Vijay G Sankaran

List of Publications by Year
in descending order

140 papers	11,889 citations	50276 46 h-index	32842 100 g-index
167 all docs	167 docs citations	167 times ranked	14742 citing authors

#	Article	IF	Citations
1	Primary HBB gene mutation severity and longâ€term outcomes in a global cohort of Î²â€thalassaemia. British Journal of Haematology, 2022, 196, 414-423.	2.5	8
2	From GWAS variant to function: A study of â¼148,000 variants for blood cell traits. Human Genetics and Genomics Advances, 2022, 3, 100063.	1.7	9
3	Germline GATA1s-generating mutations predispose toÂleukemia with acquired trisomy 21 and Down syndrome-like phenotype. Blood, 2022, 139, 3159-3165.	1.4	15
4	Clonal hematopoiesis in sickle cell disease. Journal of Clinical Investigation, 2022, 132, .	8.2	26
5	Congenital anemia reveals distinct targeting mechanisms for master transcription factor GATA1. Blood, 2022, 139, 2534-2546.	1.4	14
6	Super interactive promoters provide insight into cell type-specific regulatory networks in blood lineage cell types. PLoS Genetics, 2022, 18, e1009984.	3.5	4
7	Genome-wide association study on 13â€‰167 individuals identifies regulators of blood CD34+cell levels. Blood, 2022, 139, 1659-1669.	1.4	4
8	Functional dissection of inherited non-coding variation influencing multiple myeloma risk. Nature Communications, 2022, 13, 151.	12.8	10
9	Mapping transcriptomic vector fields of single cells. Cell, 2022, 185, 690-711.e45.	28.9	167
10	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347.	2.9	6
11	Mitochondrial variant enrichment from high-throughput single-cell RNA sequencing resolves clonal populations. Nature Biotechnology, 2022, 40, 1030-1034.	17.5	45
12	Random Forest Clustering Identifies Three Subgroups of Î²-Thalassemia with Distinct Clinical Severity. Thalassemia Reports, 2022, 12, 14-23.	0.5	3
13	A novel missense mutation outside the <scp>DNAJ</scp> domain of <scp>DNAJC21</scp> is associated with <scp>Shwachmanâ€“Diamond</scp> syndrome. British Journal of Haematology, 2022, 197, .	2.5	4
14	Patchwork Cancer Predisposition. Cancer Discovery, 2022, 12, 889-891.	9.4	1
15	Molecular and cellular mechanisms that regulate human erythropoiesis. Blood, 2022, 139, 2450-2459.	1.4	22
16	Risk of mortality from anemia and iron overload in nontransfusionâ€dependent Î²â€thalassemia. American Journal of Hematology, 2022, 97, .	4.1	19
17	Variant to function mapping at single-cell resolution through network propagation. Nature Biotechnology, 2022, 40, 1644-1653.	17.5	25
18	Genotype-phenotype association and variant characterization in Diamond-Blackfan anemia caused by pathogenic variants in <i>RPL35A</i>. Haematologica, 2021, 106, 1303-1310.	3.5	12

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19	Massively parallel single-cell mitochondrial DNA genotyping and chromatin profiling. Nature Biotechnology, 2021, 39, 451-461.	17.5	150
20	Coronavirus disease 2019 in patients with inborn errors of immunity: An international study. Journal of Allergy and Clinical Immunology, 2021, 147, 520-531.	2.9	278
21	Long-Term Patient-Customized Therapy for a Pathogenic EPO Mutation. Med, 2021, 2, 33-37.e1.	4.4	0
22	Uridineâ€responsive epileptic encephalopathy due to inherited variants in CAD : A Tale of Two Siblings. Annals of Clinical and Translational Neurology, 2021, 8, 716-722.	3.7	6
23	Familial thrombocytopenia due to a complex structural variant resulting in a WAC-ANKRD26 fusion transcript. Journal of Experimental Medicine, 2021, 218, .	8.5	20
24	Survival and causes of death in 2,033 patients with non-transfusion-dependent Î²-thalassemia. Haematologica, 2021, 106, 2489-2492.	3.5	25
25	Deciphering transcriptional and functional heterogeneity in hematopoiesis with single-cell genomics. Current Opinion in Hematology, 2021, 28, 269-276.	2.5	5
26	I SPI1 something needed for B cells. Journal of Experimental Medicine, 2021, 218, .	8.5	3
27	Scalable, multimodal profiling of chromatin accessibility, gene expression and protein levels in single cells. Nature Biotechnology, 2021, 39, 1246-1258.	17.5	244
28	Longitudinal Single-Cell Dynamics of Chromatin Accessibility and Mitochondrial Mutations in Chronic Lymphocytic Leukemia Mirror Disease History. Cancer Discovery, 2021, 11, 3048-3063.	9.4	31
29	CUT&RUNTools 2.0: a pipeline for single-cell and bulk-level CUT&RUN and CUT&Tag data analysis. Bioinformatics, 2021, 38, 252-254.	4.1	25
30	Mapping the human genetic architecture of COVID-19. Nature, 2021, 600, 472-477.	27.8	640
31	A unified model of human hemoglobin switching through single-cell genome editing. Nature Communications, 2021, 12, 4991.	12.8	22
32	Pathogenic BCL11A variants provide insights into the mechanisms of human fetal hemoglobin silencing. PLoS Genetics, 2021, 17, e1009835.	3.5	10
33	Investigating Germline Predisposition to Clonal Hematopoiesis through Perturbation of a Variant-Harboring Enhancer of TET2. Blood, 2021, 138, 3274-3274.	1.4	0
34	A Genetic Disorder Reveals a Hematopoietic Stem Cell Regulatory Network Co-Opted in Leukemia. Blood, 2021, 138, 861-861.	1.4	0
35	Stabilizing HIF to Ameliorate Anemia. Cell, 2020, 180, 6.	28.9	39
36	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388

