

David Robert Westhead

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2643222/publications.pdf>

Version: 2024-02-01

111
papers

6,026
citations

66234

42
h-index

85405

71
g-index

116
all docs

116
docs citations

116
times ranked

9484
citing authors

#	ARTICLE	IF	CITATIONS
1	Dysregulation of the miR30c/DLL4 axis by circHIPK3 is essential for KSHV lytic replication. EMBO Reports, 2022, 23, e54117.	2.0	9
2	Bridging the gap with the UK Genomics Pathology Imaging Collection. Nature Medicine, 2022, 28, 1107-1108.	15.2	7
3	Comparative analysis of gene expression platforms for cell-of-origin classification of diffuse large B-cell lymphoma shows high concordance. British Journal of Haematology, 2021, 192, 599-604.	1.2	7
4	Arabidopsis Coexpression Tool: a tool for gene coexpression analysis in Arabidopsis thaliana. IScience, 2021, 24, 102848.	1.9	11
5	Benchmarking pipelines for subclonal deconvolution of bulk tumour sequencing data. Nature Communications, 2021, 12, 6396.	5.8	10
6	Distinct genetic changes reveal evolutionary history and heterogeneous molecular grade of DLBCL with MYC/BCL2 double-hit. Leukemia, 2020, 34, 1329-1341.	3.3	66
7	Identification of gene specific cis-regulatory elements during differentiation of mouse embryonic stem cells: An integrative approach using high-throughput datasets. PLoS Computational Biology, 2019, 15, e1007337.	1.5	18
8	Ibrutinib induces chromatin reorganisation of chronic lymphocytic leukaemia cells. Oncogenesis, 2019, 8, 32.	2.1	10
9	Parsimonious Gene Correlation Network Analysis (PGCNA): a tool to define modular gene co-expression for refined molecular stratification in cancer. Npj Systems Biology and Applications, 2019, 5, 13.	1.4	22
10	Cut-and-Run: A Distinct Mechanism by which V(D)J Recombination Causes Genome Instability. Molecular Cell, 2019, 74, 584-597.e9.	4.5	20
11	Gene-expression profiling of bortezomib added to standard chemoimmunotherapy for diffuse large B-cell lymphoma (REMoDL-B): an open-label, randomised, phase 3 trial. Lancet Oncology, The, 2019, 20, 649-662.	5.1	187
12	Molecular High-Grade B-Cell Lymphoma: Defining a Poor-Risk Group That Requires Different Approaches to Therapy. Journal of Clinical Oncology, 2019, 37, 202-212.	0.8	187
13	The Role of SurA PPlase Domains in Preventing Aggregation of the Outer-Membrane Proteins tOmpA and OmpT. Journal of Molecular Biology, 2019, 431, 1267-1283.	2.0	22
14	Cell-of-origin in diffuse large B-cell lymphoma: findings from the UK's population-based Haematological Malignancy Research Network. British Journal of Haematology, 2019, 185, 781-784.	1.2	19
15	Growth Factor-like Gene Regulation Is Separable from Survival and Maturation in Antibody-Secreting Cells. Journal of Immunology, 2019, 202, 1287-1300.	0.4	11
16	Simulation of heterogeneous tumour genomes with HeteroGenesis and in silico whole exome sequencing. Bioinformatics, 2019, 35, 2850-2852.	1.8	3
17	Longitudinal Analyses of Diagnostic-Relapse Biopsies of Diffuse Large B Cell Lymphoma Reveal a Poor Risk Subset of ABC Patients Based on the Expression of a 30 Gene Panel. Blood, 2019, 134, 2769-2769.	0.6	0
18	Chromatin Accessibility-Based Characterization of the Gene Regulatory Network Underlying Plasmodium falciparum Blood-Stage Development. Cell Host and Microbe, 2018, 23, 557-569.e9.	5.1	135

