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SUPPLEMENTAL DATA

Shi et al: ST6GAL1 and LGALS3BP sialylation in colorectal cancer

Multi-omics reveals that ST6GAL1 promotes colorectal cancer progression through LGALS3BP sialylation

Yuanchao Shi[1, 2], Zhenzhong Pan[3], Jingwei Duan[4], Zexing Wang[5], Yiliang Fang[6], Bo Tang[7*], Quanlin Guan[1, 2*]

[1]The First Clinical Academy of Lanzhou University, Lanzhou University, Lanzhou, China

[2]Department of General Surgery and Gastrointestinal Oncology Surgery, Lanzhou University First Hospital, Lanzhou, China

[3]State Key Laboratory of Biotherapy and Cancer Center, West China Hospital, Sichuan University, Chengdu, China

[4]Emergency department, Peking University Third Hospital, Beijing, China

[5]School of Medicine, Chongqing University, Chongqing, China

[6]Department of Neurology, Army Medical University Xinqiao Hospital, Chongqing, China.

[7]Department of General Surgery and Center of Minimal Invasive Gastrointestinal Surgery, Third Military Medical University Southwest Hospital, Chongqing, China

[*]**Correspondence to** Quanlin Guan: guanql@lzu.edu.cn and Bo Tang: tangbo@sina.com

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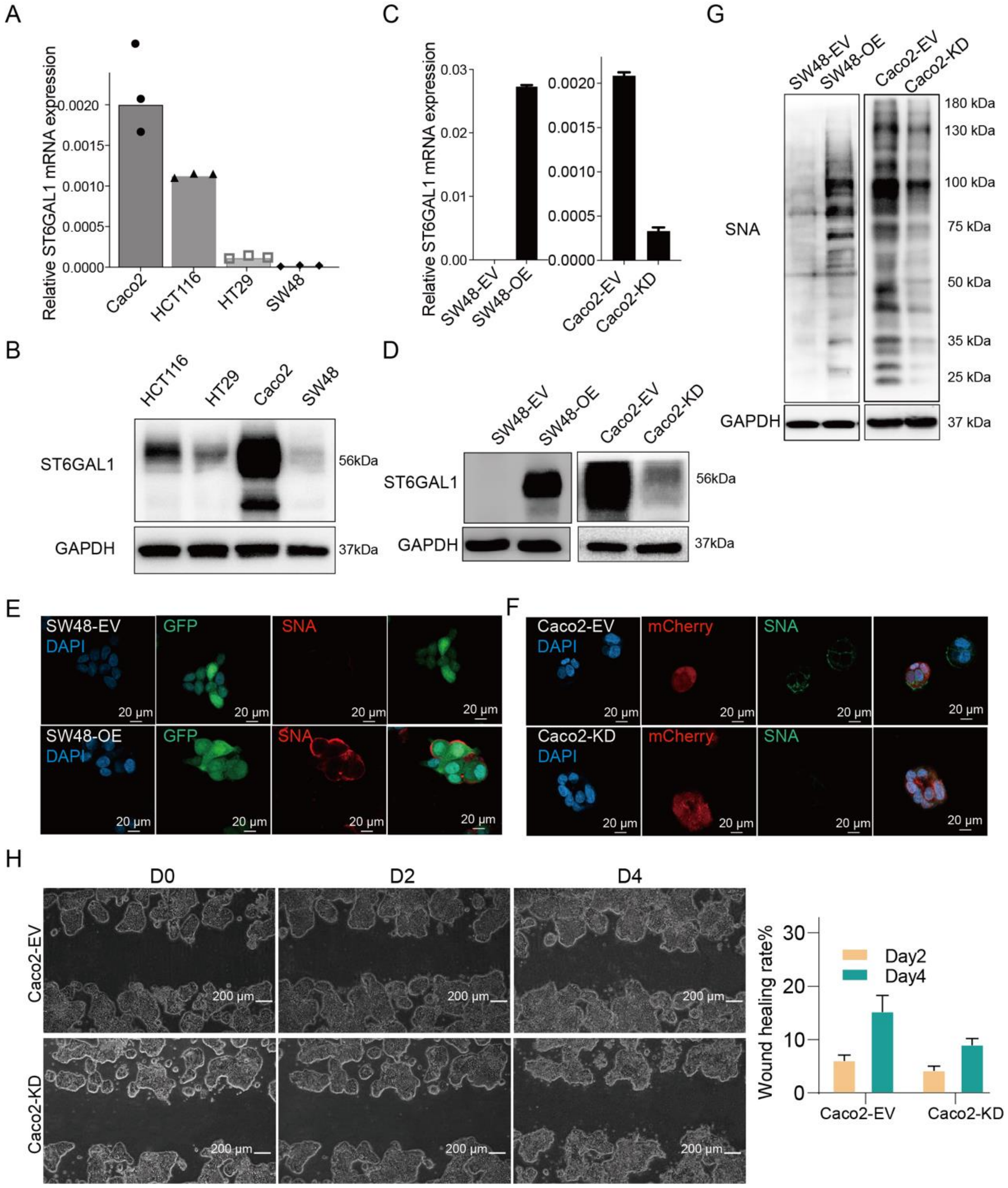

Figure S1. ST6GAL1 expression in different CRC cell lines was quantified, and cell migration was detected. After the ST6GAL1-overexpressing (OE) SW48 cell line (SW48-OE) and knockdown (KD) Caco2 cell line (Caco2-KD) as well as the related empty virus (EV)-expressing control cell lines SW48-EV and Caco2-EV were constructed, tumor cell migration was tested. (A and B) Relative ST6GAL1 expression levels were confirmed in different CRC cell lines via reverse transcription–quantitative polymerase chain reaction (RT–qPCR) (A) and Western blotting (WB) (B). (C and D) The overexpression efficiency of ST6GAL1 in the SW48 cell line and the knockdown efficiency of ST6GAL1 in the Caco2 cell line were confirmed by RT–qPCR (C) and WB (D). (E and F) Staining of SNA (red in SW48-EV and SW48-OE cells; green in Caco2-EV and Caco2-KD cells) in SW48 (E) and Caco2 (F) cell lines by immunofluorescence (IFC). Nuclei were counterstained with DAPI (blue) (magnification, ×400; scale bars, 20 μm). (G) SNA was confirmed in SW48-OE cells and Caco2-KD cells by Lectin blot. (H) Wound healing assay in Caco2-KD cells (magnification, ×400; scale bars, 20 μm) and corresponding statistical results. The data are presented as the means ± SDs of three independent experiments.

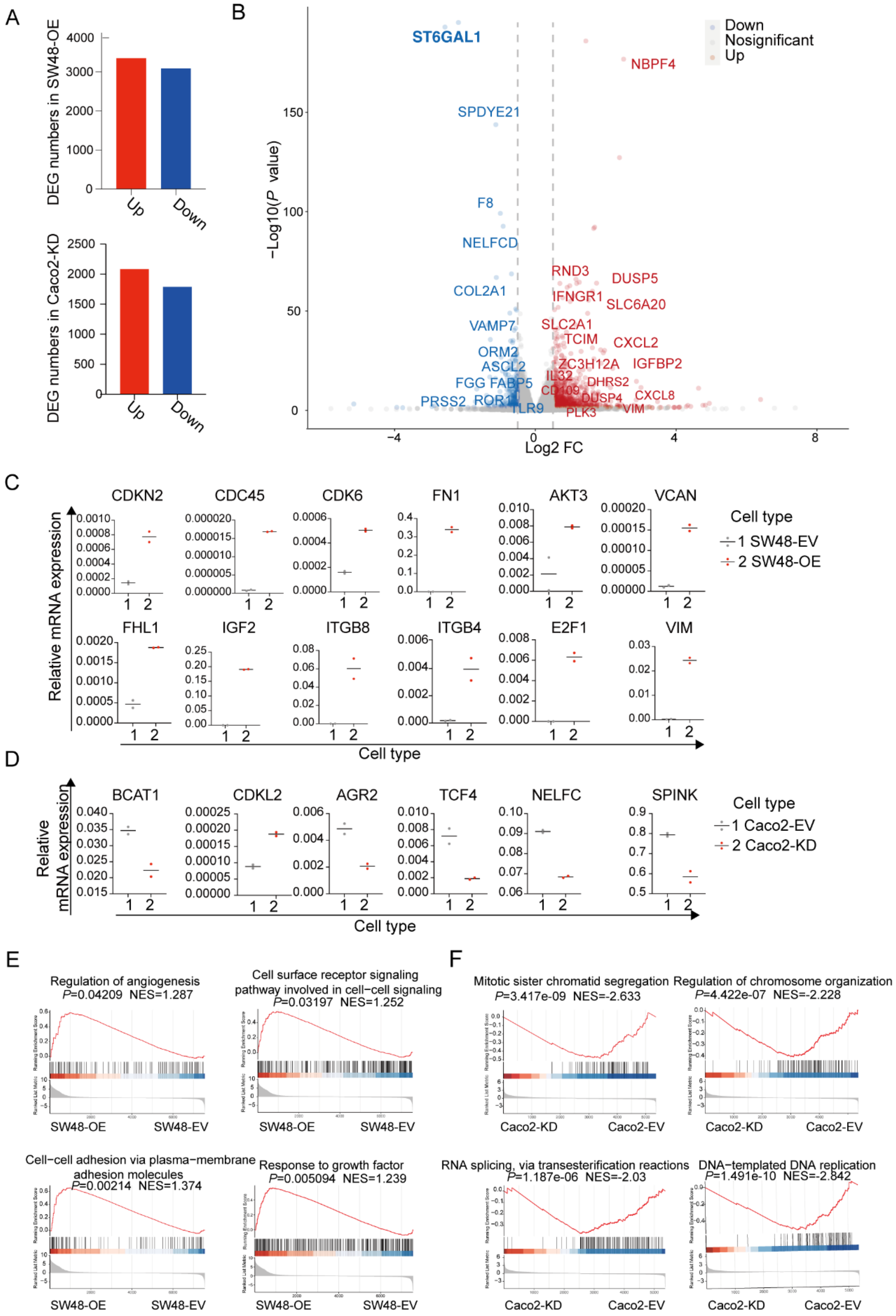

Figure S2. ST6GAL1 mediates transcriptome changes in CRC cells. Two cell line groups, SW48-EV vs. SW48-OE and Caco2-EV vs. Caco2-KD, were subjected to bulk RNA sequencing (RNA-seq). (A) Statistical results of differentially expressed gene (DEG) numbers in SW48-OE vs. SW48-EV and Caco2-KD vs. Caco2-EV (FC >

1.5, $P < 0.05$). (B) Volcano plot of all genes expressed in the Caco2-EV and Caco2-KD cell lines. The x-axis shows the $\log_2$ FC, and the y-axis shows the $-\log_{10}$ (P value), which represents the threshold values in log transformation. Each dot represents a DEG. The red dots indicate significantly upregulated DEGs, the blue dots indicate significantly downregulated DEGs, and the gray dots represent nonsignificant DEGs. (C and D) The transcript levels of several DEGs were confirmed in S6TGAL1-overexpressing cells (C) and S6TGAL1-knockdown cells (D) via RT–qPCR. (E) GSEA of SW48-OE cells compared with SW48-EV cells from GO-based enrichment analyses of RNA-seq data. (F) GSEA of the RNA-seq data of Caco2-KD cells compared with those of Caco2-EV cells from GO-based enrichment analyses. NES, normalized enrichment score.

