Research consortium starts GENImmune project for new methods to design vaccines for efficient SARS-CoV-2 immunization

Planegg/Munich, Germany, 22 February 2022 – Biomax Informatics, PEPperPRINT and PMCR today announced the launch of a joint research project with partners from the University of Bonn, the Helmholtz Munich and the Technical University of Munich.

Under the name GENImmune the consortium will develop new methods to design vaccines applied for efficient SARS-CoV-2 immunization. The project is funded by the German Federal Ministry of Education and Research and coordinated by Biomax Informatics.

The first wave of SARS-CoV-2 vaccine projects have focused on the most obvious surface antigen ignoring the vulnerability against immune evasion by the evolution of new virus variants. At the same time a detailed understanding of the full life-cycle of the virus has been generated and can now be applied to a rational vaccine design with the goal to develop a broadly active Pan-coronavirus vaccine.

GENimmune aims to employ new Artificial-Intelligence (AI)-based approaches such as machine learning and natural language processing. Additionally, computer models for an efficient understanding of interactions between pathogens such as viruses and the human immune system shall be created, enabling the development of workflows for rational vaccine design and target identification.

The project partners have long-standing experience in vaccine development and the application of computational methods for rational design. The partners are already involved in immunization projects for Hepatitis B, Norovirus and cancer immunizations as well as clinical COVID-19 analysis and contribute to the [COVID-19 Disease Map Collaboration](#), an international effort of 130 institutions that curates a detailed, computer-readable molecular and cellular map of host-pathogen interactions.

GENImmune will develop AI and text mining methods to quickly generate and refine similar disease maps for any infection. Using these methods, the COVID-19 disease map will be refined, too, integrating the growing volume of relevant literature. New methods to develop disease maps into predictive computational models need to be developed to leverage these efforts.

"Computational models for host-pathogen interaction derived from disease maps and causal linkage of vaccine composition with B- and T-cell responses will enable simplified development of new vaccines that are broadly active and robust against novel variants", explained Dr. Dieter Maier, Director Project Management at Biomax and project leader of GENImmune.

"New Machine Learning and bioinformatics methods will support the iterative optimization of the epitope selection, specific amino acid sequences, and adjuvants to trigger balanced B-/T-cell responses and to ensure robustness with respect to newly emerging SARS-CoV-2 variants of concern" added Dr. Wolfgang Schönharting, CEO of PMCR.

"In addition, AI data analysis methods will be developed to interpret the results of new biotechnology platforms relevant to immunology, for example high resolution, conformation-specific characterization of antibody responses on the epitope level combined with functional assays for precise measurement of cellular immune responses" described Dr. Volker Stadler, CEO of PEPperPRINT.

GENImmune started on 1 January 2022 and is designed to run for two years.

End of Press Release

Additional Information

The partner of the consortium:
- **Biomax Informatics AG,** coordinates the project and will use text mining tools to optimize COVID-19 disease map.
- Prof Hasenauer, **University of Bonn,** will apply computer models to predict meaningful vaccine development targets.
- Prof Frishman, **Technical University of Munich,** will develop machine learning methods to predict vaccine epitopes.

- **PCMR GmbH** will develop machine learning methods to predict clinical effects of different combinations of epitopes and adjuvants.
- **PEPperPRINT GmbH** will develop a SARS-CoV-2 specific peptide-microarray for analysis of vaccine-induced antibodies.
- Prof Protzer, **Helmholtz Munich,** will apply the methods to validate SARS-CoV-2 immunization robust against multiple escape variants in preclinical studies.

About Biomax Informatics

Biomax Informatics provides software solutions for better decision making and optimal knowledge management in the life science industry. Using the software, customers are able to add value by integrating information from proprietary and public resources to achieve a knowledge-based approach to developing innovative life science products. Biomax's global customers include hospitals, companies and research institutions. Founded in 1997, the company currently has 45 employees and is headquartered in Planegg near Munich. For more information, visit www.biomax.com.

Your contact at Biomax:

Press Contact:	**Project Leader:**
Bettina von Klitzing-Stückle	Dr. Dieter Maier
Marketing Manager	Director Project Management
Bettina.klitzing-stueckle@biomax.com	dieter.maier@biomax.com

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