The T2D Knowledge Portal (T2DKP; [www.type2diabetesgenetics.org](http://www.type2diabetesgenetics.org)), produced by the Accelerating Medicines Partnership in Type 2 Diabetes, is an open-access resource that aims to facilitate the translation of genomic data into actionable knowledge for understanding and treatment of T2D.

**Data in the T2DKP**

GWAS data for T2D and related traits
- Meta-analysis results from GWAS Consortia for 366,729 samples: MAGIC, CARDioGRAM, CKDGen, GIANT, GLGC, VATGen
- GWAS results from 12,171 cases and 56,862 controls
- GWAS data for 9,000 samples of Mexican and Latin American ancestry
- GENESIS GWAS for insulin sensitivity from over 2,700 samples
- 70KforT2D: pre-publication dataset re-analyzing >70,000 public GWAS samples
- GWAS for 3,700 samples from Cardiology and Metabolic Patient Cohort
- GWAS for 9,200 individuals from BioMe Biobank at Mt. Sinai Medical Center

Whole exome sequence data
- 19,000 T2D exomes from T2D-GENES, SIGMA, GoT2D, LuCamp

Whole genome sequence data
- whole genome sequencing results for ~3,000 individuals from GoT2D

Exome chip data
- exome chip results for ~82,000 samples of European ancestry
- exome chip results for glycemic and lipid traits from Oxford BioBank

Disease-agnostic genomic resources
- 1000 Genomes
- gnomAD exomes and whole genomes

Epigenomic data
- 11 million chromatin state annotations from the Stephen Parker lab

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**Summary visualizations distill and integrate data across disparate data sets**

Variant page
- At-a-glance section is a visual display of phenotypic associations and their significance
- Association statistics across traits table lists associations across all traits and datasets
- Epigenomic annotations section displays chromatin states across the region of the variant
- "How common is..." section shows allele frequency across different ancestry groups

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Contact us: [help@type2diabetesgenetics.org](mailto:help@type2diabetesgenetics.org)
Twitter: @T2DKP
Interactive tools for custom, real-time analysis

Interactive burden test calculates the aggregate effects of the variants in a gene
- create custom sets of variants
- filter samples by phenotype, ancestry, and more
- choose principal components
- add covariate phenotypes
- run on-the-fly association analysis
- Genetic Association Interactive Tool (GAIT) on Variant pages offers same functionality for single variant associations

LocusZoom interactive visualization displays variant associations and LD relationships across a region
- select phenotype and dataset for display
- perform on-the-fly conditional analysis to determine whether variant associations are independent
- LocusZoom on Gene pages displays chromatin states across the region in a range of tissues

Variant Finder searches across datasets to retrieve variants meeting custom criteria
- associated phenotypes
- p-value and effect size thresholds
- genomic location and consequence for encoded protein
- presence in a specific dataset or ancestry-specific cohort

More information about the T2DKP
- Data page contains information and reports on datasets
- About page describes the project
- Policies page describes data intake, analysis, and access
- Resources page links to detailed interface guides and tutorials
- Contact page lists T2DKP team and contact information
- Collaborate page presents FAQ for those interested in submitting data
- Blog presents T2DKP developments and news

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