


# Predicting multi-omics from genotypes with OmicsPred




April 3 2023, by Justin Jackson

**a**


Platforms with Genetic Scores





**Somalogic**

**Proteomics (plasma)**  
2,384 protein genetic scores, validated on the  FENLAND,  MEC and  JHS cohorts

Learn more




**Olink**

**Proteomics (plasma)**  
308 protein genetic scores, validated on the  NSPHS and  ORCADES cohorts


Learn more






**Metabolon**

**Metabolomics (plasma)**  
726 metabolite genetic scores, validated on a withheld subset of INTERVAL and  ORCADES cohort


Learn more



**Nightingale**

**Metabolomics (serum)**  
Genetic scores for 141 metabolic traits, validated on  UK Biobank,  ORCADES and  VIKING cohorts

Learn more



**RNASeq**


**Transcriptomics (whole blood)**  
13,668 gene expression genetic scores, validated on a withheld subset of INTERVAL

Learn more


**c**


Summary


Number of proteins: 2,384

Training cohort:  INTERVAL

Training sample size: 3,175

External validation in cohort 1:  FENLAND (European; 2,129 proteins; 8,832 participants)

External validation in cohort 2:  MEC (2,047 proteins) - Chinese (CN; N=645), Indian (IN; N=564) and Malay (MA; N=563)

External validation in cohort 3:  JHS (African American; 820 proteins; 1,852 participants)

Evaluation Metric: Spearman correlation coefficient (rho), Variance explained (R<sup>2</sup>)

**b**

Explore traits and their genetic scores

Find your traits quickly

OMICS PRED ID	SOMALOGIC ID	LINK ID	Gene	Protein	FGAP	Interval R <sup>2</sup>	Interval Rho	FENLAND R <sup>2</sup>	FENLAND Rho	MEC R <sup>2</sup>	MEC Rho	JHS R <sup>2</sup>	JHS Rho
OP00000001	OLEC10A.1187.11.3	CSQ029	OLEC10A	C-type lectin domain family 12 member A	134	0.765	0.864	0.127	0.841	0	0	0	0
OP00000002	SGLEC8.3007.7.2	OYV36	SGLEC8	Sialic acid-binding $\alpha$ -like lectin 3	72	0.746	0.823	0.71	0.809	0.014	0.014	0.014	0.014
OP00000003	FCGR2A.3309.2.2	P12318	FCGR2A	Low affinity immunoglobulin gamma Fc region receptor 2a	276	0.743	0.845	0.73	0.844	0.04	0.04	0.04	0.04
OP00000004	ABO.3053.30.3	P16442	ABO	Histo blood group ABO system transferase	202	0.743	0.837	0.697	0.835	0.03	0.03	0.03	0.03
OP00000005	FCGR2B.3310.02.1	P31994	FCGR2B	Low affinity immunoglobulin gamma Fc region receptor 2b	127	0.727	0.876	0.128	0.873	0.04	0.04	0.04	0.04
OP00000006	ILFNB.7015.8.3	O70023	ILFNB	Leukocyte immunoglobulin-like receptor subfamily B member 5	139	0.725	0.847	0.121	0.859	0.04	0.04	0.04	0.04
OP00000007	PLRRA.3422.8.3	GRUKJ1	PLRRA	Pancreatic immunoglobulin-like type 2 receptor alpha isoform F003-delta1M	425	0.709	0.808	0.659	0.792	0.04	0.04	0.04	0.04
OP00000008	ICAM1.4240.13.3	P05032	ICAM1	Intercellular adhesion molecule 1	165	0.689	0.805	0.712	0.841	0.010	0.010	0.010	0.010
OP00000009	PLRRA.18915.150.3	GRUKJ1	PLRRA	Pancreatic immunoglobulin-like type 2 receptor alpha isoform F003-delta1	408	0.684	0.791	0.689	0.794	0.008	0.008	0.008	0.008
OP00000010	SNRPB.13047.3	O98038	SNRPB	Splicing-related protein	180	0.681	0.850	0.128	0.873	0.161	0.161	0.161	0.161
OP00000011	MEF1A.4407.16.1	P29927	MEF1A	Hepatocyte growth factor-like protein	493	0.680	0.809	0.671	0.807	0.046	0.046	0.046	0.046

**d**

Download

Download results

Download model files

Key features of the OmicsPred portal for accessing genetic scores of multi-omic traits. a, Organization of genetic scores on the portal. b, Example of how biomolecular traits and their genetic-score-related information can be explored. c, Example of how summary statistics of training and validation cohorts are presented. d, Example of how validation results and genetic-score models can be downloaded. e, Example of how validation results and trait-related information can be visualized. Credit: *Nature* (2023). DOI: 10.1038/s41586-023-05844-9

Work by an international research team led by Yu Xu and Michael Inouye at the Department of Public Health and Primary Care, University of Cambridge, has resulted in a unique resource for predicting multi-omics data directly from genotypes. The details of how the team developed the OmicsPred resource are in an article, "An atlas of genetic scores to predict multi-omic traits," published in the journal *Nature*. A Research Briefing on the study is published in the same journal issue.

There is a vision of the future that includes a device like the medical tricorder in "Star Trek," a hand-held device or an app incorporated into a mobile device. After a quick and painless scan just by waving the device over the afflicted area, comes the prognosis—such as Barclay's protomorphosis syndrome, a pernicious DNA disease that makes one de-evolve in the most intriguing [science-fiction](#) way possible. While a device of this type remains science fiction, many of the medical tricorders' capabilities already exist in the form of bulky lab equipment and databases spread across the fields of omics.

Thorough investigation of disease, or disease susceptibility, requires a lot of different omics—genomics, epigenomics, transcriptomics, proteomics and metabolomics. The collection of multi-omics is costly and data-intensive, making it somewhat rare within research. These fields of knowledge are in databases full of detailed analyses of human cell functions and disease associations. Additionally, many multi-omics studies have been targeted at specific subset populations to interrogate disease mechanisms. A broader capture of multi-omics could confirm inferred knowledge and discover hidden biological pathways.

Xu and colleagues used a [machine-learning approach](#) to create genetic scores for 17,227 biomolecular traits from 48,813 healthy blood samples that can predict the levels of 13,668 RNA transcripts, 2,692 proteins and 867 metabolites. The genetic scores were then validated in seven diverse, independent cohorts.

The OmicsPred team anticipates that this new resource will be widely useful in investigating multi-omic traits and associations with biological traits. All the genetic scores from the study have been made public through the web portal [omicspred.org](https://omicspred.org), and the [scientific community](#) is invited to use it to predict multi-omic traits from genotypes in their own data sets.

Currently, the molecular traits that these scores predict only reflect the heritability and variability in the training data set, which was derived from healthy blood donors of predominantly white European ancestries. The creators plan to enhance and refine the range of genetic scores available in the OmicsPred resource and expand the ancestral diversity with updated training data sets.

**More information:** Yu Xu et al, An atlas of genetic scores to predict multi-omic traits, *Nature* (2023). [DOI: 10.1038/s41586-023-05844-9](https://doi.org/10.1038/s41586-023-05844-9)

Genome-based scores predict thousands of molecular traits in humans, *Nature* (2023). [DOI: 10.1038/d41586-023-00721-x](https://doi.org/10.1038/d41586-023-00721-x)

© 2023 Science X Network

Citation: Predicting multi-omics from genotypes with OmicsPred (2023, April 3) retrieved 9 May 2024 from <https://medicalxpress.com/news/2023-04-multi-omics-genotypes-omicspred.html>

<p>This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.</p>
------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------