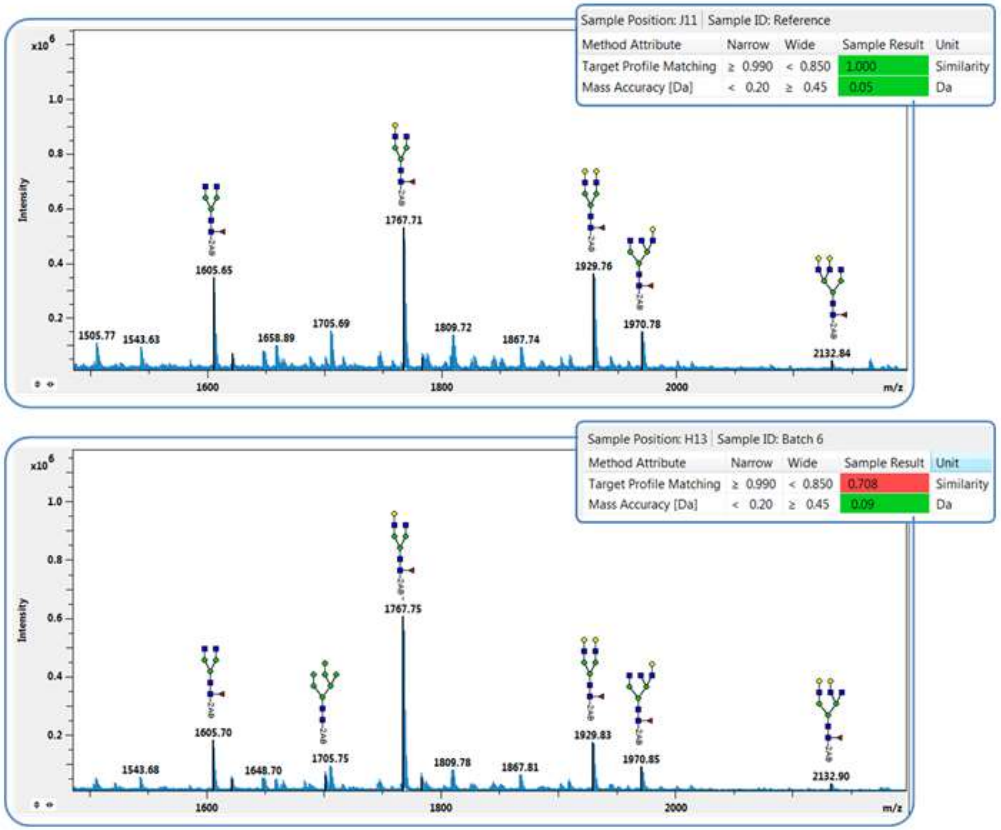

Result	Position	Sample Name	Matrix	Enzyme
	G14	Batch 1	sDHB	PNGAse F
	K13	Batch 2	sDHB	PNGAse F
	I13	Batch 3	sDHB	PNGAse F
	L13	Batch 5	sDHB	PNGAse F
	H13	Batch 6	sDHB	PNGAse F
	J10	Batch 4	sDHB	PNGaseF
	J11	Reference	sDHB	PNGAse F

Multi Target Screening MALDI Result
2AB Glycans_1.3

BRUKER

Project Info

Name: Multicompound MALDI Test Date: Jan 16, 2018

Sample Info & Protocols

Name: 2-AB Labelled Glycan Profiles Date: Mar 12, 2018

Workflow Result Info

Result: 2AB Glycans_1.3 Date: Mar 21, 2018
Location: /Multicompound MALDI Test/2-AB Labelled Glycan Profiles
Method: 2AB Glycans Version: 1.3

Results

Summary

Row	Result	Position	Sample Name	Matrix	Enzyme	Target Profile Matching	Mass Accuracy [Da]
1		J10	Batch 4	sDHB	PNGaseF	0.994	0.08
2		J11	Reference	sDHB	PNGAse F	1.000	0.05
3		G14	Batch 1	sDHB	PNGAse F	0.986	0.04
4		K13	Batch 2	sDHB	PNGAse F	0.939	0.08
5		I13	Batch 3	sDHB	PNGAse F	0.985	0.05
6		L13	Batch 5	sDHB	PNGAse F	0.418	0.09
7		H13	Batch 6	sDHB	PNGAse F	0.708	0.09

Comparison of N-glycan profiles of two batches of an IgG mAb with different intensity of G1F and the presence of high mannose glycans. N-linked glycans were released using PNGAse F and 2-AB labeled. MALDI-MS profiles were acquired within seconds in positive reflector mode and annotated spectra were analyzed using Biopharma Compass. The glycan profiles of six batches of an IgG mAb were compared to reference data and scored for similarity. Intensity profiles as well as presence and absence of certain glycan structures were included within the evaluation. Rapid evaluation via Biopharma Compass includes traffic light displays save analysis time. In this example, Batch 4 was the most similar compared to the reference batch. Reportability is improved with regulatory ready, customizable analysis summaries.