℘ Diagrams

By default only columns that are primary keys, foreign keys or indexes are shown.

Compact   Large   Compact Implied   Large Implied

tad_tbl [table]
| chr |
| start_hg38 |
| end_hg38 |
| sample_id |
| < 1 | 78.173 rows |

tad_sample_tbl [table]
| sample_id |
| ... |
| 40 rows | 1 > |

gwascatalog_associations_tbl [table]
| chr_Hg38 |
| pos_Hg38 |
| PUBMEDID |
| ... |
| < 1 | 362.557 rows |

gwascatalog_studies_tbl [table]
| PUBMEDID |
| ... |
| 5.756 rows | 1 > |

ensembl_reg_build_tbl [table]
| seqid |
| start_GRCh38 |
| end_GRCh38 |
| feature_type_id |
| ... |
| < 1 | 622.461 rows |

ensembl_reg_build_features_tbl [table]
| feature_type_id |
| ... |
| 6 rows | 1 > |

rsid_tbl [table]
| rsID |
| ... |
| 241 rows |

variation [table]
| id |
| chr |
| pos_hg38_one_based |
| rsid |
| ... |
| 20.211.833 rows | 1 > |

gwas_meta_cad [table]
| id |
| variant_id |
| ... |
| < 1 | 20.211.833 rows |

identified_proxy_SNPs_tbl [table]
| rsID |
| nearest_gene_hgnc_id |
| most_likely_causal_gene_hgnc_id |
| < 2 | 241 rows | 1 > |

linked_SNPs_tbl [table]
| proxy_rsid |
| linked_rsid |
| chr |
| pos_hg38 |
| consequence_id |
| population_id |
| ... |
| < 3 | 449.770 rows |

consequence_tbl [table]
| consequence_id |
| ... |
| 23 rows | 1 > |

population_tbl [table]
| population_id |
| ... |
| 6 rows | 1 > |

hgnc_all_symbols_tbl [table]
| all_symbols |
| hgnc_id |
| < 1 | 101.180 rows | 1 > |

ensembl_genelist_tbl [table]
| seqid |
| start_GRCh38 |
| end_GRCh38 |
| gene_symbol |
| biotype_id |
| ... |
| < 2 | 39.605 rows |

clint_miller_tbl [table]
| chrom |
| chromStart |
| chromEnd |
| biosample_id |
| ... |
| < 1 | 593.028 rows |

hgnc_approved_symbols_tbl [table]
| hgnc_id |
| ... |
| 43.135 rows | 5 > |

ensembl_genelist_biotypes_tbl [table]
| biotype_id |
| ... |
| 3 rows | 1 > |

clint_miller_biotypes_tbl [table]
| biosample_id |
| ... |
| 8 rows | 1 > |

opentarget_l2g_tbl [table]
| chrom |
| pos |
| hgnc_id |
| ... |
| < 1 | 3.580.206 rows |

catlas_tbl [table]
| chrom |
| chromStart |
| chromEnd |
| biosample_id |
| ... |
| < 1 | 15.968.759 rows |

catlas_biotypes_tbl [table]
| biosample_id |
| ... |
| 222 rows | 1 > |

tss_tbl [table]
| chr |
| pos_Hg38 |
| hgnc_id |
| ... |
| < 1 | 35.160 rows |

abc_classes_tbl [table]
| class_id |
| ... |
| 3 rows | 1 > |

abc_tbl [table]
| chr |
| start_hg38 |
| end_hg38 |
| class_id |
| TargetGene_id |
| CellType_id |
| ... |
| < 3 | 7.717.392 rows |

abc_targetgenes_tbl [table]
| TargetGene_id |
| ... |
| 23.227 rows | 1 > |

abc_celltypes_tbl [table]
| CellType_id |
| ... |
| 131 rows | 1 > |