# Obtaining data from EWAS atlas

Standard operating procedure 7

Dec 31, 2023

Download epigenomic associations from EWAS atlas <a href="https://ngdc.cncb.ac.cn/ewas/browse">https://ngdc.cncb.ac.cn/ewas/browse</a> available from China National Center for Bioinformatics.

EWAS Atlas is described in the study shown on the image below:

> Nucleic Acids Res. 2019 Jan 8;47(D1):D983-D988. doi: 10.1093/nar/gky1027.

# EWAS Atlas: a curated knowledgebase of epigenomewide association studies

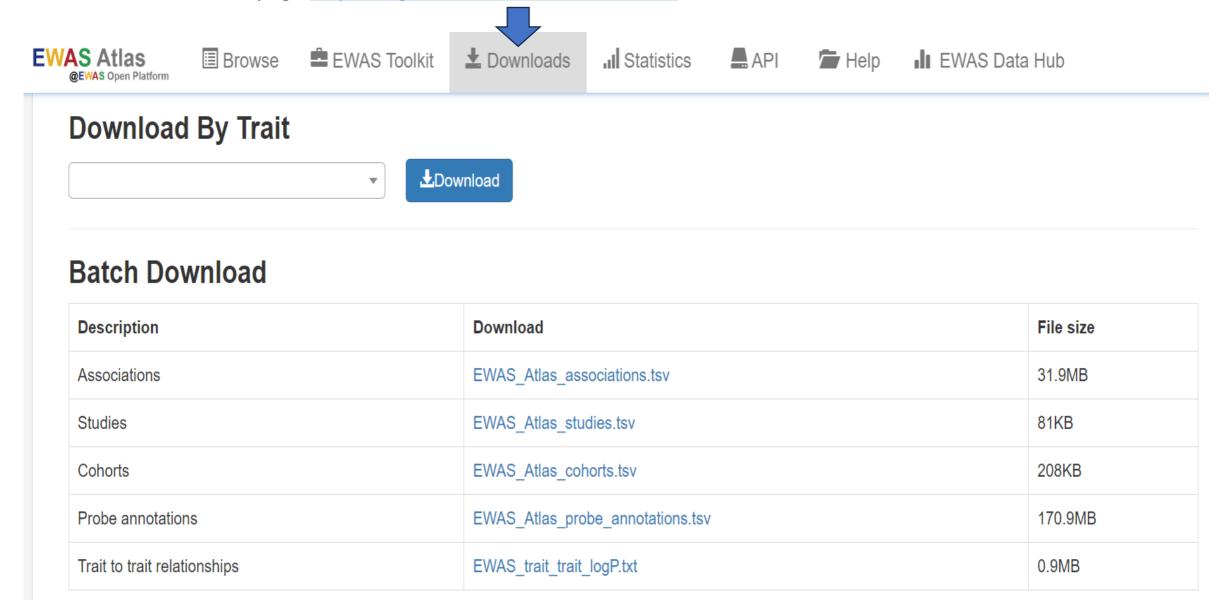
```
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```

Affiliations + expand

PMID: 30364969 PMCID: PMC6324068 DOI: 10.1093/nar/gky1027

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### Go to EWAS Atlas home page <a href="https://ngdc.cncb.ac.cn/ewas/browse">https://ngdc.cncb.ac.cn/ewas/browse</a> and click **Downloads**



#### Download EWAS atlas associations

















# **Download By Trait**



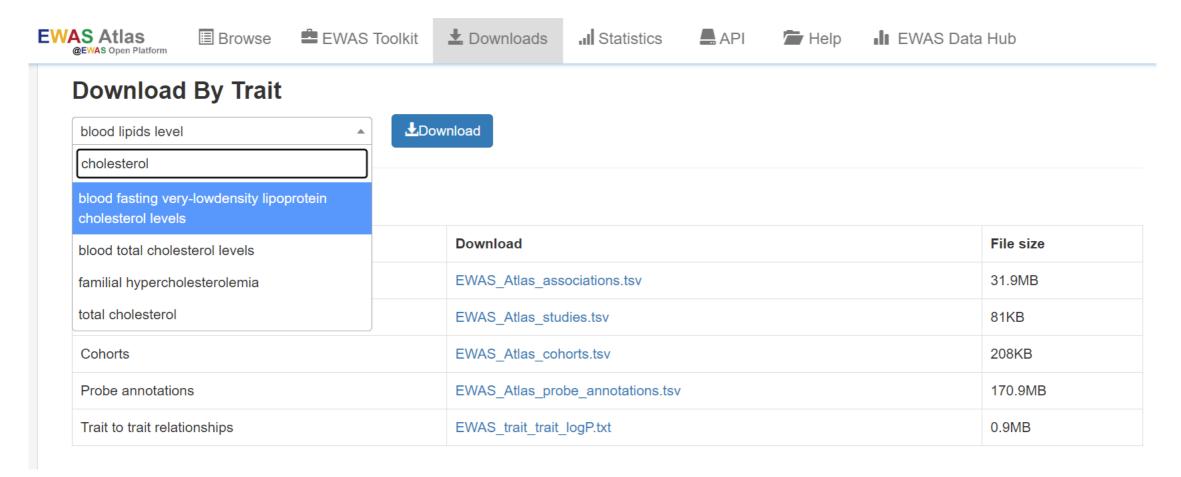


## **Batch Download**

Description	Download	File size
Associations	EWAS_Atlas_associations.tsv	31.9MB
Studies	EWAS_Atlas_studies.tsv	81KB
Cohorts	EWAS_Atlas_cohorts.tsv	208KB
Probe annotations	EWAS_Atlas_probe_annotations.tsv	170.9MB
Trait to trait relationships	EWAS_trait_trait_logP.txt	0.9MB

Use R to search *EWAS\_atlas\_associations.tsv* file and save the associations with cardiovascular conditions of interest.

Before searching in R, verify which traits are present in the dataset by entering corresponding keywords in EWAS atlas search tab as shown below:



For example, typing in **cholesterol** will reveal cholesterol-related traits present in the dataset

After verifying that relevant traits are present in the dataset, we can use R grep to search for corresponding keywords and download selected associations as CSV files

After all relevant associations were downloaded, we can join all separate CSV files into a single master table