Sheng Wang

List of Publications by Year
in descending order

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101 papers	8,215 citations	81743 39 h-index	54797 84 g-index
120 all docs	120 docs citations	120 times ranked	10103 citing authors

#	Article	IF	Citations
1	Template-based protein structure modeling using the RaptorX web server. Nature Protocols, 2012, 7, 1511-1522.	5.5	1,474
2	Accurate De Novo Prediction of Protein Contact Map by Ultra-Deep Learning Model. PLoS Computational Biology, 2017, 13, e1005324.	1.5	783
3	RaptorX-Property: a web server for protein structure property prediction. Nucleic Acids Research, 2016, 44, W430-W435.	6.5	446
4	Protein Secondary Structure Prediction Using Deep Convolutional Neural Fields. Scientific Reports, 2016, 6, 18962.	1.6	396
5	Vanillin-Derived High-Performance Flame Retardant Epoxy Resins: Facile Synthesis and Properties. Macromolecules, 2017, 50, 1892-1901.	2.2	343
6	Facile in situ preparation of high-performance epoxy vitrimer from renewable resources and its application in nondestructive recyclable carbon fiber composite. Green Chemistry, 2019, 21, 1484-1497.	4.6	333
7	Robust, Fire-Safe, Monomer-Recovery, Highly Malleable Thermosets from Renewable Bioresources. Macromolecules, 2018, 51, 8001-8012.	2.2	244
8	RaptorX server: A Resource for Template-Based Protein Structure Modeling. Methods in Molecular Biology, 2014, 1137, 17-27.	0.4	232
9	DEEPre: sequence-based enzyme EC number prediction by deep learning. Bioinformatics, 2018, 34, 760-769.	1.8	191
10	High-performance, command-degradable, antibacterial Schiff base epoxy thermosets: synthesis and properties. Journal of Materials Chemistry A, 2019, 7, 15420-15431.	5.2	180
11	Readily recyclable, high-performance thermosetting materials based on a lignin-derived spiro diacetal trigger. Journal of Materials Chemistry A, 2019, 7, 1233-1243.	5.2	142
12	Protein structure alignment beyond spatial proximity. Scientific Reports, 2013, 3, 1448.	1.6	133
13	Protein threading using context-specific alignment potential. Bioinformatics, 2013, 29, i257-i265.	1.8	129
14	Analysis of distanceâ€based protein structure prediction by deep learning in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1069-1081.	1.5	129
15	Chiron: translating nanopore raw signal directly into nucleotide sequence using deep learning. GigaScience, 2018, 7, .	3.3	123
16	Facile Preparation of Polyimine Vitrimers with Enhanced Creep Resistance and Thermal and Mechanical Properties via Metal Coordination. Macromolecules, 2020, 53, 2919-2931.	2.2	120
17	ComplexContact: a web server for inter-protein contact prediction using deep learning. Nucleic Acids Research, 2018, 46, W432-W437.	6.5	118
18	AUCpreD: proteome-level protein disorder prediction by AUC-maximized deep convolutional neural fields. Bioinformatics, 2016, 32, i672-i679.	1.8	104