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37	Calmodulin inhibitors improve erythropoiesis in Diamond-Blackfan anemia. Science Translational Medicine, 2020, 12, .	12.4	26
38	Inherited myeloproliferative neoplasm risk affects haematopoietic stem cells. Nature, 2020, 586, 769-775.	27.8	101
39	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
40	Purifying Selection against Pathogenic Mitochondrial DNA in Human T Cells. New England Journal of Medicine, 2020, 383, 1556-1563.	27.0	62
41	Sowing the Seeds of Clonal Hematopoiesis. Cell Stem Cell, 2020, 27, 195-197.	11.1	3
42	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	353
43	Unraveling Hematopoiesis through the Lens of Genomics. Cell, 2020, 182, 1384-1400.	28.9	96
44	From blood development to disease: a paradigm for clinical translation. DMM Disease Models and Mechanisms, 2020, 13, .	2.4	4
45	In The Blood: Connecting Variant to Function In Human Hematopoiesis. Trends in Genetics, 2020, 36, 563-576.	6.7	12
46	COVIDâ€19 presenting with autoimmune hemolytic anemia in the setting of underlying immune dysregulation. Pediatric Blood and Cancer, 2020, 67, e28382.	1.5	32
47	Control of human hemoglobin switching by LIN28B-mediated regulation of BCL11A translation. Nature Genetics, 2020, 52, 138-145.	21.4	73
48	Infantile Myelofibrosis and Myeloproliferation with CDC42 Dysfunction. Journal of Clinical Immunology, 2020, 40, 554-566.	3.8	27
49	CD11c regulates hematopoietic stem and progenitor cells under stress. Blood Advances, 2020, 4, 6086-6097.	5.2	13
50	Single Cell Understanding of Hematopoiesis and Myeloid Lineage Commitment. Blood, 2020, 136, SCI5-SCI5.	1.4	0
51	The genetics of human hematopoiesis and its disruption in disease. EMBO Molecular Medicine, 2019, 11, e10316.	6.9	32
52	A chance encounter changes everything. Nature Medicine, 2019, 25, 869-869.	30.7	0
53	Heritability of fetal hemoglobin, white cell count, and other clinical traits from a sickle cell disease family cohort. American Journal of Hematology, 2019, 94, 522-527.	4.1	6
54	Macrothrombocytopenia associated with a rare GFI1B missense variant confounding the presentation of immune thrombocytopenia. Pediatric Blood and Cancer, 2019, 66, e27874.	1.5	5

