# Andrew L Hopkins

## List of Publications by Year in Descending Order



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|---|---|---|---|
| 43 papers | 14,361 citations | 29 h-index | 47 g-index |
| 47 ext. papers | 16,281 ext. citations | 16.5 avg, IF | 7.04 L-index |

| # | Paper | IF | Citations |
|---|---|---|---|
| 43 | Bispecific repurposed medicines targeting the viral and immunological arms of COVID-19. *Scientific Reports*, **2021**, 11, 13208 | 4.9 | 9 |
| 42 | Surveying GPCR solubilisation conditions using surface plasmon resonance. *Analytical Biochemistry*, **2018**, 556, 23-34 | 3.1 | 4 |
| 41 | Discovery of New Bromodomain Scaffolds by Biosensor Fragment Screening. *ACS Medicinal Chemistry Letters*, **2016**, 7, 1213-1218 | 4.3 | 14 |
| 40 | Application of RNAi to Genomic Drug Target Validation in Schistosomes. *PLoS Neglected Tropical Diseases*, **2015**, 9, e0003801 | 4.8 | 24 |
| 39 | Surface plasmon resonance analysis of seven-transmembrane receptors. *Methods in Enzymology*, **2015**, 556, 499-525 | 1.7 | 19 |
| 38 | The Joint European Compound Library: boosting precompetitive research. *Drug Discovery Today*, **2015**, 20, 181-6 | 8.8 | 55 |
| 37 | Validity of ligand efficiency metrics. *ACS Medicinal Chemistry Letters*, **2014**, 5, 616-8 | 4.3 | 85 |
| 36 | The role of ligand efficiency metrics in drug discovery. *Nature Reviews Drug Discovery*, **2014**, 13, 105-21 | 64.1 | 649 |
| 35 | Fragment screening by SPR and advanced application to GPCRs. *Progress in Biophysics and Molecular Biology*, **2014**, 116, 113-23 | 4.7 | 55 |
| 34 | De Novo Design of Ligands against Multitarget Profiles **2013**, 287-309 | | |
| 33 | Discovery of 2 Adrenergic Receptor Ligands Using Biosensor Fragment Screening of Tagged Wild-Type Receptor. *ACS Medicinal Chemistry Letters*, **2013**, 4, 1005-1010 | 4.3 | 55 |
| 32 | Automated design of ligands to polypharmacological profiles. *Nature*, **2012**, 492, 215-20 | 50.4 | 535 |
| 31 | Introduction: The Case for Polypharmacology **2012**, 1-6 | | 1 |
| 30 | Quantifying the chemical beauty of drugs. *Nature Chemistry*, **2012**, 4, 90-8 | 17.6 | 664 |
| 29 | Whole organism high-content screening by label-free, image-based Bayesian classification for parasitic diseases. *PLoS Neglected Tropical Diseases*, **2012**, 6, e1762 | 4.8 | 77 |
| 28 | Screening for GPCR Ligands Using Surface Plasmon Resonance. *ACS Medicinal Chemistry Letters*, **2011**, 2, 549-554 | 4.3 | 68 |
| 27 | Emerging role of surface plasmon resonance in fragment-based drug discovery. *Future Medicinal Chemistry*, **2011**, 3, 1809-20 | 4.1 | 44 |

