

This dataset contains GWAS summary statistics on the BOLT-LMM GWAS of Multisite Chronic Pain performed October 2018, Daniel Smith Group, Glasgow UK

BOLT-LMM manual: <https://data.broadinstitute.org/alkesgroup/BOLT-LMM/>

Column names:

SNP: rs number or ID string

CHR: chromosome

BP: physical (base pair) position

GENPOS: genetic position either from bim file or interpolated from genetic map

ALLELE1: first allele in bim file (usually the minor allele), used as the effect allele

ALLELE0: second allele in bim file, used as the reference allele

A1FREQ: frequency of first allele

F\_MISS: fraction of individuals with missing genotype at this SNP

BETA: effect size from BOLT-LMM approximation to infinitesimal mixed model

SE: standard error of effect size

P\_BOLT\_LMM\_INF: infinitesimal mixed model association test p-value

P\_BOLT\_LMM: non-infinitesimal mixed model association test p-value