

## MetaDome

highly accessed

---

7 May 2020



[MetaDome](#) was recently recognized as one of the most accessed articles of 2018-2019 in *Human Mutation*.

Researchers of the Radboudumc have developed MetaDome to survey regions in proteins that tolerate genetic variation. This helps to address the pathogenicity of genetic variants of unknown clinical significance. Using evolutionary relationships between protein domain homologues, MetaDome aggregates variation onto “meta-domains”. These meta-domains make the genetic variation map richer than individual protein domains. MetaDome additionally visualizes variation into a tolerance landscape, indicating regions within protein-coding genes that are more, or less, tolerant to variation.

The MetaDome was a project developed by Laurens van de Wiel, [Christian Gilissen](#), and [Gert Vriend](#) and was first available online in spring 2018. Since then, it has been used by nearly 2,500 colleagues from various institutes across 64 countries and can be accessed [here](#).

