Douglas Higgs

List of Publications by Year in descending order

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166 papers	10,210 citations	31976 53 h-index	40979 93 g-index
236 all docs	236 docs citations	236 times ranked	11156 citing authors

#	Article	IF	Citations
1	Scalable in vitro production of defined mouse erythroblasts. PLoS ONE, 2022, 17, e0261950.	2.5	8
2	Functional impairment of erythropoiesis in Congenital Dyserythropoietic Anaemia type I arises at the progenitor level. British Journal of Haematology, 2022, , .	2.5	0
3	The chromatin remodeller ATRX facilitates diverse nuclear processes, in a stochastic manner, in both heterochromatin and euchromatin. Nature Communications, 2022, 13, .	12.8	20
4	Genetic and functional insights into CDA-I prevalence and pathogenesis. Journal of Medical Genetics, 2021, 58, 185-195.	3.2	9
5	The relationship between genome structure and function. Nature Reviews Genetics, 2021, 22, 154-168.	16.3	160
6	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
7	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
8	Enhancers predominantly regulate gene expression during differentiation via transcription initiation. Molecular Cell, 2021, 81, 983-997.e7.	9.7	27
9	Defining genome architecture at base-pair resolution. Nature, 2021, 595, 125-129.	27.8	107
10	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
11	Reactivation of a developmentally silenced embryonic globin gene. Nature Communications, 2021, 12, 4439.	12.8	19
12	Testing the super-enhancer concept. Nature Reviews Genetics, 2021, 22, 749-755.	16.3	53
13	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
14	The EHA Research Roadmap: Normal Hematopoiesis. HemaSphere, 2021, 5, e669.	2.7	1
15	Base Editing Repairs the HbE Mutation Restoring the Production of Normal Globin Chains in Severe HbE/Î²-Thalassemia Patient Hematopoietic Stem Cells and Erythroid Cells. Blood, 2021, 138, 2935-2935.	1.4	0
16	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
17	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
18	Enhancerâ€“promoter interactions and transcription. Nature Genetics, 2020, 52, 470-471.	21.4	15

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19	Dynamics of the 4D genome during in vivo lineage specification and differentiation. Nature Communications, 2020, 11, 2722.	12.8	79
20	An evolutionarily ancient mechanism for regulation of hemoglobin expression in vertebrate red cells. Blood, 2020, 136, 269-278.	1.4	16
21	An integrative view of the regulatory and transcriptional landscapes in mouse hematopoiesis. Genome Research, 2020, 30, 472-484.	5.5	38
22	A Dynamic Folded Hairpin Conformation Is Associated with Î±-Globin Activation in Erythroid Cells. Cell Reports, 2020, 30, 2125-2135.e5.	6.4	38
23	ATR-16 syndrome: mechanisms linking monosomy to phenotype. Journal of Medical Genetics, 2020, 57, 414-421.	3.2	7
24	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
25	Single-Cell Proteomics Reveal that Quantitative Changes in Co-expressed Lineage-Specific Transcription Factors Determine Cell Fate. Cell Stem Cell, 2019, 24, 812-820.e5.	11.1	99
26	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
27	The Loss of ATRX Increases Susceptibility to Pancreatic Injury and Oncogenic KRAS in Female But Not Male Mice. Cellular and Molecular Gastroenterology and Hepatology, 2019, 7, 93-113.	4.5	14
28	Beta thalassaemia intermedia due to coâ€inheritance of three unique alpha globin cluster duplications characterised by next generation sequencing analysis. British Journal of Haematology, 2018, 180, 160-164.	2.5	19
29	Molecular Basis and Genetic Modifiers of Thalassemia. Hematology/Oncology Clinics of North America, 2018, 32, 177-191.	2.2	93
30	Phenotypic and molecular characterization of a serum-free miniature erythroid differentiation system suitable for high-throughput screening and single-cell assays. Experimental Hematology, 2018, 60, 10-20.	0.4	6
31	A tissue-specific self-interacting chromatin domain forms independently of enhancer-promoter interactions. Nature Communications, 2018, 9, 3849.	12.8	62
32	Anaemia among females in child-bearing age: Relative contributions, effects and interactions of Î±- and Î²-thalassaemia. PLoS ONE, 2018, 13, e0206928.	2.5	17
33	Single-allele chromatin interactions identify regulatory hubs in dynamic compartmentalized domains. Nature Genetics, 2018, 50, 1744-1751.	21.4	150
34	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
35	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
36	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

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37	Expression of the Human Alpha-Globin Cluster in the Absence of the Major Regulatory Element Mcs-R2. Blood, 2018, 132, 3632-3632.	1.4	1
38	How best to identify chromosomal interactions: a comparison of approaches. Nature Methods, 2017, 14, 125-134.	19.0	124
39	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
40	Functional characterisation of cis-regulatory elements governing dynamic Eomes expression in the early mouse embryo. Development (Cambridge), 2017, 144, 1249-1260.	2.5	32
41	An international registry of survivors with Hb Bart's hydrops fetalis syndrome. Blood, 2017, 129, 1251-1259.	1.4	59
42	The chromatin remodelling factor <scp>ATRX</scp> suppresses Râ€loops in transcribed telomeric repeats. EMBO Reports, 2017, 18, 914-928.	4.5	99
43	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
44	Sasquatch: predicting the impact of regulatory SNPs on transcription factor binding from cell- and tissue-specific DNase footprints. Genome Research, 2017, 27, 1730-1742.	5.5	33
45	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
46	Tissue-specific CTCFâ€“cohesin-mediated chromatin architecture delimits enhancer interactions and function in vivo. Nature Cell Biology, 2017, 19, 952-961.	10.3	179
47	Between form and function: the complexity of genome folding. Human Molecular Genetics, 2017, 26, R208-R215.	2.9	20
48	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
49	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
50	Genetic dissection of the Î±-globin super-enhancer in vivo. Nature Genetics, 2016, 48, 895-903.	21.4	308
51	MicroRNAs of the miR-290â€“295 Family Maintain Bivalency in Mouse Embryonic Stem Cells. Stem Cell Reports, 2016, 6, 635-642.	4.8	24
52	KrÃ¼ppeling erythropoiesis: an unexpected broad spectrum of human red blood cell disorders due to KLF1 variants. Blood, 2016, 127, 1856-1862.	1.4	124
53	Haemoglobin Variant Screening in Jamaica: Meeting Student's Request. British Journal of Haematology, 2016, 172, 634-636.	2.5	10
54	Transcription factors LRF and BCL11A independently repress expression of fetal hemoglobin. Science, 2016, 351, 285-289.	12.6	260

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55	Multiplexed analysis of chromosome conformation at vastly improved sensitivity. Nature Methods, 2016, 13, 74-80.	19.0	225
56	Stem Cell Transplantation. , 2015, , 651-675.		1
57	Hereditary Disorders of the Red Cell Membrane and Disorders of Red Cell Metabolism. , 2015, , 114-137.		1
58	Studying epigenomics in single cells: what is feasible and what can we learn?. Epigenomics, 2015, 7, 1231-1234.	2.1	2
59	Suppression of the alternative lengthening of telomere pathway by the chromatin remodelling factor ATRX. Nature Communications, 2015, 6, 7538.	12.8	219
60	ATRX Plays a Key Role in Maintaining Silencing at Interstitial Heterochromatic Loci and Imprinted Genes. Cell Reports, 2015, 11, 405-418.	6.4	152
61	Î±-Globin as a molecular target in the treatment of Î²-thalassemia. Blood, 2015, 125, 3694-3701.	1.4	102
62	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
63	ATRX Dysfunction Induces Replication Defects in Primary Mouse Cells. PLoS ONE, 2014, 9, e92915.	2.5	84
64	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
65	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
66	Considerations when investigating lncRNA function in vivo. ELife, 2014, 3, e03058.	6.0	309
67	Regulated RNA Expression and Normal Erythropoiesis. Blood, 2014, 124, SCI-34-SCI-34.	1.4	0
68	Chromatin signatures at transcriptional start sites separate two equally populated yet distinct classes of intergenic long noncoding RNAs. Genome Biology, 2013, 14, R131.	9.6	183
69	Analysis of Sequence Variation Underlying Tissue-specific Transcription Factor Binding and Gene Expression. Human Mutation, 2013, 34, 1140-1148.	2.5	10
70	Causes and Consequences of Chromatin Variation between Inbred Mice. PLoS Genetics, 2013, 9, e1003570.	3.5	18
71	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
72	Homozygous mutations in a predicted endonuclease are a novel cause of congenital dyserythropoietic anemia type I. Haematologica, 2013, 98, 1383-1387.	3.5	71

