Search

varsomepremium

Who is it for: Researchers in need of individual gene or variant lookups.

VarSome Premium gives users powerful access to the VarSome search engine to query and work with the VarSome database at the variant and gene level. Users can search by HGVS nomenclature, rsID, gene name, transcript symbol or genome location. However, the VarSome database contains much more than just variant frequencies. Our complete search functionality supports word searches allowing you to find publications, diseases, phenotypes, genes, ClinVar & UniProt variants, and user comments.

Classifiers

The VarSome database powers the classification algorithms that apply ACMG* and AMP** interpretation guidelines to germline, somatic, and copy number variants. Every result provides clear natural language explanations as to why specific rules were triggered and the accompanying evidence. Similarly, a full explanation is provided when threshold criteria have not been met. As the rules were originally designed to be applied by clinicians with the benefit of case knowledge, VarSome allows users to adjust the weighting of rules to better fit their case.

VarSome and ClinVar

ClinVar links directly to VarSome result pages. Similarly, you can make ClinVar Submissions directly from VarSome.

Community

Over 500 000 users have visited VarSome.com, adding comments, linking publications, and providing advice. As many variants are rarely seen by any one individual, the VarSome Community ensures that knowledge and experience is shared. Users around the world have connected via VarSome to share expertise.

varsome

With access to over 140 data sources, and clear and transparent classification tools, VarSome is the most comprehensive and robust variant interpretation platform for human genome data.

*https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4544753/
**https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5707196/

HPST
a member of Altium Group

HPST, s.r.o.
Na Jetelce 69/2
190 00 Praha 9

info@hpst.cz
+420 244 001 231
www.hpst.cz