#	ARTICLE	IF	CITATIONS
19	A PQM-1-Mediated Response Triggers Transcellular Chaperone Signaling and Regulates Organismal Proteostasis. <i>Cell Reports</i> , 2018, 23, 3905-3919.	2.9	58
20	Network Analysis Identifies Proinflammatory Plasma Cell Polarization for Secretion of ISG15 in Human Autoimmunity. <i>Journal of Immunology</i> , 2016, 197, 1447-1459.	0.4	52
21	A validated microRNA profile with predictive potential in glioblastoma patients treated with bevacizumab. <i>Molecular Oncology</i> , 2016, 10, 1296-1304.	2.1	19
22	Flexible model-based clustering of mixed binary and continuous data: application to genetic regulation and cancer. <i>Nucleic Acids Research</i> , 2016, 45, gkw1270.	6.5	4
23	Cancer somatic mutations cluster in a subset of regulatory sites predicted from the ENCODE data. <i>Molecular Cancer</i> , 2016, 15, 76.	7.9	3
24	Dynamic Gene Regulatory Networks Drive Hematopoietic Specification and Differentiation. <i>Developmental Cell</i> , 2016, 36, 572-587.	3.1	213
25	Similarity Search Methods As an Alternative to Sub-Type Characterisation in Aggressive Lymphomas. <i>Blood</i> , 2016, 128, 3052-3052.	0.6	2
26	Transferring genomics to the clinic: distinguishing Burkitt and diffuse large B cell lymphomas. <i>Genome Medicine</i> , 2015, 7, 64.	3.6	20
27	Gene expression meta-analysis reveals immune response convergence on the IFN γ -STAT1-IRF1 axis and adaptive immune resistance mechanisms in lymphoma. <i>Genome Medicine</i> , 2015, 7, 96.	3.6	24
28	Chronic FLT3-ITD Signaling in Acute Myeloid Leukemia Is Connected to a Specific Chromatin Signature. <i>Cell Reports</i> , 2015, 12, 821-836.	2.9	63
29	Using common variants to indicate cancer genes. <i>International Journal of Cancer</i> , 2015, 136, 241-245.	2.3	0
30	Prediction of clinical outcome in glioblastoma using a biologically relevant nine-microRNA signature. <i>Molecular Oncology</i> , 2015, 9, 704-714.	2.1	56
31	Defining Immune Response Signatures in DLBCL As Potential Predictive Biomarkers for Outcome to Immunotherapy. <i>Blood</i> , 2015, 126, 2663-2663.	0.6	0
32	A crucial role for the ubiquitously expressed transcription factor Sp1 at early stages of hematopoietic specification. <i>Development (Cambridge)</i> , 2014, 141, 2391-2401.	1.2	51
33	SPIB and BATF provide alternate determinants of IRF4 occupancy in diffuse large B-cell lymphoma linked to disease heterogeneity. <i>Nucleic Acids Research</i> , 2014, 42, 7591-7610.	6.5	43
34	Identification of a Dynamic Core Transcriptional Network in t(8;21) AML that Regulates Differentiation Block and Self-Renewal. <i>Cell Reports</i> , 2014, 8, 1974-1988.	2.9	106
35	Prognostic microRNAs in high-grade glioma reveal a link to oligodendrocyte precursor differentiation. <i>Oncoscience</i> , 2014, 2, 252-262.	0.9	12
36	Identification of a Dynamic Core Transcriptional Network in t(8;21) AML Regulating Differentiation Block and Self-Renewal. <i>Blood</i> , 2014, 124, 1061-1061.	0.6	0