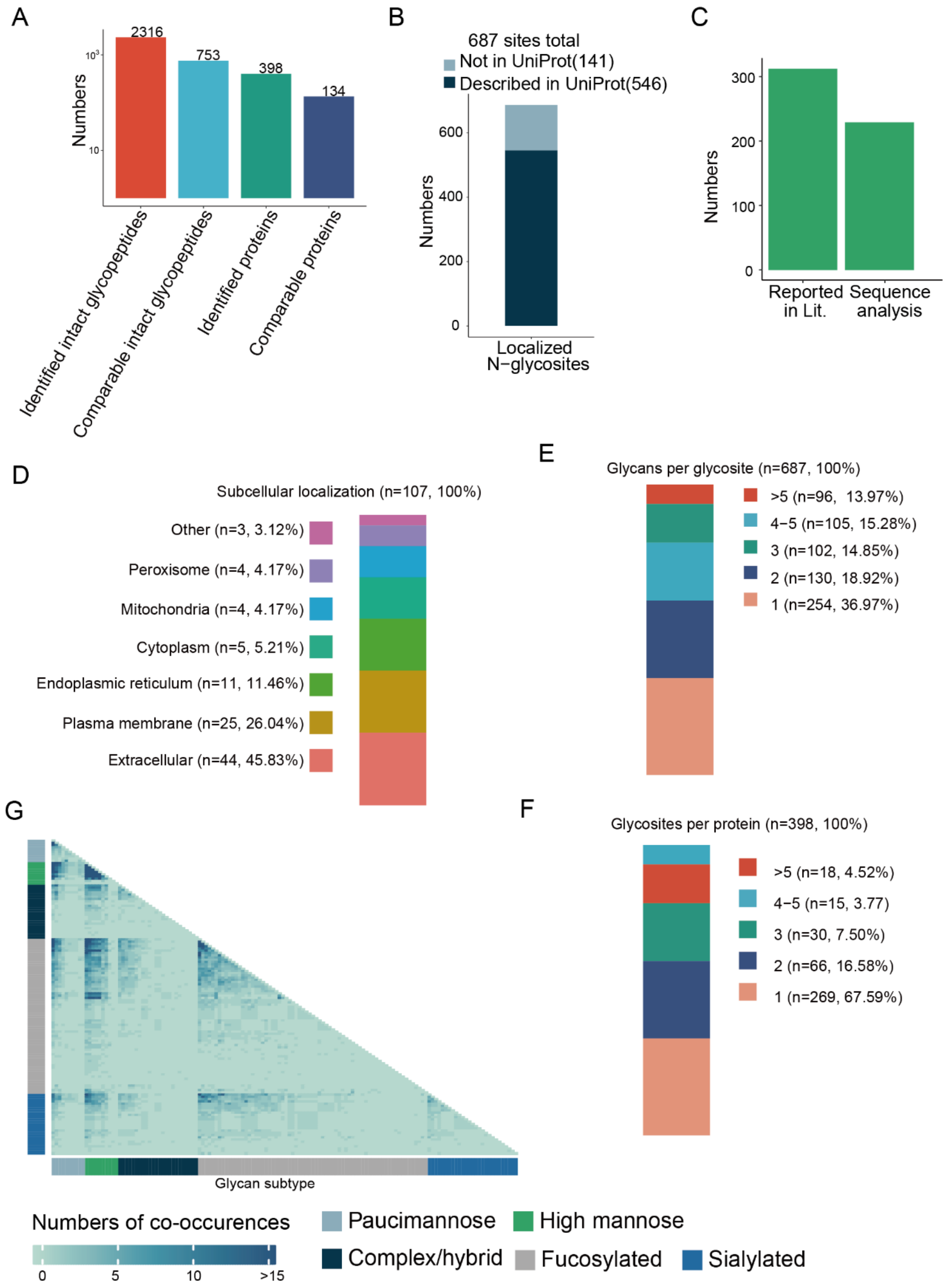

Figure S3. ST6GAL1 increases cancer cell sialylation. Modification omics was performed on SW48-EV and SW48-OE cell lines, and sialylation was analyzed. (A) The total number of identified glycopeptides and proteins. (B) The percentage of identified glycosites, which are described as known glycosites in the UniProt database. (C) Statistical results of the N-glycosite numbers, which have been reported in the literature or assigned via ‘sequence analysis. (D) Subcellular localization results of glycosylated proteins. (E) The distribution of glycans per glycosite identified. (F)

The distribution of glycosites per protein identified. (G) A glycan co-occurrence heatmap representing the number of times glycan pairs appeared together at the same glycosite.

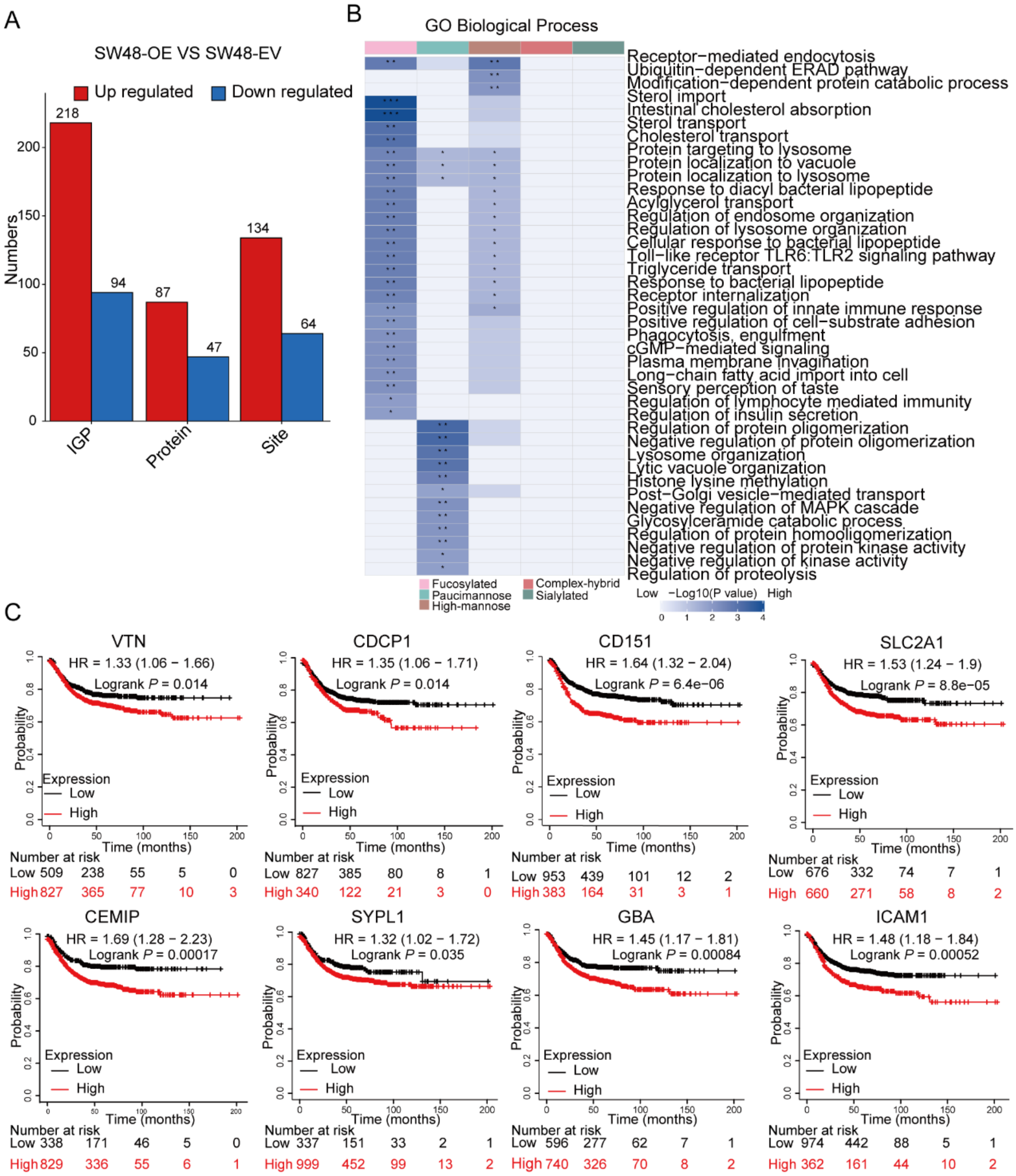

Figure S4. ST6GAL1 increases cancer cell sialylation, and sialylated substrates are correlated with tumor progression. Modification omics was performed on SW48-EV and SW48-OE cell lines, and sialylation was analyzed. (A) The number of differentially expressed glycopeptides and proteins. FC > 1.5 indicates differential upregulation, and FC < 1.5 indicates differential downregulation. (B) Heatmap of GO-based enrichment analysis results for 5 different N-glycopeptide modification types, with the aim of revealing the correlation of the corresponding protein functions among the 5 different N-glycopeptide modification types after ST6GAL1 overexpression. (Fisher test, * *P* value < 0.05, * * *P* value < 0.01, * * * *P* value < 0.001). (C) Survival analysis of molecules with sialylation modifications and Kaplan–Meier plotter database analysis using RNA-seq data from the TCGA, EGA, and GEO databases.

