

Supplementary Table S2: Quantification of glycopeptides from RNase B by mass spectrometry

Quantification by peak area

observed m/z	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan structure	interday (N)	intraday (N)	average	SD	
1295.540		3	3884.626	2668.155	1216.471	M5Gn2	3	3	0.55	0.007
1349.557		3	4046.679	2668.155	1378.524	M6Gn2	3	3	0.25	0.004
1403.574		3	4208.731	2668.155	1540.576	M7Gn2	3	3	0.06	0.001
1457.593		3	4370.786	2668.155	1702.631	M8Gn2	3	3	0.11	0.008
1511.610		3	4532.838	2668.155	1864.683	M9Gn2	3	3	0.03	0.003

observed m/z	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan structure	interday (N)	intraday (N)	average	SD	
971.905		4	3884.626	2668.155	1216.471	M5Gn2	3	3	0.40	0.007
1012.418		4	4046.678	2668.155	1378.523	M6Gn2	3	3	0.28	0.006
1052.931		4	4208.731	2668.155	1540.576	M7Gn2	3	3	0.09	0.001
1093.447		4	4370.794	2668.155	1702.639	M8Gn2	3	3	0.18	0.005
1133.958		4	4532.838	2668.155	1864.683	M9Gn2	3	3	0.06	0.004

Quantification by peak height

[M+H] ⁺	glycan structure	average	SD	interday (N)	intraday (N)
3884.626	M5Gn2	0.391	0.012	3	3
4046.678	M6Gn2	0.265	0.080	3	3
4208.731	M7Gn2	0.080	0.070	3	3
4370.794	M8Gn2	0.189	0.020	3	3
4532.838	M9Gn2	0.075	0.010	3	3

Supplementary table: Quantification of glycans from RNase B by HPLC-FD

	Average	SD	interday (N)	intraday (N)
M5Gn2	0.42	0.004	3	3
M6Gn2	0.25	0.003	3	3
M7Gn2	0.10	0.002	3	3
M8Gn2	0.16	0.001	3	3
M9Gn2	0.07	0.005	3	3

Supplementary Table S3: Quantification results for glycopeptides from ePdiP by mass spectrometry
file: PDI summary-endogeneous-Biological replicate_20131023_raw data

Site 1

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan stucture	peptide sequence	Average	SD
1492.325	3	4474.981	3258.520	1216.461	M5Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.07	0.015
1546.338	3	4637.023	3258.520	1378.503	M6Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.19	0.011
1600.357	3	4799.080	3258.520	1540.560	M7Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.49	0.013
1654.376	3	4961.135	3258.520	1702.615	M8Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.12	0.004
1708.394	3	5123.190	3258.520	1864.670	M9Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.12	0.007

Site 2

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan stucture	peptide sequence	Average	SD
1398.581	2	2796.170	1579.704	1216.466	M5Gn2	NSDVNSIDYEGPR	0.30	0.017
1479.609	2	2958.226	1579.704	1378.522	M6Gn2	NSDVNSIDYEGPR	0.28	0.004
1560.637	2	3120.282	1579.704	1540.578	M7Gn2	NSDVNSIDYEGPR	0.31	0.010
1641.666	2	3282.339	1579.704	1702.635	M8Gn2	NSDVNSIDYEGPR	0.07	0.003
1722.693	2	3444.393	1579.704	1864.689	M9Gn2	NSDVNSIDYEGPR	0.04	0.003

Site 3

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan stucture	peptide sequence	Average	SD
1477.063	3	4429.196	3212.710	1216.486	M5Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.19	0.035
1531.079	3	4591.244	3212.710	1378.534	M6Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.27	0.012
1585.098	3	4753.303	3212.710	1540.593	M7Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.29	0.024
1639.115	3	4915.353	3212.710	1702.643	M8Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.17	0.016
1693.131	3	5077.399	3212.710	1864.689	M9Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.08	0.012

Site 4

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan stucture	peptide sequence	Average	SD
1462.599	2	2924.206	1707.775	1216.431	M5Gn2	IDADFNFATFYSMANK	0.02	0.005
1543.627	2	3086.262	1707.775	1378.487	M6Gn2	IDADFNFATFYSMANK	0.07	0.015
1624.655	2	3248.318	1707.775	1540.543	M7Gn2	IDADFNFATFYSMANK	0.27	0.004
1705.683	2	3410.373	1707.775	1702.598	M8Gn2	IDADFNFATFYSMANK	0.44	0.013
1786.707	2	3572.422	1707.775	1864.647	M9Gn2	IDADFNFATFYSMANK	0.20	0.026

Site 5

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan stucture	peptide sequence	Average	SD
1228.900	3	3684.701	2468.250	1216.451	M5Gn2	LAPTYQELADTYANATSDVLIK	0.13	0.023
1282.919	3	3846.758	2468.250	1378.508	M6Gn2	LAPTYQELADTYANATSDVLIK	0.26	0.008
1336.940	3	4008.819	2468.250	1540.569	M7Gn2	LAPTYQELADTYANATSDVLIK	0.34	0.014
1390.956	3	4170.868	2468.250	1702.618	M8Gn2	LAPTYQELADTYANATSDVLIK	0.19	0.011
1444.973	3	4332.918	2468.250	1864.668	M9Gn2	LAPTYQELADTYANATSDVLIK	0.09	0.008

