

Zhang, Kaijiang (Kevin)

From: Stroncek, Jackie <jstroncek@wsgr.com>
Sent: Wednesday, October 3, 2018 11:45 AM
To: Zhang, Kaijiang (Kevin)
Cc: Alemozafar, Ali; Tiee, Nicholas
Subject: U.S. Patent Application No. 14/810337 - Interview agenda
Attachments: USSN14810337 Interview agenda-10-05-2018_final.pdf

Dear Examiner Zhang,

Please find attached an interview agenda for discussion during our interview scheduled for Friday October 5 at 3 PM Eastern Standard Time (noon PDT).

We look forward to discussing the attached claim language with you via the WebEx link circulated in the Outlook meeting invitation.

Best,
Jackie Stroncek
(Reg. No. 72,619)

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Application No: 14/810,337
Title: METHODS AND SYSTEMS FOR GENETIC ANALYSIS
Examiner: ZHANG, KAIJIANG
Attorney Docket No: 44168-702.401

Patent Examiner Interview Agenda – October 5th, 2018 at
12:00 PM PST (3:00 PM EST)

Planned attendees: Ali Alemozafar, Jacqueline Stroncek, Nicholas Tiee

Non-final Office Action mailed April 9th, 2018:

- Discuss § 102 rejection of claim 31
- Discuss proposed claim language (next page)
- Discuss double patenting rejections

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Proposed claim language

31. A method for analyzing a nucleic acid sample, comprising:
- (a) producing two or more subsets of nucleic acid molecules from a nucleic acid sample, wherein the two or more subsets differ by one or more genomic features selected from the group consisting of genomic regions, mean GC content, mean molecular size, ~~subset preparation method, methylation state, insertion or deletion, and single nucleotide variant (SNV) or combination thereof,~~ with the aid of probes that selectively enrich for the one or more genomic features in at least a first subset or a second subset of the two or more subsets of nucleic acid molecules as compared to another genomic feature(s) in the at least the first subset or the second subset;
 - (b) combining at least two of the two or more subsets of nucleic acid molecules to produce a first combined pool of nucleic acid molecules; and
 - (c) conducting one or more assays on the first combined pool of nucleic acid molecules, wherein at least one of the one or more assays comprises a sequencing reaction.