The aim of our research is the identification and functional characterization of genes for monogenic and genetically complex hair loss disorders with a major focus on the autoimmune disorder alopecia areata (AA). We have the largest sample of AA patients available worldwide, which includes a current total of more than 2,200 individuals of middle European origin. We have been able to demonstrate the contribution of the HLA-complex and the genes PTPN22, TRAF1/C5, CTLA4, IL13 and KIAA0350 to the disease risk using candidate gene studies. By the use of genome-wide association studies, meta-analyses, immunochips and functional studies, we just recently identified HLA-DR as a key etiologic driver for AA as well as two loci outside the HLA-region: ACOX1/BCL2L11 and GARP. Future analyses and functional studies will contribute to a comprehensive understanding of AA.