**Supplementary Table S4: Quantification results for glycopeptides from different domains of Pdip by mass spectrometry
file: PDI summary-endogeneous_secreted domain study 20140304-replicate**

abb' domain

Site 1

ions used for quantification	z	[M+H] ⁺	peptide [M]	glycan	glycan stucture	peptide sequence	Average	SD
1492.325	3	4474.981	3258.520	1216.461	M5Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.30	0.061
1546.338	3	4637.023	3258.520	1378.503	M6Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.22	0.010
1600.357	3	4799.080	3258.520	1540.560	M7Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.26	0.032
1654.376	3	4961.135	3258.520	1702.615	M8Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.11	0.010
1708.394	3	5123.190	3258.520	1864.670	M9Gn2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.11	0.026

Site 2

ions used for quantification	z	[M+H] ⁺	peptide [M]	glycan	glycan stucture	peptide sequence	Average	SD
1398.581	2	2796.170	1579.704	1216.466	M5Gn2	NSDVNSIDYEGPR	0.65	0.065
1479.609	2	2958.226	1579.704	1378.522	M6Gn2	NSDVNSIDYEGPR	0.19	0.028
1560.637	2	3120.282	1579.704	1540.578	M7Gn2	NSDVNSIDYEGPR	0.11	0.023
1641.666	2	3282.339	1579.704	1702.635	M8Gn2	NSDVNSIDYEGPR	0.04	0.013
1722.693	2	3444.393	1579.704	1864.689	M9Gn2	NSDVNSIDYEGPR	0.01	0.005

Site 3

ions used for quantification	z	[M+H] ⁺	peptide [M]	glycan	glycan stucture	peptide sequence	Average	SD
1477.063	3	4429.196	3212.710	1216.486	M5Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.42	0.093
1531.079	3	4591.244	3212.710	1378.534	M6Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.20	0.020
1585.098	3	4753.303	3212.710	1540.593	M7Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.15	0.032
1639.115	3	4915.353	3212.710	1702.643	M8Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.16	0.026
1693.131	3	5077.399	3212.710	1864.689	M9Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.07	0.024

Site 4

ions used for quantification	z	[M+H] ⁺	peptide [M]	glycan	glycan stucture	peptide sequence	Average	SD
1462.599	2	2924.206	1707.775	1216.431	M5Gn2	IDADF ^N NATFYSMANK	0.14	0.029
1543.627	2	3086.262	1707.775	1378.487	M6Gn2	IDADF ^N NATFYSMANK	0.20	0.012
1624.655	2	3248.318	1707.775	1540.543	M7Gn2	IDADF ^N NATFYSMANK	0.32	0.032
1705.683	2	3410.373	1707.775	1702.598	M8Gn2	IDADF ^N NATFYSMANK	0.29	0.018
1786.707	2	3572.422	1707.775	1864.647	M9Gn2	IDADF ^N NATFYSMANK	0.04	0.011

ab domain

Average	SD
0.29	0.055
0.20	0.012
0.25	0.023
0.12	0.014
0.14	0.019

Average	SD
0.59	0.061
0.16	0.026
0.13	0.027
0.09	0.014
0.03	0.006

Average	SD
0.44	0.084
0.20	0.024
0.14	0.018
0.17	0.034
0.05	0.031

Average	SD
0.14	0.024
0.19	0.016
0.25	0.019
0.36	0.013
0.06	0.011

bb' domain

Average	SD
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.

Average	SD
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.

Average	SD
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.

Average	SD
0.28	0.035
0.33	0.028
0.28	0.021
0.10	0.013
0.01	0.004

b domain

Average	SD
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.

Average	SD
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.

Average	SD
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.
n.d.	n.d.

Average	SD
0.32	0.033
0.30	0.023
0.31	0.018
0.06	0.015
0.00	0.002

Supplementary Table S5: Quantification results for glycopeptides from P dip treated with kifunensine first and mannosidase by mass spectrometry
file: PDI endo treated with Kif and MNS_20140320
three biological replicates

Site 1 (1st)

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan structure	peptide sequence	T0	T1	T3	T10	T30	T60
1492.325	3	4474.981	3258.520	1216.461	M5Gn2	NITLAQIDCTENQDLCMEHNIPGFPPLK	0.00	0.00	0.00	0.00	0.00	0.00
1546.338	3	4637.023	3258.520	1378.503	M6Gn2	NITLAQIDCTENQDLCMEHNIPGFPPLK	0.00	0.00	0.00	0.00	0.00	0.00
1600.357	3	4799.080	3258.520	1540.560	M7Gn2	NITLAQIDCTENQDLCMEHNIPGFPPLK	0.00	0.00	0.00	0.00	0.00	0.00
1654.376	3	4961.135	3258.520	1702.615	M8Gn2	NITLAQIDCTENQDLCMEHNIPGFPPLK	0.01	0.15	0.56	0.93	0.93	0.95
1708.394	3	5123.190	3258.520	1864.670	M9Gn2	NITLAQIDCTENQDLCMEHNIPGFPPLK	0.99	0.85	0.44	0.07	0.07	0.04

