# Donald E Ayer

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 46 papers | 7,832 citations | 117625 34 h-index | 233421 45 g-index |
| 54 all docs | 54 docs citations | 54 times ranked | 8189 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Age-associated decline of MondoA drives cellular senescence through impaired autophagy and mitochondrial homeostasis. Cell Reports, 2022, 38, 110444. | 6.4 | 27 |
| 2 | The glucose-sensing transcription factor MLX balances metabolism and stress to suppress apoptosis and maintain spermatogenesis. PLoS Biology, 2021, 19, e3001085. | 5.6 | 7 |
| 3 | Protein synthesis inhibitors stimulate MondoA transcriptional activity by driving an accumulation of glucose 6-phosphate. Cancer & Metabolism, 2020, 8, 27. | 5.0 | 9 |
| 4 | MondoA drives muscle lipid accumulation and insulin resistance. JCI Insight, 2019, 4, . | 5.0 | 22 |
| 5 | Cellular acidosis triggers human MondoA transcriptional activity by driving mitochondrial ATP production. ELife, 2019, 8, . | 6.0 | 41 |
| 6 | Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2. | 6.2 | 284 |
| 7 | Extracellular Matrix Remodeling Regulates Glucose Metabolism through TXNIP Destabilization. Cell, 2018, 175, 117-132.e21. | 28.9 | 180 |
| 8 | Ras Suppresses TXNIP Expression by Restricting Ribosome Translocation. Molecular and Cellular Biology, 2018, 38, . | 2.3 | 12 |
| 9 | Deregulated Myc Requires MondoA/Mlx for Metabolic Reprogramming and Tumorigenesis. Cancer Cell, 2015, 27, 271-285. | 16.8 | 172 |
| 10 | MondoA-Mlx Transcriptional Activity Is Limited by mTOR-MondoA Interaction. Molecular and Cellular Biology, 2015, 35, 101-110. | 2.3 | 34 |
| 11 | Metabolic reprogramming in triple-negative breast cancer through Myc suppression of TXNIP. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 5425-5430. | 7.1 | 190 |
| 12 | Interactions between Myc and MondoA transcription factors in metabolism and tumourigenesis. British Journal of Cancer, 2015, 113, 1529-1533. | 6.4 | 50 |
| 13 | Foxk proteins repress the initiation of starvation-induced atrophy and autophagy programs. Nature Cell Biology, 2014, 16, 1202-1214. | 10.3 | 120 |
| 14 | Response of BRAF-Mutant Melanoma to BRAF Inhibition Is Mediated by a Network of Transcriptional Regulators of Glycolysis. Cancer Discovery, 2014, 4, 423-433. | 9.4 | 242 |
| 15 | Response to Acidity: The MondoAâ€“TXNIP Checkpoint Couples the Acidic Tumor Microenvironment to Cell Metabolism. , 2014, , 69-100. | | 0 |
| 16 | Adaptive metabolic response to 4Âweeks of sugar-sweetened beverage consumption in healthy, lightly active individuals and chronic high glucose availability in primary human myotubes. European Journal of Nutrition, 2013, 52, 937-948. | 3.9 | 12 |
| 17 | MondoA senses adenine nucleotides: transcriptional induction of thioredoxin-interacting protein. Biochemical Journal, 2013, 453, 209-218. | 3.7 | 13 |
| 18 | Coordination of Nutrient Availability and Utilization by MAX- and MLX-Centered Transcription Networks. Cold Spring Harbor Perspectives in Medicine, 2013, 3, a014258-a014258. | 6.2 | 43 |