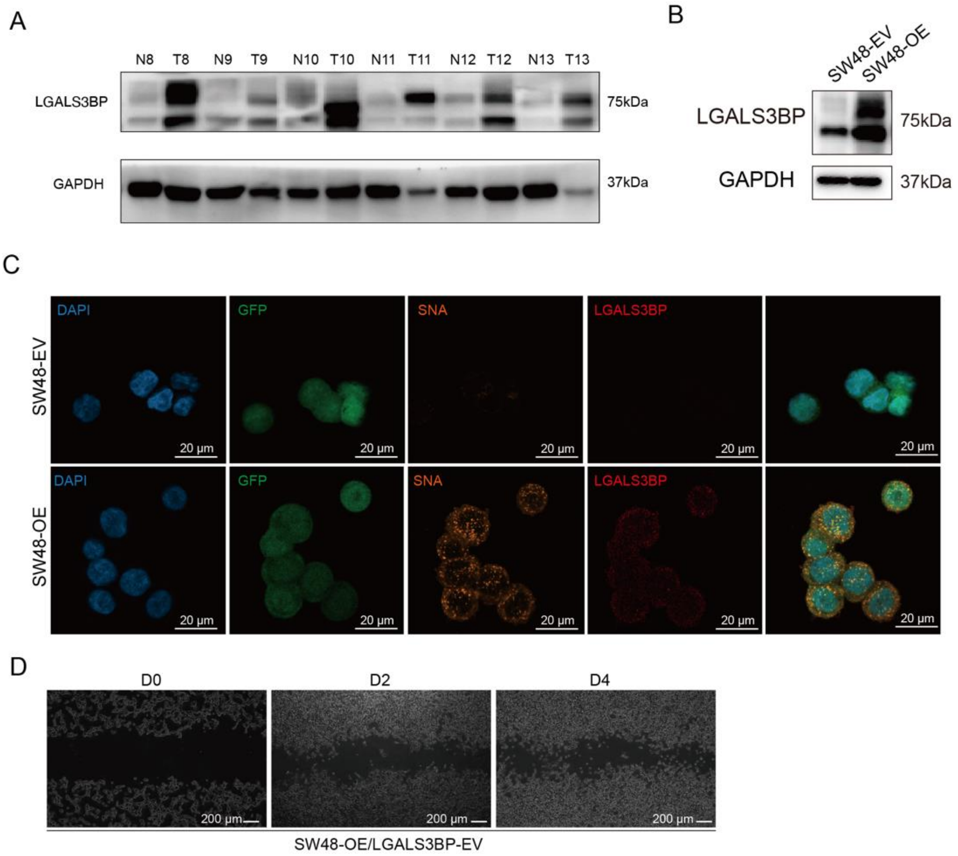

Figure S5. Sialylation of LGALS3BP promotes the migration of ST6GAL1-overexpressing cells. (A) LGALS3BP expression in tumor and paired normal tissues in clinical CRC samples, as determined by WB. (B) LGALS3BP expression in SW48-EV and SW48-OE cell lines determined by WB. (C) Staining of SNA (orange) and LGALS3BP (red) in SW48-EV (GFP, green) and SW48-OE (GFP, green) cell lines by IFC. Nuclei were counterstained with DAPI (blue) (magnification, ×400; scale bars, 20 μm). (D) Wound healing assay of LGALS3BP-EV in SW48-OE cell line on Days 0, 2 and 4 (magnification, ×40; scale bars, 200 μm). The data are presented as the means ± SDs of three independent experiments.

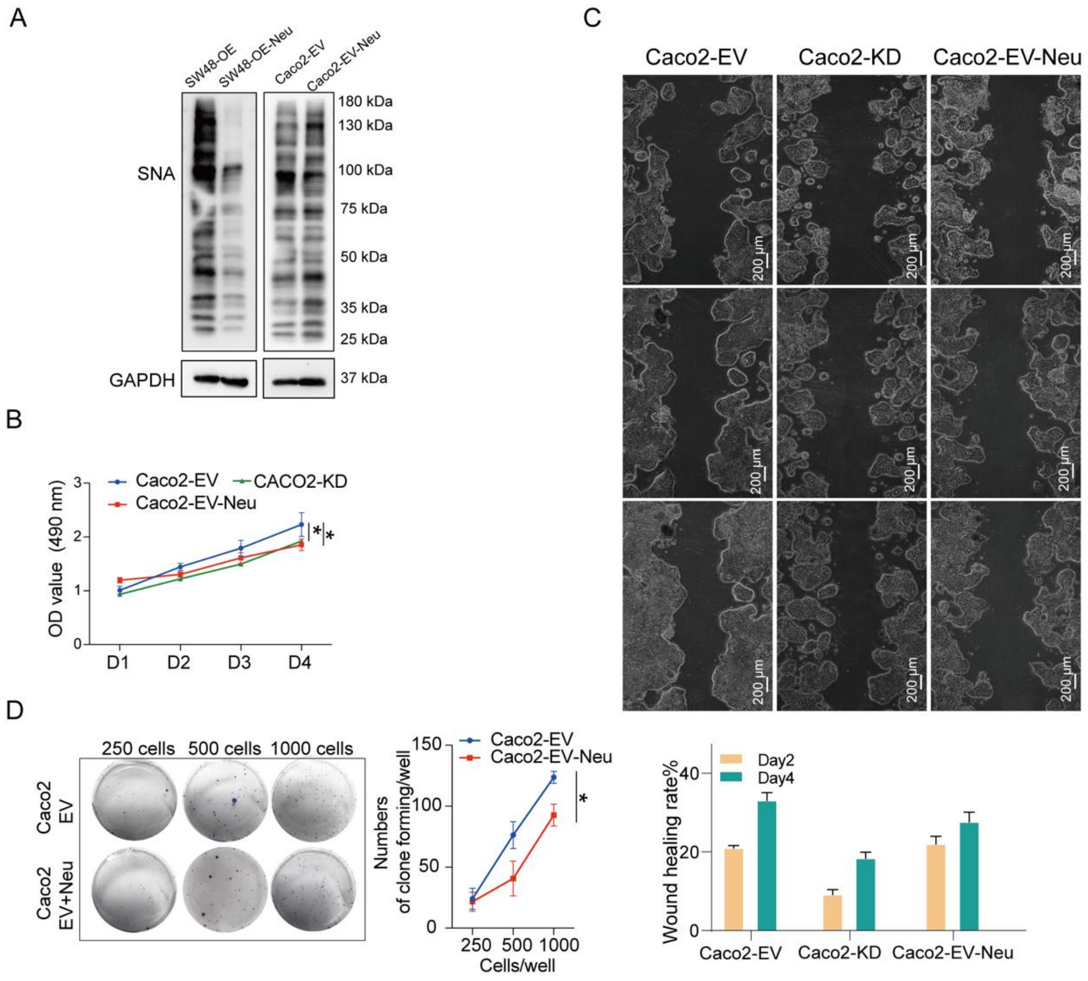

Figure S6. Desialylation blocks CRC cell proliferation, migration, and chemoresistance. SW48-OE or Caco2-EV cells were treated with α-(2-3, 6, 8, 9) neuraminidase (NA) for 24 hours at a concentration of 5 μg/ml. (A) After NA treatment (5 μg/ml, 37 °C, 24 hours) in SW48-OE or Caco2-EV cells, the SNA level was detected via lectin blotting. (B) MTT assay in Caco2-EV cells. (C) Wound healing assay in Caco2-EV cells (magnification, ×400; scale bars, 20 μm) and statistical results. (D) Colony formation assay results and statistical analysis of Caco2-EV cells. * *P* value < 0.05, * * *P* value < 0.01, * * * *P* value < 0.001, by Student's *t* test (B and D). The data are presented as the means ± SDs of three independent experiments.

Supplementary tables

Table S1. Clinical characteristics of the included patients.

	1	2	3	4	5	6	7	8	9	10	11
Age, year	70	50	67	58	82	63	36	78	73	61	55
Sex	Male	Female	Female	Female	Male	Female	Female	Female	Male	Male	Male
ECOG	1	0	0	0	1	0	0	0	0	0	0
TNM											
T	T3	T4a	T4b	T3	T3	T3	T4b	T3	T3	T3	T2
N	N0	N2a	N2b	N2a	N1a	N2b	N0	N0	N0	N0	N0
M	M1	M0	M0	M0	M0	M1	M0	M0	M0	M0	M0
Grade	IVA	IIIC	IIIC	IIIB	IIIB	IV	IIC	IIA	IIA	IIA	I
NAC	No	No	No	No	No	No	No	No	No	No	No
Metastatic	Yes	No	No	No	No	Yes	No	No	No	No	No
Location	Sigmoid	Rectum	Rectum	Colon	Rectum	Colon	Sigmoid	Colon	Colon	Rectum	Rectum
Tumor volume (cm*cm*cm)	3*2.8*2.5	4.8*4.2*1.5	3.8*2.7*1	5*3*2.5	3.3*2.5*0.7	7*4.5*2	5*4.5*3	5.5*5*4.5	5.5*3*2.5	6*4*3	6.5*5*2
Pathological	AD	AD	SRCC	AD	AD	SRCC	SRCC	AD	AD	AD	AD
Diagnosis type	Ulcer	Ulcer	Ulcer	Bulge	Ulcer	Bulge	Bulge	Bulge	Ulcer	Bulge	Ulcer
Differentiation	Medium	Low	Medium	Low	Low	Low	High	Low	Low	Low	Medium
MSI	MSS	-	MSS	MSS	-	-	MSI-H	-	-	-	MSS
Ki67 (%)	90	80	90	70	50	90	60	60	80	60	40
Vascular	No	Yes	Yes	Yes	No	Yes	No	No	No	No	No
Nerve	Yes	Yes	Yes	Yes	No	No	Yes	Yes	No	No	No
ST6GAL1											
mRNA-T	0.012605	0.004677	0.007642	0.004597	0.003512	0.009222	0.002632	0.002061	0.001921	0.001819	0.000876
mRNA-N	0.002054	0.000272	0.003011	0.000006	0.001052	0.000283	0.001565	0.000140	0.004627	0.001453	0.000370
Protein-T	5.251710	5.655562	4.045227	6.523537	4.597119	6.318852	4.286396	3.134481	4.374308	3.352297	5.156293
Protein-N	1.262119	1.107384	0.893455	1.046707	1.257260	1.278934	1.818954	0.788114	0.259621	0.404422	1.794062

