Jane S Richardson

List of Publications by Citations

130 papers	52,159 citations	52 h-index	142 g-index
142 ext. papers	60,549 ext. citations	8.1 avg, IF	7.16 L-index

#	Paper	IF	Citations
130	PHENIX: a comprehensive Python-based system for macromolecular structure solution. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 213-21		16067
129	MolProbity: all-atom structure validation for macromolecular crystallography. *Acta Crystallographica Section D: Biological Crystallography*, **2010**, 66, 12-21		9600
128	Structure validation by Calpha geometry: phi,psi and Cbeta deviation. *Proteins: Structure, Function and Bioinformatics*, **2003**, 50, 437-50	4.2	3522
127	MolProbity: all-atom contacts and structure validation for proteins and nucleic acids. *Nucleic Acids Research*, **2007**, 35, W375-83	20.1	3030
126	The anatomy and taxonomy of protein structure. *Advances in Protein Chemistry*, **1981**, 34, 167-339		2607
125	Macromolecular structure determination using X-rays, neutrons and electrons: recent developments in Phenix. *Acta Crystallographica Section D: Structural Biology*, **2019**, 75, 861-877	5.5	1527
124	Amino acid preferences for specific locations at the ends of alpha helices. *Science*, **1988**, 240, 1648-52	33.3	1337
123	MolProbity: More and better reference data for improved all-atom structure validation. *Protein Science*, **2018**, 27, 293-315	6.3	1169
122	Asparagine and glutamine: using hydrogen atom contacts in the choice of side-chain amide orientation. *Journal of Molecular Biology*, **1999**, 285, 1735-47	6.5	1064
121	Determination and analysis of the 2 A-structure of copper, zinc superoxide dismutase. *Journal of Molecular Biology*, **1982**, 160, 181-217	6.5	879
120	The penultimate rotamer library. *Proteins: Structure, Function and Bioinformatics*, **2000**, 40, 389-408	4.2	849
119	MOLPROBITY: structure validation and all-atom contact analysis for nucleic acids and their complexes. *Nucleic Acids Research*, **2004**, 32, W615-9	20.1	816
118	Structure and mechanism of copper, zinc superoxide dismutase. *Nature*, **1983**, 306, 284-7	50.4	797
117	Natural beta-sheet proteins use negative design to avoid edge-to-edge aggregation. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 2754-9	11.5	660
116	The Phenix software for automated determination of macromolecular structures. *Methods*, **2011**, 55, 94-106	4.6	580
115	beta-Sheet topology and the relatedness of proteins. *Nature*, **1977**, 268, 495-500	50.4	512
114	Electrostatic recognition between superoxide and copper, zinc superoxide dismutase. *Nature*, **1983** , 306, 287-90	50.4	498

113	Visualizing and quantifying molecular goodness-of-fit: small-probe contact dots with explicit hydrogen atoms. *Journal of Molecular Biology*, **1999**, 285, 1711-33	6.5	445
112	Crystal structure of bovine Cu,Zn superoxide dismutase at 3 A resolution: chain tracing and metal ligands. *Proceedings of the National Academy of Sciences of the United States of America*, **1975**, 72, 1349-53	11.5	381
111	A new generation of crystallographic validation tools for the protein data bank. *Structure*, **2011**, 19, 1395-412	5.2	335
110	Structures of the bacterial ribosome in classical and hybrid states of tRNA binding. *Science*, **2011**, 332, 981-4	33.3	285
109	Principles and Patterns of Protein Conformation **1989**, 1-98		227
108	Three dimensional structure of erabutoxin b neurotoxic protein: inhibitor of acetylcholine receptor. *Proceedings of the National Academy of Sciences of the United States of America*, **1976**, 73, 2991-4	11.5	225
107	The beta bulge: a common small unit of nonrepetitive protein structure. *Proceedings of the National Academy of Sciences of the United States of America*, **1978**, 75, 2574-8	11.5	223
106	Alternate states of proteins revealed by detailed energy landscape mapping. *Journal of Molecular Biology*, **2011**, 405, 607-18	6.5	207
105	The backrub motion: how protein backbone shrugs when a sidechain dances. *Structure*, **2006**, 14, 265-74	5.2	197
104	RNA backbone: consensus all-angle conformers and modular string nomenclature (an RNA Ontology Consortium contribution). *Rna*, **2008**, 14, 465-81	5.8	188
103	The kinemage: a tool for scientific communication. *Protein Science*, **1992**, 1, 3-9	6.3	175
102	The de novo design of protein structures. *Trends in Biochemical Sciences*, **1989**, 14, 304-9	10.3	170
101	Scientific benchmarks for guiding macromolecular energy function improvement. *Methods in Enzymology*, **2013**, 523, 109-43	1.7	164
100	Handedness of crossover connections in beta sheets. *Proceedings of the National Academy of Sciences of the United States of America*, **1976**, 73, 2619-23	11.5	160
99	Use of knowledge-based restraints in phenix.refine to improve macromolecular refinement at low resolution. *Acta Crystallographica Section D: Biological Crystallography*, **2012**, 68, 381-90		156
98	RNA backbone is rotameric. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 13904-9	11.5	154
97	Similarity of three-dimensional structure between the immunoglobulin domain and the copper, zinc superoxide dismutase subunit. *Journal of Molecular Biology*, **1976**, 102, 221-35	6.5	145
96	Betadoublet: de novo design, synthesis, and characterization of a beta-sandwich protein. *Proceedings of the National Academy of Sciences of the United States of America*, **1994**, 91, 8747-51	11.5	138

