# Douglas R Higgs

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 155 papers | 15,300 citations | 14655 66 h-index | 19749 117 g-index |
| 167 all docs | 167 docs citations | 167 times ranked | 14287 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Distinct Factors Control Histone Variant H3.3 Localization at Specific Genomic Regions. Cell, 2010, 140, 678-691. | 28.9 | 1,069 |
| 2 | Mutations in a putative global transcriptional regulator cause X-linked mental retardation with Î±-thalassemia (ATR-X syndrome). Cell, 1995, 80, 837-845. | 28.9 | 583 |
| 3 | Transcription of antisense RNA leading to gene silencing and methylation as a novel cause of human genetic disease. Nature Genetics, 2003, 34, 157-165. | 21.4 | 505 |
| 4 | Mutations in ATRX, encoding a SWI/SNF-like protein, cause diverse changes in the pattern of DNA methylation. Nature Genetics, 2000, 24, 368-371. | 21.4 | 476 |
| 5 | Î±-thalassaemia. Orphanet Journal of Rare Diseases, 2010, 5, 13. | 2.7 | 417 |
| 6 | Analysis of hundreds of cis-regulatory landscapes at high resolution in a single, high-throughput experiment. Nature Genetics, 2014, 46, 205-212. | 21.4 | 417 |
| 7 | Thalassaemia. Lancet, The, 2012, 379, 373-383. | 13.7 | 371 |
| 8 | ATR-X Syndrome Protein Targets Tandem Repeats and Influences Allele-Specific Expression in a Size-Dependent Manner. Cell, 2010, 143, 367-378. | 28.9 | 365 |
| 9 | Genetic dissection of the Î±-globin super-enhancer in vivo. Nature Genetics, 2016, 48, 895-903. | 21.4 | 308 |
| 10 | The Interaction of Alpha-Thalassemia and Homozygous Sickle-Cell Disease. New England Journal of Medicine, 1982, 306, 1441-1446. | 27.0 | 305 |
| 11 | A truncated human chromosome 16 associated with Î± thalassaemia is stabilized by addition of telomeric repeat (TTAGGG)n. Nature, 1990, 346, 868-871. | 27.8 | 300 |
| 12 | Transcription factors LRF and BCL11A independently repress expression of fetal hemoglobin. Science, 2016, 351, 285-289. | 12.6 | 260 |
| 13 | A Regulatory SNP Causes a Human Genetic Disease by Creating a New Transcriptional Promoter. Science, 2006, 312, 1215-1217. | 12.6 | 254 |
| 14 | Intragenic Enhancers Act as Alternative Promoters. Molecular Cell, 2012, 45, 447-458. | 9.7 | 237 |
| 15 | Association between active genes occurs at nuclear speckles and is modulated by chromatin environment. Journal of Cell Biology, 2008, 182, 1083-1097. | 5.2 | 231 |
| 16 | Multiplexed analysis of chromosome conformation at vastly improved sensitivity. Nature Methods, 2016, 13, 74-80. | 19.0 | 225 |
| 17 | Long-range chromosomal interactions regulate the timing of the transition between poised and active gene expression. EMBO Journal, 2007, 26, 2041-2051. | 7.8 | 224 |
| 18 | Suppression of the alternative lengthening of telomere pathway by the chromatin remodelling factor ATRX. Nature Communications, 2015, 6, 7538. | 12.8 | 219 |

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|---|---|---|---|
| 19 | Molecular-clinical spectrum of the ATR-X syndrome. American Journal of Medical Genetics Part A, 2000, 97, 204-212. | 2.4 | 208 |
| 20 | Mutations in transcriptional regulator ATRX establish the functional significance of a PHD-like domain. Nature Genetics, 1997, 17, 146-148. | 21.4 | 196 |
| 21 | Globin gene activation during haemopoiesis is driven by protein complexes nucleated by GATA-1 and GATA-2. EMBO Journal, 2004, 23, 2841-2852. | 7.8 | 193 |