Site 2 (1st)

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan structure	peptide sequence	T0	T1	T3	T10	T30	T60
1398.581	2	2796.170	1579.704	1216.466	M5Gn2	NSDVNSIDYEGPR	0.00	0.00	0.01	0.01	0.01	0.01
1479.609	2	2958.226	1579.704	1378.522	M6Gn2	NSDVNSIDYEGPR	0.01	0.00	0.01	0.01	0.01	0.01
1560.637	2	3120.282	1579.704	1540.578	M7Gn2	NSDVNSIDYEGPR	0.01	0.01	0.01	0.01	0.02	0.03
1641.666	2	3282.339	1579.704	1702.635	M8Gn2	NSDVNSIDYEGPR	0.03	0.38	0.83	0.83	0.96	0.95
1722.693	2	3444.393	1579.704	1864.689	M9Gn2	NSDVNSIDYEGPR	0.96	0.61	0.14	0.14	0.00	0.00

Site 3 (1st)

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan structure	peptide sequence	T0	T1	T3	T10	T30	T60
1477.063	3	4429.196	3212.710	1216.486	M5Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.00	0.00	0.00	0.00	0.00	0.00
1531.079	3	4591.244	3212.710	1378.534	M6Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.00	0.00	0.00	0.00	0.00	0.00
1585.098	3	4753.303	3212.710	1540.593	M7Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.00	0.00	0.01	0.01	0.02	0.02
1639.115	3	4915.353	3212.710	1702.643	M8Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.02	0.28	0.78	0.96	0.98	0.98
1693.131	3	5077.399	3212.710	1864.689	M9Gn2	QSQPAVAVVADLPAYLANETFVTPVIVQSGK	0.98	0.72	0.21	0.03	0.00	0.00

Site 4 (1st)

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan structure	peptide sequence	T0	T1	T3	T10	T30	T60
1462.599	2	2924.206	1707.775	1216.431	M5Gn2	IDADFNATFYSMANK	0.00	0.00	0.00	0.00	0.00	0.00
1543.627	2	3086.262	1707.775	1378.487	M6Gn2	IDADFNATFYSMANK	0.00	0.00	0.00	0.00	0.00	0.00
1624.655	2	3248.318	1707.775	1540.543	M7Gn2	IDADFNATFYSMANK	0.01	0.01	0.01	0.01	0.02	0.02
1705.683	2	3410.373	1707.775	1702.598	M8Gn2	IDADFNATFYSMANK	0.01	0.09	0.35	0.66	0.91	0.96
1786.707	2	3572.422	1707.775	1864.647	M9Gn2	IDADFNATFYSMANK	0.98	0.90	0.64	0.33	0.07	0.01

Site 5 (1st)

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan structure	peptide sequence	T0	T1	T3	T10	T30	T60
1228.900	3	3684.701	2468.250	1216.451	M5Gn2	LAPTYQELADTYANATSDVLIK	0.00	0.00	0.00	0.00	0.00	0.00
1282.919	3	3846.758	2468.250	1378.508	M6Gn2	LAPTYQELADTYANATSDVLIK	0.00	0.00	0.00	0.00	0.01	0.01
1336.940	3	4008.819	2468.250	1540.569	M7Gn2	LAPTYQELADTYANATSDVLIK	0.00	0.01	0.01	0.03	0.03	0.04
1390.956	3	4170.868	2468.250	1702.618	M8Gn2	LAPTYQELADTYANATSDVLIK	0.02	0.22	0.62	0.94	0.95	0.93
1444.973	3	4332.918	2468.250	1864.668	M9Gn2	LAPTYQELADTYANATSDVLIK	0.97	0.77	0.36	0.03	0.01	0.01

Site 1 (2nd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.21	0.51	0.91	0.91	0.90
1.00	0.79	0.49	0.09	0.09	0.09

Site 2 (2nd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.01	0.01	0.01
0.00	0.00	0.00	0.01	0.01	0.01
0.00	0.01	0.02	0.02	0.02	0.03
0.03	0.42	0.79	0.96	0.96	0.96
0.96	0.57	0.19	0.00	0.00	0.00

Site 3 (2nd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.01	0.00
0.01	0.01	0.02	0.02	0.01	0.02
0.03	0.35	0.74	0.98	0.98	0.97
0.96	0.64	0.24	0.00	0.00	0.00

Site 4 (2nd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.00	0.00	0.01
0.00	0.00	0.00	0.00	0.00	0.00
0.01	0.01	0.01	0.02	0.01	0.02
0.01	0.13	0.33	0.66	0.89	0.95
0.97	0.86	0.66	0.31	0.09	0.02