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19	Protein contact prediction by integrating joint evolutionary coupling analysis and supervised learning. Bioinformatics, 2015, 31, 3506-3513.	1.8	101
20	Itaconic Acid as a Green Alternative to Acrylic Acid for Producing a Soybean Oil-Based Thermoset: Synthesis and Properties. ACS Sustainable Chemistry and Engineering, 2017, 5, 1228-1236.	3.2	94
21	Analysis of deep learning methods for blind protein contact prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 67-77.	1.5	89
22	Facile catalyst-free synthesis, exchanging, and hydrolysis of an acetal motif for dynamic covalent networks. Journal of Materials Chemistry A, 2019, 7, 18039-18049.	5.2	81
23	Green and Facile Preparation of Readily Dual-Recyclable Thermosetting Polymers with Superior Stability Based on Asymmetric Acetal. Macromolecules, 2020, 53, 1474-1485.	2.2	80
24	A conditional neural fields model for protein threading. Bioinformatics, 2012, 28, i59-i66.	1.8	77
25	Dihydrazone-based dynamic covalent epoxy networks with high creep resistance, controlled degradability, and intrinsic antibacterial properties from bioresources. Journal of Materials Chemistry A, 2020, 8, 11261-11274.	5.2	72
26	Upcycling of Polyethylene Terephthalate to Continuously Reprocessable Vitrimers through Reactive Extrusion. Macromolecules, 2021, 54, 703-712.	2.2	71
27	MRFalign: Protein Homology Detection through Alignment of Markov Random Fields. PLoS Computational Biology, 2014, 10, e1003500.	1.5	68
28	Protein threading using residue co-variation and deep learning. Bioinformatics, 2018, 34, i263-i273.	1.8	66
29	DeepSimulator: a deep simulator for Nanopore sequencing. Bioinformatics, 2018, 34, 2899-2908.	1.8	65
30	DeepCNF-D: Predicting Protein Order/Disorder Regions by Weighted Deep Convolutional Neural Fields. International Journal of Molecular Sciences, 2015, 16, 17315-17330.	1.8	64
31	Facile synthesis of â€œdigestibleâ€, rigid-and-flexible, bio-based building block for high-performance degradable thermosetting plastics. Green Chemistry, 2020, 22, 1275-1290.	4.6	64
32	Folding Membrane Proteins by Deep Transfer Learning. Cell Systems, 2017, 5, 202-211.e3.	2.9	63
33	Biosourced Acetal and Dielsâ€“Alder Adduct Concurrent Polyurethane Covalent Adaptable Network. Macromolecules, 2021, 54, 1742-1753.	2.2	63
34	2,5-Furandicarboxylic Acid- and Itaconic Acid-Derived Fully Biobased Unsaturated Polyesters and Their Cross-Linked Networks. Industrial & Engineering Chemistry Research, 2017, 56, 2650-2657.	1.8	58
35	High-Performance, Biobased, Degradable Polyurethane Thermoset and Its Application in Readily Recyclable Carbon Fiber Composites. ACS Sustainable Chemistry and Engineering, 2020, 8, 11162-11170.	3.2	58
36	Alignment of distantly related protein structures: algorithm, bound and implications to homology modeling. Bioinformatics, 2011, 27, 2537-2545.	1.8	57

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37	CoinFold: a web server for protein contact prediction and contact-assisted protein folding. Nucleic Acids Research, 2016, 44, W361-W366.	6.5	57
38	CMsearch: simultaneous exploration of protein sequence space and structure space improves not only protein homology detection but also protein structure prediction. Bioinformatics, 2016, 32, i332-i340.	1.8	52
39	RaptorX-Angle: real-value prediction of protein backbone dihedral angles through a hybrid method of clustering and deep learning. BMC Bioinformatics, 2018, 19, 100.	1.2	44
40	Sustainable valorization of lignin with levulinic acid and its application in polyimine thermosets. Green Chemistry, 2019, 21, 4964-4970.	4.6	43
41	Lynx: a database and knowledge extraction engine for integrative medicine. Nucleic Acids Research, 2014, 42, D1007-D1012.	6.5	40
42	Algorithms, Applications, and Challenges of Protein Structure Alignment. Advances in Protein Chemistry and Structural Biology, 2014, 94, 121-175.	1.0	40
43	Vanillinâ€derived phosphorusâ€containing compounds and ammonium polyphosphate as green fireâ€resistant systems for epoxy resins with balanced properties. Polymers for Advanced Technologies, 2019, 30, 264-278.	1.6	40
44	Prediction of the remaining useful life of cutting tool using the Hurst exponent and CNN-LSTM. International Journal of Advanced Manufacturing Technology, 2021, 112, 2277-2299.	1.5	40
45	Upcycling of post-consumer polyolefin plastics to covalent adaptable networks via in situ continuous extrusion cross-linking. Green Chemistry, 2021, 23, 2931-2937.	4.6	39
46	High-performance bio-based epoxies from ferulic acid and furfuryl alcohol: synthesis and properties. Green Chemistry, 2021, 23, 1772-1781.	4.6	38
47	Conserved salt-bridge competition triggered by phosphorylation regulates the protein interactome. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 13453-13458.	3.3	35
48	Extracellular vesicles in gastrointestinal cancer in conjunction with microbiota: On the border of Kingdoms. Biochimica Et Biophysica Acta: Reviews on Cancer, 2017, 1868, 372-393.	3.3	35
49	When homologous sequences meet structural decoys: Accurate contact prediction by <scp>tFold</scp> in <scp>CASP14</scp>â€”(<scp>tFold</scp> for <scp>CASP14</scp> contact) Tj ETQq1 1 0.784314 rgBT /Overlock		
50	CLePAPS: FAST PAIR ALIGNMENT OF PROTEIN STRUCTURES BASED ON CONFORMATIONAL LETTERS. Journal of Bioinformatics and Computational Biology, 2008, 06, 347-366.	0.3	34
51	Deep learning based multi-label classification for surgical tool presence detection in laparoscopic videos. , 2017, , .		34
52	Concurrent thiolâ€“ene competitive reactions provide reprocessable, degradable and creep-resistant dynamicâ€“permanent hybrid covalent networks. Green Chemistry, 2020, 22, 7769-7777.	4.6	34
53	DeepSimulator1.5: a more powerful, quicker and lighter simulator for Nanopore sequencing. Bioinformatics, 2020, 36, 2578-2580.	1.8	33
54	A systematic selective disassembly approach for Waste Electrical and Electronic Equipment with case study on liquid crystal display televisions. Proceedings of the Institution of Mechanical Engineers, Part B: Journal of Engineering Manufacture, 2017, 231, 2261-2278.	1.5	27