| 22 | Coregulated human globin genes are frequently in spatial proximity when active. Journal of Cell Biology, 2006, 172, 177-187. | 5.2 | 192 |
| 23 | Combinatorial readout of histone H3 modifications specifies localization of ATRX to heterochromatin. Nature Structural and Molecular Biology, 2011, 18, 777-782. | 8.2 | 187 |
| 24 | Tissue-specific CTCFâ€“cohesin-mediated chromatin architecture delimits enhancer interactions and function in vivo. Nature Cell Biology, 2017, 19, 952-961. | 10.3 | 179 |
| 25 | An interspecies analysis reveals a key role for unmethylated CpG dinucleotides in vertebrate Polycomb complex recruitment. EMBO Journal, 2012, 31, 317-329. | 7.8 | 173 |
| 26 | Stable length polymorphism of up to 260 kb at the tip of the short arm of human chromosome 16. Cell, 1991, 64, 595-606. | 28.9 | 169 |
| 27 | The chromatin-remodeling protein ATRX is critical for neuronal survival during corticogenesis. Journal of Clinical Investigation, 2005, 115, 258-267. | 8.2 | 169 |
| 28 | The relationship between genome structure and function. Nature Reviews Genetics, 2021, 22, 154-168. | 16.3 | 160 |
| 29 | ATRX Plays a Key Role in Maintaining Silencing at Interstitial Heterochromatic Loci and Imprinted Genes. Cell Reports, 2015, 11, 405-418. | 6.4 | 152 |
| 30 | Comparative genome analysis delimits a chromosomal domain and identifies key regulatory elements in the alpha globin cluster. Human Molecular Genetics, 2001, 10, 371-382. | 2.9 | 151 |
| 31 | Manipulating the Mouse Genome to Engineer Precise Functional Syntenic ReplacementsÂwith Human Sequence. Cell, 2007, 128, 197-209. | 28.9 | 150 |
| 32 | Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. Nature Genetics, 2018, 50, 1744-1751. | 21.4 | 150 |
| 33 | The relationship between chromosome structure and function at a human telomeric region. Nature Genetics, 1997, 15, 252-257. | 21.4 | 143 |
| 34 | Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. Nature Genetics, 2011, 43, 295-301. | 21.4 | 142 |
| 35 | Loss of Atrx Affects Trophoblast Development and the Pattern of X-Inactivation in Extraembryonic Tissues. PLoS Genetics, 2006, 2, e58. | 3.5 | 140 |
| 36 | Expression of Î±- and Î²-globin genes occurs within different nuclear domains in haemopoietic cells. Nature Cell Biology, 2001, 3, 602-606. | 10.3 | 139 |

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| 37 | Structural consequences of disease-causing mutations in the ATRX-DNMT3-DNMT3L (ADD) domain of the chromatin-associated protein ATRX. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 11939-11944. | 7.1 | 138 |
| 38 | Annotation of cis-regulatory elements by identification, subclassification, and functional assessment of multispecies conserved sequences. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 9830-9835. | 7.1 | 133 |
| 39 | Identification of acquired somatic mutations in the gene encoding chromatin-remodeling factor ATRX in the Î±-thalassemia myelodysplasia syndrome (ATMDS). Nature Genetics, 2003, 34, 446-449. | 21.4 | 132 |
| 40 | DNA methylation of intragenic CpG islands depends on their transcriptional activity during differentiation and disease. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E7526-E7535. | 7.1 | 125 |
| 41 | KrÃ¼ppeling erythropoiesis: an unexpected broad spectrum of human red blood cell disorders due to KLF1 variants. Blood, 2016, 127, 1856-1862. | 1.4 | 124 |
