Nigel P Brown

List of Publications by Year in Descending Order

17 papers	1,159 citations	13 h-index	17 g-index
17 ext. papers	1,271 ext. citations	10.1 avg, IF	3.37 L-index

#	Paper	IF	Citations
17	How to learn about gene function: text-mining or ontologies?. *Methods*, **2015**, 74, 3-15	4.6	18
16	Proteome analysis of the HIV-1 Gag interactome. *Virology*, **2014**, 460-461, 194-206	3.6	34
15	Automated Annotation of Scientific Documents: Increasing Access to Biological Knowledge **2013**, 869-900		
14	Martini: using literature keywords to compare gene sets. *Nucleic Acids Research*, **2010**, 38, 26-38	20.1	32
13	From experimental setup to bioinformatics: an RNAi screening platform to identify host factors involved in HIV-1 replication. *Biotechnology Journal*, **2010**, 5, 39-49	5.6	36
12	Reflect: augmented browsing for the life scientist. *Nature Biotechnology*, **2009**, 27, 508-10	44.5	78
11	Understanding eukaryotic linear motifs and their role in cell signaling and regulation. *Frontiers in Bioscience - Landmark*, **2008**, 13, 6580-603	2.8	230
10	Non-parametric classification of protein secondary structures. *Computers in Biology and Medicine*, **2006**, 36, 145-56	7	8
9	Quest **2002**, 67-82		
8	Protein structure: geometry, topology and classification. *Reports on Progress in Physics*, **2001**, 64, 517-590	24.4	43
7	The GeneQuiz web server: protein functional analysis through the Web. *Trends in Biochemical Sciences*, **2000**, 25, 33-5	10.3	44
6	Iterated sequence databank search methods. *Computers & Chemistry*, **1999**, 23, 365-85		8
5	Metabolism and evolution of Haemophilus influenzae deduced from a whole-genome comparison with Escherichia coli. *Current Biology*, **1996**, 6, 279-91	6.3	270
4	A protein structure comparison methodology. *Computers & Chemistry*, **1996**, 20, 359-380		37
3	The protein phosphatase 2C (PP2C) superfamily: detection of bacterial homologues. *Protein Science*, **1996**, 5, 1421-5	6.3	169
2	Identification and analysis of multigene families by comparison of exon fingerprints. *Journal of Molecular Biology*, **1995**, 249, 342-59	6.5	26
1	Fast structure alignment for protein databank searching. *Proteins: Structure, Function and Bioinformatics*, **1992**, 14, 139-67	4.2	126