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|---|---|---|---|
| 19 | An extended Myc network contributes to glucose homeostasis in cancer and diabetes. Frontiers in Bioscience - Landmark, 2011, 16, 2206. | 3.0 | 43 |
| 20 | MondoA Senses Non-glucose Sugars. Journal of Biological Chemistry, 2011, 286, 38027-38034. | 3.4 | 60 |
| 21 | Glucose Controls Nuclear Accumulation, Promoter Binding, and Transcriptional Activity of the MondoA-Mlx Heterodimer. Molecular and Cellular Biology, 2010, 30, 2887-2895. | 2.3 | 84 |
| 22 | Myc, Mondo, and Metabolism. Genes and Cancer, 2010, 1, 587-596. | 1.9 | 35 |
| 23 | Transcriptional and Translational Downregulation of Thioredoxin Interacting Protein Is Required for Metabolic Reprogramming during G1. Genes and Cancer, 2010, 1, 893-907. | 1.9 | 67 |
| 24 | Coordination of glucose and glutamine utilization by an expanded Myc network. Transcription, 2010, 1, 36-40. | 3.1 | 28 |
| 25 | Glutamine-dependent anapleurosis dictates glucose uptake and cell growth by regulating MondoA transcriptional activity. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 14878-14883. | 7.1 | 142 |
| 26 | Over-expression of the BRMS1 family member SUDS3 does not suppress metastasis of human cancer cells. Cancer Letters, 2009, 276, 32-37. | 7.2 | 17 |
| 27 | Glucose sensing by MondoA:Mlx complexes: A role for hexokinases and direct regulation of thioredoxin-interacting protein expression. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 6912-6917. | 7.1 | 238 |
| 28 | A C. elegans Myc-like network cooperates with semaphorin and Wnt signaling pathways to control cell migration. Developmental Biology, 2007, 310, 226-239. | 2.0 | 37 |
| 29 | MondoA-Mlx Heterodimers Are Candidate Sensors of Cellular Energy Status: Mitochondrial Localization and Direct Regulation of Glycolysis. Molecular and Cellular Biology, 2006, 26, 4863-4871. | 2.3 | 101 |
| 30 | ING2 PHD domain links histone H3 lysine 4 methylation to active gene repression. Nature, 2006, 442, 96-99. | 27.8 | 851 |
| 31 | The Polybasic Region That Follows the Plant Homeodomain Zinc Finger 1 of Pf1 Is Necessary and Sufficient for Specific Phosphoinositide Binding. Journal of Biological Chemistry, 2006, 281, 28831-28836. | 3.4 | 65 |
| 32 | Identification and Characterization of Three New Components of the mSin3A Corepressor Complex. Molecular and Cellular Biology, 2003, 23, 3456-3467. | 2.3 | 164 |
| 33 | Role for the Mortality Factors MORF4, MRGX, and MRG15 in Transcriptional Repression via Associations with Pf1, mSin3A, and Transducin-Like Enhancer of Split. Molecular and Cellular Biology, 2002, 22, 7868-7876. | 2.3 | 89 |
| 34 | A Novel Heterodimerization Domain, CRM1, and 14-3-3 Control Subcellular Localization of the MondoA-Mlx Heterocomplex. Molecular and Cellular Biology, 2002, 22, 8514-8526. | 2.3 | 45 |
| 35 | Pf1, a Novel PHD Zinc Finger Protein That Links the TLE Corepressor to the mSin3A-Histone Deacetylase Complex. Molecular and Cellular Biology, 2001, 21, 4110-4118. | 2.3 | 80 |
| 36 | MondoA, a Novel Basic Helix-Loop-Helixâ€“Leucine Zipper Transcriptional Activator That Constitutes a Positive Branch of a Max-Like Network. Molecular and Cellular Biology, 2000, 20, 8845-8854. | 2.3 | 118 |

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|---|---|---|---|
| 37 | Î²-Cateninâ€“Histone Deacetylase Interactions Regulate the Transition of LEF1 from a Transcriptional Repressor to an Activator. Molecular and Cellular Biology, 2000, 20, 6882-6890. | 2.3 | 200 |
| 38 | Solution Structure of the Interacting Domains of the Madâ€“Sin3 Complex. Cell, 2000, 103, 655-665. | 28.9 | 95 |
| 39 | Mlx, a Novel Max-like BHLHZip Protein That Interacts with the Max Network of Transcription Factors. Journal of Biological Chemistry, 1999, 274, 36344-36350. | 3.4 | 89 |
| 40 | A 13-Amino Acid Amphipathic Î±-Helix Is Required for the Functional Interaction between the Transcriptional Repressor Mad1 and mSin3A. Journal of Biological Chemistry, 1999, 274, 32750-32756. | 3.4 | 58 |
| 41 | Histone deacetylases: transcriptional repression with SINers and NuRDs. Trends in Cell Biology, 1999, 9, 193-198. | 7.9 | 257 |
| 42 | SAP30, a Component of the mSin3 Corepressor Complex Involved in N-CoR-Mediated Repression by Specific Transcription Factors. Molecular Cell, 1998, 2, 33-42. | 9.7 | 196 |
| 43 | Histone Deacetylase Activity Is Required for Full Transcriptional Repression by mSin3A. Cell, 1997, 89, 341-347. | 28.9 | 705 |
| 44 | Nuclear Receptor Repression Mediated by a Complex Containing SMRT, mSin3A, and Histone Deacetylase. Cell, 1997, 89, 373-380. | 28.9 | 1,206 |
| 45 | Mad-max transcriptional repression is mediated by ternary complex formation with mammalian homologs of yeast repressor Sin3. Cell, 1995, 80, 767-776. | 28.9 | 585 |
| 46 | Mad: A heterodimeric partner for Max that antagonizes Myc transcriptional activity. Cell, 1993, 72, 211-222. | 28.9 | 717 |