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55	Structures and mechanism of transcription initiation by bacterial ECF factors. Nucleic Acids Research, 2019, 47, 7094-7104.	6.5	27
56	AcconPred: Predicting Solvent Accessibility and Contact Number Simultaneously by a Multitask Learning Framework under the Conditional Neural Fields Model. BioMed Research International, 2015, 2015, 1-10.	0.9	25
57	PredMP: a web server for de novo prediction and visualization of membrane proteins. Bioinformatics, 2019, 35, 691-693.	1.8	25
58	Heterogeneous sensors-based feature optimisation and deep learning for tool wear prediction. International Journal of Advanced Manufacturing Technology, 2021, 114, 2651-2675.	1.5	25
59	Amino acids as latent curing agents and their application in fully bio-based epoxy resins. Green Chemistry, 2021, 23, 6566-6575.	4.6	24
60	Exploring the functional impact of alternative splicing on human protein isoforms using available annotation sources. Briefings in Bioinformatics, 2019, 20, 1754-1768.	3.2	23
61	Crystal structure of steroid reductase SRD5A reveals conserved steroid reduction mechanism. Nature Communications, 2021, 12, 449.	5.8	23
62	Comparison of Hydrogenated Bisphenol A and Bisphenol A Epoxies: Curing Behavior, Thermal and Mechanical Properties, Shape Memory Properties. Macromolecular Research, 2018, 26, 529-538.	1.0	22
63	PointSite: A Point Cloud Segmentation Tool for Identification of Protein Ligand Binding Atoms. Journal of Chemical Information and Modeling, 2022, 62, 2835-2845.	2.5	22
64	An accurate and rapid continuous wavelet dynamic time warping algorithm for end-to-end mapping in ultra-long nanopore sequencing. Bioinformatics, 2018, 34, i722-i731.	1.8	21
65	AUC-Maximized Deep Convolutional Neural Fields for Protein Sequence Labeling. Lecture Notes in Computer Science, 2016, 9852, 1-16.	1.0	20
66	Long-read individual-molecule sequencing reveals CRISPR-induced genetic heterogeneity in human ESCs. Genome Biology, 2020, 21, 213.	3.8	20
67	Dissociate transfer exchange of tandem dynamic bonds endows covalent adaptable networks with fast reprocessability and high performance. Polymer Chemistry, 2021, 12, 5217-5228.	1.9	19
68	A Study on Physical Parameters of Local Landâ€Surface Processes on the Gobi in Northwest China. Chinese Journal of Geophysics, 2003, 46, 883-895.	0.2	16
69	AuTom-dualx: a toolkit for fully automatic fiducial marker-based alignment of dual-axis tilt series with simultaneous reconstruction. Bioinformatics, 2019, 35, 319-328.	1.8	15
70	DeepBound: accurate identification of transcript boundaries via deep convolutional neural fields. Bioinformatics, 2017, 33, i267-i273.	1.8	14
71	Novel algorithms for efficient subsequence searching and mapping in nanopore raw signals towards targeted sequencing. Bioinformatics, 2020, 36, 1333-1343.	1.8	14
72	Facile synthesis of hemiacetal ester-based dynamic covalent polymer networks combining fast reprocessability and high performance. Green Chemistry, 2021, 23, 9061-9070.	4.6	14

