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# 2016

## Notable Articles

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Scientists

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# 1 Analysis of protein-coding genetic variation in 60,706 humans.



**Pamela Sklar, Psychiatry, PROFESSOR**



**Shaun Purcell, Psychiatry, ASSOCIATE PROFESSOR**

This study analyzes vast amounts of shared data—from the Exome Aggregation Consortium and the 23andMe database—to provide insights into genetic-variant penetrance and possible treatment approaches for a rare, fatal genetic prion disease.



Analysis of protein-coding genetic variation in 60,706 humans.

Citation data: Nature, ISSN: 1476-4687, Vol: 536, Issue: 7616, Page: 285-91

Publication Year: 2016

Researchers: Shaun Purcell, Pamela Sklar

USAGE	852	CAPTURES	651	MENTIONS	274	SOCIAL MEDIA	3834	CITATIONS	67
Clicks	817	Readers	651	Comments	223	Shares, Likes & Comments	2775	Citation Indexes	67
Abstract Views	29			News Mentions	38	Tweets	783		
Link-outs	6			Blog Mentions	13	Scores	276		

Nature, ISSN: 1476-4687, Vol: 536,  
Issue: 7616, Page: 285-91

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## 2 E-Waste and Harm to Vulnerable Populations: A Growing Global Problem



**Philip J. Landrigan,**  
**DEAN FOR GLOBAL HEALTH; PROFESSOR**  
**Preventive Medicine**

This article reviews international efforts concerned with environmental hazards, especially affecting children, as a preface to presenting next steps in addressing health issues stemming from the global e-waste problem.



E-Waste and Harm to Vulnerable Populations: A Growing Global Problem.

Citation data: Environmental health perspectives, ISSN: 1552-9924, Vol: 124, Issue: 5, Page: 550-5  
Publication Year: 2016

USAGE	25455	CAPTURES	191	SOCIAL MEDIA	47	CITATIONS	3
HTML Views	13008	Exports-Saves	145	Tweets	24	Citation Indexes	3
Abstract Views	12397	Readers	46	Shares, Likes & Comments	23		
Clicks	42						
Link-outs	8						

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Environmental health perspectives, ISSN: 1552-9924, Vol: 124, Issue: 5, Page: 550-5

## 3 The genetic architecture of type 2 diabetes.



**Ruth Loos**  
**PROFESSOR, Environmental Medicine &**  
**Public Health**

This study tested the GoT2D and T2D-GENES and performed whole-genome sequencing in 2,657 European individuals with and without diabetes, and exome sequencing in 12,940 individuals from five ancestry groups. The study was expanded the sample size via genotyping and imputation in a further 111,548 subjects. Variants associated with type 2 diabetes after sequencing were found to be overwhelmingly common and most fell within regions previously identified by genome-wide association studies.



The genetic architecture of type 2 diabetes.

Citation data: Nature, ISSN: 1476-4687, Vol: 536, Issue: 7614, Page: 41-7  
Publication Year: 2016  
Researchers: Ruth Loos

USAGE	283	CAPTURES	285	MENTIONS	8	SOCIAL MEDIA	1898	CITATIONS	16
Clicks	241	Readers	285	Blog Mentions	5	Shares, Likes & Comments	1562	Citation Indexes	16
Abstract Views	40			News Mentions	2	Tweets	334		
Link-outs	2			Comments	1	Scores	2		

Nature, ISSN: 1476-4687, Vol: 536, Issue: 7614, Page: 41-7

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