Kim Henrick

List of Publications by Year
in descending order

39 papers	14,279 citations	270111 25 h-index	355658 38 g-index
42 all docs	42 docs citations	42 times ranked	25194 citing authors

#	Article	IF	Citations
1	Structure of the signal transduction protein TRAP (target of RNAIII-activating protein). Acta Crystallographica Section F: Structural Biology Communications, 2012, 68, 744-750.	0.7	11
2	The Protein Information Management System (PiMS): a generic tool for any structural biology research laboratory. Acta Crystallographica Section D: Biological Crystallography, 2011, 67, 249-260.	2.5	18
3	EMDataBank.org: unified data resource for CryoEM. Nucleic Acids Research, 2011, 39, D456-D464.	6.5	246
4	EUROCarbDB: An open-access platform for glycoinformatics. Glycobiology, 2011, 21, 493-502.	1.3	116
5	Straightforward and complete deposition of NMR data to the PDBe. Journal of Biomolecular NMR, 2010, 48, 85-92.	1.6	7
6	Data Deposition and Annotation at the Worldwide Protein Data Bank. Molecular Biotechnology, 2009, 42, 1-13.	1.3	113
7	Chemical Substructure Search in SQL. Journal of Chemical Information and Modeling, 2009, 49, 22-27.	2.5	36
8	BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions. Journal of Biomolecular NMR, 2008, 40, 153-155.	1.6	117
9	Representation of viruses in the remediated PDB archive. Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 874-882.	2.5	35
10	MSDmotif: exploring protein sites and motifs. BMC Bioinformatics, 2008, 9, 312.	1.2	119
11	Data Deposition and Annotation at the Worldwide Protein Data Bank. Methods in Molecular Biology, 2008, 426, 81-101.	0.4	17
12	The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. Nucleic Acids Research, 2007, 35, D301-D303.	6.5	992
13	Remediation of the protein data bank archive. Nucleic Acids Research, 2007, 36, D426-D433.	6.5	136
14	Inference of Macromolecular Assemblies from Crystalline State. Journal of Molecular Biology, 2007, 372, 774-797.	2.0	8,484
15	Structural bioinformatics: from protein structure to function. NATO Science Series Series II, Mathematics, Physics and Chemistry, 2007, , 165-179.	0.1	0
16	Realism about PDB. Nature Biotechnology, 2007, 25, 845-846.	9.4	17
17	Reply to: Building meaningful models of glycoproteins. Nature Structural and Molecular Biology, 2007, 14, 354-355.	3.6	24
18	Using MSDchem to Search the PDB Ligand Dictionary. , 2006, Chapter 14, Unit14.3.		26

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19	Reply to: Is one solution good enough?. Nature Structural and Molecular Biology, 2006, 13, 185-185.	3.6	3
20	Outcome of a Workshop on Archiving Structural Models of Biological Macromolecules. Structure, 2006, 14, 1211-1217.	1.6	60
21	The Protein Data Bank (PDB) and the Worldwide PDB http://www.wwpdb.org. , 2005, , .		2
22	Detection of Protein Assemblies in Crystals. Lecture Notes in Computer Science, 2005, , 163-174.	1.0	133
23	PDBML: the representation of archival macromolecular structure data in XML. Bioinformatics, 2005, 21, 988-992.	1.8	154
24	MSDsite: A database search and retrieval system for the analysis and viewing of bound ligands and active sites. Proteins: Structure, Function and Bioinformatics, 2004, 58, 190-199.	1.5	98
25	Design of a data model for developing laboratory information management and analysis systems for protein production. Proteins: Structure, Function and Bioinformatics, 2004, 58, 278-284.	1.5	27
26	Common subgraph isomorphism detection by backtracking search. Software - Practice and Experience, 2004, 34, 591-607.	2.5	78
27	Announcing the worldwide Protein Data Bank. Nature Structural and Molecular Biology, 2003, 10, 980-980.	3.6	2,355
28	New electron microscopy database and deposition system. Trends in Biochemical Sciences, 2002, 27, 589.	3.7	131
29	Discriminating between homodimeric and monomeric proteins in the crystalline state. Proteins: Structure, Function and Bioinformatics, 2000, 41, 47-57.	1.5	217
30	Deposition of Macromolecular Structures. Acta Crystallographica Section D: Biological Crystallography, 1998, 54, 1105-1108.	2.5	13
31	Crystal Structure of a Supramolecular Dimer Formed byÏ€ï£¿Ï€ Interactions between Two Interlocked Cyclic Zinc Porphyrin Trimers. Angewandte Chemie International Edition in English, 1994, 33, 429-431.	4.4	59
32	Complexes of ruthenium(II) with the mono-oximes of 1,2-naphthoquinone: X-ray crystal structure of bis (1,2-naphthoquinone 1-oximato)dipyridine ruthenium(II). Polyhedron, 1989, 8, 103-107.	1.0	17
33	Complexes of rhodium(III) and iridium(III) with the mono-oximes of 1,2-naphthoquinone: X-ray crystal structure of pyridinium trichloro(1,2-naphthoquinone 1-oximato)(pyridine)iridate(III). Polyhedron, 1987, 6, 1509-1512.	1.0	17
34	The synthesis and X-ray structure analysis of dichloro {1,3-bis(disphenylphosphino)propane}digold(I). Inorganica Chimica Acta, 1984, 84, L9-L10.	1.2	42
35	Specification of the bonding cavities available in metal-binding sites: a comparative study of a series of quadridentate macrocyclic ligands. Journal of the American Chemical Society, 1984, 106, 1641-1645.	6.6	52
36	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. Inorganic Chemistry, 1982, 21, 3261-3264.	1.9	40

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37	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. Inorganic Chemistry, 1982, 21, 3923-3927.	1.9	50
38	The synthesis and X-ray structure of trichloro-1,1,1-(diphenylphosphinomethyl)ethanetrigold(I). Inorganica Chimica Acta, 1982, 65, L185-L186.	1.2	31
39	The Specification of Bonding Cavities in Macrocyclic Ligands. Progress in Inorganic Chemistry, 0, , 1-58.	3.0	45