Table S1. Continued

	12	13	14	15	16	17	18	19	20	21	22
Age, year	52	76	75	50	76	61	55	36	78	50	73
Sex	Female	Male	Male	Female	Male	Male	Male	Female	Female	Female	Male
ECOG	0	1	0	1	0	1	0	1	0	0	0
TNM											
T	T3b	T3	T3	T2	T3	T2a	T2b	T3a	T3	T3	T3
N	N0	N0	N1	N2	N2a	N2a	N0	N2a	N2b	N1	N0
M	M0	M0	M0	M0	M0	M0	M0	M0	M0	M0	M0
Grade	IIC	IIA	IIB	IIB	IIA	I	I	IIA	IIA	IIB	IIA
NAC	No	No	No	No	No	No	No	No	No	No	No

Metastatic	No	No	No	No	No	No	No	No	Yes	Yes	No
Location	Colon	Colon	Rectum	Rectum	Colon	Rectum	Rectum	Sigmoid	Colon	Rectum	Sigmoid
Tumor volume (cm*cm*cm)	4.5*3*1.5	5*3*2.5	3*4*2	4.5*2.6*3	5*3*2.5	6*4*3	6.5*5*2	5*4.5*3	5.5*5*4.5	2.5*2*1.5	5*4.5*1.5
Pathological	AD	AD	AD	AD	AD	AD	AD	AD	AD	SRCC	AD
Diagnosis type	Ulcer	Ulcer	Ulcer	Ulcer	Ulcer	Bulge	Ulcer	Bulge	Bulge	Bulge	Ulcer
Differentiation	Low	Medium	Low	Medium	Medium	Low	High	Low	Medium	Medium	Low
MSI	MSS	-	-	-	-	MSS	MSS	-	-	MSI	-
Ki67 (%)	50	30	80	40	60	40	50	70	60	50	60
Vascular	Yes	No	No	No	Yes	Yes	No	No	Yes	No	Yes
Nerve	Yes	No	Yes	Yes	No	Yes	Yes	No	Yes	Yes	Yes
ST6GAL1											
mRNA-T	0.001363	0.001124	0.003908	0.000079	0.000120	0.000077	0.000026	0.000587	0.000278	0.000318	0.000213
mRNA-N	0.001931	0.003627	0.000583	0.000018	0.000034	0.000009	0.000013	0.000035	0.000103	0.000011	0.000057
Protein-T	5.405488	3.388203	4.042280	1.194106	0.215596	0.861418	0.602790	1.048834	0.903418	0.941649	1.194106
Protein-N	2.402110	1.159582	1.014609	0.112667	0.139519	0.253215	0.116694	0.404944	0.114364	0.262619	0.112667

Table S2. Sequence of primers used in article.

Gene	Sequence
ST6GAL1	Forward: ATCGTAAGCTGCACCCCAAT
	Reverse: ATGATACCAAGCATCCCAGAGG
GAPDH	Forward: GGAGCGAGATCCCTCCAAAAT
	Reverse: GGCTGTTGTCATACTTCTCATGG
VIM	Forward: AGTCCACTGAGTACCGGAGAC
	Reverse: CATTTCACGCATCTGGCGTTC
CDKN2A	Forward: GGGTTTTCGTGGTTCACATCC
	Reverse: CTAGACGCTGGCTCCTCAGTA
Gene	Sequence
FHL1	Forward: TGCTGCCTGAAATGCTTTGAC
	Reverse: GCCAGAAGCGGTTCTTATAGTG
ITGB8	Forward: GTGAAAGTCATATCGGATGGCG
	Reverse: GCTATCAAGAGCGAGATGAGACG
ITGB4	Forward: CTCCACCGAGTCAGCCTTC
	Reverse: CGGGTAGTCCTGTGTCCTGTA
CDK6	Forward: TCTTCATTCACACCGAGTAGTGC
	Reverse: TGAGGTTAGAGCCATCTGGAAA
AKT3	Forward: AATGGACAGAAGCTATCCAGGC
	Reverse: TGATGGGTTGTAGAGGCATCC
METTL17	Forward: GCGGCACTGAAGTGTCTACTG
	Reverse: GGTCACTCCGGGTACTAAGG
COL4A1	Forward: GGGATGCTGTTGAAAGGTGAA

	Reverse: GGTGGTCCGGTAAATCCTGG
CKB	Forward: GCTGCGACTTCAGAAGCGA
	Reverse: GGCATGAGGTCGTCGATGG
E2F1	Forward: CATCCCAGGAGGTCACTTCTG
	Reverse: GACAACAGCGGTTCTTGCTC
TFF3	Forward: CCAAGCAAACAATCCAGAGCA
	Reverse: GCTCAGGACTCGCTTCATGG
IGF2	Forward: GTGGCATCGTTGAGGAGTG
	Reverse: CACGTCCCTCTCGGACTTG
FN1	Forward: CGGTGGCTGTCAGTCAAAG
	Reverse: AAACCTCGGCTTCCTCCATAA
CDC45	Forward: CTTGAAGTTCCCGCCTATGAAG
	Reverse: GCATGGTTTGCTCCACTATCTC
NELFCD	Forward: CCGAGTGGCTCATTCAGACAG
	Reverse: GGGGTCTCTCCTTCTTCAGTAA
SPINK1	Forward: TCTATCTGGTAACACTGGAGCTG
	Reverse: ACACGCATTCATTGGGATAAGT
TCF4	Forward: CAAGCACTGCCGACTACAATA
	Reverse: CCAGGCTGATTCATCCCACTG
AGR2	Forward: CGCGAGTGCATTCCATCCT
	Reverse: TCCAAAGTCTTTTAGGTGGCAG
VCAN	Forward: GTAACCCATGCGCTACATAAAGT
	Reverse: GGCAAAGTAGGCATCGTTGAAA
CDKL2	Forward: TCTCCCAGTCTGGCGTTGT
	Reverse: ACCATCGGGTTGCCACATAAT
BCAT1	Forward: AGCCCTGCTCTTTGTACTCTT
Gene	Sequence
	Reverse: CCAGGCTCTTACATACTTGGGA

Table S3. Bulk RNA-seq original data of SW48-EV and SW48-OE.

Gene Symbol	SW48-EV1	SW48-EV2	SW48-EV3	SW48-0E1	SW48-OE2	SW48-OE3	log2FC	P-value
SORBS2	156	209	172	1	0	1	-8.113351109	4.98E-15
LRATD1	39	39	39	0	0	0	-7.77213995	2.94E-10
ODAM	33	38	45	0	0	0	-7.759911003	3.40E-10
CLEC2B	48	32	27.03	0	0	0	-7.642566013	8.45E-10
PID1	53	63	54	0	1	0	-7.349684859	1.54E-09
HAS2	173	124	147	1	1	1	-7.252933957	2.51E-17
TMPRSS2	75	71	92	1	0	1	-6.938709835	4.43E-11
CLCN4	37	42	41	0	1	0	-6.847069671	2.70E-08
PRODH	13.57	11.47	24.02	0	0	0	-6.48632454	9.50E-07
PTPN20	20	9	14	0	0	0	-6.326735248	2.18E-06
AMELX	9.33	14	15.04	0	0	0	-6.15029933	5.04E-06
DNAJC25-GNG10	7.36	8.68	14.16	0	0	0	-5.75975657	3.93E-05
CFTR	11	7	10	0	0	0	-5.708379142	4.62E-05
B3GALT5	328.63	357.66	314.07	3.65	11.44	7.82	-5.61624872	4.22E-61
TRIM73	16.08	4.15	5.59	0	0	0	-5.543264084	1.55E-04
IL1R2	8	16	20	0	0	1	-5.400200243	4.94E-05

