Recon3D enables a three-dimensional view of gene variation in human metabolism

Recon3D enables a three-dimensional view of gene variation in human metabolism

Genome-scale network reconstructions have helped uncover the molecular basis of metabolism. Here we present Recon3D, a computational resource that includes three-dimensional (3D) metabolite and protein structure data and enables integrated analyses of metabolic functions in humans. We use Recon3D to functionally characterize mutations associated with disease, and identify metabolic response signatures that are caused by exposure to certain drugs. Recon3D represents the most comprehensive human metabolic network model to date, accounting for 3,288 open reading frames (representing 17% of functionally annotated human genes), 13,543 metabolic reactions involving 4,140 unique metabolites, and 12,890 protein structures. These data provide a unique resource for investigating molecular mechanisms of human metabolism. Recon3D is available at http://vmh.life.

General information
State: Published
Organisations: Novo Nordisk Foundation Center for Biosustainability, Yeast Cell Factories, Big Data 2 Knowledge, Network Reconstruction in Silico Biology, Technical University of Denmark, University of Luxembourg, University of California at San Diego, University of Tübingen, Chalmers University of Technology
Pages: 272-281
Publication date: 2018
Peer-reviewed: Yes

Publication information
Journal: Nature Biotechnology
Volume: 36
Issue number: 3
ISSN (Print): 1087-0156
Ratings:
BFI (2018): BFI-level 3
Web of Science (2018): Indexed yes
BFI (2017): BFI-level 2
Scopus rating (2017): CiteScore 12.94 SJR 18.252 SNIP 6.062
Web of Science (2017): Impact factor 35.724
Web of Science (2017): Indexed yes
BFI (2016): BFI-level 2
Scopus rating (2016): CiteScore 13.16 SJR 20.666 SNIP 6.42
Web of Science (2016): Impact factor 41.667
Web of Science (2016): Indexed yes
BFI (2015): BFI-level 2
Scopus rating (2015): CiteScore 11.88 SJR 18.263 SNIP 5.553
Web of Science (2015): Impact factor 43.113
Web of Science (2015): Indexed yes
BFI (2014): BFI-level 2
Scopus rating (2014): CiteScore 11.4 SJR 16.609 SNIP 5.37
Web of Science (2014): Impact factor 41.514
Web of Science (2014): Indexed yes
BFI (2013): BFI-level 2
Scopus rating (2013): CiteScore 10.45 SJR 13.974 SNIP 5.364
Web of Science (2013): Impact factor 39.08
ISI indexed (2013): ISI indexed yes
Web of Science (2013): Indexed yes
BFI (2012): BFI-level 2
Scopus rating (2012): CiteScore 8.44 SJR 10.87 SNIP 4.914
Web of Science (2012): Impact factor 32.438
ISI indexed (2012): ISI indexed yes
Web of Science (2012): Indexed yes