#	ARTICLE	IF	CITATIONS
37	Identification of a dynamic core transcriptional regulatory network for t(8;21) AML. <i>Experimental Hematology</i> , 2013, 41, S16.	0.2	0
38	A Microarray Platform-Independent Classification Tool for Cell of Origin Class Allows Comparative Analysis of Gene Expression in Diffuse Large B-cell Lymphoma. <i>PLoS ONE</i> , 2013, 8, e55895.	1.1	64
39	Development Of A Cross Platform, 2-Way Gene Expression Classifier To Distinguish Burkitt Lymphoma From DLBCL, and Assessment Of The Potential Impact Of Its Use In Treatment Decision Making. <i>Blood</i> , 2013, 122, 74-74.	0.6	7
40	RUNX1 reshapes the epigenetic landscape at the onset of haematopoiesis. <i>EMBO Journal</i> , 2012, 31, 4318-4333.	3.5	158
41	Whole genome expression profiling based on paraffin embedded tissue can be used to classify diffuse large B-cell lymphoma and predict clinical outcome. <i>British Journal of Haematology</i> , 2012, 159, 441-453.	1.2	81
42	In Vitro Generation of Long-lived Human Plasma Cells. <i>Journal of Immunology</i> , 2012, 189, 5773-5785.	0.4	111
43	Depletion of RUNX1/ETO in t(8;21) AML cells leads to genome-wide changes in chromatin structure and transcription factor binding. <i>Leukemia</i> , 2012, 26, 1829-1841.	3.3	161
44	Two distinct auto-regulatory loops operate at the PU.1 locus in B cells and myeloid cells. <i>Blood</i> , 2011, 117, 2827-2838.	0.6	120
45	Meta-Analysis of Diffuse Large B-Cell Lymphoma Gene Expression Identifies Novel and Recurrent Biological Connections. <i>Blood</i> , 2011, 118, 3682-3682.	0.6	0
46	PlasmoPredict: a gene function prediction website for <i>Plasmodium falciparum</i> . <i>Trends in Parasitology</i> , 2010, 26, 107-110.	1.5	3
47	KvDB; mining and mapping sequence variants in voltage-gated potassium channels. <i>Human Mutation</i> , 2010, 31, 908-917.	1.1	3
48	GO-At–in silico prediction of gene function in <i>Arabidopsis thaliana</i> by combining heterogeneous data. <i>Plant Journal</i> , 2010, 61, 713-721.	2.8	17
49	An extended set of PRDM1/BLIMP1 target genes links binding motif type to dynamic repression. <i>Nucleic Acids Research</i> , 2010, 38, 5336-5350.	6.5	52
50	MetNetMaker: a free and open-source tool for the creation of novel metabolic networks in SBML format. <i>Bioinformatics</i> , 2010, 26, 2352-2353.	1.8	17
51	Gene function prediction using semantic similarity clustering and enrichment analysis in the malaria parasite <i>Plasmodium falciparum</i> . <i>Bioinformatics</i> , 2010, 26, 2431-2437.	1.8	17
52	Simple sequence-based kernels do not predict protein-protein interactions. <i>Bioinformatics</i> , 2010, 26, 2610-2614.	1.8	98
53	Transferomics: Seeing the Evolutionary Forest Using Phylogenetic Trees. , 2010, , 101-114.		0
54	metaTIGER: a metabolic evolution resource. <i>Nucleic Acids Research</i> , 2009, 37, D531-D538.	6.5	32