SEMA3A	267	261	232	7	6	6	-5.365977733	7.70E-50
ARHGAP6	6	7	7	0	0	0	-5.223935845	4.06E-04
KCTD14	5.42	5.48	10.16	0	0	0	-5.223506844	4.55E-04
ITGB6	112	134	112	4	3	3	-5.206279791	3.62E-25
ALDH1A1	71	64	62	3	1	2	-5.080986789	6.03E-15
NPY4R	364	356.18	351.39	10.31	19	11.12	-4.786848876	1.26E-76
ACTL8	70	59	47	5	1	2	-4.503265498	3.64E-14
IGFBP3	392	368	391	19	21	26	-4.168205143	2.59E-86
CALCA	3.1	9.08	6.17	0	0	1	-4.111577506	0.006169154
SUCNR1	7	6	5	0	0	1	-4.109694225	0.005632225
GADD45G	15	13	5	1	0	1	-4.088300134	9.45E-04
NAV3	116.07	139.65	135	7.87	12.19	7.42	-3.951244291	3.26E-30
FAM174B	158	157	133	15	11	4	-3.944616773	1.30E-33
DPEP1	712.48	785.72	802.64	58.31	47.98	59.77	-3.853430253	1.60E-161
SLC6A20	1438.86	1415.91	1433.61	104.42	96.96	106.6	-3.852050796	1.05E-307
STC1	13	23	19	3	1.01	0	-3.826423205	2.02E-05
AFAP1L2	65	55	61	7	3	6.03	-3.543609726	1.09E-14
SLCO3A1	62	65	80	8	4	7	-3.489612061	2.63E-16
ADPRH	51	67	64	7	2	8	-3.46475166	2.98E-14
TCHH	18	19	15	3	2	0	-3.42283904	4.13E-05
ETV1	362	337	335	31	39	31	-3.399764873	5.02E-74
KRT20	16	10	20	1	4	0	-3.245059092	2.05E-04
MME	569	509.02	550	55	58	65	-3.237003044	3.91E-110
NDUFC2-KCTD14	262.21	293.51	283.09	37.48	42.25	22.26	-3.09689085	6.15E-54
INSC	53.49	61.04	49.61	6.12	4	10.27	-3.071055562	2.86E-12
SYT13	275.09	311.68	314.52	37.04	42.72	33.39	-3.050679851	1.83E-59
RGS4	9	13	10	1	1	2	-3.04460161	0.001715094
VWA2	167.25	132.5	162.99	21.93	17.7	20.99	-3.034294964	2.82E-31
MARCHF4	9	10.51	12	0	0	4.02	-2.998003384	0.003135887
TSSK2	7.5	9.92	7.54	0.99	3.5	0	-2.983275282	0.010178632
PMEPA1	181	199	192	23	21	31	-2.975220252	2.84E-38
TPRG1	165.84	170.61	156.28	21.59	18.62	26.9	-2.961301229	2.54E-33
IFI27	11	8	11	1	1	2	-2.950348501	0.002678183
FCRLB	4	9	9	0	1	2	-2.919380188	0.011892443
HGF	7	9	6	1	2	0	-2.919184351	0.011072488
GOLT1A	10	13	13	0	2	3	-2.892289263	0.00129865
PLSCR4	25	31	23	3	4	4	-2.888799317	1.50E-06
SERPINA1	247	249	270	37	37	34	-2.870367768	6.50E-50
PIP5K1B	61	68	62	11	8	8	-2.866799493	8.85E-14
TESC	38	42	40	5	6	6	-2.863630747	2.94E-09
LCP1	46	39	36	9	5	4	-2.792809048	6.46E-09
TMEM61	5	7	8	2	1	0	-2.781595154	0.017748834
SCN1A	8.24	10.15	7.18	2	2	0	-2.688528482	0.009160781
CNTNAP2	581.08	524.18	558.21	92.66	93.89	82.19	-2.682774783	8.14E-97
ANO1	358	340.03	315	48	48	73	-2.627467886	1.10E-54
SH3RF3	122	110	118	24	23	17	-2.495135416	5.96E-21
BLK	8	12	7	4	0	1	-2.477912499	0.011321727
WNT16	488	432	433	84	87	89	-2.423439954	4.61E-71
SSTR1	227	214	195	48	40	37	-2.391107157	2.99E-34
ABCA12	51	48	38	4	10	13	-2.387057094	2.59E-08
ZBTB20	258	269.42	181.53	58	31.72	51.02	-2.382535499	5.34E-29
PDE10A	151	157.03	139	25	29	35.67	-2.37250411	1.12E-24
THSD4	372	339.01	371	77	66.86	76	-2.348586038	3.25E-56
PSD3	315	317	343	66.01	62	70	-2.343933135	2.99E-51
ST18	25.85	22.56	16.15	2.89	9.4	2.01	-2.320865655	2.50E-04
FBN3	24	11	18	1	7	3	-2.311347345	8.29E-04
THRB	81	80	72	19	17	13	-2.293578171	2.39E-13
CXXC4	29	37	31	10	5	6	-2.252088841	3.33E-06
CD99	2235.7	2216.28	2362.48	530.29	515.32	470.04	-2.213015749	3.40E-268
FZD7	2603.69	2538.11	2545.36	633.62	549.85	542.61	-2.200503093	9.45E-287
TSPOAP1	29	40	38	12	4	9	-2.142123511	3.57E-06
NHS	32	35	27	10	6	6	-2.139452258	8.50E-06
TSPAN8	1752	1632	1676	378	401	412	-2.130892749	1.35E-206
EPHA4	212	207	232	61	44	51	-2.105108356	4.82E-30
S100A5	351	340	339	113	61	76	-2.086675817	1.99E-37
CYP26B1	257	239	252	76	48	58	-2.083043726	2.21E-32
EFNA2	68.15	73.96	64.78	18.62	11	21.23	-2.079759365	1.76E-10
ADGRL2	431.09	440.92	413.73	103.81	102.51	109.79	-2.075899489	4.02E-58
HLA-G	53.9	28.85	40.81	9.9	9.71	13.78	-2.007652528	2.84E-06
GLRA3	19.14	16.3	23.13	7.72	4.18	4.77	-1.994879009	8.04E-04

Table S4. Bulk RNA-seq original data of Caco2-EV and Caco2-KD.

Gene Symbol	caco2_EV1	caco2_EV2	caco2_EV3	Caco2 _KD1	caco2 _KD2	caco2 _KD3	log2 (T / con)	P-value (T / con)
SPDYE21	0.05	0.18	0.12	0	0	0	-5.089025052	8.48E-04
F8	0.17	0.11	0.17	0.01	0.04	0.01	-2.868914348	0.00466506
ST6GAL1	38.25	38.75	37.24	8.88	8.45	8.75	-2.186550276	1.62E-307
SSTR3	0.52	0.45	0.57	0.18	0.16	0.16	-1.736947716	3.95E-05
HP	5.79	5.67	4.47	1.29	2.53	1.24	-1.673461839	3.34E-11
HPR	1.11	1.08	0.92	0.33	0.35	0.54	-1.468649843	0.004615968
ANKRD37	3.79	4.22	3.73	1.62	1.46	1.46	-1.409592765	3.38E-05

ZBTB16	0.64	0.58	0.72	0.25	0.25	0.27	-1.375702356	5.35E-08
VAMP7	14.44	14.73	13.95	5.64	5.53	6.07	-1.343262292	3.76E-43
SLC26A8	0.64	0.47	0.48	0.2	0.14	0.3	-1.34281307	0.002417421
NUTM2D	0.78	0.68	0.87	0.38	0.14	0.33	-1.322975008	1.45E-04
SYT15	0.94	0.99	1.16	0.67	0.55	0.57	-1.310874015	8.95E-05
FGG	67.44	64.82	48.33	25.41	24.96	23.91	-1.295477223	1.53E-17
ORM1	67.65	67.5	57.33	28.88	28.56	22.8	-1.279172705	8.04E-36
DIO1	2.16	2.13	1.99	0.9	1.14	0.85	-1.221897846	3.16E-05
FGA	10.51	11.3	10.05	4.96	4.45	4.78	-1.187087579	1.54E-23
SERPIND1	0.71	0.76	1.27	0.41	0.24	0.61	-1.164007384	0.006610617
SERPINA11	1.11	0.98	1.5	0.57	0.66	0.65	-1.154734683	0.008080576
ORM2	46.71	42.94	40.9	21.09	22.16	16.7	-1.141050958	1.23E-23
KIF26B	1.93	1.75	1.67	0.65	0.98	0.81	-1.133798226	1.92E-16
H3-3A	413.14	421.41	384.11	194.89	187.02	185.72	-1.123225366	1.16E-145
THSD7B	1.43	1.14	1.24	0.66	0.63	0.48	-1.122832654	2.09E-06
COL2A1	25.15	26.17	22.46	11.9	11.29	11.57	-1.109877345	2.77E-67
P2RY6	2.66	2	2.68	1.11	1.14	1.06	-1.085590255	3.00E-06
BCL2L2-PABPN1	4.16	4.37	4.22	3.08	1.17	2.05	-1.039656932	0.004513972
ROR1	1.1	1.22	0.93	0.51	0.65	0.54	-1.030334172	1.54E-05
ARPIN-AP3S2	2.72	1.95	2.73	1.35	1.3	1.07	-1.015147411	3.52E-10
NELFCD	114.26	120.61	109.7	57.4	58.15	59.92	-0.995309638	4.24E-100
SMLR1	7.58	8.32	7.86	4.36	3.8	3.98	-0.988312853	3.29E-15
APOH	41.76	39.19	36.85	19.23	22.13	19.4	-0.975473626	5.16E-27
GABRA4	0.29	0.27	0.32	0.16	0.16	0.15	-0.974547431	0.00110476
NPR2	3.08	3.48	3.01	1.26	1.63	1.65	-0.964817868	3.80E-07
AMBP	2.53	1.98	2.17	1.31	0.99	1.19	-0.964071303	0.003301491
PMF1-BGLAP	3.57	3.4	3.44	1.36	2.49	1.7	-0.960926505	0.001882049
C1S	11.88	10.93	10.74	5.84	6	5.91	-0.940585855	2.15E-20
LAMA1	0.49	0.56	0.43	0.23	0.26	0.32	-0.939121211	1.94E-04
FAM107B	68.94	71.59	71.02	38.34	37.77	37.43	-0.915200542	2.13E-93
ASCL2	15.29	15.86	12.82	8.14	7.84	7.91	-0.904948103	3.17E-13
PRSS2	11.5	8.82	9.59	5.01	7.09	4.49	-0.870250783	3.84E-05
TLR9	0.88	1.22	1	0.6	0.54	0.59	-0.858793489	0.003129678
APOC1	74.72	72.58	74.62	41.29	45.32	39.01	-0.850488129	3.25E-19
ADH4	4.1	4.21	3.49	2.11	2.35	2.23	-0.84647486	9.34E-06
BNIP3	21.26	20.81	22.48	12	12.24	12.29	-0.842940581	1.61E-18
ATG4C	1.72	1.86	1.79	0.93	0.96	1.17	-0.830763004	6.49E-04
SLC9B2	4.5	4.64	4.15	2.59	2.81	2.53	-0.828060883	1.60E-14
BHLHE40	6.25	6.62	9.79	4.2	4.28	4.5	-0.82427776	2.13E-08
LOC112268052	2.59	2.14	2.48	1.42	1.18	1.55	-0.822659574	0.007509723
PLA2G7	1.45	1.45	1.8	0.68	0.9	1.2	-0.807517552	0.005105327
SPINK1	61.61	57.94	54.39	36.05	36	28.9	-0.804765019	6.01E-11
TUSC2	21.16	22.96	19.8	12.94	12.11	12.18	-0.800927977	6.22E-17
NTN4	21.21	20.47	19.27	12.27	11.75	11.44	-0.800225964	4.48E-31
UQCR10	50.63	48.8	47.54	29.46	28.95	28.33	-0.789829932	1.69E-21
PAH	11.9	13.19	12.61	7.42	7.01	7.42	-0.767954209	1.86E-18
CHST9	3.38	3.04	3.85	1.51	1.82	2.51	-0.762522837	1.89E-10
H2BC21	5.36	5.16	2.92	2.46	2.57	3.03	-0.761902588	2.59E-04
MED31	2.13	2.94	2.29	1.34	1.65	1.48	-0.750633997	0.005488554
EML5	0.46	0.61	0.4	0.31	0.32	0.25	-0.747960496	0.003079828
INSIG1	11.53	10.77	11.3	6.79	7.31	6.27	-0.74462806	1.86E-14
TCF4	3.69	3.32	3.2	2.02	2.02	2.27	-0.738686956	3.13E-11
ABCA1	6.72	7.1	6.41	4.24	3.83	4.25	-0.736612969	4.59E-25
APOA2	182.84	176.83	210.19	116.05	122.1	108.7	-0.736198928	4.27E-22
SGMS2	2.9	2.73	3.01	1.8	1.83	1.65	-0.726910926	9.53E-09
STK32B	1.47	1.93	1.68	0.81	0.98	1.18	-0.726528689	0.00324988
KCND1	1.24	1.47	1.14	0.71	0.88	0.81	-0.725200591	0.001636795
MOB1A	47.55	44.92	43.67	28.96	27.86	26.7	-0.724562677	1.13E-49
REEP1	1.82	1.47	1.74	0.89	1.04	1.19	-0.721351052	6.61E-04
UQCC2	17.69	18.13	17.63	11.56	10.04	11.32	-0.72059081	1.97E-10
IGDCC3	13.95	15.05	14.11	9.17	8.66	8.74	-0.719846087	2.24E-23
CHST15	0.73	1	0.78	0.45	0.44	0.55	-0.71182975	0.009706312
SERPINA6	20.17	20.26	20.97	12.04	13.12	12.9	-0.711036727	4.45E-13
LIN7A	1.77	1.64	1.69	1.06	1.06	1.03	-0.710263244	1.06E-05
SP8	2.28	2.67	2.22	1.28	1.56	1.61	-0.705584175	1.05E-04
COL12A1	5.81	6.08	6.23	4.03	3.69	3.69	-0.704330784	3.08E-21
MBNL3	12.96	12.65	11.68	7.71	7.7	7.62	-0.703135119	2.02E-35
SMIM4	13.26	12.34	10.86	9.4	6.56	8.85	-0.700898831	2.71E-04
SERPINC1	5.03	6.02	8.57	3.74	4.47	4.17	-0.69634712	4.13E-04
FUT11	4.84	4.53	4.67	3.09	2.97	3.13	-0.693645545	6.23E-05
PCYT1B	4.97	4.84	4.55	2.93	2.84	3.28	-0.687885475	6.07E-11
CPS1	10.4	10.37	8.32	6.15	5.93	6.22	-0.687531836	4.05E-15
CAB39L	5.27	5.62	5.05	3.19	3.59	3.32	-0.68215856	1.63E-08
RBBP8NL	25.59	25.32	22.61	15.93	14.82	15.75	-0.681772492	4.13E-21

Table S5. Original data of quantitative proteomics.

	MS/MS Counts	Peptides	Unique peptides	LFQ intensity SW48 OE	LFQ intensity SW48 EV	SW48_OE	SW48_EV	SW48_OE/SW 48 EV Ratio
TRAV18	8	1	1	0	0			
PPIAL4C	1	3	1	0	0			
GATD3	33	9	9	169730000	180940000	0.968032623	1.031967377	0.938045761
GNG5B	8	2	2	255620000	311290000	0.901800991	1.098199009	0.821163545
RBM47	12	6	6	45967000	35958000	1.122172719	0.877827281	1.278352522
UBA6	65	22	22	85942000	83577000	1.013951239	0.986048761	1.028297259
ESYT2	46	16	16	46635000	48740000	0.977929227	1.022070773	0.956811654
MED19	3	1	1	0	0			
SHTN1	32	13	13	69307000	82843000	0.911035163	1.088964837	0.836606593
ILVBL	25	7	7	87674000	80066000	1.045355908	0.954644092	1.095021607
ANKRD18A	1	2	2	0	0			
VWA8	16	5	5	34289000	32356000	1.029004426	0.970995574	1.059741624
SBNO1	8	5	5	24446000	28388000	0.925388954	1.074611046	0.861138509
GTPBP10	5	3	3	19376000	15525000	1.110340678	0.889659322	1.24805153
LRRD1	3	1	1	0	0			
WDR91	4	1	1	0	0			
CNOT1	62	24	24	73699000	71821000	1.012905443	0.987094557	1.026148341
MAP1LC3B	5	1	1	0	0			
PGP	15	4	4	61274000	46605000	1.135976418	0.864023582	1.314751636
DPRX	0	1	1	0	0			
TUBAL3	4	5	1	0	0			
FBLL1	5	3	1	0	0			
SMCHD1	24	14	14	36844000	41959000	0.935091304	1.064908696	0.878095283
UNC119B	24	7	6	54266000	61650000	0.936298699	1.063701301	0.880227088
RAP1B	17	4	3	133620000	157280000	0.918666208	1.081333792	0.84956765
COL6A6	0	1	1	0	0			
ANKRD36B	1	1	1	0	0			
POM121C	12	5	1	65272000	48847000	1.143928706	0.856071294	1.336254018
CYSRT1	1	1	1	0	0			
GNAT3	65	18	16	762690000	1302700000	0.738543326	1.261456674	0.585468642
SNRPG	8	2	2	840860000	750730000	1.056628906	0.943371094	1.120056478
NUDT19	20	7	7	49888000	48856000	1.010451268	0.989548732	1.021123301
MIF4GD	1	1	1	0	0			
WDR64	0	2	2	0	0			
WASH3P	2	2	2	0	0			
NACA	45	4	4	870130000	848070000	1.012839018	0.987160982	1.026012004
C11orf98	5	2	2	0	0			
SLC35A4	12	4	4	57656000	80495000	0.834680893	1.165319107	0.716268091
DNASE2	12	4	4	37884000	62991000	0.751107807	1.248892193	0.60141925
AGPS	34	12	12	89917000	89702000	1.001196978	0.998803022	1.002396825
KIF2A	8	3	3	25330000	38424000	0.794616808	1.205383192	0.659223402
DDX39A	24	17	7	151330000	179340000	0.915293193	1.084706807	0.843816215
PDLIM1	9	7	7	0	0			
ACOT7	58	11	11	310850000	417550000	0.853514552	1.146485448	0.744461741
MYO1C	90	27	27	553030000	760670000	0.841942605	1.158057395	0.727030118
SNAP23	5	2	2	0	0			
HAX1	6	3	3	23481000	25608000	0.956670537	1.043329463	0.916940019
AIP	44	14	14	144480000	125490000	1.070341149	0.929658851	1.151326799
GTPBP1	7	3	3	25866000	26074000	0.995995379	1.004004621	0.992022705
STXBP3	20	8	8	45300000	38470000	1.081532768	0.918467232	1.177540941
ARVCF	1	1	1	0	0			
SMAP	4	2	2	0	0			
AP3B1	41	12	12	52775000	63247000	0.909741256	1.090258744	0.834426929
SULT2B1	15	6	6	35822000	50016000	0.834642	1.165358	0.716210813
LGALS8	9	5	5	67124000	42301000	1.22684944	0.77315056	1.586818279
NDUFS8	17	5	5	86477000	76935000	1.058392285	0.941607715	1.124026776

TNFRSF10A	4	1	1	0	0				
PSMD11	90	22	22	309980000	332890000	0.964362935	1.035637065	0.931178467	
PSMD12	59	18	18	201460000	188670000	1.032783944	0.967216056	1.067790322	
PSMD9	37	10	10	436670000	441860000	0.994092404	1.005907596	0.988254198	
ATOX1	4	1	1	0	0				
MEN1	2	1	1	0	0				
PGRMC1	27	6	5	125540000	109520000	1.068152812	0.931847188	1.146274653	
SUPT5H	26	11	11	72703000	65095000	1.055211251	0.944788749	1.116875336	
TAF4	2	1	1	0	0				
DFFA	19	5	5	180310000	141020000	1.122273053	0.877726947	1.278612963	
HIP1	21	12	12	27288000	41402000	0.794526132	1.205473868	0.659098594	
CLIC1	70	14	14	676590000	789160000	0.923199727	1.076800273	0.857354656	
EIF3F	44	11	11	209650000	183670000	1.066053087	0.933946913	1.141449338	
PDHX	12	4	4	25551000	24924000	1.012421991	0.987578009	1.025156476	
DCTN6	3	1	1	0	0				
SLC33A1	1	1	1	0	0				
WASL	8	4	4	0	0				
IPO5	162	39	39	475550000	384940000	1.105300468	0.894699532	1.235387333	

Table S6. Original data of N-glycopeptide modification omics.

Modification sites information							Protein quantitation		Normalized modification sites quantitation		
Protein accession	Position	Amino acid	Protein description	Gene name	Assigned Modification	Observed Modification	SW48_EV	SW48_OE	SW48_EV	SW48_OE	SW48_OE/SW48 EV Ratio
A0A2R8Y4L2	223	N	Heterogeneous nuclear ribonucleoprotein A1-like 3 OS=Homo sapiens OX=9606 GN=HNRNPA1L3 PE=4 SV=1	HNRNPA1L3	714.2695	HexNAc(2)Hex(1)Fuc(1)					
O00115	212	N	Deoxyribonuclease-2-alpha OS=Homo sapiens OX=9606 GN=DNASE2 PE=1 SV=2	DNASE2	1054.37	HexNAc(2)Hex(4)	1.248892193	0.751107807	0.925815227	1.123349515	1.213
O00115	212	N	Deoxyribonuclease-2-alpha OS=Homo sapiens OX=9606 GN=DNASE2 PE=1 SV=2	DNASE2	1216.4228	HexNAc(2)Hex(5)	1.248892193	0.751107807	0.955416569	1.074130368	1.124
O00115	212	N	Deoxyribonuclease-2-alpha OS=Homo sapiens OX=9606 GN=DNASE2 PE=1 SV=2	DNASE2	1378.4757	HexNAc(2)Hex(6)	1.248892193	0.751107807			

O00115	212	N	Deoxyribonuclease-2-alpha OS=Homo sapiens OX=9606 GN=DNASE2 PE=1 SV=2	DNASE2	892.3172	HexNAc(2)Hex(3)	1.248892193	0.751107807	0.87084833	1.214744822	1.395
O00462	77	N	Beta-mannosidase OS=Homo sapiens OX=9606 GN=MANBA PE=1 SV=3	MANBA	892.3172	HexNAc(2)Hex(3)					
O00584	106	N	Ribonuclease T2 OS=Homo sapiens OX=9606 GN=RNASET2 PE=1 SV=2	RNASET2	1054.37	HexNAc(2)Hex(4)	0.937268398	1.062731602	0.804900508	1.172066577	1.456
O00584	106	N	Ribonuclease T2 OS=Homo sapiens OX=9606 GN=RNASET2 PE=1 SV=2	RNASET2	1216.4228	HexNAc(2)Hex(5)	0.937268398	1.062731602	1.460304637	0.594037677	0.407
O00584	106	N	Ribonuclease T2 OS=Homo sapiens OX=9606 GN=RNASET2 PE=1 SV=2	RNASET2	1378.4757	HexNAc(2)Hex(6)	0.937268398	1.062731602	1.486068436	0.571315482	0.384
O00584	106	N	Ribonuclease T2 OS=Homo sapiens OX=9606 GN=RNASET2 PE=1 SV=2	RNASET2	1458.442	HexNAc(2)Hex(6) Phospho(1)	0.937268398	1.062731602	0.758783321	1.212739293	1.598
O00584	106	N	Ribonuclease T2 OS=Homo sapiens OX=9606 GN=RNASET2 PE=1 SV=2	RNASET2	1540.5285	HexNAc(2)Hex(7)	0.937268398	1.062731602	1.066930243		
O00584	106	N	Ribonuclease T2 OS=Homo sapiens OX=9606 GN=RNASET2 PE=1 SV=2	RNASET2	1702.5813	HexNAc(2)Hex(8)	0.937268398	1.062731602	1.066930243		
O00584	106	N	Ribonuclease T2 OS=Homo sapiens OX=9606 GN=RNASET2 PE=1 SV=2	RNASET2	1864.6341	HexNAc(2)Hex(9)	0.937268398	1.062731602	0.974120767	1.022824001	1.05
O00584	212	N	Ribonuclease T2 OS=Homo sapiens OX=9606 GN=RNASET2 PE=1 SV=2	RNASET2	1702.5813	HexNAc(2)Hex(8)	0.937268398	1.062731602	1.066930243		
O00592	360	N	Podocalyxin OS=Homo sapiens OX=9606 GN=PODXL PE=1 SV=2	PODXL	2117.7768	HexNAc(5)Hex(5)Fuc(2)	0.978956648	1.021043352	1.021495694		
O00754	133	N	Lysosomal alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B1 PE=1 SV=3	MAN2B1	1038.3751	HexNAc(2)Hex(3)Fuc(1)					
O00754	692	N	Lysosomal alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B1 PE=1 SV=3	MAN2B1	892.3172	HexNAc(2)Hex(3)					
O00754	766	N	Lysosomal alpha-mannosidase OS=Homo sapiens OX=9606 GN=MAN2B1 PE=1 SV=3	MAN2B1	1038.3751	HexNAc(2)Hex(3)Fuc(1)					

O14524	125	N	Nuclear envelope integral membrane protein 1 OS=Homo sapiens OX=9606 GN=NEMP1 PE=1 SV=2	NEMP1	1702.5813	HexNAc(2)Hex(8)					
O14524	125	N	Nuclear envelope integral membrane protein 1 OS=Homo sapiens OX=9606 GN=NEMP1 PE=1 SV=2	NEMP1	1864.6341	HexNAc(2)Hex(9)					
O14656	158	N	Torsin-1A OS=Homo sapiens OX=9606 GN=TOR1A PE=1 SV=1	TOR1A	1864.6341	HexNAc(2)Hex(9)					
O14657	64	N	Torsin-1B OS=Homo sapiens OX=9606 GN=TOR1B PE=1 SV=2	TOR1B	1378.4757	HexNAc(2)Hex(6)	1.36852736	0.63147264	0.730712465		
O14657	64	N	Torsin-1B OS=Homo sapiens OX=9606 GN=TOR1B PE=1 SV=2	TOR1B	1702.5813	HexNAc(2)Hex(8)	1.36852736	0.63147264	1.355669597	0.229192932	0.169
O14657	64	N	Torsin-1B OS=Homo sapiens OX=9606 GN=TOR1B PE=1 SV=2	TOR1B	1864.6341	HexNAc(2)Hex(9)	1.36852736	0.63147264	1.057948957	0.874413034	0.827
O14672	267	N	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	ADAM10	1216.4228	HexNAc(2)Hex(5)	1.29163291	0.70836709	0.65910721	1.621582159	2.46
O14672	278	N	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	ADAM10	1702.5813	HexNAc(2)Hex(8)	1.29163291	0.70836709	0.981899722	1.033003953	1.052
O14672	278	N	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	ADAM10	1864.6341	HexNAc(2)Hex(9)	1.29163291	0.70836709	0.834949492	1.300952247	1.558
O14672	439	N	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	ADAM10	1216.4228	HexNAc(2)Hex(5)	1.29163291	0.70836709	0.802475078	1.360165928	1.695
O14672	439	N	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	ADAM10	1378.4757	HexNAc(2)Hex(6)	1.29163291	0.70836709	0.85930499	1.256542557	1.462
O14672	439	N	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	ADAM10	1540.5285	HexNAc(2)Hex(7)	1.29163291	0.70836709	0.805379713	1.35486963	1.682
O14672	439	N	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	ADAM10	1702.5813	HexNAc(2)Hex(8)	1.29163291	0.70836709	0.926682797	1.133686211	1.223
O14672	439	N	Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens OX=9606 GN=ADAM10 PE=1 SV=1	ADAM10	1864.6341	HexNAc(2)Hex(9)	1.29163291	0.70836709	0.868644111	1.239513653	1.427

O14773	443	N	Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=2	TPP1	1038.3751	HexNAc(2)Hex(3)Fuc(1)	1.078330253	0.921669747	0.779410787	1.258083791	1.614
O14773	443	N	Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=2	TPP1	1403.5073	HexNAc(3)Hex(4)Fuc(1)	1.078330253	0.921669747	0.927359681		
O14773	443	N	Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=2	TPP1	1864.6341	HexNAc(2)Hex(9)	1.078330253	0.921669747	0.898178319	1.119128788	1.246
O14773	443	N	Tripeptidyl-peptidase 1 OS=Homo sapiens OX=9606 GN=TPP1 PE=1 SV=2	TPP1	892.3172	HexNAc(2)Hex(3)	1.078330253	0.921669747	0.763832706	1.276309751	1.671
O14974	384	N	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens OX=9606 GN=PPP1R12A PE=1 SV=1	PPP1R12A	203.0794	HexNAc(1)	0.891401135	1.108598865	0.9049806	1.07640311	1.189
O15031	127	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1038.3751	HexNAc(2)Hex(3)Fuc(1)	1.107541303	0.892458697	0.902900865		
O15031	127	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1540.5285	HexNAc(2)Hex(7)	1.107541303	0.892458697	0.903570648	1.119668832	1.239
O15031	127	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1702.5813	HexNAc(2)Hex(8)	1.107541303	0.892458697	0.957640055	1.052568694	1.099
O15031	127	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1864.6341	HexNAc(2)Hex(9)	1.107541303	0.892458697	0.944046692	1.069438059	1.133
O15031	528	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1864.6341	HexNAc(2)Hex(9)	1.107541303	0.892458697		1.120500034	
O15031	528	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	892.3172	HexNAc(2)Hex(3)	1.107541303	0.892458697	0.902900865		
O15031	733	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1038.3751	HexNAc(2)Hex(3)Fuc(1)	1.107541303	0.892458697	1.280857722	0.651455548	0.509
O15031	733	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1702.5813	HexNAc(2)Hex(8)	1.107541303	0.892458697	0.967650168	1.040146144	1.075
O15031	733	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1768.6395	HexNAc(4)Hex(5)Fuc(1)	1.107541303	0.892458697	0.902900865		