Site 5 (2nd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.01	0.00	0.00
0.01	0.01	0.02	0.02	0.03	0.03
0.03	0.24	0.59	0.93	0.95	0.95
0.96	0.75	0.38	0.04	0.01	0.01

Site 1 (3rd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.02	0.05
0.00	0.22	0.55	0.94	0.98	0.95
1.00	0.78	0.45	0.06	0.00	0.00

Site 2 (3rd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.01	0.00	0.01
0.00	0.00	0.00	0.01	0.01	0.01
0.00	0.01	0.01	0.02	0.03	0.03
0.03	0.49	0.89	0.96	0.96	0.95
0.96	0.50	0.10	0.00	0.00	0.00

Site 3 (3rd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.02
0.02	0.01	0.02	0.01	0.02	0.02
0.03	0.39	0.86	0.97	0.98	0.95
0.96	0.60	0.12	0.02	0.00	0.00

Site 4 (3rd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.01	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00
0.01	0.00	0.01	0.01	0.02	0.02
0.01	0.13	0.42	0.71	0.90	0.95
0.98	0.86	0.56	0.27	0.07	0.02

Site 5 (3rd)

T0	T1	T3	T10	T30	T60
0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.01	0.01	0.01	0.01
0.01	0.01	0.02	0.02	0.03	0.03
0.03	0.26	0.65	0.94	0.96	0.96
0.96	0.73	0.32	0.03	0.01	0.01

Supplementary Table S6: Quantification results for glycopeptides from sPdp B by mass spectrometry
file: #LY3LY6 raw

Site 1

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan sturcture	peptide sequence	Average	SD
1384.28	3	4150.84	3258.52	892.32	(HexNAc2Hex3)	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.15	0.012
1432.97	3	4296.91	3258.52	1038.39	(HexNAc2Hex3)Fuc	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.08	0.005
1451.98	3	4353.94	3258.52	1095.42	(HexNAc2Hex3)HexNAc	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.29	0.021
1481.65	3	4442.95	3258.52	1184.43	(HexNAc2Hex3)Fuc2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.02	0.004
1492.32	3	4474.98	3258.52	1216.46	(HexNAc2Hex3)Hex2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.20	0.028
1500.67	3	4500.01	3258.52	1241.49	(HexNAc2Hex3)FucHexNAc	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.13	0.014
1546.34	3	4637.02	3258.52	1378.50	(HexNAc2Hex3)Hex3	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.07	0.008
1568.36	3	4703.08	3258.52	1444.56	(HexNAc2Hex3)FucHexNAc2	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.02	0.001
1600.36	3	4799.08	3258.52	1540.56	(HexNAc2Hex3)Hex4	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.05	0.009
1654.38	3	4961.14	3258.52	1702.62	(HexNAc2Hex3)Hex5	NITLAQIDCTENQDLCMEHNIPGFPSLK	0.01	0.004

Site 2

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan sturcture	peptide sequence	Average	SD
1228.52	2	2456.03	1579.70	876.33	(HexNAc2Hex2)Fuc	NSDVNNSIDYEGPR	0.03	0.004
1236.51	2	2472.03	1579.70	892.32	(HexNAc2Hex3)	NSDVNNSIDYEGPR	0.07	0.005
1301.55	2	2602.09	1579.70	1022.39	HexNAc2Hex2Fuc2	NSDVNNSIDYEGPR	0.01	0.003
1309.55	2	2618.09	1579.70	1038.39	(HexNAc2Hex3)Fuc	NSDVNNSIDYEGPR	0.11	0.007
1317.54	2	2634.09	1579.70	1054.38	(HexNAc2Hex3)Hex	NSDVNNSIDYEGPR	0.01	0.001
1338.05	2	2675.10	1579.70	1095.40	(HexNAc2Hex3)HexNAc	NSDVNNSIDYEGPR	0.10	0.005
1382.57	2	2764.15	1579.70	1184.44	(HexNAc2Hex3)Fuc2	NSDVNNSIDYEGPR	0.07	0.006
1390.56	2	2780.13	1579.70	1200.42	(HexNAc2Hex3)HexFuc	NSDVNNSIDYEGPR	0.00	0.002
1398.57	2	2796.15	1579.70	1216.45	(HexNAc2Hex3)Hex2	NSDVNNSIDYEGPR	0.11	0.014
1411.09	2	2821.17	1579.70	1241.47	(HexNAc2Hex3)FucHexNAc	NSDVNNSIDYEGPR	0.17	0.005
1439.59	2	2878.18	1579.70	1298.48	(HexNAc2Hex3)HexNAc	NSDVNNSIDYEGPR	0.03	0.009
1479.59	2	2958.19	1579.70	1378.48	(HexNAc2Hex3)Hex3	NSDVNNSIDYEGPR	0.04	0.009
1484.11	2	2967.23	1579.70	1387.52	(HexNAc2Hex3)Fuc2HexNAc	NSDVNNSIDYEGPR	0.08	0.005
1492.11	2	2983.22	1579.70	1403.51	(HexNAc2Hex3)HexHexNAcFuc	NSDVNNSIDYEGPR	0.02	0.000
1512.63	2	3024.25	1579.70	1444.55	(HexNAc2Hex3)FucHexNAc2	NSDVNNSIDYEGPR	0.06	0.011
1560.62	2	3120.24	1579.70	1540.54	(HexNAc2Hex3)Hex4	NSDVNNSIDYEGPR	0.03	0.009
1585.65	2	3170.30	1579.70	1590.60	(HexNAc2Hex3)Fuc2HexNAc2	NSDVNNSIDYEGPR	0.04	0.007
1641.65	2	3282.30	1579.70	1702.59	(HexNAc2Hex3)Hex5	NSDVNNSIDYEGPR	0.01	0.002
1722.68	2	3444.37	1579.70	1864.66	(HexNAc2Hex3)Hex6	NSDVNNSIDYEGPR	0.00	0.001

