

Wim F Vranken

List of Publications by Year in descending order

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104
papers

10,199
citations

87723

38
h-index

37111

96
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119
all docs

119
docs citations

119
times ranked

13831
citing authors

#	ARTICLE	IF	CITATIONS
1	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	6.5	46
2	Prediction of Disordered Regions in Proteins with Recurrent Neural Networks and Protein Dynamics. <i>Journal of Molecular Biology</i> , 2022, 434, 167579.	2.0	22
3	MobiDB: intrinsically disordered proteins in 2021. <i>Nucleic Acids Research</i> , 2021, 49, D361-D367.	6.5	183
4	Interpreting a black box predictor to gain insights into early folding mechanisms. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 4919-4930.	1.9	5
5	Computational resources for identifying and describing proteins driving liquid-liquid phase separation. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	40
6	Online biophysical predictions for SARS-CoV-2 proteins. <i>BMC Molecular and Cell Biology</i> , 2021, 22, 23.	1.0	1
7	b2bTools: online predictions for protein biophysical features and their conservation. <i>Nucleic Acids Research</i> , 2021, 49, W52-W59.	6.5	9
8	MutaFrame—an interpretative visualization framework for deleteriousness prediction of missense variants in the human exome. <i>Bioinformatics</i> , 2021, 38, 265-266.	1.8	2
9	Megabodies expand the nanobody toolkit for protein structure determination by single-particle cryo-EM. <i>Nature Methods</i> , 2021, 18, 60-68.	9.0	79
10	Massively parallel interrogation of protein fragment secretability using SECRIFY reveals features influencing secretory system transit. <i>Nature Communications</i> , 2021, 12, 6414.	5.8	5
11	DisProt: intrinsic protein disorder annotation in 2020. <i>Nucleic Acids Research</i> , 2020, 48, D269-D276.	6.5	141
12	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	6.5	87
13	Accurate prediction of protein beta-aggregation with generalized statistical potentials. <i>Bioinformatics</i> , 2020, 36, 2076-2081.	1.8	20
14	ShiftCrypt: a web server to understand and biophysically align proteins through their NMR chemical shift values. <i>Nucleic Acids Research</i> , 2020, 48, W36-W40.	6.5	1
15	Scop3P: A Comprehensive Resource of Human Phosphosites within Their Full Context. <i>Journal of Proteome Research</i> , 2020, 19, 3478-3486.	1.8	19
16	Distance-Based Metrics for Comparing Conformational Ensembles of Intrinsically Disordered Proteins. <i>Biophysical Journal</i> , 2020, 118, 2952-2965.	0.2	17
17	Structural Basis of the Subcellular Topology Landscape of <i>Escherichia coli</i> . <i>Frontiers in Microbiology</i> , 2019, 10, 1670.	1.5	25
18	Auto-encoding NMR chemical shifts from their native vector space to a residue-level biophysical index. <i>Nature Communications</i> , 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. <i>Bioinformatics</i> , 2019, 35, 4617-4623.	1.8	45
20	Exploring the limitations of biophysical propensity scales coupled with machine learning for protein sequence analysis. <i>Scientific Reports</i> , 2019, 9, 16932.	1.6	19
21	An intrinsically disordered proteins community for ELIXIR. <i>F1000Research</i> , 2019, 8, 1753.	0.8	12
22	Lexicon Visualization Library and JavaScript for Scientific Data Visualization. <i>Computing in Science and Engineering</i> , 2018, 20, 50-65.	1.2	3
23	RINspecter: a Cytoscape app for centrality analyses and DynaMine flexibility prediction. <i>Bioinformatics</i> , 2018, 34, 294-296.	1.8	23
24	AmyPro: a database of proteins with validated amyloidogenic regions. <i>Nucleic Acids Research</i> , 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. <i>Scientific Reports</i> , 2018, 8, 16980.	1.6	7
26	Ultra-fast global homology detection with Discrete Cosine Transform and Dynamic Time Warping. <i>Bioinformatics</i> , 2018, 34, 3118-3125.	1.8	13
27	MobiDB 3.0: more annotations for intrinsic disorder, conformational diversity and interactions in proteins. <i>Nucleic Acids Research</i> , 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. <i>Bioinformatics</i> , 2017, 33, 1479-1487.	1.8	66
29	DisProt 7.0: a major update of the database of disordered proteins. <i>Nucleic Acids Research</i> , 2017, 45, D219-D227.	6.5	242
30	Exploring the Sequence-based Prediction of Folding Initiation Sites in Proteins. <i>Scientific Reports</i> , 2017, 7, 8826.	1.6	39
31	SVM-dependent pairwise HMM: an application to protein pairwise alignments. <i>Bioinformatics</i> , 2017, 33, 3902-3908.	1.8	8
32	DEOGEN2: prediction and interactive visualization of single amino acid variant deleteriousness in human proteins. <i>Nucleic Acids Research</i> , 2017, 45, W201-W206.	6.5	114
33	Investigating the Molecular Mechanisms Behind Uncharacterized Cysteine Losses from Prediction of Their Oxidation State. <i>Human Mutation</i> , 2017, 38, 86-94.	1.1	4
34	Start2Fold: a database of hydrogen/deuterium exchange data on protein folding and stability. <i>Nucleic Acids Research</i> , 2016, 44, D429-D434.	6.5	28
35	Observation selection bias in contact prediction and its implications for structural bioinformatics. <i>Scientific Reports</i> , 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. <i>Bioinformatics</i> , 2016, 32, 1797-1804.	1.8	32

