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Genocea Presents Data at AACR Annual Meeting Further Highlighting Advantages of ATLAS Platform in Identification of Neoantigens over in silico Methods

- ATLAS data demonstrate in silico *methods miss most empirically confirmed neoantigens -*
- ATLAS able to identify inhibitory neoantigens -
- Mouse ATLAS melanoma model developed to study mechanism of inhibitory antigens -

CAMBRIDGE, Mass., April 18, 2018 (GLOBE NEWSWIRE) -- Genocea Biosciences, Inc. (NASDAQ:GNCA), a biopharmaceutical company developing neoantigen cancer vaccines, today announced highlights from its scientific presentations at the 2018 Annual Meeting of the American Association for Cancer Research (AACR 2018), taking place April 14-18, 2018 in Chicago, IL.

Jessica Flechtner, Ph.D., Genocea's chief scientific officer commented on the AACR presentations: "We continue to generate data that demonstrate the versatility of our ATLAS platform. As the studies presented at AACR indicate, ATLAS is a differentiator for Genocea - allowing us to do what *in silico* approaches cannot - to both identify and characterize neoantigens for use in personalized cancer vaccines. We believe that our ability to find stimulatory and inhibitory antigens during the neoantigen selection process combined with our capacity to explore mechanisms of inhibitory antigens in a murine model, may enable us to help cure cancer by pioneering next-generation cancer vaccines."

Summary of AACR Poster #730, "Empirical neoantigen identification using the ATLAS™ platform across thousands of mutations and multiple tumor types highlights advantages over algorithmic prediction methods":

- ATLAS enables identification of biologically relevant $CD4^+$ and $CD8^+$ T cell neoantigens in subjects in an unbiased manner, by using subjects' own antigen-presenting cells (APCs) and T cells rather than predictive algorithms to identify and characterize T cell responses to all candidate neoantigens.
- Neoantigen screening was performed on 23 individuals across eight tumor types with mutational burden ranging from 9 to 319 unique mutations.
- Empiric identification of neoantigens derived from somatic mutations from each patient's tumor independently of HLA type and without predictions resulted in the following observations:
  - ATLAS identified stimulatory neoantigens of both $CD4^+$ and $CD8^+$ T cells, which Genocea believes confirms the importance of including antigens of relevance for both T cell subsets in neoantigen vaccines;
  - There is little overlap between CD4+ and CD8+ T cell neoantigens; fewer than 2% of empirically confirmed neoantigens were shared between T cell subsets;
  - Prediction algorithms missed up to 69% of ATLAS-identified neoantigens, with only 2% of CD8+ neoantigens and 24% of CD4+ neoantigens accurately predicted;
  - The major histocompatibility complex (MHC) class I algorithm appeared to better predict CD4+, not CD8+, neoantigens;
  - ATLAS also identified inhibitory neoantigens of both $CD4^+$ and $CD8^+$ T cells
    - Inhibitory neoantigens outnumbered stimulatory neoantigens more than three-fold in aggregate in the screened patients;
    - Inhibitory antigens currently cannot be identified using *in silico* approaches.

Summary of Poster #5718, "*ex vivo* ATLAS™ identification of neoantigens for personalized cancer immunotherapy in mouse melanoma":

- The B16F10 mouse melanoma model was utilized to characterize neoantigens. More than 1,600 tumor-specific mutations (possible neoantigens) were interrogated using the ATLAS technology and $CD8^+$ T cells from tumor-bearing C57BL/6 mice.
- Similar to human neoantigen screens, mouse ATLAS (mATLAS) identified both stimulatory and inhibitory neoantigens:
  - 99% of mutations identified using whole exome sequencing were screened;
  - 68 stimulatory (4% of total mutations) and 57 inhibitory (3% of total mutations) neoantigens were identified.
- NetMHCPan, a MHC-binding prediction algorithm, failed to identify the majority of mATLAS-identified neoantigens:

    - Only 2% of B16F10 neoantigens predicted by algorithms were empirically confirmed to be stimulatory antigens;
    - 91% of stimulatory neoantigens empirically identified with mATLAS were not predicted;
    - 6% of algorithm-predicted neoantigens were inhibitory.
- These data demonstrate that inhibitory antigens can be identified in mouse models, allowing for future research into the mechanism of ATLAS-identified inhibitory responses and their relationship to stimulatory neoantigens in mediating tumor control.

About Genocea Biosciences, Inc.
Genocea's mission is to help conquer cancer by designing and delivering targeted vaccines and immunotherapies. While traditional immunotherapy discovery methods have largely used predictive methods to propose T cell targets, or antigens, Genocea has developed ATLAS™, its proprietary technology platform, to identify clinically relevant antigens of T cells based on actual human immune responses. Genocea is using ATLAS in immuno-oncology applications to develop neoantigen cancer vaccines, while also exploring partnership opportunities for general cancer vaccines and a vaccine targeting cancers caused by Epstein-Barr Virus. Genocea expects to begin clinical development of its first neoantigen cancer vaccine, GEN-009, in 2018. For more information, please visit www.genocea.com.

Forward-Looking Statements
This press release includes forward-looking statements, including statements relating to the expected clinical development of GEN-009, within the meaning of the Private Securities Litigation Reform Act. Such forward-looking statements are subject to risks and uncertainties that could cause actual results to differ materially from those expressed or implied in such statements. Genocea cautions that these forward-looking statements are subject to numerous assumptions, risks and uncertainties, which change over time. Applicable risks and uncertainties include those identified under the heading "Risk Factors" included in Genocea's Annual Report on Form 10-K for the year ended December 31, 2017 and any subsequent SEC filings. These forward-looking statements speak only as of the date of this press release and Genocea assumes no duty to update forward-looking statements, except as may be required by law.

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