| 42 | How best to identify chromosomal interactions: a comparison of approaches. Nature Methods, 2017, 14, 125-134. | 19.0 | 124 |
| 43 | The chromatin-remodeling protein ATRX is critical for neuronal survival during corticogenesis. Journal of Clinical Investigation, 2005, 115, 258-267. | 8.2 | 119 |
| 44 | The Molecular Basis of Â-Thalassemia. Cold Spring Harbor Perspectives in Medicine, 2013, 3, a011718-a011718. | 6.2 | 106 |
| 45 | RNA discrimination. Nature, 2012, 482, 310-311. | 27.8 | 104 |
| 46 | The chromatin remodeller ATRX: a repeat offender in human disease. Trends in Biochemical Sciences, 2013, 38, 461-466. | 7.5 | 103 |
| 47 | Evaluation of alpha hemoglobin stabilizing protein (AHSP) as a genetic modifier in patients with Î² thalassemia. Blood, 2004, 103, 3296-3299. | 1.4 | 102 |
| 48 | Î±-Globin as a molecular target in the treatment of Î²-thalassemia. Blood, 2015, 125, 3694-3701. | 1.4 | 102 |
| 49 | Loss of Extreme Long-Range Enhancers in Human Neural Crest Drives a Craniofacial Disorder. Cell Stem Cell, 2020, 27, 765-783.e14. | 11.1 | 101 |
| 50 | The chromatin remodelling factor <scp>ATRX</scp> suppresses Râ€loops in transcribed telomeric repeats. EMBO Reports, 2017, 18, 914-928. | 4.5 | 99 |
| 51 | Acquired Î±-thalassemia in association with myelodysplastic syndrome and other hematologic malignancies. Blood, 2005, 105, 443-452. | 1.4 | 95 |
| 52 | Global gene expression analysis of human erythroid progenitors. Blood, 2011, 117, e96-e108. | 1.4 | 95 |
| 53 | 5 Î±-Thalassaemia. Best Practice and Research: Clinical Haematology, 1993, 6, 117-150. | 1.1 | 94 |
| 54 | Do LCRs Open Chromatin Domains?. Cell, 1998, 95, 299-302. | 28.9 | 94 |

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|---|---|---|---|
| 55 | Molecular Basis and Genetic Modifiers of Thalassemia. Hematology/Oncology Clinics of North America, 2018, 32, 177-191. | 2.2 | 93 |
| 56 | SW-ARRAY: a dynamic programming solution for the identification of copy-number changes in genomic DNA using array comparative genome hybridization data. Nucleic Acids Research, 2005, 33, 3455-3464. | 14.5 | 87 |
| 57 | Editing an Î±-globin enhancer in primary human hematopoietic stem cells as a treatment for Î²-thalassemia. Nature Communications, 2017, 8, 424. | 12.8 | 85 |
| 58 | Acquired somatic ATRX mutations in myelodysplastic syndrome associated with Î± thalassemia (ATMDS) convey a more severe hematologic phenotype than germline ATRX mutations. Blood, 2004, 103, 2019-2026. | 1.4 | 84 |
| 59 | ATRX Dysfunction Induces Replication Defects in Primary Mouse Cells. PLoS ONE, 2014, 9, e92915. | 2.5 | 84 |
| 60 | Sequence, structure and pathology of the fully annotated terminal 2 Mb of the short arm of human chromosome 16. Human Molecular Genetics, 2001, 10, 339-352. | 2.9 | 81 |
| 61 | Chromosome looping at the human Î±-globin locus is mediated via the major upstream regulatory element (HS â^'40). Blood, 2009, 114, 4253-4260. | 1.4 | 79 |
| 62 | Dynamics of the 4D genome during in vivo lineage specification and differentiation. Nature Communications, 2020, 11, 2722. | 12.8 | 79 |
| 63 | Polycomb eviction as a new distant enhancer function. Genes and Development, 2011, 25, 1583-1588. | 5.9 | 78 |
| 64 | Adventitious changes in long-range gene expression caused by polymorphic structural variation and promoter competition. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 21771-21776. | 7.1 | 77 |