Site 3

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan sturcture	peptide sequence	Average	SD
1363.69	3	4089.07	3212.71	876.36	HexNAc2Hex2Fuc	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.03	0.006
1369.02	3	4105.07	3212.71	892.36	HexNAc2Hex3	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.07	0.009
1412.38	3	4235.13	3212.71	1022.42	HexNAc2Hex2Fuc2	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.01	0.002
1417.71	3	4251.13	3212.71	1038.42	(HexNAc2Hex3)Fuc	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.19	0.029
1466.40	3	4397.19	3212.71	1184.48	(HexNAc2Hex3)Fuc2	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.14	0.015
1477.06	3	4429.18	3212.71	1216.47	(HexNAc2Hex3)Hex2	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.10	0.018
1485.40	3	4454.20	3212.71	1241.49	(HexNAc2Hex3)FucHexNAc	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.21	0.018
1531.07	3	4591.22	3212.71	1378.51	(HexNAc2Hex3)Hex3	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.06	0.004
1534.09	3	4600.26	3212.71	1387.55	(HexNAc2Hex3)Fuc2HexNAc	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.09	0.014
1585.09	3	4753.28	3212.71	1540.57	(HexNAc2Hex3)Hex4	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.06	0.012
1601.78	3	4803.34	3212.71	1590.63	(HexNAc2Hex3)Fuc2HexNAc2	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.02	0.003
1639.11	3	4915.34	3212.71	1702.63	(HexNAc2Hex3)Hex5	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.03	0.007
1693.13	3	5077.39	3212.71	1864.68	(HexNAc2Hex3)Hex6	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.01	0.003

Site 4

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan sturcture	peptide sequence	Average	SD
1300.55	2	2600.10	1707.78	892.33	(HexNAc2Hex3)	IDADFNATFYSMANK	0.06	0.017
1373.58	2	2746.15	1707.78	1038.38	(HexNAc2Hex3)Fuc	IDADFNATFYSMANK	0.00	0.000
1402.09	2	2803.18	1707.78	1095.41	(HexNAc2Hex3)HexNAc	IDADFNATFYSMANK	0.14	0.033
1462.60	2	2924.20	1707.78	1216.43	(HexNAc2Hex3)Hex2	IDADFNATFYSMANK	0.04	0.007
1475.12	2	2949.23	1707.78	1241.46	(HexNAc2Hex3)HexNAcFuc	IDADFNATFYSMANK	0.00	0.000
1483.12	2	2965.23	1707.78	1257.46	(HexNAc2Hex3)HexNAc1Hex1	IDADFNATFYSMANK	0.17	0.016
1543.62	2	3086.24	1707.78	1378.47	(HexNAc2Hex3)Hex3	IDADFNATFYSMANK	0.08	0.013
1564.14	2	3127.28	1707.78	1419.51	(HexNAc2Hex3)HexNAcHex2	IDADFNATFYSMANK	0.06	0.014
1624.65	2	3248.31	1707.78	1540.53	(HexNAc2Hex3)Hex4	IDADFNATFYSMANK	0.30	0.032
1645.17	2	3289.33	1707.78	1581.56	(HexNAc2Hex3)HexNAcHex3	IDADFNATFYSMANK	0.02	0.006
1705.68	2	3410.36	1707.78	1702.58	(HexNAc2Hex3)Hex5	IDADFNATFYSMANK	0.10	0.011
1786.71	2	3572.41	1707.78	1864.64	(HexNAc2Hex3)Hex6	IDADFNATFYSMANK	0.02	0.006