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73	The Molecular Basis of Â-Thalassemia. Cold Spring Harbor Perspectives in Medicine, 2013, 3, a011718-a011718.	6.2	106
74	Dynamics and Mechanics Of KLF1 Regulation In Erythropoiesis. Blood, 2013, 122, 2176-2176.	1.4	11
75	Thalassaemia. Lancet, The, 2012, 379, 373-383.	13.7	371
76	Intragenic Enhancers Act as Alternative Promoters. Molecular Cell, 2012, 45, 447-458.	9.7	237
77	Nprl3 is required for normal development of the cardiovascular system. Mammalian Genome, 2012, 23, 404-415.	2.2	38
78	Global gene expression analysis of human erythroid progenitors. Blood, 2011, 117, e96-e108.	1.4	95
79	Codanin-1 mutations in congenital dyserythropoietic anemia type 1 affect HP1Î± localization in erythroblasts. Blood, 2011, 117, 6928-6938.	1.4	58
80	Systematic documentation and analysis of human genetic variation in hemoglobinopathies using the microattribution approach. Nature Genetics, 2011, 43, 295-301.	21.4	142
81	Î±-thalassaemia. Orphanet Journal of Rare Diseases, 2010, 5, 13.	2.7	417
82	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
83	A Developmental Approach to Hematopoiesis. , 2009, , 3-23.		0
84	The Erythrocyte Membrane. , 2009, , 158-184.		3
85	The Molecular Basis of Î± Thalassemia. , 2009, , 241-265.		1
86	Dyshemoglobinemias. , 2009, , 607-622.		11
87	Transfusion and Iron Chelation Therapy in Thalassemia and Sickle Cell Disease. , 2009, , 689-744.		2
88	Prospects for Gene Therapy of Sickle Cell Disease and Thalassemia. , 2009, , 791-814.		0
89	Foreword, by H. Franklin Bunn. , 2009, , xv-xvi.		0
90	Nuclear Factors That Regulate Erythropoiesis. , 2009, , 62-85.		3

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91	Rheology and Vascular Pathobiology in Sickle Cell Disease and Thalassemia. , 2009, , 139-157.		1
92	Novel Approaches to Treatment. , 2009, , 755-773.		0
93	Stem Cell Transplantation. , 2009, , 774-790.		0
94	THE Î² THALASSEMIAS. , 2009, , 321-322.		0
95	Clinical Aspects of Î² Thalassemia and Related Disorders. , 2009, , 357-416.		10
96	THE MOLECULAR, CELLULAR, AND GENETIC BASIS OF HEMOGLOBIN DISORDERS. , 2009, , 1-2.		0
97	Mechanisms and Clinical Complications of Hemolysis in Sickle Cell Disease and Thalassemia. , 2009, , 201-224.		9
98	The Pathophysiology and Clinical Features of Î± Thalassaemia. , 2009, , 266-295.		7
99	The Molecular Basis of Î² Thalassemia, ÎÎ² Thalassemia, and Hereditary Persistence of Fetal Hemoglobin. , 2009, , 323-356.		34
100	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
101	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
102	Clinical and Pathophysiological Aspects of Sickle Cell Anemia. , 2009, , 437-496.		3
103	PATHOPHYSIOLOGY OF HEMOGLOBIN AND ITS DISORDERS. , 2009, , 137-138.		0
104	Genetic Modulation of Sickle Cell Disease and Thalassemia. , 2009, , 638-657.		4
105	Sickle Cell Trait. , 2009, , 549-563.		0
106	SPECIAL TOPICS IN HEMOGLOBINOPATHIES. , 2009, , 623-624.		0
107	NEW APPROACHES TO THE TREATMENT OF HEMOGLOBINOPATHIES AND THALASSEMIA. , 2009, , 687-688.		0
108	OTHER CLINICALLY IMPORTANT DISORDERS OF HEMOGLOBIN. , 2009, , 587-588.		0

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109	Erythropoiesis. , 2009, , 24-45.		1
110	Hemoglobins of the Embryo, Fetus, and Adult. , 2009, , 119-136.		10
111	Hemoglobin E Disorders. , 2009, , 417-434.		10
112	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
113	Chapter 5 Longâ€Range Regulation of Î±â€Globin Gene Expression. Advances in Genetics, 2008, 61, 143-173.	1.8	30
114	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
115	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
116	A New Dawn for Stem-Cell Therapy. New England Journal of Medicine, 2008, 358, 964-966.	27.0	12
117	Long-range regulation of ?? globin gene expression during erythropoiesis. Current Opinion in Hematology, 2008, 15, 176-183.	2.5	66
118	Switching Genes On and Off During Hematopoiesis.. Blood, 2008, 112, sci-17-sci-17.	1.4	0
119	Analysis of DNA Methylation at the Human Alpha Globin Cluster during Hematopoiesis.. Blood, 2008, 112, 1861-1861.	1.4	0
120	Manipulating the Mouse Genome to Engineer Precise Functional Syntenic ReplacementsÂwith Human Sequence. Cell, 2007, 128, 197-209.	28.9	150
121	Tissue-specific histone modification and transcription factor binding in Î± globin gene expression. Blood, 2007, 110, 4503-4510.	1.4	69
122	Using Genomics to Study How Chromatin Influences Gene Expression. Annual Review of Genomics and Human Genetics, 2007, 8, 299-325.	6.2	33
123	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
124	A Regulatory SNP Causes a Human Genetic Disease by Creating a New Transcriptional Promoter. Science, 2006, 312, 1215-1217.	12.6	254
125	A lack of border guards?. Blood, 2006, 108, 1121-1121.	1.4	0
126	5-Azacytidine treatment of the patient with ATMDS. European Journal of Haematology, 2006, 76, 453-453.	2.2	0