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55	Transcriptional States and Chromatin Accessibility Underlying Human Erythropoiesis. Cell Reports, 2019, 27, 3228-3240.e7.	6.4	122
56	Topological control of cytokine receptor signaling induces differential effects in hematopoiesis. Science, 2019, 364, .	12.6	89
57	Impaired human hematopoiesis due to a cryptic intronic GATA1 splicing mutation. Journal of Experimental Medicine, 2019, 216, 1050-1060.	8.5	27
58	Interrogation of human hematopoiesis at single-cell and single-variant resolution. Nature Genetics, 2019, 51, 683-693.	21.4	147
59	Deubiquitylase USP7 regulates human terminal erythroid differentiation by stabilizing GATA1. Haematologica, 2019, 104, 2178-2188.	3.5	28
60	Lineage Tracing in Humans Enabled by Mitochondrial Mutations and Single-Cell Genomics. Cell, 2019, 176, 1325-1339.e22.	28.9	345
61	Longitudinal assessment of clonal mosaicism in human hematopoiesis via mitochondrial mutation tracking. Blood Advances, 2019, 3, 4161-4165.	5.2	10
62	A mummy emerges from the grave: Scurvy confounding the clinical presentation of a child with Fanconi anemia. American Journal of Hematology, 2019, 94, 506-507.	4.1	1
63	Gene-centric functional dissection of human genetic variation uncovers regulators of hematopoiesis. ELife, 2019, 8, .	6.0	14
64	HRI coordinates translation necessary for protein homeostasis and mitochondrial function in erythropoiesis. ELife, 2019, 8, .	6.0	47
65	Functional Assays to Screen and Dissect Genomic Hits. Circulation Genomic and Precision Medicine, 2018, 11, e002178.	3.6	18
66	A chance to cut (the genome) is a chance to cure. Blood, 2018, 131, 1884-1885.	1.4	0
67	Ribosome Levels Selectively Regulate Translation and Lineage Commitment in Human Hematopoiesis. Cell, 2018, 173, 90-103.e19.	28.9	296
68	Thrombopoietin: tickling the HSC's fancy. EMBO Molecular Medicine, 2018, 10, 10-12.	6.9	6
69	The Genetic Landscape of Diamond-Blackfan Anemia. American Journal of Human Genetics, 2018, 103, 930-947.	6.2	184
70	Common Î±-globin variants modify hematologic and other clinical phenotypes in sickle cell trait and disease. PLoS Genetics, 2018, 14, e1007293.	3.5	45
71	Ribonuclease inhibitor 1 regulates erythropoiesis by controlling GATA1 translation. Journal of Clinical Investigation, 2018, 128, 1597-1614.	8.2	20
72	Transcriptional Signaling Centers Govern Human Erythropoiesis and Harbor Genetic Variations of Red Blood Cell Traits. Blood, 2018, 132, 1277-1277.	1.4	0

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73	Functional Selectivity in Cytokine Signaling Revealed Through a Pathogenic EPO Mutation. Cell, 2017, 168, 1053-1064.e15.	28.9	98
74	Confounding in ex vivo models of Diamond-Blackfan anemia. Blood, 2017, 130, 1165-1168.	1.4	11
75	Unexpected role for p19INK4d in posttranscriptional regulation of GATA1 and modulation of human terminal erythropoiesis. Blood, 2017, 129, 226-237.	1.4	21
76	Comprehensive population-based genome sequencing provides insight into hematopoietic regulatory mechanisms. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E327-E336.	7.1	39
77	Developmentallyâ€faithful and effective human erythropoiesis in immunodeficient and Kit mutant mice. American Journal of Hematology, 2017, 92, E513-E519.	4.1	20
78	Whole-exome sequencing identifies an Î±-globin cluster triplication resulting in increased clinical severity of Î²-thalassemia. Journal of Physical Education and Sports Management, 2017, 3, a001941.	1.2	13
79	Regulation of the fetal hemoglobin silencing factor BCL11A. Annals of the New York Academy of Sciences, 2016, 1368, 25-30.	3.8	39
80	Advances in understanding erythropoiesis: evolving perspectives. British Journal of Haematology, 2016, 173, 206-218.	2.5	109
81	Exome sequencing results in successful diagnosis and treatment of a severe congenital anemia. Journal of Physical Education and Sports Management, 2016, 2, a000885.	1.2	10
82	Normal hematologic parameters and fetal hemoglobin silencing with heterozygous IKZF1 mutations. Blood, 2016, 128, 2100-2103.	1.4	7
83	Insight into GATA1 transcriptional activity through interrogation of cis elements disrupted in human erythroid disorders. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 4434-4439.	7.1	56
84	A novel pathogenic mutation in RPL11 identified in a patient diagnosed with diamond Blackfan anemia as a young adult. Blood Cells, Molecules, and Diseases, 2016, 61, 46-47.	1.4	9
85	Development of autologous blood cell therapies. Experimental Hematology, 2016, 44, 887-894.	0.4	6
86	Whole-Exome Sequencing Identifies Loci Associated with Blood Cell Traits and Reveals a Role for Alternative GFI1B Splice Variants in Human Hematopoiesis. American Journal of Human Genetics, 2016, 99, 481-488.	6.2	45
87	Adenosine-to-inosine RNA editing by ADAR1 is essential for normal murine erythropoiesis. Experimental Hematology, 2016, 44, 947-963.	0.4	52
88	The severity of hereditary porphyria is modulated by the porphyrin exporter and Lan antigen ABCB6. Nature Communications, 2016, 7, 12353.	12.8	37
89	Emerging cellular and gene therapies for congenital anemias. American Journal of Medical Genetics, Part C: Seminars in Medical Genetics, 2016, 172, 332-348.	1.6	6
90	Systematic Functional Dissection of Common Genetic Variation Affecting Red Blood Cell Traits. Cell, 2016, 165, 1530-1545.	28.9	294

