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	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
2	Prior knowledge facilitates low homologous protein secondary structure prediction with DSM distillation. Bioinformatics, 2022, 38, 3574-3581.	1.8	6
3	Deep Ensemble Learning with Atrous Spatial Pyramid Networks for Protein Secondary Structure Prediction. Biomolecules, 2022, 12, 774.	1.8	3
4	Structure prediction of the entire proteome of monkeypox variants. , 2022, 1, .		6
5	Amino acids as latent curing agents and their application in fully bio-based epoxy resins. Green Chemistry, 2021, 23, 6566-6575.	4.6	24
6	Upcycling of Polyethylene Terephthalate to Continuously Reprocessable Vitrimers through Reactive Extrusion. Macromolecules, 2021, 54, 703-712.	2.2	71
7	Crystal structure of steroid reductase SRD5A reveals conserved steroid reduction mechanism. Nature Communications, 2021, 12, 449.	5.8	23
8	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
9	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
10	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
11	High-performance bio-based epoxies from ferulic acid and furfuryl alcohol: synthesis and properties. Green Chemistry, 2021, 23, 1772-1781.	4.6	38
12	Biosourced Acetal and Dielsâ€“Alder Adduct Concurrent Polyurethane Covalent Adaptable Network. Macromolecules, 2021, 54, 1742-1753.	2.2	63
13	EPTool: A New Enhancing PSSM Tool for Protein Secondary Structure Prediction. Journal of Computational Biology, 2021, 28, 362-364.	0.8	8
14	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
15	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
16	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
17	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 /Overlo		
18	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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19	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
20	Novel algorithms for efficient subsequence searching and mapping in nanopore raw signals towards targeted sequencing. Bioinformatics, 2020, 36, 1333-1343.	1.8	14
21	DeepSimulator1.5: a more powerful, quicker and lighter simulator for Nanopore sequencing. Bioinformatics, 2020, 36, 2578-2580.	1.8	33
22	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
23	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
24	Long-read individual-molecule sequencing reveals CRISPR-induced genetic heterogeneity in human ESCs. Genome Biology, 2020, 21, 213.	3.8	20
25	Conductive vitrimer nanocomposites enable advanced and recyclable thermo-sensitive materials. Journal of Materials Chemistry C, 2020, 8, 11681-11686.	2.7	12
26	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
27	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
28	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
29	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
30	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
31	A Web-Based Protocol for Interprotein Contact Prediction by Deep Learning. Methods in Molecular Biology, 2020, 2074, 67-80.	0.4	13
32	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
33	PredMP: a web server for de novo prediction and visualization of membrane proteins. Bioinformatics, 2019, 35, 691-693.	1.8	25
34	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
35	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
36	Sustainable valorization of lignin with levulinic acid and its application in polyimine thermosets. Green Chemistry, 2019, 21, 4964-4970.	4.6	43

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37	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
38	Transmembrane Topology Identification by Fusing Evolutionary and Co-evolutionary Information with Cascaded Bidirectional Transformers. , 2019, , .		0
39	Analysis of distanceâ€based protein structure prediction by deep learning in CASP13. Proteins: Structure, Function and Bioinformatics, 2019, 87, 1069-1081.	1.5	129
40	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
41	Structures and mechanism of transcription initiation by bacterial ECF factors. Nucleic Acids Research, 2019, 47, 7094-7104.	6.5	27
42	High-performance, command-degradable, antibacterial Schiff base epoxy thermosets: synthesis and properties. Journal of Materials Chemistry A, 2019, 7, 15420-15431.	5.2	180
43	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
44	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
45	Analysis of deep learning methods for blind protein contact prediction in CASP12. Proteins: Structure, Function and Bioinformatics, 2018, 86, 67-77.	1.5	89
46	Chiron: translating nanopore raw signal directly into nucleotide sequence using deep learning. GigaScience, 2018, 7, .	3.3	123
47	DeepSimulator: a deep simulator for Nanopore sequencing. Bioinformatics, 2018, 34, 2899-2908.	1.8	65
48	PRIM: An Efficient Preconditioning Iterative Reweighted Least Squares Method for Parallel Brain MRI Reconstruction. Neuroinformatics, 2018, 16, 425-430.	1.5	6
49	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
50	DEEPre: sequence-based enzyme EC number prediction by deep learning. Bioinformatics, 2018, 34, 760-769.	1.8	191
51	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
52	A Membrane Burial Potential with H-Bonds and Applications to Curved Membranes and Fast Simulations. Biophysical Journal, 2018, 115, 1872-1884.	0.2	9
53	Robust, Fire-Safe, Monomer-Recovery, Highly Malleable Thermosets from Renewable Bioresources. Macromolecules, 2018, 51, 8001-8012.	2.2	244
54	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

