

Bode SIMS – User Specification Worksheet

Extraction

Are robot workstations utilized for extraction? If yes, please specify. If no, please specify manual method(s). If both methods are used please specify.

Additional comments: _____

Quantification

Bode SIMS supports Applied Biosystems QuantifilerTM or Quantifiler[®] Duo or Plexor HY. (Please contact Bode Technical Services if another platform is desired.)

What quantification platform is your lab using? _____

Please select from the following options for desired features:

___ Quant Standards evaluated for pass/fail

___ Dilution chart

___ CT value evaluation for inhibition/clean up

___ Sample data evaluation for concentration

___ If your lab uses a concentration/clean up method and you want that worksheet incorporated in SIMS, please indicate which method(s)

___ Data output file for robotic normalization, If yes, please specify workstation:

Additional comments: _____

STR Multiplex Amplification Set up

Please specify multiplex STR system(s) and PCR reaction volume(s):

____ Profiler Plus/COfiler reaction volume(s) _____

____ Identifiler reaction volume(s) _____

____ PowerPlex 16 reaction volume(s) _____

____ MiniFiler reaction volume(s) _____

____ Y Filer reaction volume(s) _____

(If additional STR systems are required please contact Bode Technical Services.)

If you perform robotic PCR tray set up, please specify workstation: _____

Additional comments: _____

Capillary Electrophoresis Genetic Analysis Tray Set up

Bode SIMS supports the ABI PRISM® 3100, 3130, and 3130xl genetic analyzers. Please contact Bode Technical Services if another platform is desired.

Which genetic analyzer(s) does your lab use? _____

Additional comments: _____

Sample Tracking Features

Bode SIMS selects samples for quantification, normalization, PCR set up and CE based on the sample list and order generated from extraction. This ensures efficient sample tracking of batched samples. If you would prefer to customize your SIMS so that each laboratory step is independent, please specify.

Allele Tables/CODIS CMF files

If different from Amplification set up, please specify multiplex STR system(s):

Please specify interpretation features you would like incorporated:

- RFU values above or below specific thresholds (different for homozygous and heterozygous loci)
- Peak height ratio imbalance
- Sort samples based on sample name
- Verify control allele calls (9947 or 007)
- List homozygotes as one or two allele calls

Additional comments: _____

Additional Notes:
