Application: 4508

BostonGene AI-based digital pathology platform

Page: General Information

Provide information about the company to be considered for the award. If you will be nominating an individual, specify the nominee's employer.

Name of Organization/Company

BostonGene

Additional Contacts

I do not wish to list additional contacts

Page: Entry Information

Entry Title

BostonGene AI-based digital pathology platform

Category

P05. New Product of the Year - Healthcare Technology

New Product Submission Format

Written Answers

a. Briefly describe the organization that developed the nominated new product: its history and past performance (up to 200 words). Required

BostonGene is a company at the intersection of technology and biology, dedicated to advancing and personalizing cancer medicine. Founded in 2015, BostonGene has continually pushed the boundaries of innovation to improve cancer patient care and accelerate research and drug development through cutting-edge solutions. Leveraging our AI-powered multiomics platform, we digitize and comprehensively analyze the molecular profiles of cancer patients, including the immune system and tumor microenvironment. Our software solutions, indication-specific cancer library and advanced bioanalytics, enable us to discover multiparametric signatures, identify targets, match them to relevant indications for biopharma and recommend the most effective treatments for patients.

BostonGene's flagship product, the Tumor Portrait™ test, combines DNA and RNA sequencing results with patient clinical profiles, the latest ▮▮▮▮▮▮▮▮ and available clinical trials to generate a comprehensive report. This approach ensures personalized and effective treatment options for each patient based on data-driven insights.

BostonGene's unwavering commitment to innovation and excellence has earned a strong reputation within the clinical and pharma community. By continuously advancing the capabilities of personalized cancer treatment, BostonGene remains a trusted partner for healthcare professionals striving to elevate patient care and treatment efficacy.

b. Specify the date on which this nominated product was introduced to the marketplace. Outline the nominated product's features, functions, benefits and novelty (up to 250 words). Required

Histopathologic evaluation of tumor tissue slides is crucial for cancer patient management: it specifies the cancer diagnosis and identifies therapy response biomarkers. However, traditional pathology has limitations due to potential human error in manual slide examination, risking missed biomarkers and depriving patients of beneficial therapies.

BostonGene introduced an AI-based digital pathology platform that eliminates the need for manual analysis and reduces variability for various types of pathology data.

1) H&E (hematoxylin and eosin) is used for evaluating tissue structure. For example: tertiary lymphoid structure (TLS) and stromal tumor infiltrating lymphocytes (sTILs) are potential biomarkers of therapy response and are associated with better patient prognosis. BostonGene's analysis of H&E slides from lung and breast cancer patients showed that patients with high TLS or TILs had longer survival compared to patients with low TLS or TILs. Accurate identification of TLS and TILs was independently validated by an orthogonal method - RNA sequencing.

2) IHC (immunohistochemistry) is used for identifying single proteins and biomarkers in tumor tissue. **[REDACTED FOR PUBLICATION]** ▮▮▮

3) MxIF (multiplex immunofluorescence) is used for identifying multiple biomarkers and TME characterization on one slide to gain insights into tissue architecture, cell subtyping and cell-to-cell interactions. For example, in breast cancer patients treated with palbociclib+anastrazole, there currently are no biomarkers predicting response.However, BostonGene's AI-based analysis of MxIF slides stained with 21 different markers identified 3 cellular neighborhoods significantly increased in patients resistant to therapy, suggesting these can be biomarkers predicting treatment response.

c. Explain why the nominated product is unique or significant. If possible compare the product to competitors' offerings and/or to the organization's other or past products (up to 250 words). Required

Manual assessment of TILs and TLS structures from H&E slides is prone to variability, as shown in several independent studies: the same slides can be evaluated as TLS / TILs positive or negative by different pathologists. AI-based tools can solve this reproducibility challenge; however, the results of automated TLS / TILs identification need to correlate with clinical outcomes in order to be used in clinical practice. BostonGene's model highly correlated with clinical outcomes in patients with lung adenocarcinoma and breast cancer.

Spatial proteomics provides an overview of tissue composition based on multiplex immunofluorescence (MxIF) detection of up to 40 biomarkers with single-cell resolution. BostonGene's customizable AI-powered pipeline characterizes tumor cells, immune cell infiltration, stroma, vasculature and cell-cell interactions, offering valuable insights into complex tissue architecture and spatial relationships.

This complex analysis starts with cell segmentation to correctly identify each cell. The accuracy of cell segmentation directly impacts the validity and interpretation of the results obtained from subsequent analysis (determination of cell types and their interaction). BostonGene compared the performance of its proprietary cell segmentation tool with three other algorithms ███████████████████ and showed superior accuracy. The F1 score of the BostonGene tool was 0.91 versus 0.55 - 0.86 for other tools (the F1 score is a measure of how good a model is at making accurate predictions, ideally is close to 1).

d. Reference any attachments of supporting materials throughout this nomination and how they provide evidence of the claims you have made in this nomination (up to 250 words). Optional

1. Publication in a high-impact scientific journal: spatial proteomics analysis conducted by BostonGene contributed to the identification of high-risk follicular lymphoma patients almost 2 years prior to the progression of their disease. https://www.cell.com/cancer-cell/abstract/S1535-6108(24)00045-X

2. Conference abstract: BostonGene AI-based analysis identifies TLS and TILs in breast cancer patients and predicts survival outcomes https://aacrjournals.org/cancerres/article/83/7_Supplement/5444/720667

3. Conference abstract: BostonGene AI-based analysis identifies TLS and TILs in lung adenocarcinoma patients and predicts survival outcomes https://ascopubs.org/doi/10.1200/JCO.2022.40.16_suppl.3142

4. Conference abstract: BostonGene AI-based MxIF analysis reveals biomarkers of response to neoadjuvant therapy in breast cancer patients. https://aacrjournals.org/cancerres/article/82/12_Supplement/6151/701657/Abstract-6151-Tumor-microenvironment-heterogeneity?searchresult=1

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Webpage Link

Would you like to add an additional webpage link?

Supporting Document

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Would you like to add an additional supporting document?

Yes

Supporting Document 2

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Would you like to add an additional supporting document?

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No

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