For Immediate Release
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Genomenon Wins $1.8M NIH Grant to Automatically Curate Genomic Literature

Fast track SBIR grant will accelerate publication-driven genomic analysis

ANN ARBOR, Mich., April 25 2017 - Genomenon® Inc., a genomic interpretation software company, today announced a $1.8M grant awarded by the National Institutes of Health. The fast-track Small Business Innovation Research (SBIR) grant, awarded by the National Human Genome Research Institute, will fund Genomenon's further innovation in genomic analysis, efficiently streamlining the laborious literature research and curation process leading to faster patient diagnosis.

"This grant recognizes the solid approach and great potential of Genomenon's technology to drive rapid improvements in automating accurate gene and variant curation" Genomenon co-founder and CSO Dr. Mark Kiel said.

Genomenon's initial product, Mastermind, is a novel analytic and data visualization tool that accelerates gene and variant curation by providing immediate insight into millions of scientific articles from the primary medical literature. The grant will help Genomenon in its quest to assemble the most comprehensive database of genomic knowledge ever created by expanding its Mastermind database with millions of additional articles covering genetic disease.

The funds for Phase I of this grant will be used to perform concordance testing between the Mastermind database and current gold-standard references of genomic knowledge. Phase II will focus on refining various applications using the Mastermind database including the development of ancillary software to inform patient diagnosis and research discovery.

Genomenon recently announced the completion of its latest financing round in the 4th quarter of 2016. The financing fueled the completion and launch of Mastermind, which was officially released in February.

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About Genomenon:
Genomenon has eliminated the manual search process for gene and variant curation with a scientific literature database and software for use in clinical decision-making. We have mined the full text of millions of genomic-related scientific articles to create a comprehensive genomic knowledge base that enables pathologists and geneticists to quickly and accurately curate disease-causing variants from genomic-sequencing datasets. With the comprehensive dataset and deep insight into the genomic literature, we're able to provide fascinating results – from accelerated gene and variant curation to evidence-based panel design – by scouring the literature to find genes and variants linked to specific diseases within the literature.
For more information, visit www.genomenon.com or email sales@genomenon.com.

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