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91	Defining the Minimal Factors Required for Erythropoiesis through Direct Lineage Conversion. Cell Reports, 2016, 15, 2550-2562.	6.4	48
92	Characterization of Deletions of the HBA and HBB Loci by Array Comparative Genomic Hybridization. Journal of Molecular Diagnostics, 2016, 18, 92-99.	2.8	17
93	Mutations in the substrate binding glycine-rich loop of the mitochondrial processing peptidase-Î± protein (PMPCA) cause a severe mitochondrial disease. Journal of Physical Education and Sports Management, 2016, 2, a000786.	1.2	33
94	Society for Pediatric Research 2015 Young Investigator Award: genetics of human hematopoiesisâ€"what patients can teach us about blood cell production. Pediatric Research, 2016, 79, 366-370.	2.3	0
95	Targeted Application of Human Genetic Variation Can Improve Red Blood Cell Production from Stem Cells. Cell Stem Cell, 2016, 18, 73-78.	11.1	78
96	Genomeâ€wide association study followâ€up identifies cyclin A2 as a regulator of the transition through cytokinesis during terminal erythropoiesis. American Journal of Hematology, 2015, 90, 386-391.	4.1	15
97	Anemia: progress in molecular mechanisms and therapies. Nature Medicine, 2015, 21, 221-230.	30.7	209
98	Inducible Gata1 suppression expands megakaryocyte-erythroid progenitors from embryonic stem cells. Journal of Clinical Investigation, 2015, 125, 2369-2374.	8.2	29
99	X-linked macrocytic dyserythropoietic anemia in females with an ALAS2 mutation. Journal of Clinical Investigation, 2015, 125, 1665-1669.	8.2	43
100	BCL11A deletions result in fetal hemoglobin persistence and neurodevelopmental alterations. Journal of Clinical Investigation, 2015, 125, 2363-2368.	8.2	122
101	Biallelic Mutations in PARP4 Are Linked to a Variant Form of Congenital Dyserythropoietic Anemia. Blood, 2015, 126, 272-272.	1.4	2
102	Temporally Distinct Developmental Waves of Erythropoiesis from Human Pluripotent Stem Cells. Blood, 2015, 126, 1170-1170.	1.4	0
103	Altered Chromatin Occupancy of Master Regulators Underlies Evolutionary Divergence in the Transcriptional Landscape of Erythroid Differentiation. PLoS Genetics, 2014, 10, e1004890.	3.5	42
104	Transcriptional divergence and conservation of human and mouse erythropoiesis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4103-4108.	7.1	76
105	Altered translation of GATA1 in Diamond-Blackfan anemia. Nature Medicine, 2014, 20, 748-753.	30.7	243
106	Post-Transcriptional Defects and Erythroid Pathobiology. Blood, 2014, 124, SCI-35-SCI-35.	1.4	0
107	Direct Lineage Reprogramming of Murine Fibroblasts to Erythroid Progenitor Cells By Defined Factors. Blood, 2014, 124, 246-246.	1.4	0
108	Applications of high-throughput DNA sequencing to benign hematology. Blood, 2013, 122, 3575-3582.	1.4	25