Site 5

ions used for quantification	z	[M+H] ⁺	peptide [M+H] ⁺	glycan	glycan sturcture	peptide sequence	Average	SD
1169.55	3	3506.66	2468.25	1038.41	(HexNAc2Hex3)Fuc	LAPTYQELADTYANATSDVLIK	0.05	0.020
1188.56	3	3563.68	2468.25	1095.43	(HexNAc2Hex3)HexNAc	LAPTYQELADTYANATSDVLIK	0.27	0.052
1218.24	3	3652.71	2468.25	1184.46	(HexNAc2Hex3)Fuc2	LAPTYQELADTYANATSDVLIK	0.02	0.004
1228.90	3	3684.70	2468.25	1216.45	(HexNAc2Hex3)Hex2	LAPTYQELADTYANATSDVLIK	0.15	0.064
1237.25	3	3709.74	2468.25	1241.49	(HexNAc2Hex3)FucHexNAc	LAPTYQELADTYANATSDVLIK	0.30	0.027
1256.25	3	3766.75	2468.25	1298.50	(HexNAc2Hex3)HexNAc2	LAPTYQELADTYANATSDVLIK	0.07	0.023
1285.93	3	3855.79	2468.25	1387.54	(HexNAc2Hex3)Fuc2HexNAc	LAPTYQELADTYANATSDVLIK	0.04	0.010
1304.94	3	3912.81	2468.25	1444.56	(HexNAc2Hex3)FucHexNAc2	LAPTYQELADTYANATSDVLIK	0.07	0.009
1339.95	3	4017.84	2468.25	1549.59	(HexNAc2Hex3)Fuc2HexNAcHex	LAPTYQELADTYANATSDVLIK	0.00	0.001
1353.62	3	4058.87	2468.25	1590.62	(HexNAc2Hex3)Fuc2HexNAc2	LAPTYQELADTYANATSDVLIK	0.02	0.002

Supplementary Table S7: Quantification results for glycopeptides from sPdp B by mass spectrometry
file: PDI summary-secreted-GalT_Biological replicate_20140729_raw data with chart

Site 1

ions used for quantification	z	[M+H] ⁺	peptide [M]	glycan	glycan structure	peptide sequence	EV		Gal	
							Average	SD	Average	SD
1384.28	3	4150.84	3258.52	892.32	(HexNAc2Hex3)	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.159754	0.003302	0.179435	0.004265
1432.97	3	4296.91	3258.52	1038.39	(HexNAc2Hex3)Fuc	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.118021	0.001748	0.113831	0.002365
1451.98	3	4353.94	3258.52	1095.42	(HexNAc2Hex3)HexNAc	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.288007	0.010657	0.323587	0.005687
1481.65	3	4442.95	3258.52	1184.43	(HexNAc2Hex3)Fuc2	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.037979	0.002873	0.010813	0.000675
1492.3245	3	4474.981	3258.52	1216.461	(HexNAc2Hex3)Hex2	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.122997	0.003081	0.12757	0.006444
1500.67	3	4500.01	3258.52	1241.49	(HexNAc2Hex3)FucHexNAc	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.159509	0.00244	0.117712	0.000797
1505.9965	3	4515.99	3258.52	1257.47	(HexNAc2Hex3)HexHexNAc	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.021392	0.001972	0.025992	0.001366
1546.3384	3	4637.023	3258.52	1378.503	(HexNAc2Hex3)Hex3	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.037595	0.001405	0.038577	0.001724
1560.0152	3	4678.054	3258.52	1419.534	(HexNAc2Hex3)Hex2HexNAc	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.002996	0.001274	0.006373	0.000501
1568.36	3	4703.08	3258.52	1444.56	(HexNAc2Hex3)FucHexNAc2	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.024324	0.005213	0.020237	0.004043
1600.3572	3	4799.08	3258.52	1540.56	(HexNAc2Hex3)Hex4	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.024086	0.003187	0.032711	0.001753
1654.3757	3	4961.135	3258.52	1702.615	(HexNAc2Hex3)Hex5	NTLAQIDCTENQDLCLMEHNIPGFPSLK	0.00334	0.000915	0.003162	0.001878