| 65 | Mutations in KrÃ¼ppel-like factor 1 cause transfusion-dependent hemolytic anemia and persistence of embryonic globin gene expression. Blood, 2014, 123, 1586-1595. | 1.4 | 76 |
| 66 | The IL-9 Receptor Gene (IL9R): Genomic Structure, Chromosomal Localization in the Pseudoautosomal Region of the Long Arm of the Sex Chromosomes, and Identification of IL9R Pseudogenes at 9qter, 10pter, 16pter, and 18pter. Genomics, 1995, 29, 371-382. | 2.9 | 72 |
| 67 | A nonsense mutation of theATRX gene causing mild mental retardation and epilepsy. Annals of Neurology, 2000, 47, 117-121. | 5.3 | 72 |
| 68 | Homozygous mutations in a predicted endonuclease are a novel cause of congenital dyserythropoietic anemia type I. Haematologica, 2013, 98, 1383-1387. | 3.5 | 71 |
| 69 | Tissue-specific histone modification and transcription factor binding in Î± globin gene expression. Blood, 2007, 110, 4503-4510. | 1.4 | 69 |
| 70 | Long-range regulation of ?? globin gene expression during erythropoiesis. Current Opinion in Hematology, 2008, 15, 176-183. | 2.5 | 66 |
| 71 | Comparison of the human and murine ATRX gene identifies highly conserved, functionally important domains. Mammalian Genome, 1998, 9, 400-403. | 2.2 | 64 |
| 72 | A tissue-specific self-interacting chromatin domain forms independently of enhancer-promoter interactions. Nature Communications, 2018, 9, 3849. | 12.8 | 62 |

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| 73 | Neuronal Death Resulting from Targeted Disruption of the Snf2 Protein ATRX Is Mediated by p53. Journal of Neuroscience, 2008, 28, 12570-12580. | 3.6 | 61 |
| 74 | The bipartite TAD organization of the X-inactivation center ensures opposing developmental regulation of Tsix and Xist. Nature Genetics, 2019, 51, 1024-1034. | 21.4 | 60 |
| 75 | A revised model for promoter competition based on multi-way chromatin interactions at the Î±-globin locus. Nature Communications, 2019, 10, 5412. | 12.8 | 60 |
| 76 | An international registry of survivors with Hb Bart's hydrops fetalis syndrome. Blood, 2017, 129, 1251-1259. | 1.4 | 59 |
| 77 | Codanin-1 mutations in congenital dyserythropoietic anemia type 1 affect HP1Î± localization in erythroblasts. Blood, 2011, 117, 6928-6938. | 1.4 | 58 |
| 78 | Conservation of Position and Sequence of a Novel, Widely Expressed Gene Containing the Major Human Î±-Globin Regulatory Element. Genomics, 1995, 29, 679-689. | 2.9 | 56 |
| 79 | Generation of bivalent chromatin domains during cell fate decisions. Epigenetics and Chromatin, 2011, 4, 9. | 3.9 | 54 |
| 80 | Structure and expression of the human Î¸ globin gene. Nature, 1988, 331, 94-96. | 27.8 | 53 |
| 81 | Deletion of the mouse Î±-globin regulatory element (HS â^'26) has an unexpectedly mild phenotype. Blood, 2002, 100, 3450-3456. | 1.4 | 53 |
| 82 | A conserved truncated isoform of the ATR-X syndrome protein lacking the SWI/SNF-homology domain. Gene, 2004, 326, 23-34. | 2.2 | 53 |
| 83 | Testing the super-enhancer concept. Nature Reviews Genetics, 2021, 22, 749-755. | 16.3 | 53 |
| 84 | The role of the polycomb complex in silencing Î±-globin gene expression in nonerythroid cells. Blood, 2008, 112, 3889-3899. | 1.4 | 51 |
| 85 | X-linked Î±-thalassemia/mental retardation (ATR-X) syndrome: A new kindred with severe genital anomalies and mild hematologic expression. American Journal of Medical Genetics Part A, 1995, 55, 302-306. | 2.4 | 50 |
| 86 | Î±-Thalassemia resulting from a negative chromosomal position effect. Blood, 2000, 96, 800-807. | 1.4 | 50 |
