P1	Amrhein, Lisa	Probability distributions for scRNA-Seq
P2	Banck, Jan C.	A model-based comparison of 7+3 and S-HAM: Potential improvement of induction therapy usage in acute myeloid leukemia (AML)
P3	Bast, Lisa	Computational Modeling of Hematopoiesis in Myelodysplastic Syndromes and Age-Matched Healthy Individuals
P4	Baumann, Ursula	HAX1 is an essential regulator of CXCR4 endocytosis that determines sensitivity to BTK-inhibiton in B-cell lymphoma
P5	Baygun, Seren	Investigating the evolution of follicular lymphoma by using in vivo genetic screens
P6	Blundell, Jamie	The dynamics of adaptive genetic diversity during the early stages of clonal evolution
P7	Bultmann, S.	TET2 is critical for the generation of 5-formylcytosine in the transition from naive to primed pluripotency
P8	Colomé-Tatché, M.	Computational single cell genomics and low input epigenomics
P9	Domínguez M., H.	Evolution of the regulatory landscape in hematopoietic malignancies
P10	Dutta, Sayantanee	Acute myeloid leukemia with isolated trisomy 4 is characterized by frequent mutations of TET2
P11	Götze, Katharina	Azacitidine Acts on the Mesenchymaal Stromal Cell Compartment in Myelodysplastic Syndromes to alter Niche Function and Suppress Malignant HSPC
P12	Graf, Alexander	IT infrastructure for handling and analysis of sequencing data and related metadata
P13	Grath, Sonja	The evolution of DNA methylation – what insects can tell us about cancer
P43	Greif, Philipp	Clonal heterogeneity of FLT3-ITD correlates with adverse prognosis in acute myeloid leukemia
P14	Grosser, Konrad	Reversible Jump Markov Chain Monte Carlo based inference of phylogeny of cell samples based on single cell methylation data
P15	Hanekamp, Diana	A dynamic epigenetic landscape in genetic and immunophenotypic generally stable pediatric AML
P16	Haubner, Sascha	Coexpression Profile of Leukemic Stem Cell Markers for Combinatorial Targeted Therapy in AML
P17	Hellmann, Ines	*zUMIs* - A fast and flexible pipeline to process RNA sequencing data with UMIs
P44	Helma-Smets, J.	Next-generation Antibody Drug Conjugates (ADCs) for targeted therapy of Acute Myeloid Leukemia (AML)
P18	Herrmann, Monika	Novel PD-1 fusion protein to enhance cytolysis of Acute Myeloid Leukemia cells and reduce adverse events
P19	Hettler, Franziska	Evolution of the bone marrow microenvironment in a myeloid leukemogenesis
P20	Jayavelu, Ashok K.	Ybx1-dependent signaling maintains Jak2-mutated MPN
P21	Keay, William	Redefining the Molecular Ontogeny of Follicular Lymphoma
P22	Kempf, Julia M.	Inactivation of the histone methyltransferase EZH2 induces resistance towards cytarabine in AML
P23	Kerbs, Paul	Allele-specific transcription in AML
P24	Khandanpour, C.	Alteration of the transcription factor GFI1 as a driver of genetic instability of leukemia development
P25	Köhnke, Thomas	Identification of Novel Targets for Antibody or Chimeric Antigen Receptor (CAR) based Immunotherapy in AML: Characterizing the Surfaceome from Primary Patient Samples
P26	Kozik, Jan-H.	SIRPα-αCD33 LicMABs Enhance Killing and Phagocytosis of $CD47^{high}$ Primary, Patient-derived Acute Myeloid Leukemia Cells
P28	Krebs, Stefan	Nanopore sequencing provides new tools for analysis of haematological malignancies
P29	Kuhn, Laura	The non-canonical NF-kB signaling pathway contributes to the expansion and lymphomagenesis of CD40 activated B cells
P30	Leubolt, Georg	Functional investigation of GATA2 mutations in hematological malignancies