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127	Coregulated human globin genes are frequently in spatial proximity when active. Journal of Cell Biology, 2006, 172, 177-187.	5.2	192
128	How transcriptional and epigenetic programmes are played out on an individual mammalian gene cluster during lineage commitment and differentiation. Biochemical Society Symposia, 2006, 73, 11-22.	2.7	7
129	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
130	An Entirely Novel Form of Î± Thalassemia in Patients from the South Pacific Linked to Chromosome 16.. Blood, 2005, 106, 2688-2688.	1.4	4
131	Ham-Wasserman Lecture. Hematology American Society of Hematology Education Program, 2004, 2004, 1-13.	2.5	25
132	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
133	A Novel Splicing Mutation in the Gene Encoding the Chromatin-Associated Factor ATRX Associated with Acquired Hemoglobin H Disease in Myelodysplastic Syndrome (ATMDS).. Blood, 2004, 104, 3606-3606.	1.4	3
134	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
135	Functional and comparative analysis of globin loci in pufferfish and humans. Blood, 2003, 101, 2842-2849.	1.4	53
136	Deletion of the mouse Î±-globin regulatory element (HS â^'26) has an unexpectedly mild phenotype. Blood, 2002, 100, 3450-3456.	1.4	53
137	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
138	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
139	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
140	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
141	A nonsense mutation of theATRX gene causing mild mental retardation and epilepsy. Annals of Neurology, 2000, 47, 117-121.	5.3	72
142	Comparison of the human and murine ATRX gene identifies highly conserved, functionally important domains. Mammalian Genome, 1998, 9, 400-403.	2.2	64
143	The relationship between chromosome structure and function at a human telomeric region. Nature Genetics, 1997, 15, 252-257.	21.4	143
144	Mutations in transcriptional regulator ATRX establish the functional significance of a PHD-like domain. Nature Genetics, 1997, 17, 146-148.	21.4	196

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145	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
146	5 Î±-Thalassaemia. Best Practice and Research: Clinical Haematology, 1993, 6, 117-150.	1.1	94
147	A base substitution (Tâ†'C) in codon 29 of the Î±2â€globin gene causes Î± thalassaemia. British Journal of Haematology, 1993, 85, 546-552.	2.5	47
148	The haematology of homozygous sickle cell disease after the age of 40 years. British Journal of Haematology, 1991, 77, 382-385.	2.5	44
149	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
150	Individual specific DNA fingerprints from a hypervariable region probe: alpha-globin 3?HVR. Human Genetics, 1988, 79, 142-146.	3.8	71
151	Structure and expression of the human Î¸l globin gene. Nature, 1988, 331, 94-96.	27.8	53
152	Hemoglobin SC Disease and Hemoglobin C Disorders. , 0, , 525-548.		4
153	Molecular and Cellular Basis of Hemoglobin Switching. , 0, , 86-100.		3
154	Introduction, by David J. Weatherall. , 0, , xix-xx.		0
155	The Biology of Vascular Nitric Oxide. , 0, , 185-200.		0
156	Animal Models of Hemoglobinopathies and Thalassemia. , 0, , 225-238.		0
157	Î± THALASSEMIA. , 0, , 239-240.		6
158	Structure and Function of Hemoglobin and Its Dysfunction in Sickle Cell Disease. , 0, , 101-118.		0
159	Unusual Types of Î± Thalassemia. , 0, , 296-320.		2
160	Population Genetics and Global Health Burden. , 0, , 625-637.		1
161	Induction of Fetal Hemoglobin in the Treatment of Sickle Cell Disease and Î² Thalassemia. , 0, , 745-754.		6
162	Unstable Hemoglobins, Hemoglobins with Altered Oxygen Affinity, Hemoglobin M, and Other Variants of Clinical and Biological Interest. , 0, , 589-606.		6

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163	Sickle Cell Pain: Biology, Etiology, and Treatment. , 0, , 497-524.		5
164	Laboratory Methods for Diagnosis and Evaluation of Hemoglobin Disorders. , 0, , 658-686.		3
165	Other Sickle Hemoglobinopathies. , 0, , 564-586.		4
166	The Normal Structure and Regulation of Human Globin Gene Clusters. , 0, , 46-61.		8