| 87 | Clinical features and molecular analysis of acquired hemoglobin H disease. American Journal of Medicine, 1983, 75, 181-191. | 1.5 | 49 |
| 88 | Analysis of a 70 kb segment of DNA containing the human Î¶ and Î±-globin genes linked to their regulatory element (HS-40) in transgenic mice. Nucleic Acids Research, 1994, 22, 4139-4147. | 14.5 | 48 |
| 89 | Population analysis of the alpha hemoglobin stabilizing protein (AHSP) gene identifies sequence variants that alter expression and function. American Journal of Hematology, 2008, 83, 103-108. | 4.1 | 48 |
| 90 | Monosomy for the most telomeric, gene-rich region of the short arm of human chromosome 16 causes minimal phenotypic effects. European Journal of Human Genetics, 2001, 9, 217-225. | 2.8 | 47 |

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| 91 | Functional significance of mutations in the Snf2 domain of ATRX. Human Molecular Genetics, 2011, 20, 2603-2610. | 2.9 | 46 |
| 92 | Understanding Î±â€globin gene regulation and implications for the treatment of Î²â€thalassemia. Annals of the New York Academy of Sciences, 2016, 1368, 16-24. | 3.8 | 44 |
| 93 | Genetic complexity in sickle cell disease. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11595-11596. | 7.1 | 43 |
| 94 | Nprl3 is required for normal development of the cardiovascular system. Mammalian Genome, 2012, 23, 404-415. | 2.2 | 38 |
| 95 | An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Research, 2020, 30, 472-484. | 5.5 | 38 |
| 96 | A Dynamic Folded Hairpin Conformation Is Associated with Î±-Globin Activation in Erythroid Cells. Cell Reports, 2020, 30, 2125-2135.e5. | 6.4 | 38 |
| 97 | De novo deletion within the telomeric region flanking the human Î± globin locus as a cause of Î± thalassaemia. British Journal of Haematology, 2003, 120, 867-875. | 2.5 | 36 |
| 98 | The Molecular Basis of Î±-Thalassemia: A Model for Understanding Human Molecular Genetics. Hematology/Oncology Clinics of North America, 2010, 24, 1033-1054. | 2.2 | 36 |
| 99 | Deletion of the Î±-globin gene cluster as a cause of acquired Î±-thalassemia in myelodysplastic syndrome. Blood, 2004, 103, 1518-1520. | 1.4 | 34 |
| 100 | A novel deletion causing Î± thalassemia clarifies the importance of the major human alpha globin regulatory element. Blood, 2006, 107, 3811-3812. | 1.4 | 34 |
| 101 | Using Genomics to Study How Chromatin Influences Gene Expression. Annual Review of Genomics and Human Genetics, 2007, 8, 299-325. | 6.2 | 33 |
| 102 | Selective silencing of Î±-globin by the histone demethylase inhibitor IOX1: a potentially new pathway for treatment of Î²-thalassemia. Haematologica, 2017, 102, e80-e84. | 3.5 | 33 |
| 103 | Defining the Cause of Skewed X-Chromosome Inactivation in X-Linked Mental Retardation by Use of a Mouse Model. American Journal of Human Genetics, 2007, 80, 1138-1149. | 6.2 | 32 |
| 104 | Functional characterisation of cis-regulatory elements governing dynamic Eomes expression in the early mouse embryo. Development (Cambridge), 2017, 144, 1249-1260. | 2.5 | 32 |
| 105 | Characterization of a Widely Expressed Gene (LUC7-LIKE; LUC7L) Defining the Centromeric Boundary of the Human Î±-Globin Domain. Genomics, 2001, 71, 307-314. | 2.9 | 31 |
| 106 | Chapter 5 Longâ€Range Regulation of Î±â€Globin Gene Expression. Advances in Genetics, 2008, 61, 143-173. | 1.8 | 30 |
