

Junke Wang

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

177
citations

1684188

5
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1281871

11
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#	ARTICLE	IF	CITATIONS
1	Genome-Wide Non-HLA Mismatches Correlate with Overall Survival and Cause Specific Mortality after Unrelated Donor Allogeneic HCT. <i>Transplantation and Cellular Therapy</i> , 2021, 27, S61-S62.	1.2	0
2	Impact of Common Graft Versus Leukemia Minor Histocompatibility Antigens on the Outcomes of Allogeneic Hematopoietic Cell Transplantation (alloHCT). <i>Transplantation and Cellular Therapy</i> , 2021, 27, S156-S158.	1.2	0
3	Genome-Wide Association Analyses Identify Variants in IRF4 Associated With Acute Myeloid Leukemia and Myelodysplastic Syndrome Susceptibility. <i>Frontiers in Genetics</i> , 2021, 12, 554948.	2.3	8
4	Association of CXCR6 with COVID-19 severity: delineating the host genetic factors in transcriptomic regulation. <i>Human Genetics</i> , 2021, 140, 1313-1328.	3.8	33
5	Prognostic impact of pre-transplant chromosomal aberrations in peripheral blood of patients undergoing unrelated donor hematopoietic cell transplant for acute myeloid leukemia. <i>Scientific Reports</i> , 2021, 11, 15004.	3.3	4
6	Novel genetic variants associated with mortality after unrelated donor allogeneic hematopoietic cell transplantation. <i>EClinicalMedicine</i> , 2021, 40, 101093.	7.1	8
7	Pre-HCT mosaicism increases relapse risk and lowers survival in acute lymphoblastic leukemia patients post-unrelated HCT. <i>Blood Advances</i> , 2021, 5, 66-70.	5.2	6
8	Genome-wide association study identifies susceptibility loci for acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 6233.	12.8	17
9	Prognostic Impact of Pre-Transplant Chromosomal Aberrations Detected By SNP-Array in Patients Undergoing Unrelated Donor Hematopoietic Cell Transplant for Acute Myeloid Leukemia. <i>Biology of Blood and Marrow Transplantation</i> , 2020, 26, S12-S13.	2.0	0
10	Meta-Analysis of Genome-Wide Association Studies of Acute Myeloid Leukemia (AML) Patients Identifies Variants Associated with Risk of 11q23/KMT2A-Translocated and Core-Binding Factor (CBF) AML and Suggests a Role for Transcription Elongation in Leukemogenesis. <i>Blood</i> , 2020, 136, 29-30.	1.4	0
11	Population Distribution of GvL and GvH Minor Histocompatibility Antigens. <i>Blood</i> , 2020, 136, 23-25.	1.4	0
12	Associations of Clinical Outcomes after Allogeneic Hematopoietic Cell Transplantation with Number of Predicted Class II Restricted mHA. <i>Blood</i> , 2020, 136, 2-2.	1.4	0
13	Pre-Transplant Clonal Mosaicism Is Associated with Increased Relapse and Lower Survival in Acute Lymphoblastic Leukemia Patients Undergoing Allogeneic Hematopoietic Cell Transplant. <i>Blood</i> , 2020, 136, 9-10.	1.4	0
14	Validation of genetic associations with acute GVHD and nonrelapse mortality in DISCOVeRY-BMT. <i>Blood Advances</i> , 2019, 3, 2337-2341.	5.2	8
15	Multiple functional variants in the IL1RL1 region are pretransplant markers for risk of GVHD and infection deaths. <i>Blood Advances</i> , 2019, 3, 2512-2524.	5.2	7
16	gwasurvivr: an R package for genome-wide survival analysis. <i>Bioinformatics</i> , 2019, 35, 1968-1970.	4.1	72
17	De Novo and Therapy-Related Acute Myeloid Leukemia and Myelodysplastic Syndrome: Similarities and Differences in SNP-Array Detected Chromosomal Aberrations in Pre-Transplant Blood Samples. <i>Blood</i> , 2019, 134, 1430-1430.	1.4	2
18	Genome Wide Interaction Analysis Identifies Expression Quantitative Trait Loci Associated with Reduced Survival after Reduced Intensity Conditioning HLA-Matched Unrelated Donor Allogeneic Hematopoietic Cell Transplant. <i>Blood</i> , 2019, 134, 4595-4595.	1.4	0

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19	Genome Wide Association Analyses Identify Pleiotropic Variants Associated with Acute Myeloid Leukemia (AML) and Myelodysplastic Syndrome (MDS) Susceptibility. <i>Blood</i> , 2018, 132, 1500-1500.	1.4	0
20	Multiple Functional Donor Polymorphisms in IL1RL1 region Associate with Death Due to GvHD or Infection after Unrelated Donor Allogeneic Hematopoietic Stem Cell Transplantation (HCT) for AML and MDS. <i>Blood</i> , 2018, 132, 312-312.	1.4	0