Site 2

1228.517	2	2456.034	1579.704	876.33	HexNAc2Hex2Fuc	NSDVNSIDYEGPR	0.042156	0.000435	0.026961	0.000514
1236.5135	2	2472.027	1579.704	892.323	(HexNAc2Hex3)	NSDVNSIDYEGPR	0.050402	0.00078	0.064341	0.001376
1301.545	2	2602.09	1579.704	1022.386	HexNAc2Hex2Fuc2	NSDVNSIDYEGPR	0.031554	0.001169	0.012228	0.000386
1309.545	2	2618.09	1579.704	1038.386	(HexNAc2Hex3)Fuc	NSDVNSIDYEGPR	0.128126	0.003714	0.119859	0.002087
1317.5444	2	2634.089	1579.704	1054.385	(HexNAc2Hex3)Hex	NSDVNSIDYEGPR	0.00197	0.000165	0.002973	0.000115
1338.0523	2	2675.105	1579.704	1095.401	(HexNAc2Hex3)HexNAc	NSDVNSIDYEGPR	0.089328	0.000974	0.125141	0.001334
1382.574	2	2764.148	1579.704	1184.444	(HexNAc2Hex3)Fuc2	NSDVNSIDYEGPR	0.129149	0.002859	0.067568	0.000297
1390.5625	2	2780.125	1579.704	1200.421	(HexNAc2Hex3)HexFuc	NSDVNSIDYEGPR	0	0	0.038724	0.001049
1398.5749	2	2796.15	1579.704	1216.446	(HexNAc2Hex3)Hex2	NSDVNSIDYEGPR	0.036887	0.001021	0.060806	0.001315
1411.085	2	2821.17	1579.704	1241.466	(HexNAc2Hex3)FucHexNAc	NSDVNSIDYEGPR	0.209022	0.003922	0.141399	0.00542
1419.0801	2	2837.16	1579.704	1257.456	(HexNAc2Hex3)HexHexNAc	NSDVNSIDYEGPR	0.00897	0.000447	0.017975	0.000525
1439.59	2	2878.18	1579.704	1298.476	(HexNAc2Hex3)HexNAc2	NSDVNSIDYEGPR	0.010556	0.000673	0.019586	0.000714
1463.6097	2	2926.219	1579.704	1346.515	(HexNAc2Hex3)Fuc2Hex	NSDVNSIDYEGPR	0	0	0.059509	0.001235
1479.5942	2	2958.188	1579.704	1378.484	(HexNAc2Hex3)Hex3	NSDVNSIDYEGPR	0.008675	0.001606	0.014786	0.000324
1484.114	2	2967.228	1579.704	1387.524	(HexNAc2Hex3)Fuc2HexNAc	NSDVNSIDYEGPR	0.145619	0.001217	0.074585	0.000445
1492.1089	2	2983.218	1579.704	1403.514	(HexNAc2Hex3)HexHexNAcFuc	NSDVNSIDYEGPR	0.010662	0.000771	0.0783	0.001901
1512.625	2	3024.25	1579.704	1444.546	(HexNAc2Hex3)FucHexNAc2	NSDVNSIDYEGPR	0.0487	0.002327	0.040732	0.000977
1560.6196	2	3120.239	1579.704	1540.535	(HexNAc2Hex3)Hex4	NSDVNSIDYEGPR	0.006095	0.000913	0.00967	0.000802
1585.65	2	3170.3	1579.704	1590.596	(HexNAc2Hex3)Fuc2HexNAc2	NSDVNSIDYEGPR	0.040016	0.001522	0.021248	0.000721
1641.6477	2	3282.295	1579.704	1702.591	(HexNAc2Hex3)Hex5	NSDVNSIDYEGPR	0.001595	0.000297	0.02856	0.000309
1722.6834	2	3444.367	1579.704	1864.663	(HexNAc2Hex3)Hex6	NSDVNSIDYEGPR	0.000518	0.000236	0.000754	0.000168

Site 3

1363.69	3	4089.07	3212.71	876.36	HexNAc2Hex2Fuc	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.033813	0.001039	0.022373	0.00219
1369.0233	3	4105.07	3212.71	892.3599	HexNAc2Hex3	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.046167	0.000961	0.065114	0.002353
1412.377	3	4235.131	3212.71	1022.421	HexNAc2Hex2Fuc2	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.022478	0.002667	0.010305	0.004935
1417.709	3	4251.127	3212.71	1038.417	(HexNAc2Hex3)Fuc	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.184693	0.003419	0.151288	0.012552
1466.397	3	4397.191	3212.71	1184.481	(HexNAc2Hex3)Fuc2	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.200042	0.010334	0.115713	0.004015
1471.7288	3	4413.186	3212.71	1200.476	(HexNAc2Hex3)FucHex	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0	0	0.090432	0.003262
1477.0585	3	4429.176	3212.71	1216.466	(HexNAc2Hex3)Hex2	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.061768	0.00206	0.087111	0.004426
1520.4165	3	4559.25	3212.71	1346.54	(HexNAc2Hex3)Fuc2Hex	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.248142	0.008437	0.15652	0.007659
1485.4	3	4454.2	3212.71	1241.49	(HexNAc2Hex3)FucHexNAc	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.024198	0.002561	0.038354	0.002533
1531.0749	3	4591.225	3212.71	1378.515	(HexNAc2Hex3)Hex3	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0	0	0.150302	0.009504
1534.087	3	4600.261	3212.71	1387.551	(HexNAc2Hex3)Fuc2HexNAc	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.12478	0.006383	0.066304	0.001971
1585.0931	3	4753.279	3212.71	1540.569	(HexNAc2Hex3)Hex4	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.018621	0.001266	0.029509	0.002085
1601.779	3	4803.337	3212.71	1590.627	(HexNAc2Hex3)Fuc2HexNAc2	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.026296	0.001862	0.007486	0.001743
1639.1118	3	4915.335	3212.71	1702.625	(HexNAc2Hex3)Hex5	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.007815	0.001847	0.006616	0.001291
1693.1306	3	5077.392	3212.71	1864.682	(HexNAc2Hex3)Hex6	QSQPAVAVVADLPAYLANETFTVPVIVQSGK	0.001188	0.001396	0.002573	0.000707