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73	WaveNano: a signalâ€level nanopore baseâ€caller via simultaneous prediction of nucleotide labels and move labels through biâ€directional WaveNets. Quantitative Biology, 2018, 6, 359-368.	0.3	13
74	A Web-Based Protocol for Interprotein Contact Prediction by Deep Learning. Methods in Molecular Biology, 2020, 2074, 67-80.	0.4	13
75	Preparation of Non-Planar-Ring Epoxy Thermosets Combining Ultra-Strong Shape Memory Effects and High Performance. Macromolecular Research, 2020, 28, 480-493.	1.0	12
76	Conductive vitrimer nanocomposites enable advanced and recyclable thermo-sensitive materials. Journal of Materials Chemistry C, 2020, 8, 11681-11686.	2.7	12
77	Characteristics of hydrologie transfer between soil and atmosphere over Gobi near oasis at the end of summer. Advances in Atmospheric Sciences, 2003, 20, 442-452.	1.9	11
78	The functional domains for Baxâˆ†2 aggregate-mediated caspase 8-dependent cell death. Experimental Cell Research, 2017, 359, 342-355.	1.2	11
79	Marine microalgae bioengineered Schizochytrium sp. meal hydrolysates inhibits acute inflammation. Scientific Reports, 2018, 8, 9848.	1.6	10
80	A Membrane Burial Potential with H-Bonds and Applications to Curved Membranes and Fast Simulations. Biophysical Journal, 2018, 115, 1872-1884.	0.2	9
81	Hierarchical ZSM-5 Supported CoMn Catalyst for the Production of Middle Distillate from Syngas. Industrial & Engineering Chemistry Research, 2021, 60, 5783-5791.	1.8	9
82	Lynx: a knowledge base and an analytical workbench for integrative medicine. Nucleic Acids Research, 2016, 44, D882-D887.	6.5	8
83	EPTool: A New Enhancing PSSM Tool for Protein Secondary Structure Prediction. Journal of Computational Biology, 2021, 28, 362-364.	0.8	8
84	Bagging MSA Learning: Enhancing Low-Quality PSSM with Deep Learning for Accurate Protein Structure Property Prediction. Lecture Notes in Computer Science, 2020, , 88-103.	1.0	8
85	Research Progress on Vanillin-based Thermosets. Current Green Chemistry, 2018, 5, 138-149.	0.7	8
86	Incorporating Ab Initio energy into threading approaches for protein structure prediction. BMC Bioinformatics, 2011, 12, S54.	1.2	7
87	An Integrative Computational Approach for Prioritization of Genomic Variants. PLoS ONE, 2014, 9, e114903.	1.1	7
88	PRIM: An Efficient Preconditioning Iterative Reweighted Least Squares Method for Parallel Brain MRI Reconstruction. Neuroinformatics, 2018, 16, 425-430.	1.5	6
89	The effect of the particle size on Fischerâ€“Tropsch synthesis for ZSM-5 zeolite supported cobalt-based catalysts. Chemical Communications, 2021, 57, 13522-13525.	2.2	6
90	Prior knowledge facilitates low homologous protein secondary structure prediction with DSM distillation. Bioinformatics, 2022, 38, 3574-3581.	1.8	6

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91	Structure prediction of the entire proteome of monkeypox variants. , 2022, 1, .		6
92	De Novo Protein Structure Prediction by Big Data and Deep Learning. Biophysical Journal, 2017, 112, 55a.	0.2	3
93	Strategic Integration of Multiple Bioinformatics Resources for System Level Analysis of Biological Networks. Methods in Molecular Biology, 2017, 1613, 85-99.	0.4	3
94	Comprehensive Study on Enhancing Low-Quality Position-Specific Scoring Matrix with Deep Learning for Accurate Protein Structure Property Prediction: Using Bagging Multiple Sequence Alignment Learning. Journal of Computational Biology, 2021, 28, 346-361.	0.8	3
95	Deep Ensemble Learning with Atrous Spatial Pyramid Networks for Protein Secondary Structure Prediction. Biomolecules, 2022, 12, 774.	1.8	3
96	PredMP: A Web Resource for Computationally Predicted Membrane Proteins via Deep Learning. Biophysical Journal, 2018, 114, 573a.	0.2	2
97	Predicting diverse M-best protein contact maps. , 2015, , .		0
98	Folding Membrane Proteins by Contacts Inferred from Non-Membrane Proteins and Near-Atomic Level Refinement. Biophysical Journal, 2017, 112, 204a-205a.	0.2	0
99	A Phospho-Induced Theft of a Salt Bridge in RKIP Links Map Kinase and G Protein-Mediated Signaling. Biophysical Journal, 2017, 112, 63a-64a.	0.2	0
100	Specific and intrinsic sequence patterns extracted by deep learning from intra-protein binding and non-binding peptide fragments. Scientific Reports, 2017, 7, 14916.	1.6	0
101	Transmembrane Topology Identification by Fusing Evolutionary and Co-evolutionary Information with Cascaded Bidirectional Transformers. , 2019, , .		0