
48	NMR structure validation in relation to dynamics and structure determination. Progress in Nuclear Magnetic Resonance Spectroscopy, 2014, 82, 27-38.	3.9	12
49	Improving 3D structure prediction from chemical shift data. Journal of Biomolecular NMR, 2013, 57, 27-35.	1.6	25
50	From protein sequence to dynamics and disorder with DynaMine. Nature Communications, 2013, 4, 2741.	5.8	139
51	Recommendations of the wwPDB NMR Validation Task Force. Structure, 2013, 21, 1563-1570.	1.6	151
52	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
53	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2012, 40, D445-D452.	6.5	166
54	Determination of Secondary Structure Populations in Disordered States of Proteins Using Nuclear Magnetic Resonance Chemical Shifts. Biochemistry, 2012, 51, 2224-2231.	1.2	316

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55	WeNMR: Structural Biology on the Grid. Journal of Grid Computing, 2012, 10, 743-767.	2.5	170
56	CING: an integrated residue-based structure validation program suite. Journal of Biomolecular NMR, 2012, 54, 267-283.	1.6	106
57	Protein Structure Validation Using Side-Chain Chemical Shifts. Journal of Physical Chemistry B, 2012, 116, 4754-4759.	1.2	5
58	ACPYPE - AnteChamber PYthon Parser interfacE. BMC Research Notes, 2012, 5, 367.	0.6	1,864
59	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. Structure, 2012, 20, 227-236.	1.6	75
60	Structure-based prediction of methyl chemical shifts in proteins. Journal of Biomolecular NMR, 2011, 50, 331-346.	1.6	65
61	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
62	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
63	EUROCarbDB: An open-access platform for glycoinformatics. Glycobiology, 2011, 21, 493-502.	1.3	116
64	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2011, 39, D402-D410.	6.5	64
65	MEMOPS: Data modelling and automatic code generation. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	2
66	Straightforward and complete deposition of NMR data to the PDBe. Journal of Biomolecular NMR, 2010, 48, 85-92.	1.6	7
67	Validation of archived chemical shifts through atomic coordinates. Proteins: Structure, Function and Bioinformatics, 2010, 78, 2482-2489.	1.5	31
68	PDBe: Protein Data Bank in Europe. Nucleic Acids Research, 2010, 38, D308-D317.	6.5	108
69	MEMOPS: data modelling and automatic code generation. Journal of Integrative Bioinformatics, 2010, 7, .	1.0	2
70	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
71	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
72	Relationship between chemical shift value and accessible surface area for all amino acid atoms. BMC Structural Biology, 2009, 9, 20.	2.3	26

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73	CASD-NMR: critical assessment of automated structure determination by NMR. Nature Methods, 2009, 6, 625-626.	9.0	80
74	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
75	Remediation of the protein data bank archive. Nucleic Acids Research, 2007, 36, D426-D433.	6.5	136
76	A global analysis of NMR distance constraints from the PDB. Journal of Biomolecular NMR, 2007, 39, 303-314.	1.6	10
77	SPINE bioinformatics and data-management aspects of high-throughput structural biology. Acta Crystallographica Section D: Biological Crystallography, 2006, 62, 1184-1195.	2.5	19
78	A nomenclature and data model to describe NMR experiments. Journal of Biomolecular NMR, 2006, 36, 147-155.	1.6	17
79	E-MSD: improving data deposition and structure quality. Nucleic Acids Research, 2006, 34, D287-D290.	6.5	38
80	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
81	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
82	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
83	A framework for scientific data modeling and automated software development. Bioinformatics, 2005, 21, 1678-1684.	1.8	42
84	E-MSD: an integrated data resource for bioinformatics. Nucleic Acids Research, 2004, 32, 211D-216.	6.5	90
85	DRESS: a database of REfined solution NMR structures. Proteins: Structure, Function and Bioinformatics, 2004, 55, 483-486.	1.5	91
86	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
87	E-MSD: the European Bioinformatics Institute Macromolecular Structure Database. Nucleic Acids Research, 2003, 31, 458-462.	6.5	93
88	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
89	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
90	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

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91	Pescador: the PEptides in Solution ConformAtion Database: Online Resource. Journal of Biomolecular NMR, 2002, 23, 85-102.	1.6	2
92	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
93	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
94	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
95	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
96	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
97	The three-dimensional solution structure ofAesculus hippocastanum antimicrobial protein 1 determined by1H nuclear magnetic resonance. , 1999, 37, 388-403.		62
98	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
99	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
100	An NMR-based identification of peptide fragments mimicking the interactions of the cathepsin B propeptide. FEBS Letters, 1998, 429, 9-16.	1.3	9
101	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
102	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
103	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
104	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