#	ARTICLE	IF	CITATIONS
55	Small RNA analysis in <i>Petunia hybrida</i> identifies unusual tissue-specific expression patterns of conserved miRNAs and of a 24mer RNA. <i>Rna</i> , 2009, 15, 1012-1020.	1.6	9
56	Alio intuitu: the automated reconstruction of the metabolic networks of parasites. <i>Trends in Parasitology</i> , 2009, 25, 396-397.	1.5	2
57	From gene expression to gene regulatory networks in <i>Arabidopsis thaliana</i> . <i>BMC Systems Biology</i> , 2009, 3, 85.	3.0	38
58	Combining the interactome and deleterious SNP predictions to improve disease gene identification. <i>Human Mutation</i> , 2009, 30, 485-492.	1.1	18
59	\hat{I}^2 Edge strands in protein structure prediction and aggregation. <i>Protein Science</i> , 2009, 12, 2348-2359.	3.1	48
60	The transcriptional regulation of protein complexes; a cross-species perspective. <i>Genomics</i> , 2009, 94, 369-376.	1.3	18
61	The fibril_one on-line database: Mutations, experimental conditions, and trends associated with amyloid fibril formation. <i>Protein Science</i> , 2009, 11, 1862-1866.	3.1	10
62	The transferome of metabolic genes explored: analysis of the horizontal transfer of enzyme encoding genes in unicellular eukaryotes. <i>Genome Biology</i> , 2009, 10, R36.	13.9	56
63	Prediction of horizontal gene transfers in eukaryotes: approaches and challenges. <i>Biochemical Society Transactions</i> , 2009, 37, 792-795.	1.6	19
64	Bayesian Data Integration and Enrichment Analysis for Predicting Gene Function in Malaria. <i>Lecture Notes in Computer Science</i> , 2009, , 457-466.	1.0	1
65	A Unique Dual Activity Amino Acid Hydroxylase in <i>Toxoplasma gondii</i> . <i>PLoS ONE</i> , 2009, 4, e4801.	1.1	238
66	Heat Stress Enhances the Accumulation of Polyadenylated Mitochondrial Transcripts in <i>Arabidopsis thaliana</i> . <i>PLoS ONE</i> , 2008, 3, e2889.	1.1	23
67	Bioinformatic approaches to biological systems. <i>SEB Experimental Biology Series</i> , 2008, 61, 1-16.	0.1	0
68	Conservation, Convergence, and Divergence of Light-Responsive, Circadian-Regulated, and Tissue-Specific Expression Patterns during Evolution of the <i>Arabidopsis</i> GATA Gene Family. <i>Plant Physiology</i> , 2007, 143, 941-958.	2.3	87
69	Deleterious SNP prediction: be mindful of your training data!. <i>Bioinformatics</i> , 2007, 23, 664-672.	1.8	54
70	Modelling the pH-dependent Properties of Kv1 Potassium Channels. <i>Journal of Molecular Biology</i> , 2007, 368, 328-335.	2.0	8
71	Functional Gene Networks: A Preliminary Study on a Modified Genetic Algorithm for Candidate Discovery in Large Microarray Datasets. , 2007, , .		0
72	A consensus algorithm to screen genomes for novel families of transmembrane \hat{I}^2 barrel proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 69, 8-18.	1.5	7

#	ARTICLE	IF	CITATIONS
73	Bayesian refinement of protein functional site matching. BMC Bioinformatics, 2007, 8, 257.	1.2	9
74	Metabolic reconstruction and analysis for parasite genomes. Trends in Parasitology, 2007, 23, 548-554.	1.5	33
75	A Primer on Learning in Bayesian Networks for Computational Biology. PLoS Computational Biology, 2007, 3, e129.	1.5	220
76	Insights into Protein-Protein Interfaces using a Bayesian Network Prediction Method. Journal of Molecular Biology, 2006, 362, 365-386.	2.0	99
77	The Arabidopsis co-expression tool (act): a WWW-based tool and database for microarray-based gene expression analysis. Plant Journal, 2006, 46, 336-348.	2.8	69
78	Inference in Bayesian networks. Nature Biotechnology, 2006, 24, 51-53.	9.4	77
79	Predicting the effect of missense mutations on protein function: analysis with Bayesian networks. BMC Bioinformatics, 2006, 7, 405.	1.2	21
80	Identification of the REST regulon reveals extensive transposable element-mediated binding site duplication. Nucleic Acids Research, 2006, 34, 3862-3877.	6.5	121
81	metaSHARK: a WWW platform for interactive exploration of metabolic networks. Nucleic Acids Research, 2006, 34, W725-W728.	6.5	23
82	Arabidopsis Co-expression Tool (ACT): web server tools for microarray-based gene expression analysis. Nucleic Acids Research, 2006, 34, W504-W509.	6.5	145
83	Automated derivation and refinement of sequence length patterns for protein sequences using evolutionary computation. BioSystems, 2005, 81, 247-254.	0.9	0
84	TmaDB: a repository for tissue microarray data. BMC Bioinformatics, 2005, 6, 218.	1.2	18
85	TMB-Hunt: an amino acid composition based method to screen proteomes for beta-barrel transmembrane proteins. BMC Bioinformatics, 2005, 6, 56.	1.2	59
86	Differential expression and extent of fungal/plant and fungal/bacterial chitinases of Aspergillus fumigatus. Archives of Microbiology, 2005, 184, 78-81.	1.0	19
87	metaSHARK: software for automated metabolic network prediction from DNA sequence and its application to the genomes of Plasmodium falciparum and Eimeria tenella. Nucleic Acids Research, 2005, 33, 1399-1409.	6.5	91
88	TMB-Hunt: a web server to screen sequence sets for transmembrane β -barrel proteins. Nucleic Acids Research, 2005, 33, W188-W192.	6.5	51
89	Improved prediction of protein-protein binding sites using a support vector machines approach. Bioinformatics, 2005, 21, 1487-1494.	1.8	347
90	Fundamentals of protein structure and function. , 2005, , .		0

