Agilent mAb-Glyco Chip (G4240-64020)

Quick Start Guide

Important

The Agilent mAb-Glyco Chip Quick Start Guide is designed for fast and easy check of the HPLC-Chip/MS system before running the mAb-Glyco Chip. Incorrect system configuration can lead to signal loss or significant decrease in chip lifetime. For details please refer to the mAb-Glyco Chip User's Guide, P/N G4240-90020.

Agilent mAb-Glyco Chip Acquisition Checklist

Please check the following points before running the mAb-Glyco Chip.

- ☐ Chip Cube is in backflush mode (User's Guide section 2).
- ☐ 8 µL injection loop (P/N G1375-87315) is installed (User's Guide section 2).
- ☐ The yellow 25 µm x 105 cm PEEK coated fused silica capillary (P/N G4240-87301) is installed between the Micro HiP Sampler and the Chip Cube (User's Guide section 2).
- ☐ The mAb-Glyco Chip Enablement Kit (G4240-64025) is installed (User's Guide section 2).
- ☐ Deglycosylation Buffer is installed on channel A1 of the Capillary Pump. Buffer is not older than 3 months and acetonitrile was added (User's Guide section 2 and 3).
- ☐ Chip.ini file and firmware have been updated (required only once, User's Guide section 2).
- ☐ Acquisition methods are copied into \MassHunter\Methods (User's Guide section 2 and 4)
- ☐ System has been initially conditioned, no parts in the sample flow have been changed since (User's Guide section 6).
- ☐ Correct method file is loaded (User's Guide section 4).
- ☐ Injection flush volume (IFV) is set to match method used (User's Guide section 4).
- ☐ Sample injection volume is set to 2 µL (User's Guide section 7).
- ☐ Chip was properly stored (User's Guide section 8).
- ☐ The sample has been centrifuged before injection.

Agilent mAb-Glyco Chip Data Analysis Checklist

Please check the following points before analyzing mAb-Glyco Chip data.

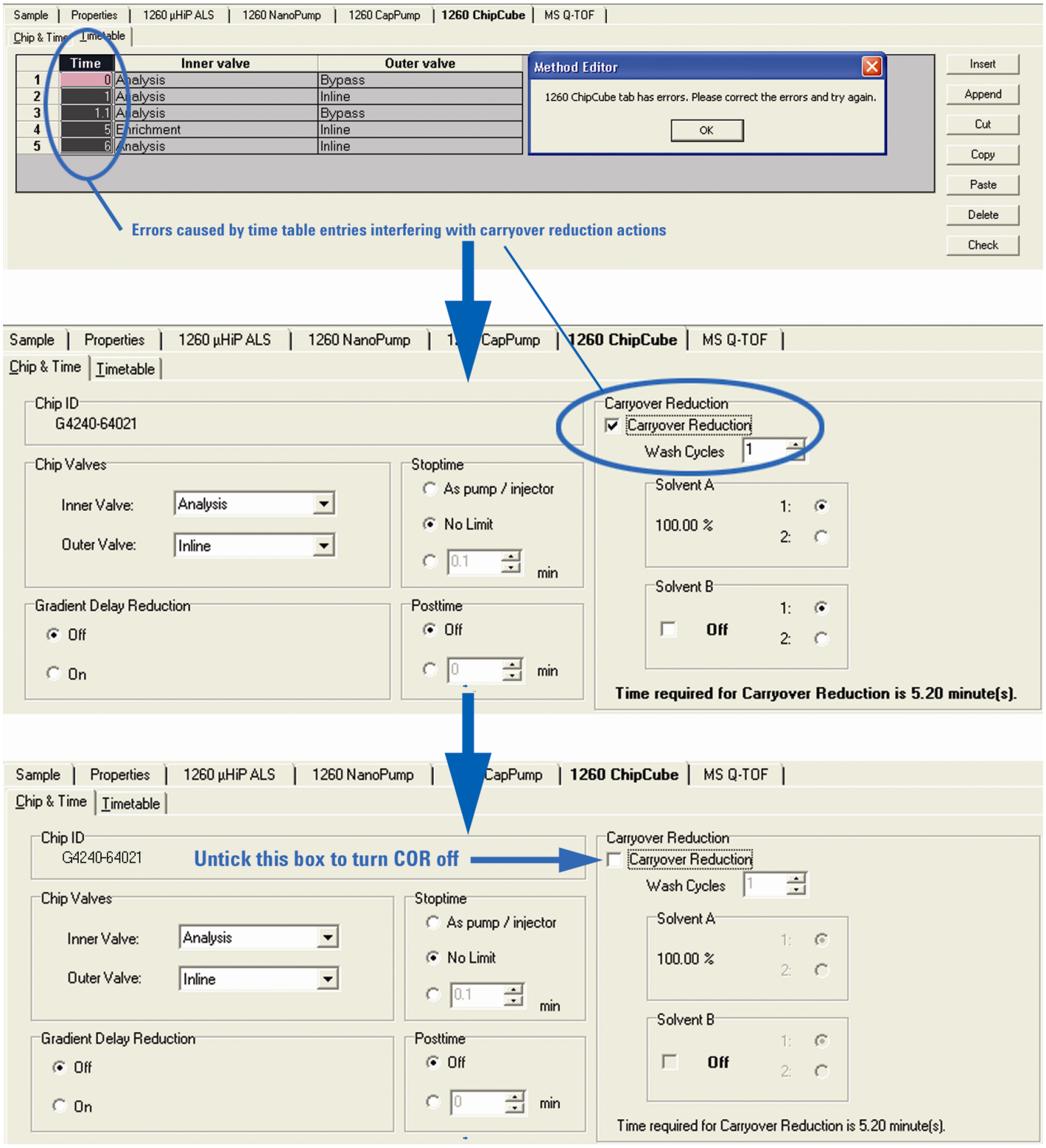
Before starting Mass Hunter Qualitative Analysis software

- ☐ Mass Hunter Analysis Software and the respective version of Personal Compound and Database Library Software are installed (User's Guide section 10).
- ☐ Data analysis method is copied into *\MassHunter\Methods* (User's Guide section 4 and 10)
- ☐ Reporting templates ***Glycan_Template_Letter.xltx*** and ***Glycan_Screening_Template_Letter.xltx*** are copied into respective folders (User's Guide section 10)
- ☐ Service Pack 3 is installed (for MassHunter B.03.01 only) (User's Guide section 10).
- ☐ Glycan Database is installed (User's Guide section 10).

After starting Mass Hunter Qualitative Analysis software

- ☐ The method ***Agilent mAb_Glycan_DataAnalysis.m*** is loaded (User's Guide section 10).
- ☐ **Agilent mAb_Glyco_AM_PCD.cdb** file is defined as database (User's Guide section 10).
- ☐ Compound reporting template is defined (User's Guide section 10).
- ☐ Sample file to be analyzed is not write-protected.

Do not use Carryover Reduction as it will result in Time Table Errors



G4240-90021

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