Dunedin Study Participation in the ENIGMA (Enhancing NeuroImaging Genetics through Meta Analysis) Consortium

(https://enigma.ini.usc.edu/)

Project	Lead(s)	Status	Timeline	Brain data	Genetic data	Pre-registration?
E5 - ENIGMA-GWAS of Cerebellum	Sarah Medland and Ian Harding	Sent summary statistics July 2023	Sites complete GWAS by 10/31/22	Regional cerebellar volumes calculated with ENIGMA tool	Imputed GWAS data (unfiltered, including chr X)	Limited; links to download protocol on ENIGMA site
ENIGMA Brain Age GWAS	Vilte Baltramonaityte, Esther Walton, Danai Dima	Generated Brain Age, awaiting further instructions for GWAS	?	Brain Age generated per ENIGMA protocol (using standard FreeSurfer measures)	Presumably imputed GWAS, have not released instructions	BrainAGE page on ENIGMA site (no preregistration, per correspondence with project lead)
ENIGMA-COINSTAC APOE2	Vince Calhoun and Jessica Turner	Analyses completed April 2023 (using COINSTAC; no need to send data), no word from organizers since	?	T1 anatomical scan, run through COINSTAC VBM pipeline	APOE Genotype	?
ENIGMA-tbfMRI	Henrik Walter, Ilya Veer, Lea Waller, and Susanne Erk	Working on GWAS step March 2024	ASAP	task-fMRI for emotion and reward task, processed with ENIGMA tool	Imputed GWAS (1000 genomes, continuous dosage in vcf format, from Michigan Imputation Server)	Page on ENIGMA site
ENIGMA-GWAS of DTI/White Matter	Barbara Franke and Neda Jahanshad	Have not received communication since opting in –project lead mentioned there's been a delay	?	DTI; WM measures from Freesurfer	Presumably imputed GWAS	Page on ENIGMA site
ENIGMA-Epigenetics	Sylvane Desrivières	Sent summary statistics September 2023	-	Cortical and Subcortical measures from Fressurfer	methylation	limited page on ENIGMA site
ENIGMA-dcSBM	Eimhear Davis	Awaiting instructions & further information	?	?	?	?

| ENIGMA-CNV | Ole Andreassen and Ida Elken Sønderby | Decided that it's not feasible | Asking for results from sites by 10/20/22 (not a final freeze) | Standard measures from recent version of FreeSurer | Genotype calling intensity data - "b allele freq" and "log r ratio" | - |