Site 4

1300.55	2	2600.1	1707.775	892.325	(HexNAc2Hex3)	IDADF ^N NATFYSMANK	0.115639	0.004286	0.106979	0.004031
1373.577	2	2746.154	1707.775	1038.379	(HexNAc2Hex3)Fuc	IDADF ^N NATFYSMANK	0.001084	0.000108	0.001543	0.002378
1402.09	2	2803.18	1707.775	1095.405	(HexNAc2Hex3)HexNAc	IDADF ^N NATFYSMANK	0.333244	0.007417	0.301583	0.006088
1462.6	2	2924.2	1707.775	1216.425	(HexNAc2Hex3)Hex2	IDADF ^N NATFYSMANK	0.029004	0.001184	0.032676	0.000998
1475.1172	2	2949.234	1707.775	1241.459	(HexNAc2Hex3)HexNAcFuc	IDADF ^N NATFYSMANK	0	0	0.002297	0.001636
1483.117	2	2965.234	1707.775	1257.459	(HexNAc2Hex3)HexNAc1Hex1	IDADF ^N NATFYSMANK	0.270982	0.004411	0.296225	0.002721
1543.62	2	3086.24	1707.775	1378.465	(HexNAc2Hex3)Hex3	IDADF ^N NATFYSMANK	0.05332	0.004046	0.054224	0.002388
1564.141	2	3127.282	1707.775	1419.507	(HexNAc2Hex3)HexNAcHex2	IDADF ^N NATFYSMANK	0.053893	0.001712	0.058782	0.001724
1624.654	2	3248.308	1707.775	1540.533	(HexNAc2Hex3)Hex4	IDADF ^N NATFYSMANK	0.100303	0.001988	0.100694	0.000869
1645.167	2	3289.334	1707.775	1581.559	(HexNAc2Hex3)HexNAcHex3	IDADF ^N NATFYSMANK	0.011802	7.15E-05	0.014013	0.001139
1705.6785	2	3410.357	1707.775	1702.582	(HexNAc2Hex3)Hex5	IDADF ^N NATFYSMANK	0.026752	0.000477	0.026192	0.000643
1786.7071	2	3572.414	1707.775	1864.639	(HexNAc2Hex3)Hex6	IDADF ^N NATFYSMANK	0.003978	0.000179	0.004793	0.000195

Site 5

1164.219	3	3490.657	2468.25	1022.407	HexNAc2Hex2Fuc2	LAPTYQELADTYANATSDVLIK	0.007498	0.00042	0.002823	0.00055
1169.552	3	3506.656	2468.25	1038.406	(HexNAc2Hex3)Fuc	LAPTYQELADTYANATSDVLIK	0.083747	0.003574	0.07038	0.001489
1188.559	3	3563.677	2468.25	1095.427	(HexNAc2Hex3)HexNAc	LAPTYQELADTYANATSDVLIK	0.140543	0.012651	0.236625	0.011667
1218.238	3	3652.714	2468.25	1184.464	(HexNAc2Hex3)Fuc2	LAPTYQELADTYANATSDVLIK	0.105352	0.005199	0.060391	0.002118
1223.5721	3	3668.716	2468.25	1200.466	(HexNAc2Hex3)FucHex	LAPTYQELADTYANATSDVLIK	0	0	0.027782	0.002503
1228.901	3	3684.703	2468.25	1216.453	(HexNAc2Hex3)Hex2	LAPTYQELADTYANATSDVLIK	0.050608	0.002317	0.087444	0.002141
1237.246	3	3709.738	2468.25	1241.488	(HexNAc2Hex3)FucHexNAc	LAPTYQELADTYANATSDVLIK	0.280134	0.013315	0.199494	0.003925
1256.2498	3	3766.749	2468.25	1298.499	(HexNAc2Hex3)HexNAc2	LAPTYQELADTYANATSDVLIK	0.128149	0.010493	0.09749	0.005034
1272.2555	3	3814.767	2468.25	1346.517	(HexNAc2Hex3)Fuc2Hex	LAPTYQELADTYANATSDVLIK	0	0	0.029434	0.002086
1285.931	3	3855.793	2468.25	1387.543	(HexNAc2Hex3)Fuc2HexNAc	LAPTYQELADTYANATSDVLIK	0.108701	0.004155	0.063348	0.002127
1304.937	3	3912.811	2468.25	1444.561	(HexNAc2Hex3)FucHexNAc2	LAPTYQELADTYANATSDVLIK	0.037111	0.005158	0.054704	0.00606
1339.9481	3	4017.844	2468.25	1549.594	(HexNAc2Hex3)Fuc2HexNAcHex	LAPTYQELADTYANATSDVLIK	0.008525	0.000268	0.045152	0.021125
1353.623	3	4058.869	2468.25	1590.619	(HexNAc2Hex3)Fuc2HexNAc2	LAPTYQELADTYANATSDVLIK	0.04963	0.001221	0.024934	0.008275