| 107 | Comparative Analysis of the Â-Like Globin Clusters in Mouse, Rat, and Human Chromosomes Indicates a Mechanism Underlying Breaks in Conserved Synteny. Genome Research, 2004, 14, 623-630. | 5.5 | 29 |
| 108 | Robust detection of chromosomal interactions from small numbers of cells using low-input Capture-C. Nucleic Acids Research, 2017, 45, e184-e184. | 14.5 | 27 |

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| 109 | Enhancers predominantly regulate gene expression during differentiation via transcription initiation. Molecular Cell, 2021, 81, 983-997.e7. | 9.7 | 27 |
| 110 | A large deletion in the human Â-globin cluster caused by a replication error is associated with an unexpectedly mild phenotype. Human Molecular Genetics, 2008, 17, 3084-3093. | 2.9 | 26 |
| 111 | Ham-Wasserman Lecture. Hematology American Society of Hematology Education Program, 2004, 2004, 1-13. | 2.5 | 25 |
| 112 | Potential new approaches to the management of the Hb Bartâ€™s hydrops fetalis syndrome: the most severe form of Î±-thalassemia. Hematology American Society of Hematology Education Program, 2018, 2018, 353-360. | 2.5 | 25 |
| 113 | The Î±-Thalassemia/Mental Retardation Syndromes. Medicine (United States), 1996, 75, 45-52. | 1.0 | 24 |
| 114 | MicroRNAs of the miR-290â€“295 Family Maintain Bivalency in Mouse Embryonic Stem Cells. Stem Cell Reports, 2016, 6, 635-642. | 4.8 | 24 |
| 115 | The mouse alpha-globin cluster: a paradigm for studying genome regulation and organization. Current Opinion in Genetics and Development, 2021, 67, 18-24. | 3.3 | 21 |
| 116 | Between form and function: the complexity of genome folding. Human Molecular Genetics, 2017, 26, R208-R215. | 2.9 | 20 |
| 117 | The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. Nature Communications, 2022, 13, . | 12.8 | 20 |
| 118 | Reactivation of a developmentally silenced embryonic globin gene. Nature Communications, 2021, 12, 4439. | 12.8 | 19 |
| 119 | Causes and Consequences of Chromatin Variation between Inbred Mice. PLoS Genetics, 2013, 9, e1003570. | 3.5 | 18 |
| 120 | A gain-of-function single nucleotide variant creates a new promoter which acts as an orientation-dependent enhancer-blocker. Nature Communications, 2021, 12, 3806. | 12.8 | 18 |
| 121 | An unusually large (CA)n repeat in the region of divergence between subtelomeric alleles of human chromosome 16p. Genomics, 1992, 13, 81-88. | 2.9 | 17 |
| 122 | Robust CRISPR/Cas9 Genome Editing of the HUDEP-2 Erythroid Precursor Line Using Plasmids and Single-Stranded Oligonucleotide Donors. Methods and Protocols, 2018, 1, 28. | 2.0 | 17 |
| 123 | An evolutionarily ancient mechanism for regulation of hemoglobin expression in vertebrate red cells. Blood, 2020, 136, 269-278. | 1.4 | 16 |
| 124 | Human ARHGDIG, a GDP-Dissociation Inhibitor for Rho Proteins: Genomic Structure, Sequence, Expression Analysis, and Mapping to Chromosome 16p13.3. Genomics, 1998, 53, 104-109. | 2.9 | 14 |
| 125 | Prevalence of erythrocyte haemoglobin H inclusions in unselected patients with clonal myeloid disorders. British Journal of Haematology, 2007, 139, 439-442. | 2.5 | 12 |
| 126 | A New Dawn for Stem-Cell Therapy. New England Journal of Medicine, 2008, 358, 964-966. | 27.0 | 12 |

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| 127 | High-resolution analysis of cis -acting regulatory networks at the Î±-globin locus. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120361. | 4.0 | 12 |
