Kim Henrick

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

40 11,261 26 42 g-index

42 12,907 8.9 6.66 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
40	Structure of the signal transduction protein TRAP (target of RNAIII-activating protein). <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012 , 68, 744-50		10
39	The Protein Information Management System (PiMS): a generic tool for any structural biology research laboratory. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2011 , 67, 249-60		17
38	EMDataBank.org: unified data resource for CryoEM. <i>Nucleic Acids Research</i> , 2011 , 39, D456-64	20.1	209
37	EUROCarbDB: An open-access platform for glycoinformatics. <i>Glycobiology</i> , 2011 , 21, 493-502	5.8	108
36	Straightforward and complete deposition of NMR data to the PDBe. <i>Journal of Biomolecular NMR</i> , 2010 , 48, 85-92	3	7
35	Data deposition and annotation at the worldwide protein data bank. <i>Molecular Biotechnology</i> , 2009 , 42, 1-13	3	104
34	Chemical substructure search in SQL. Journal of Chemical Information and Modeling, 2009, 49, 22-7	6.1	31
33	MSDmotif: exploring protein sites and motifs. <i>BMC Bioinformatics</i> , 2008 , 9, 312	3.6	108
32	Data deposition and annotation at the worldwide protein data bank. <i>Methods in Molecular Biology</i> , 2008 , 426, 81-101	1.4	15
31	BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions. <i>Journal of Biomolecular NMR</i> , 2008 , 40, 153-5	3	99
30	Representation of viruses in the remediated PDB archive. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2008 , D64, 874-82		27
29	Remediation of the protein data bank archive. <i>Nucleic Acids Research</i> , 2008 , 36, D426-33	20.1	124
28	Realism about PDB. <i>Nature Biotechnology</i> , 2007 , 25, 845-6; author reply 846	44.5	15
27	Reply to: Building meaningful models of glycoproteins. <i>Nature Structural and Molecular Biology</i> , 2007 , 14, 354-355	17.6	22
26	The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. <i>Nucleic Acids Research</i> , 2007 , 35, D301-3	20.1	807
25	Inference of macromolecular assemblies from crystalline state. <i>Journal of Molecular Biology</i> , 2007 , 372, 774-97	6.5	6659
24	Structural bioinformatics: from protein structure to function. <i>NATO Science Series Series II,</i> Mathematics, Physics and Chemistry, 2007 , 165-179		

[1984-2006]

23	Outcome of a workshop on archiving structural models of biological macromolecules. <i>Structure</i> , 2006 , 14, 1211-7	5.2	49
22	Using MSDchem to search the PDB ligand dictionary. <i>Current Protocols in Bioinformatics</i> , 2006 , Chapter 14, Unit14.3	24.2	24
21	Reply to: Is one solution good enough?. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 185-185	17.6	3
20	MSDsite: a database search and retrieval system for the analysis and viewing of bound ligands and active sites. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 190-9	4.2	83
19	Design of a data model for developing laboratory information management and analysis systems for protein production. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 58, 278-84	4.2	21
18	The Protein Data Bank (PDB) and the Worldwide PDB http://www.wwpdb.org 2005,		2
17	Detection of Protein Assemblies in Crystals. Lecture Notes in Computer Science, 2005, 163-174	0.9	93
16	PDBML: the representation of archival macromolecular structure data in XML. <i>Bioinformatics</i> , 2005 , 21, 988-92	7.2	130
15	Common subgraph isomorphism detection by backtracking search. <i>Software - Practice and Experience</i> , 2004 , 34, 591-607	2.5	63
14	Announcing the worldwide Protein Data Bank. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 980	17.6	1724
14	Announcing the worldwide Protein Data Bank. <i>Nature Structural and Molecular Biology</i> , 2003 , 10, 980 New electron microscopy database and deposition system. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 589	•	1724
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13	New electron microscopy database and deposition system. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 589 Discriminating between homodimeric and monomeric proteins in the crystalline state. <i>Proteins</i> :	10.3	101
13	New electron microscopy database and deposition system. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 589 Discriminating between homodimeric and monomeric proteins in the crystalline state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 47-57 Deposition of macromolecular structures. <i>Acta Crystallographica Section D: Biological</i>	10.3	101
13 12 11	New electron microscopy database and deposition system. <i>Trends in Biochemical Sciences</i> , 2002 , 27, 589 Discriminating between homodimeric and monomeric proteins in the crystalline state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000 , 41, 47-57 Deposition of macromolecular structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998 , 54, 1105-8 Crystal Structure of a Supramolecular Dimer Formed by Interactions between Two Interlocked Cyclic Zinc Porphyrin Trimers. <i>Angewandte Chemie International Edition in English</i> , 1994 , 33, 429-431 Kristallstruktur eines durch Elwechselwirkungen zwischen zwei ineinandergebakten cyclischen	10.3	101 196 11
13 12 11	New electron microscopy database and deposition system. <i>Trends in Biochemical Sciences</i> , 2002, 27, 589 Discriminating between homodimeric and monomeric proteins in the crystalline state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 47-57 Deposition of macromolecular structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1105-8 Crystal Structure of a Supramolecular Dimer Formed by Interactions between Two Interlocked Cyclic Zinc Porphyrin Trimers. <i>Angewandte Chemie International Edition in English</i> , 1994, 33, 429-431 Kristallstruktur eines durch IWechselwirkungen zwischen zwei ineinandergehakten cyclischen	4.2	101 196 11
13 12 11 10	New electron microscopy database and deposition system. <i>Trends in Biochemical Sciences</i> , 2002, 27, 589 Discriminating between homodimeric and monomeric proteins in the crystalline state. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 41, 47-57 Deposition of macromolecular structures. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1105-8 Crystal Structure of a Supramolecular Dimer Formed by Elinteractions between Two Interlocked Cyclic Zinc Porphyrin Trimers. <i>Angewandte Chemie International Edition in English</i> , 1994, 33, 429-431 Kristallstruktur eines durch Eliwechselwirkungen zwischen zwei ineinandergehakten cyclischen Zinkporphyrin-Trimeren gebildeten supramolekularen Dimers. <i>Angewandte Chemie</i> , 1994, 106, 445-447 Complexes of ruthenium(II) with the mono-oximes of 1,2-naphthoquinone: X-ray crystal structure	4.2	101 196 11 44

5	Specification of the bonding cavities available in metal-binding sites: a comparative study of a series of quadridentate macrocyclic ligands. <i>Journal of the American Chemical Society</i> , 1984 , 106, 1641-7	1645 ⁴	41
4	Studies of macrocyclic ligand hole sizes. 1. X-ray structures of the nickel bromide complexes of the diimine and reduced forms of a 16-membered macrocyclic ring incorporating O2N2 donors. <i>Inorganic Chemistry</i> , 1982 , 21, 3261-3264	5.1	35
3	Studies of macrocyclic ligand hole sizes. 2. X-ray structures of the nickel chloride complexes of analogous 15-membered macrocycles containing O2N2-, N4-, and S2N2-donor sets. <i>Inorganic Chemistry</i> , 1982 , 21, 3923-3927	5.1	35
2	The synthesis and X-ray structure of trichloro-1,1,1-(diphenylphosphinomethyl)ethanetrigold(I). <i>Inorganica Chimica Acta</i> , 1982 , 65, L185-L186	2.7	27
1	The Specification of Bonding Cavities in Macrocyclic Ligands. <i>Progress in Inorganic Chemistry</i> ,1-58		40