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|---|---|---|---|
| 26 | Rapid analysis of pharmacology for infectious diseases. *Current Topics in Medicinal Chemistry*, **2011**, 11, 1292-300 | 3 | 15 |
| 25 | An Ontology for Description of Drug Discovery Investigations. *Journal of Integrative Bioinformatics*, **2010**, 7, | 3.8 | 11 |
| 24 | Fragment screening by surface plasmon resonance. *ACS Medicinal Chemistry Letters*, **2010**, 1, 44-8 | 4.3 | 112 |
| 23 | An ontology for description of drug discovery investigations. *Journal of Integrative Bioinformatics*, **2010**, 7, | 3.8 | 20 |
| 22 | A crowdsourcing evaluation of the NIH chemical probes. *Nature Chemical Biology*, **2009**, 5, 441-7 | 11.7 | 97 |
| 21 | Network pharmacology: the next paradigm in drug discovery. *Nature Chemical Biology*, **2008**, 4, 682-90 | 11.7 | 2255 |
| 20 | Genomic-scale prioritization of drug targets: the TDR Targets database. *Nature Reviews Drug Discovery*, **2008**, 7, 900-7 | 64.1 | 244 |
| 19 | Pharmacological Space **2008**, 521-532 | | 2 |
| 18 | Pharmacological Space **2008**, 395-408 | | |
| 17 | Mission possible. *Nature*, **2007**, 449, 166-9 | 50.4 | 41 |
| 16 | Network pharmacology. *Nature Biotechnology*, **2007**, 25, 1110-1 | 44.5 | 598 |
| 15 | Can we rationally design promiscuous drugs?. *Current Opinion in Structural Biology*, **2006**, 16, 127-36 | 8.1 | 421 |
| 14 | Knowledge and Intelligence in Drug Design. *Annual Reports in Medicinal Chemistry*, **2006**, 425-437 | 1.6 | 6 |
| 13 | Global mapping of pharmacological space. *Nature Biotechnology*, **2006**, 24, 805-15 | 44.5 | 686 |
| 12 | How many drug targets are there?. *Nature Reviews Drug Discovery*, **2006**, 5, 993-6 | 64.1 | 2624 |
| 11 | Ligand efficiency: a useful metric for lead selection. *Drug Discovery Today*, **2004**, 9, 430-1 | 8.8 | 1500 |
| 10 | Design of non-nucleoside inhibitors of HIV-1 reverse transcriptase with improved drug resistance properties. 2. *Journal of Medicinal Chemistry*, **2004**, 47, 5923-36 | 8.3 | 58 |
| 9 | Design of non-nucleoside inhibitors of HIV-1 reverse transcriptase with improved drug resistance properties. 1. *Journal of Medicinal Chemistry*, **2004**, 47, 5912-22 | 8.3 | 79 |

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|---|---|---|---|
| 8 | Structural bioinformatics in drug discovery. *Methods of Biochemical Analysis*, **2003**, 44, 477-97 | | 8 |
| 7 | Protein kinase drugs--optimism doesn't wait on facts. *Drug Discovery Today*, **2002**, 7, 801-2 | 8.8 | 14 |
| 6 | The druggable genome. *Nature Reviews Drug Discovery*, **2002**, 1, 727-30 | 64.1 | 2427 |
| 5 | Design of MKC-442 (emivirine) analogues with improved activity against drug-resistant HIV mutants. *Journal of Medicinal Chemistry*, **1999**, 42, 4500-5 | 8.3 | 124 |
| 4 | Crystallographic analysis of the binding modes of thiazoloisoindolinone non-nucleoside inhibitors to HIV-1 reverse transcriptase and comparison with modeling studies. *Journal of Medicinal Chemistry*, **1999**, 42, 3845-51 | 8.3 | 38 |
| 3 | Crystal structures of HIV-1 reverse transcriptase in complex with carboxanilide derivatives. *Biochemistry*, **1998**, 37, 14394-403 | 3.2 | 93 |
| 2 | 3'-Azido-3'-deoxythymidine drug resistance mutations in HIV-1 reverse transcriptase can induce long range conformational changes. *Proceedings of the National Academy of Sciences of the United States of America*, **1998**, 95, 9518-23 | 11.5 | 67 |
| 1 | Complexes of HIV-1 reverse transcriptase with inhibitors of the HEPT series reveal conformational changes relevant to the design of potent non-nucleoside inhibitors. *Journal of Medicinal Chemistry*, **1996**, 39, 1589-600 | 8.3 | 326 |