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109	The Switch from Fetal to Adult Hemoglobin. Cold Spring Harbor Perspectives in Medicine, 2013, 3, a011643-a011643.	6.2	214
110	Genome-wide association studies of hematologic phenotypes: a window into human hematopoiesis. Current Opinion in Genetics and Development, 2013, 23, 339-344.	3.3	31
111	Stimulating erythropoiesis in neonates. American Journal of Hematology, 2013, 88, 930-931.	4.1	1
112	Clinical experience with fetal hemoglobin induction therapy in patients with Î²-thalassemia. Blood, 2013, 121, 2199-2212.	1.4	154
113	Rare complete loss of function provides insight into a pleiotropic genome-wide association study locus. Blood, 2013, 122, 3845-3847.	1.4	25
114	Cyclin D3 coordinates the cell cycle during differentiation to regulate erythrocyte size and number. Genes and Development, 2012, 26, 2075-2087.	5.9	100
115	Fetal hemoglobin levels and morbidity in untransfused patients with Î²-thalassemia intermedia. Blood, 2012, 119, 364-367.	1.4	85
116	Persistence of Fetal Hemoglobin Expression in an Older Child with Trisomy 13. Journal of Pediatrics, 2012, 160, 352.	1.8	5
117	Exome sequencing identifies GATA1 mutations resulting in Diamond-Blackfan anemia. Journal of Clinical Investigation, 2012, 122, 2439-2443.	8.2	292
118	Correction of Sickle Cell Disease in Adult Mice by Interference with Fetal Hemoglobin Silencing. Science, 2011, 334, 993-996.	12.6	281
119	Targeted Therapeutic Strategies for Fetal Hemoglobin Induction. Hematology American Society of Hematology Education Program, 2011, 2011, 459-465.	2.5	78
120	MicroRNA-15a and -16-1 act via MYB to elevate fetal hemoglobin expression in human trisomy 13. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 1519-1524.	7.1	186
121	A Functional Element Necessary for Fetal Hemoglobin Silencing. New England Journal of Medicine, 2011, 365, 807-814.	27.0	161
122	Therapeutic levels of fetal hemoglobin in erythroid progeny of Î²-thalassemic CD34+ cells after lentiviral vector-mediated gene transfer. Blood, 2011, 117, 2817-2826.	1.4	96
123	Erythropoietin couples erythropoiesis, B-lymphopoiesis, and bone homeostasis within the bone marrow microenvironment. Blood, 2011, 117, 5631-5642.	1.4	123
124	Heterozygous disruption of human SOX6 is insufficient to impair erythropoiesis or silencing of fetal hemoglobin. Blood, 2011, 117, 4396-4397.	1.4	5
125	Correction of Murine Sickle Cell Disease Through Interference with Fetal Hemoglobin Silencing. Blood, 2011, 118, 351-351.	1.4	1
126	Advances in the understanding of haemoglobin switching. British Journal of Haematology, 2010, 149, 181-194.	2.5	180

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127	Fine-mapping at three loci known to affect fetal hemoglobin levels explains additional genetic variation. Nature Genetics, 2010, 42, 1049-1051.	21.4	243
128	Transcriptional silencing of fetal hemoglobin by BCL11A. Annals of the New York Academy of Sciences, 2010, 1202, 64-68.	3.8	50
129	Modifier genes in Mendelian disorders: the example of hemoglobin disorders. Annals of the New York Academy of Sciences, 2010, 1214, 47-56.	3.8	27
130	Transcriptional silencing of Î³-globin by BCL11A involves long-range interactions and cooperation with SOX6. Genes and Development, 2010, 24, 783-798.	5.9	304
131	Reversing the Hemoglobin Switch. New England Journal of Medicine, 2010, 363, 2258-2260.	27.0	38
132	Thalassemia: An Overview of 50 Years of Clinical Research. Hematology/Oncology Clinics of North America, 2010, 24, 1005-1020.	2.2	62
133	Developmental and species-divergent globin switching are driven by BCL11A. Nature, 2009, 460, 1093-1097.	27.8	339
134	Rb and hematopoiesis: stem cells to anemia. Cell Division, 2008, 3, 13.	2.4	17
135	Genome-wide association study shows BCL11A associated with persistent fetal hemoglobin and amelioration of the phenotype of Î²-thalassemia. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 1620-1625.	7.1	561
136	DNA polymorphisms at the BCL11A , HBS1L-MYB , and Î²- globin loci associate with fetal hemoglobin levels and pain crises in sickle cell disease. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 11869-11874.	7.1	510
137	Human Fetal Hemoglobin Expression Is Regulated by the Developmental Stage-Specific Repressor BCL11A. Science, 2008, 322, 1839-1842.	12.6	759
138	Rb intrinsically promotes erythropoiesis by coupling cell cycle exit with mitochondrial biogenesis. Genes and Development, 2008, 22, 463-475.	5.9	118
139	Human Fetal Hemoglobin Expression Is Regulated by the Developmental Stage-Specific Repressor BCL11A. Blood, 2008, 112, 487-487.	1.4	1
140	Rb Intrinsically Promotes Erythropoiesis by Coupling Cell Cycle Exit with Mitochondrial Biogenesis.. Blood, 2007, 110, 638-638.	1.4	0