NuProbe

Multiplex Real-Time PCR Research Scientist/Assay Developer

NuProbe USA is seeking to hire a Multiplex Real-Time PCR Research Scientist/Assay Developer. The successful candidate will focus on NuProbe's multiplex real-time PCR product design, development, testing and launch. The successful candidate is expected to start between July 16 and October 15, 2018.

Location: Cambridge, MA or Houston, TX

Required qualifications and experience:

- Ph.D. in Molecular Biology, Genetics, Bioengineering or related field
- Expert in multiplex real-time PCR
- Proven ability in detection and profiling of nucleic acid sequence variations (PCR, NGS, hybridization, etc.), as evidenced by lead-author publications or published patents
- Computer-aided DNA primer/probe sequence design (MATLAB preferred)
- Working experience with cell culture and various cell lines

Preferred qualifications and experience:

- 2 years industrial experience in a related biotechnology position (leading to a commercialized successful product is a plus)
- Experience with next-generation sequencing (NGS), specifically with Illumina platforms, and downstream data analysis
- Working experience with at least one programming language (MATLAB, Python, R, Bash, etc.)
- Familiarity with mutation databases (1000 Genome, COSMIC, NCBI, etc.)

About NuProbe USA: NuProbe USA is the US-based R&D subsidiary of NuProbe Global, a company that recently raised $11M in Series A fundraising to develop novel non-invasive DNA. Its technology enables precise and comprehensive capturing of disease signatures with uniquely high sensitivity and multiplexing capability. NuProbe is co-founded by Prof. Peng Yin at Harvard University, Prof. David Zhang at Rice University, and Dr. Victor Shi (former founding president of Qiagen Asia).

Contact Information: Please email Helen Yan at helen.yan@nuprobe.com with applications. Please include an up-to-date resume or C.V., and title your email "Multiplex PCR scientist application for NuProbe + ANSWER1 + ANSWER2"

Please replace (ANSWER) with the answers of the following questions:

1. Rounding to the nearest integer, what is the number of haploid genomic copies in 15pg of human genomic DNA?
2. Assuming PCR amplification efficiency is 100%, if a primer pair can generate a Ct of 22.5 in qPCR when the sample input is 6000 copies/well, what's the theoretical Ct value if the input is 20000 copies/well (round to the nearest tenth)?

Applications and emails not conforming to this format will be deleted without review.