95	Recommendations of the wwPDB NMR Validation Task Force. *Structure*, **2013**, 21, 1563-70	5.2	117
94	Simultaneous comparison of three protein sequences. *Proceedings of the National Academy of Sciences of the United States of America*, **1985**, 82, 3073-7	11.5	117
93	The Alacoil: a very tight, antiparallel coiled-coil of helices. *Protein Science*, **1995**, 4, 2252-60	6.3	102
92	The tyrosine corner: a feature of most Greek key beta-barrel proteins. *Protein Science*, **1994**, 3, 1927-37	6.3	102
91	Graphical tools for macromolecular crystallography in PHENIX. *Journal of Applied Crystallography*, **2012**, 45, 581-586	3.8	95
90	OSPREY: protein design with ensembles, flexibility, and provable algorithms. *Methods in Enzymology*, **2013**, 523, 87-107	1.7	94
89	phenix.model_vs_data: a high-level tool for the calculation of crystallographic model and data statistics. *Journal of Applied Crystallography*, **2010**, 43, 669-676	3.8	91
88	Molecular conformation of erabutoxin b; atomic coordinates at 2.5 A resolution. *Biochemical and Biophysical Research Communications*, **1979**, 88, 950-9	3.4	81
87	Advances, interactions, and future developments in the CNS, Phenix, and Rosetta structural biology software systems. *Annual Review of Biophysics*, **2013**, 42, 265-87	21.1	76
86	The other 90% of the protein: assessment beyond the Calphas for CASP8 template-based and high-accuracy models. *Proteins: Structure, Function and Bioinformatics*, **2009**, 77 Suppl 9, 29-49	4.2	70
85	Molprobity's ultimate rotamer-library distributions for model validation. *Proteins: Structure, Function and Bioinformatics*, **2016**, 84, 1177-89	4.2	69
84	Schematic drawings of protein structures. *Methods in Enzymology*, **1985**, 115, 359-80	1.7	67
83	Sculpting proteins interactively: continual energy minimization embedded in a graphical modeling system. *Protein Science*, **1994**, 3, 198-210	6.3	66
82	Alpha-carbon coordinates for bovine Cu,Zn superoxide dismutase. *Biochemical and Biophysical Research Communications*, **1975**, 63, 986-92	3.4	64
81	The extracellular nuclease of Staphylococcus aureus: structures of the native enzyme and an enzyme-inhibitor complex at 4 A resolution. *Proceedings of the National Academy of Sciences of the United States of America*, **1969**, 64, 420-7	11.5	64
80	Algorithm for backrub motions in protein design. *Bioinformatics*, **2008**, 24, i196-204	7.2	63
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72	Describing patterns of protein tertiary structure. *Methods in Enzymology*, **1985**, 115, 341-58	1.7	40
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70	Autofix for backward-fit sidechains: using MolProbity and real-space refinement to put misfits in their place. *Journal of Structural and Functional Genomics*, **2009**, 10, 83-93		33
69	"Active" conformation of an inactive semi-synthetic ribonuclease-S. *Journal of Molecular Biology*, **1981**, 149, 313-7	6.5	33
68	Multiscale conformational heterogeneity in staphylococcal protein a: possible determinant of functional plasticity. *Structure*, **2014**, 22, 1467-77	5.2	31
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55	Cryo-EM model validation recommendations based on outcomes of the 2019 EMDataResource challenge. *Nature Methods*, **2021**, 18, 156-164	21.6	22
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44	KinImmerse: Macromolecular VR for NMR ensembles. *Source Code for Biology and Medicine*, **2009**, 4, 3	1.9	17
43	Structural genomics of Pyrococcus furiosus: X-ray crystallography reveals 3D domain swapping in rubrerythrin. *Proteins: Structure, Function and Bioinformatics*, **2004**, 57, 878-82	4.2	17
42	Kinetic role of helix caps in protein folding is context-dependent. *Biochemistry*, **2004**, 43, 3814-23	3.2	17

41	Interpretation of electron density maps. *Methods in Enzymology*, **1985**, 115, 189-206	1.7	16
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31	Biophysical highlights from 54 years of macromolecular crystallography. *Biophysical Journal*, **2014**, 106, 510-25	2.9	9
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1 THE DE NOVO DESIGN OF PROTEIN STRUCTURES **1990**, 173-182