P31	Liu, Wen-Hsin	Re-expression of KLF4 impairs growth of patient-derived acute lymphoma leukemia cells in vivo and sensitizes towards chemotherapy

P32	Matek, Christian	Recognising and classifying cell populations characteristic of Acute Myeloid Leukemia in digitized blood smears
P33	Niggemeyer, Julia	Single-cell RNA-sequencing to Elucidate Clonal Heterogeneity in Acute Myeloid Leukemia
P34	Opatz, Sabrina	The clinical mutatome of core binding factor leukemia
P35	Pfaus, Anja	*PiggyBac* transposon mutagenesis to identify cancer genes and regulatory elements in leukemia
P36	Redondo M., E.	Leukaemia-specific ZBTB7A mutations – implications in clonal expansion, cell metabolism and lineage fate decisions
P37	Richter, Carmen	A systematic CRISPR/Cas9-based screening approach for components of the ubiquitin signaling network involved in the pathophysiology of multiple myeloma and bortezomib resistance
P38	Richter, Daniel	Studying clonal dynamics in cytogenetically normal AML through sensitive backtracking of relapse-associated mutations
P39	Rosemann, M.	Osteosarcoma stem cells and radiation response: a study of function and predictive value
P40	Rühland, Svenja	Therapeutic potential of mesenchymal stem cells and cytotoxic T cells analyzed using tumor spheroids
P41	Ryan, Joel	Live-cell and single-molecule imaging reveal contrasting localization and kinetics of Tet proteins in naive mouse embryonic stem cells
P43	Schranz, Katrin	Clonal heterogeneity of FLT3-ITD correlates with adverse prognosis in acute myeloid leukemia
P44	Schumacher, D.	Next-generation Antibody Drug Conjugates (ADCs) for targeted therapy of Acute Myeloid Leukemia (AML)
P45	Soberon, Valeria	NF-kappaB involvement in CLL pathogenesis
P4	Spallek, Ria	HAX1 is an essential regulator of CXCR4 endocytosis that determines sensitivity to BTK-inhibiton in B-cell lymphoma
P46	Sperling, Stefanie	Chronic CD30 Signaling results in B Cell Lymphoma Development by driving the Expansion of pre-Plasmablasts and B1 cells
P47	Stief, Sophie	Loss of KDM6A function induces resistance to cytarabine in acute myeloid leukemia
P48	Trummer, Carina	Impact of metabolism on epigenetic regulation
P49	Valtierra G., I. A.	Inferring clonal phylogenies of acute myeloid leukemia using single-cell RNA-seq
P50	Vieth, Beate	powsimR: Statistical power analysis for bulk and single cell RNA-seq experiments
P51	Völse, Kerstin	A target-specific reporter system to identify CRISPR/Cas9-induced knockouts
P52	von Neubeck, B.	An inhibitory antibody targeting Carbonic Anhydrase XII abrogates chemoresistance and significantly reduces lung metastases in vivo
P53	Vosberg, S.	Relapse of Acute Myeloid Leukemia after Allogeneic Stem Cell Transplantation is Associated with Gain of WT1 Alterations and High Mutation Load
P54	Wange, Lucas E.	Single cell RNA sequencing of primary ALL samples before and after treatment
P55	Weser, Sabrina	DNA methylation alters the disease phenotype in acute myeloid leukemia
P56	Wichmann, C.	A t(11;19) out-of-frame MLL fusion gene expands human CD34+ blood progenitor cells resembling acute myelomonoblastic leukemia AML M4/5
P57	Wierzbinska, J.	A novel strategy for identification of CLL-specific methylation events with a focus on epigenetic deregulation of microRNAs in CLL
P58	Wilding, Anja	The role of ZBTB7A mutations in DNA repair
P59	Wirth, Anna-K.	Analysis of treatment-induced evolution in AML within a patient derived xenograft mouse model and standard induction chemotherapy
P60	Zeller, Christina	The patient derived xenograft mouse model as a tool to investigate cancer evolution