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37	Early Folding Events, Local Interactions, and Conservation of Protein Backbone Rigidity. <i>Biophysical Journal</i> , 2016, 110, 572-583.	0.2	23
38	Computational approaches for inferring the functions of intrinsically disordered proteins. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 45.	1.6	37
39	NMR Exchange Format: a unified and open standard for representation of NMR restraint data. <i>Nature Structural and Molecular Biology</i> , 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. <i>Bioinformatics</i> , 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. <i>Journal of Biomolecular NMR</i> , 2015, 62, 413-424.	1.6	27
42	Analysis of the structural quality of the CASD-NMR 2013 entries. <i>Journal of Biomolecular NMR</i> , 2015, 62, 527-540.	1.6	4
43	NMR-Based Modeling and Refinement of Protein 3D Structures. <i>Methods in Molecular Biology</i> , 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. <i>PLoS ONE</i> , 2015, 10, e0131792.	1.1	11
45	The DynaMine webserver: predicting protein dynamics from sequence. <i>Nucleic Acids Research</i> , 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. <i>Structure</i> , 2014, 22, 854-865.	1.6	61
47	Study of the Structural and Dynamic Effects in the FimH Adhesin upon $\hat{\pm}$ -Heptyl Mannose Binding. <i>Journal of Medicinal Chemistry</i> , 2014, 57, 1416-1427.	2.9	43
48	NMR structure validation in relation to dynamics and structure determination. <i>Progress in Nuclear Magnetic Resonance Spectroscopy</i> , 2014, 82, 27-38.	3.9	12
49	Improving 3D structure prediction from chemical shift data. <i>Journal of Biomolecular NMR</i> , 2013, 57, 27-35.	1.6	25
50	From protein sequence to dynamics and disorder with DynaMine. <i>Nature Communications</i> , 2013, 4, 2741.	5.8	139
51	Recommendations of the wwPDB NMR Validation Task Force. <i>Structure</i> , 2013, 21, 1563-1570.	1.6	151
52	NRG-CING: integrated validation reports of remediated experimental biomolecular NMR data and coordinates in wwPDB. <i>Nucleic Acids Research</i> , 2012, 40, D519-D524.	6.5	34
53	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2012, 40, D445-D452.	6.5	166
54	Determination of Secondary Structure Populations in Disordered States of Proteins Using Nuclear Magnetic Resonance Chemical Shifts. <i>Biochemistry</i> , 2012, 51, 2224-2231.	1.2	316