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55	ComplexContact: a web server for inter-protein contact prediction using deep learning. Nucleic Acids Research, 2018, 46, W432-W437.	6.5	118
56	Marine microalgae bioengineered Schizochytrium sp. meal hydrolysates inhibits acute inflammation. Scientific Reports, 2018, 8, 9848.	1.6	10
57	Protein threading using residue co-variation and deep learning. Bioinformatics, 2018, 34, i263-i273.	1.8	66
58	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
59	PredMP: A Web Resource for Computationally Predicted Membrane Proteins via Deep Learning. Biophysical Journal, 2018, 114, 573a.	0.2	2
60	Research Progress on Vanillin-based Thermosets. Current Green Chemistry, 2018, 5, 138-149.	0.7	8
61	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
62	Vanillin-Derived High-Performance Flame Retardant Epoxy Resins: Facile Synthesis and Properties. Macromolecules, 2017, 50, 1892-1901.	2.2	343
63	De Novo Protein Structure Prediction by Big Data and Deep Learning. Biophysical Journal, 2017, 112, 55a.	0.2	3
64	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
65	Folding Membrane Proteins by Contacts Inferred from Non-Membrane Proteins and Near-Atomic Level Refinement. Biophysical Journal, 2017, 112, 204a-205a.	0.2	0
66	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
67	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
68	Folding Membrane Proteins by Deep Transfer Learning. Cell Systems, 2017, 5, 202-211.e3.	2.9	63
69	Strategic Integration of Multiple Bioinformatics Resources for System Level Analysis of Biological Networks. Methods in Molecular Biology, 2017, 1613, 85-99.	0.4	3
70	The functional domains for Baxâˆ†2 aggregate-mediated caspase 8-dependent cell death. Experimental Cell Research, 2017, 359, 342-355.	1.2	11
71	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
72	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

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73	Deep learning based multi-label classification for surgical tool presence detection in laparoscopic videos. , 2017, , .		34
74	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
75	DeepBound: accurate identification of transcript boundaries via deep convolutional neural fields. Bioinformatics, 2017, 33, i267-i273.	1.8	14
76	Accurate De Novo Prediction of Protein Contact Map by Ultra-Deep Learning Model. PLoS Computational Biology, 2017, 13, e1005324.	1.5	783
77	Protein Secondary Structure Prediction Using Deep Convolutional Neural Fields. Scientific Reports, 2016, 6, 18962.	1.6	396
78	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
79	RaptorX-Property: a web server for protein structure property prediction. Nucleic Acids Research, 2016, 44, W430-W435.	6.5	446
80	AUC-Maximized Deep Convolutional Neural Fields for Protein Sequence Labeling. Lecture Notes in Computer Science, 2016, 9852, 1-16.	1.0	20
81	AUCpreD: proteome-level protein disorder prediction by AUC-maximized deep convolutional neural fields. Bioinformatics, 2016, 32, i672-i679.	1.8	104
82	CoinFold: a web server for protein contact prediction and contact-assisted protein folding. Nucleic Acids Research, 2016, 44, W361-W366.	6.5	57
83	Lynx: a knowledge base and an analytical workbench for integrative medicine. Nucleic Acids Research, 2016, 44, D882-D887.	6.5	8
84	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
85	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
86	Protein contact prediction by integrating joint evolutionary coupling analysis and supervised learning. Bioinformatics, 2015, 31, 3506-3513.	1.8	101
87	Predicting diverse M-best protein contact maps. , 2015, , .		0
88	MRFalign: Protein Homology Detection through Alignment of Markov Random Fields. PLoS Computational Biology, 2014, 10, e1003500.	1.5	68
89	Lynx: a database and knowledge extraction engine for integrative medicine. Nucleic Acids Research, 2014, 42, D1007-D1012.	6.5	40
90	Algorithms, Applications, and Challenges of Protein Structure Alignment. Advances in Protein Chemistry and Structural Biology, 2014, 94, 121-175.	1.0	40

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91	RaptorX server: A Resource for Template-Based Protein Structure Modeling. Methods in Molecular Biology, 2014, 1137, 17-27.	0.4	232
92	An Integrative Computational Approach for Prioritization of Genomic Variants. PLoS ONE, 2014, 9, e114903.	1.1	7
93	Protein threading using context-specific alignment potential. Bioinformatics, 2013, 29, i257-i265.	1.8	129
94	Protein structure alignment beyond spatial proximity. Scientific Reports, 2013, 3, 1448.	1.6	133
95	A conditional neural fields model for protein threading. Bioinformatics, 2012, 28, i59-i66.	1.8	77
96	Template-based protein structure modeling using the RaptorX web server. Nature Protocols, 2012, 7, 1511-1522.	5.5	1,474
97	Incorporating Ab Initio energy into threading approaches for protein structure prediction. BMC Bioinformatics, 2011, 12, S54.	1.2	7
98	Alignment of distantly related protein structures: algorithm, bound and implications to homology modeling. Bioinformatics, 2011, 27, 2537-2545.	1.8	57
99	CLePAPS: FAST PAIR ALIGNMENT OF PROTEIN STRUCTURES BASED ON CONFORMATIONAL LETTERS. Journal of Bioinformatics and Computational Biology, 2008, 06, 347-366.	0.3	34
100	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
101	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