| 128 | Differential regulation of the Î±-globin locus by KrÃ¼ppel-like factor 3 in erythroid and non-erythroid cells. BMC Molecular Biology, 2014, 15, 8. | 3.0 | 11 |
| 129 | A novel mutation in the last exon of ATRX in a patient with alpha-thalassemia myelodysplastic syndrome. European Journal of Haematology, 2006, 76, 432-435. | 2.2 | 10 |
| 130 | Analysis of Sequence Variation Underlying Tissue-specific Transcription Factor Binding and Gene Expression. Human Mutation, 2013, 34, 1140-1148. | 2.5 | 10 |
| 131 | Recapitulation of erythropoiesis in congenital dyserythropoietic anemia type I (CDA-I) identifies defects in differentiation and nucleolar abnormalities. Haematologica, 2021, 106, 2960-2970. | 3.5 | 10 |
| 132 | The role of Xâ€inactivation in the gender bias of patients with acquired Î±â€thalassaemia and myelodysplastic syndrome (ATMDS). British Journal of Haematology, 2009, 144, 538-545. | 2.5 | 9 |
| 133 | Genetic and functional insights into CDA-I prevalence and pathogenesis. Journal of Medical Genetics, 2021, 58, 185-195. | 3.2 | 9 |
| 134 | The Normal Structure and Regulation of Human Globin Gene Clusters. , 0, , 46-61. | | 8 |
| 135 | Systematic integration of GATA transcription factors and epigenomes via IDEAS paints the regulatory landscape of hematopoietic cells. IUBMB Life, 2020, 72, 27-38. | 3.4 | 8 |
| 136 | Scalable in vitro production of defined mouse erythroblasts. PLoS ONE, 2022, 17, e0261950. | 2.5 | 8 |
| 137 | The Pathophysiology and Clinical Features of Î± Thalassaemia. , 2009, , 266-295. | | 7 |
| 138 | An international effort to cure a global health problem: A report on the 19th Hemoglobin Switching Conference. Experimental Hematology, 2015, 43, 821-837. | 0.4 | 7 |
| 139 | How to Tackle Challenging ChIP-Seq, with Long-Range Cross-Linking, Using ATRX as an Example. Methods in Molecular Biology, 2018, 1832, 105-130. | 0.9 | 7 |
| 140 | ATR-16 syndrome: mechanisms linking monosomy to phenotype. Journal of Medical Genetics, 2020, 57, 414-421. | 3.2 | 7 |
| 141 | Î± THALASSEMIA. , 0, , 239-240. | | 6 |
| 142 | Switching genes on and off in haemopoiesis. Biochemical Society Transactions, 2008, 36, 613-618. | 3.4 | 6 |
| 143 | A remarkable case of HbH disease illustrates the relative contributions of the Î±-globin enhancers to gene expression. Blood, 2021, 137, 572-575. | 1.4 | 6 |
| 144 | Genetic Modulation of Sickle Cell Disease and Thalassemia. , 2009, , 638-657. | | 4 |

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| 145 | Other Sickle Hemoglobinopathies. , 0, , 564-586. | | 4 |
| 146 | ATRX: Taming tandem repeats. Cell Cycle, 2010, 9, 4605-4606. | 2.6 | 4 |
| 147 | Molecular and Cellular Basis of Hemoglobin Switching. , 0, , 86-100. | | 3 |
| 148 | Nuclear Factors That Regulate Erythropoiesis. , 2009, , 62-85. | | 3 |
| 149 | Unusual Types of Î± Thalassemia. , 0, , 296-320. | | 2 |
| 150 | Î±-Thalassemia resulting from a negative chromosomal position effect. Blood, 2000, 96, 800-807. | 1.4 | 2 |
| 151 | The Molecular Basis of Î± Thalassemia. , 2009, , 241-265. | | 1 |
| 152 | THE MOLECULAR, CELLULAR, AND GENETIC BASIS OF HEMOGLOBIN DISORDERS. , 2009, , 1-2. | | 0 |
| 153 | Research Highlights. Epigenomics, 2009, 1, 231-234. | 2.1 | 0 |
| 154 | SPECIAL TOPICS IN HEMOGLOBINOPATHIES. , 2009, , 623-624. | | 0 |
| 155 | Switching Genes On and Off During Hematopoiesis.. Blood, 2008, 112, sci-17-sci-17. | 1.4 | 0 |