#	ARTICLE	IF	CITATIONS
91	TOPS: an enhanced database of protein structural topology. <i>Nucleic Acids Research</i> , 2004, 32, 251D-254.	6.5	96
92	Annotating the Plasmodium genome and the enigma of the shikimate pathway. <i>Trends in Parasitology</i> , 2004, 20, 60-65.	1.5	70
93	Ligand binding: functional site location, similarity and docking. <i>Current Opinion in Structural Biology</i> , 2003, 13, 389-395.	2.6	191
94	Asymmetric mutation rates at enzyme-inhibitor interfaces: Implications for the protein-protein docking problem. <i>Protein Science</i> , 2003, 12, 2099-2103.	3.1	20
95	Calculation of helix packing angles in protein structures. <i>Bioinformatics</i> , 2003, 19, 1298-1299.	1.8	30
96	A computer system to perform structure comparison using TOPS representations of protein structure. <i>Computers & Chemistry</i> , 2001, 26, 23-30.	1.2	35
97	AI-based algorithms for protein surface comparisons. <i>Computers & Chemistry</i> , 2001, 26, 79-84.	1.2	17
98	Protein structural topology: Automated analysis and diagrammatic representation. <i>Protein Science</i> , 1999, 8, 897-904.	3.1	101
99	An atlas of protein topology cartoons available on the world-wide web. <i>Trends in Biochemical Sciences</i> , 1998, 23, 35-36.	3.7	55
100	Flexible docking using tabu search and an empirical estimate of binding affinity. , 1998, 33, 367-382.		328
101	Protein structure prediction. <i>Current Opinion in Biotechnology</i> , 1998, 9, 383-389.	3.3	38
102	New Tools and Resources for Analysing Protein Structures and Their Interactions. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1998, 54, 1132-1138.	2.5	19
103	A comparison of heuristic search algorithms for molecular docking. <i>Journal of Computer-Aided Molecular Design</i> , 1997, 11, 209-228.	1.3	106
104	PRO_SELECT: combining structure-based drug design and combinatorial chemistry for rapid lead discovery. 1. Technology. <i>Journal of Computer-Aided Molecular Design</i> , 1997, 11, 193-207.	1.3	65
105	Active-site-directed 3D database searching: Pharmacophore extraction and validation of hits. <i>Journal of Computer-Aided Molecular Design</i> , 1996, 10, 397-416.	1.3	24
106	Evolutionary algorithms in computer-aided molecular design. <i>Journal of Computer-Aided Molecular Design</i> , 1996, 10, 337-358.	1.3	119
107	PRO_LIGAND: An approach to de novo molecular design. 1. Application to the design of organic molecules. <i>Journal of Computer-Aided Molecular Design</i> , 1995, 9, 13-32.	1.3	118
108	PRO_LIGAND: An approach to de novo molecular design. 3. A genetic algorithm for structure refinement. <i>Journal of Computer-Aided Molecular Design</i> , 1995, 9, 139-148.	1.3	56

#	ARTICLE	IF	CITATIONS
109	PRO_LIGAND: An approach to de novo molecular design. 4. Application to the design of peptides. Journal of Computer-Aided Molecular Design, 1995, 9, 213-225.	1.3	31
110	Ligand: A new automated system for de novo drug design. AIP Conference Proceedings, 1995, , .	0.3	0
111	PRO_LIGAND: An Approach to de Novo Molecular Design. 2. Design of Novel Molecules from Molecular Field Analysis (MFA) Models and Pharmacophores. Journal of Medicinal Chemistry, 1994, 37, 3994-4002.	2.9	56