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55	WeNMR: Structural Biology on the Grid. <i>Journal of Grid Computing</i> , 2012, 10, 743-767.	2.5	170
56	CING: an integrated residue-based structure validation program suite. <i>Journal of Biomolecular NMR</i> , 2012, 54, 267-283.	1.6	106
57	Protein Structure Validation Using Side-Chain Chemical Shifts. <i>Journal of Physical Chemistry B</i> , 2012, 116, 4754-4759.	1.2	5
58	ACPYPE - AnteChamber PYthon Parser interfacE. <i>BMC Research Notes</i> , 2012, 5, 367.	0.6	1,864
59	Blind Testing of Routine, Fully Automated Determination of Protein Structures from NMR Data. <i>Structure</i> , 2012, 20, 227-236.	1.6	75
60	Structure-based prediction of methyl chemical shifts in proteins. <i>Journal of Biomolecular NMR</i> , 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. <i>Proteins: Structure, Function and Bioinformatics</i> , 2011, 79, 1525-1537.	1.5	23
62	Using Side-Chain Aromatic Proton Chemical Shifts for a Quantitative Analysis of Protein Structures. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 9620-9623.	7.2	20
63	EUROCarbDB: An open-access platform for glycoinformatics. <i>Glycobiology</i> , 2011, 21, 493-502.	1.3	116
64	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2011, 39, D402-D410.	6.5	64
65	MEMOPS: Data modelling and automatic code generation. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	2
66	Straightforward and complete deposition of NMR data to the PDBe. <i>Journal of Biomolecular NMR</i> , 2010, 48, 85-92.	1.6	7
67	Validation of archived chemical shifts through atomic coordinates. <i>Proteins: Structure, Function and Bioinformatics</i> , 2010, 78, 2482-2489.	1.5	31
68	PDBe: Protein Data Bank in Europe. <i>Nucleic Acids Research</i> , 2010, 38, D308-D317.	6.5	108
69	MEMOPS: data modelling and automatic code generation. <i>Journal of Integrative Bioinformatics</i> , 2010, 7, .	1.0	2
70	The NMR restraints grid at BMRB for 5,266 protein and nucleic acid PDB entries. <i>Journal of Biomolecular NMR</i> , 2009, 45, 389-396.	1.6	26
71	COCO: A simple tool to enrich the representation of conformational variability in NMR structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 75, 206-216.	1.5	17
72	Relationship between chemical shift value and accessible surface area for all amino acid atoms. <i>BMC Structural Biology</i> , 2009, 9, 20.	2.3	26

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73	CASD-NMR: critical assessment of automated structure determination by NMR. <i>Nature Methods</i> , 2009, 6, 625-626.	9.0	80
74	Accurate Random Coil Chemical Shifts from an Analysis of Loop Regions in Native States of Proteins. <i>Journal of the American Chemical Society</i> , 2009, 131, 16332-16333.	6.6	85
75	Remediation of the protein data bank archive. <i>Nucleic Acids Research</i> , 2007, 36, D426-D433.	6.5	136
76	A global analysis of NMR distance constraints from the PDB. <i>Journal of Biomolecular NMR</i> , 2007, 39, 303-314.	1.6	10
77	SPINE bioinformatics and data-management aspects of high-throughput structural biology. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2006, 62, 1184-1195.	2.5	19
78	A nomenclature and data model to describe NMR experiments. <i>Journal of Biomolecular NMR</i> , 2006, 36, 147-155.	1.6	17
79	E-MSD: improving data deposition and structure quality. <i>Nucleic Acids Research</i> , 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. <i>Journal of Biomolecular NMR</i> , 2005, 32, 1-12.	1.6	50
81	RECOORD: A recalculated coordinate database of 500+ proteins from the PDB using restraints from the BioMagResBank. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 662-672.	1.5	323
82	The CCPN data model for NMR spectroscopy: Development of a software pipeline. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 59, 687-696.	1.5	2,805
83	A framework for scientific data modeling and automated software development. <i>Bioinformatics</i> , 2005, 21, 1678-1684.	1.8	42
84	E-MSD: an integrated data resource for bioinformatics. <i>Nucleic Acids Research</i> , 2004, 32, 211D-216.	6.5	90
85	DRESS: a database of Refined solution NMR structures. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 483-486.	1.5	91
86	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 58, 278-284.	1.5	27
87	E-MSD: the European Bioinformatics Institute Macromolecular Structure Database. <i>Nucleic Acids Research</i> , 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 Properties. <i>Biochemistry</i> , 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. <i>Biochemistry</i> , 2002, 41, 8570-8579.	1.2	41
90	Solution structures of a 30-residue amino-terminal domain of the carp granulins protein and its amino-terminally truncated 3-30 subfragment: Implications for the conformational stability of the stack of two β -hairpins. <i>Proteins: Structure, Function and Bioinformatics</i> , 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 A. 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 of Aesculus hippocastanum antimicrobial protein 1 determined by 1H 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 Interface. 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