# Kim Henrick

## List of Publications by Citations

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|---|---|---|---|
| **40** papers | **11,261** citations | **26** h-index | **42** g-index |
| **42** ext. papers | **12,907** ext. citations | **8.9** avg, IF | **6.66** L-index |

| # | Paper | IF | Citations |
|---|-------|----|-----------|
| 40 | Inference of macromolecular assemblies from crystalline state. *Journal of Molecular Biology*, **2007**, 372, 774-97 | 6.5 | 6659 |
| 39 | Announcing the worldwide Protein Data Bank. *Nature Structural and Molecular Biology*, **2003**, 10, 980 | 17.6 | 1724 |
| 38 | The worldwide Protein Data Bank (wwPDB): ensuring a single, uniform archive of PDB data. *Nucleic Acids Research*, **2007**, 35, D301-3 | 20.1 | 807 |
| 37 | EMDataBank.org: unified data resource for CryoEM. *Nucleic Acids Research*, **2011**, 39, D456-64 | 20.1 | 209 |
| 36 | Discriminating between homodimeric and monomeric proteins in the crystalline state. *Proteins: Structure, Function and Bioinformatics*, **2000**, 41, 47-57 | 4.2 | 196 |
| 35 | PDBML: the representation of archival macromolecular structure data in XML. *Bioinformatics*, **2005**, 21, 988-92 | 7.2 | 130 |
| 34 | Remediation of the protein data bank archive. *Nucleic Acids Research*, **2008**, 36, D426-33 | 20.1 | 124 |
| 33 | EUROCarbDB: An open-access platform for glycoinformatics. *Glycobiology*, **2011**, 21, 493-502 | 5.8 | 108 |
| 32 | MSDmotif: exploring protein sites and motifs. *BMC Bioinformatics*, **2008**, 9, 312 | 3.6 | 108 |
| 31 | Data deposition and annotation at the worldwide protein data bank. *Molecular Biotechnology*, **2009**, 42, 1-13 | 3 | 104 |
| 30 | New electron microscopy database and deposition system. *Trends in Biochemical Sciences*, **2002**, 27, 589 | 10.3 | 101 |
| 29 | BioMagResBank (BMRB) as a partner in the Worldwide Protein Data Bank (wwPDB): new policies affecting biomolecular NMR depositions. *Journal of Biomolecular NMR*, **2008**, 40, 153-5 | 3 | 99 |
| 28 | Detection of Protein Assemblies in Crystals. *Lecture Notes in Computer Science*, **2005**, 163-174 | 0.9 | 93 |
| 27 | MSDsite: a database search and retrieval system for the analysis and viewing of bound ligands and active sites. *Proteins: Structure, Function and Bioinformatics*, **2005**, 58, 190-9 | 4.2 | 83 |
| 26 | Common subgraph isomorphism detection by backtracking search. *Software - Practice and Experience*, **2004**, 34, 591-607 | 2.5 | 63 |
| 25 | Outcome of a workshop on archiving structural models of biological macromolecules. *Structure*, **2006**, 14, 1211-7 | 5.2 | 49 |
| 24 | Crystal Structure of a Supramolecular Dimer Formed by Interactions between Two Interlocked Cyclic Zinc Porphyrin Trimers. *Angewandte Chemie International Edition in English*, **1994**, 33, 429-431 | | 44 |

| 23 | 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 | 16.4 | 41 |
| 22 | The Specification of Bonding Cavities in Macrocyclic Ligands. *Progress in Inorganic Chemistry*,1-58 | | 40 |
| 21 | The synthesis and X-ray structure analysis of dichloro {1,3-bis(disphenylphosphino)propane}digold(I). *Inorganica Chimica Acta*, **1984**, 84, L9-L10 | 2.7 | 35 |
| 20 | 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 | 5.1 | 35 |
| 19 | 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 | 5.1 | 35 |
| 18 | Chemical substructure search in SQL. *Journal of Chemical Information and Modeling*, **2009**, 49, 22-7 | 6.1 | 31 |
| 17 | Representation of viruses in the remediated PDB archive. *Acta Crystallographica Section D: Biological Crystallography*, **2008**, D64, 874-82 | | 27 |
| 16 | The synthesis and X-ray structure of trichloro-1,1,1-(diphenylphosphinomethyl)ethanetrigold(I). *Inorganica Chimica Acta*, **1982**, 65, L185-L186 | 2.7 | 27 |
| 15 | Using MSDchem to search the PDB ligand dictionary. *Current Protocols in Bioinformatics*, **2006**, Chapter 14, Unit14.3 | 24.2 | 24 |
| 14 | Reply to: Building meaningful models of glycoproteins. *Nature Structural and Molecular Biology*, **2007**, 14, 354-355 | 17.6 | 22 |
| 13 | Design of a data model for developing laboratory information management and analysis systems for protein production. *Proteins: Structure, Function and Bioinformatics*, **2005**, 58, 278-84 | 4.2 | 21 |
| 12 | The Protein Information Management System (PiMS): a generic tool for any structural biology research laboratory. *Acta Crystallographica Section D: Biological Crystallography*, **2011**, 67, 249-60 | | 17 |
| 11 | Kristallstruktur eines durch ⊞Wechselwirkungen zwischen zwei ineinandergehakten cyclischen Zinkporphyrin-Trimeren gebildeten supramolekularen Dimers. *Angewandte Chemie*, **1994**, 106, 445-447 | 3.6 | 17 |
| 10 | Data deposition and annotation at the worldwide protein data bank. *Methods in Molecular Biology*, **2008**, 426, 81-101 | 1.4 | 15 |
| 9 | Realism about PDB. *Nature Biotechnology*, **2007**, 25, 845-6; author reply 846 | 44.5 | 15 |
| 8 | 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 | 2.7 | 15 |
| 7 | 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 | 2.7 | 12 |
| 6 | Deposition of macromolecular structures. *Acta Crystallographica Section D: Biological Crystallography*, **1998**, 54, 1105-8 | | 11 |

5    Structure of the signal transduction protein TRAP (target of RNAIII-activating protein). *Acta Crystallographica Section F: Structural Biology Communications*, **2012**, 68, 744-50          10

4    Straightforward and complete deposition of NMR data to the PDBe. *Journal of Biomolecular NMR*, **2010**, 48, 85-92          3    7

3    Reply to: Is one solution good enough?. *Nature Structural and Molecular Biology*, **2006**, 13, 185-185          17.6    3

2    The Protein Data Bank (PDB) and the Worldwide PDB http://www.wwpdb.org **2005**,          2

1    Structural bioinformatics: from protein structure to function. *NATO Science Series Series II, Mathematics, Physics and Chemistry*, **2007**, 165-179