O15031	733	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1864.6341	HexNAc(2)Hex(9)	1.107541303	0.892458697	0.823582069	1.218934664	1.48
O15031	733	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1914.6974	HexNAc(4)Hex(5)Fuc(2)	1.107541303	0.892458697	1.019909917	0.975291791	0.956
O15031	733	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	2060.7553	HexNAc(4)Hex(5)Fuc(3)	1.107541303	0.892458697			
O15031	733	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	2133.7717	HexNAc(5)Hex(6)Fuc(1)	1.107541303	0.892458697	0.902900865		
O15031	759	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1216.4228	HexNAc(2)Hex(5)	1.107541303	0.892458697	0.812812107	1.232300188	1.516
O15031	759	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1378.4757	HexNAc(2)Hex(6)	1.107541303	0.892458697	0.797585762	1.251196083	1.569
O15031	759	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1864.6341	HexNAc(2)Hex(9)	1.107541303	0.892458697	0.85000412	1.186144897	1.395
O15031	844	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1702.5813	HexNAc(2)Hex(8)	1.107541303	0.892458697	0.902900865		
O15031	844	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1864.6341	HexNAc(2)Hex(9)	1.107541303	0.892458697	0.867777341	1.164088329	1.341
O15031	1002	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1702.5813	HexNAc(2)Hex(8)	1.107541303	0.892458697	0.929085419	1.088005	1.171
O15031	1002	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1864.6341	HexNAc(2)Hex(9)	1.107541303	0.892458697	0.951045628	1.060752378	1.115
O15031	1049	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	2117.7768	HexNAc(5)Hex(5)Fuc(2)	1.107541303	0.892458697	0.902900865		
O15031	1099	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	1914.6974	HexNAc(4)Hex(5)Fuc(2)	1.107541303	0.892458697			
O15031	1099	N	Plexin-B2 OS=Homo sapiens OX=9606 GN=PLXNB2 PE=1 SV=3	PLXNB2	2117.7768	HexNAc(5)Hex(5)Fuc(2)	1.107541303	0.892458697			

O15230	95	N	Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	LAMA5	1702.5813	HexNAc(2)Hex(8)					
O15230	1330	N	Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	LAMA5	1864.6341	HexNAc(2)Hex(9)					
O15230	1330	N	Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	LAMA5	876.3223	HexNAc(2)Hex(2)Fuc(1)					
O15230	2423	N	Laminin subunit alpha-5 OS=Homo sapiens OX=9606 GN=LAMA5 PE=1 SV=8	LAMA5	1702.5813	HexNAc(2)Hex(8)					
O15342	70	N	V-type proton ATPase subunit e 1 OS=Homo sapiens OX=9606 GN=ATP6V0E1 PE=1 SV=2	ATP6V0E1	1378.4757	HexNAc(2)Hex(6)					
O15342	70	N	V-type proton ATPase subunit e 1 OS=Homo sapiens OX=9606 GN=ATP6V0E1 PE=1 SV=2	ATP6V0E1	1702.5813	HexNAc(2)Hex(8)					
O15342	70	N	V-type proton ATPase subunit e 1 OS=Homo sapiens OX=9606 GN=ATP6V0E1 PE=1 SV=2	ATP6V0E1	1864.6341	HexNAc(2)Hex(9)					
O15460	264	N	Prolyl 4-hydroxylase subunit alpha-2 OS=Homo sapiens OX=9606 GN=P4HA2 PE=1 SV=1	P4HA2	1216.4228	HexNAc(2)Hex(5)	1.251535826	0.748464174			
O15460	264	N	Prolyl 4-hydroxylase subunit alpha-2 OS=Homo sapiens OX=9606 GN=P4HA2 PE=1 SV=1	P4HA2	1378.4757	HexNAc(2)Hex(6)	1.251535826	0.748464174	0.725045815	1.459761502	2.013
O15460	264	N	Prolyl 4-hydroxylase subunit alpha-2 OS=Homo sapiens OX=9606 GN=P4HA2 PE=1 SV=1	P4HA2	1540.5285	HexNAc(2)Hex(7)	1.251535826	0.748464174			
O15460	264	N	Prolyl 4-hydroxylase subunit alpha-2 OS=Homo sapiens OX=9606 GN=P4HA2 PE=1 SV=1	P4HA2	1702.5813	HexNAc(2)Hex(8)	1.251535826	0.748464174			
O43303	257	N	Centriolar coiled-coil protein of 110 kDa OS=Homo sapiens OX=9606 GN=CCP110 PE=1 SV=3	CCP110	1864.6341	HexNAc(2)Hex(9)					
O43657	134	N	Tetraspanin-6 OS=Homo sapiens OX=9606 GN=TSPAN6 PE=1 SV=1	TSPAN6	1038.3751	HexNAc(2)Hex(3)Fuc(1)	1.081428385	0.918571615	0.68803957	1.367268985	1.987
O43657	134	N	Tetraspanin-6 OS=Homo sapiens OX=9606 GN=TSPAN6 PE=1 SV=1	TSPAN6	1702.5813	HexNAc(2)Hex(8)	1.081428385	0.918571615	1.022813177	0.973142195	0.951

O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1038.3751	HexNAc(2)Hex(3)Fuc(1)	1.228153608	0.771846392	1.128245524	0.795937112	0.705
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1054.37	HexNAc(2)Hex(4)	1.228153608	0.771846392			
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1216.4228	HexNAc(2)Hex(5)	1.228153608	0.771846392	0.985929183	1.022389332	1.037
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1241.4545	HexNAc(3)Hex(3)Fuc(1)	1.228153608	0.771846392	1.057017462	0.909274433	0.86
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1257.4494	HexNAc(3)Hex(4)	1.228153608	0.771846392			
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1378.4757	HexNAc(2)Hex(6)	1.228153608	0.771846392	0.814230397		
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1444.5338	HexNAc(4)Hex(3)Fuc(1)	1.228153608	0.771846392	1.002256171	0.996410005	0.994
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1460.5288	HexNAc(4)Hex(4)	1.228153608	0.771846392			
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1540.5285	HexNAc(2)Hex(7)	1.228153608	0.771846392	0.814230397		
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1647.6132	HexNAc(5)Hex(3)Fuc(1)	1.228153608	0.771846392	0.938068859	1.09854416	1.171
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1663.6081	HexNAc(5)Hex(4)	1.228153608	0.771846392			
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1702.5813	HexNAc(2)Hex(8)	1.228153608	0.771846392	1.174080091	0.723005647	0.616
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1850.6926	HexNAc(6)Hex(3)Fuc(1)	1.228153608	0.771846392	0.890670936	1.173963221	1.318
O43852	131	N	Calumenin OS=Homo sapiens OX=9606 GN=CALU PE=1 SV=2	CALU	1866.6875	HexNAc(6)Hex(4)	1.228153608	0.771846392			

O60487	39	N	Myelin protein zero-like protein 2 OS=Homo sapiens OX=9606 GN=MPZL2 PE=1 SV=1	MPZL2	1038.3751	HexNAc(2)Hex(3)Fuc(1)					
O60487	39	N	Myelin protein zero-like protein 2 OS=Homo sapiens OX=9606 GN=MPZL2 PE=1 SV=1	MPZL2	1971.7189	HexNAc(5)Hex(5)Fuc(1)					
O60487	39	N	Myelin protein zero-like protein 2 OS=Homo sapiens OX=9606 GN=MPZL2 PE=1 SV=1	MPZL2	2117.7768	HexNAc(5)Hex(5)Fuc(2)					
O60487	39	N	Myelin protein zero-like protein 2 OS=Homo sapiens OX=9606 GN=MPZL2 PE=1 SV=1	MPZL2	892.3172	HexNAc(2)Hex(3)					
O60487	118	N	Myelin protein zero-like protein 2 OS=Homo sapiens OX=9606 GN=MPZL2 PE=1 SV=1	MPZL2	1216.4228	HexNAc(2)Hex(5)					
O60487	118	N	Myelin protein zero-like protein 2 OS=Homo sapiens OX=9606 GN=MPZL2 PE=1 SV=1	MPZL2	1378.4757	HexNAc(2)Hex(6)					
O60487	118	N	Myelin protein zero-like protein 2 OS=Homo sapiens OX=9606 GN=MPZL2 PE=1 SV=1	MPZL2	1540.5285	HexNAc(2)Hex(7)					
O60568	63	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1216.4228	HexNAc(2)Hex(5)	1.16006599	0.83993401	1.201557717	0.721620686	0.601
O60568	63	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1378.4757	HexNAc(2)Hex(6)	1.16006599	0.83993401	0.872338535	1.176318285	1.348
O60568	63	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1444.5338	HexNAc(4)Hex(3)Fuc(1)	1.16006599	0.83993401	0.862019927		
O60568	63	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1540.5285	HexNAc(2)Hex(7)	1.16006599	0.83993401	1.074476635	0.897137382	0.835
O60568	63	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1647.6132	HexNAc(5)Hex(3)Fuc(1)	1.16006599	0.83993401	0.862019927		
O60568	63	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1702.5813	HexNAc(2)Hex(8)	1.16006599	0.83993401	0.997192545	1.003877487	1.007
O60568	63	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1864.6341	HexNAc(2)Hex(9)	1.16006599	0.83993401	0.762632094	1.327838178	1.741

O60568	548	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1216.4228	HexNAc(2)Hex(5)	1.16006599	0.83993401	0.862019927		
O60568	548	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1378.4757	HexNAc(2)Hex(6)	1.16006599	0.83993401	0.764848329	1.324777248	1.732
O60568	548	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1444.5338	HexNAc(4)Hex(3)Fuc(1)	1.16006599	0.83993401	0.862019927		
O60568	548	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1501.5553	HexNAc(5)Hex(3)	1.16006599	0.83993401	0.862019927		
O60568	548	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1540.5285	HexNAc(2)Hex(7)	1.16006599	0.83993401	1.00056875	0.999214476	0.999
O60568	548	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1647.6132	HexNAc(5)Hex(3)Fuc(1)	1.16006599	0.83993401	0.862019927		
O60568	548	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1702.5813	HexNAc(2)Hex(8)	1.16006599	0.83993401	1.015154517	0.979069499	0.964
O60568	548	N	Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 OS=Homo sapiens OX=9606 GN=PLOD3 PE=1 SV=1	PLOD3	1864.6341	HexNAc(2)Hex(9)	1.16006599	0.83993401	0.805177624	1.269076868	1.576
O60637	127	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1038.3751	HexNAc(2)Hex(3)Fuc(1)					
O60637	127	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	2498.9039	HexNAc(6)Hex(7)Fuc(1)					
O60637	127	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	2791.0197	HexNAc(6)Hex(7)Fuc(3)					
O60637	127	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	892.3172	HexNAc(2)Hex(3)					
O60637	152	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1038.3751	HexNAc(2)Hex(3)Fuc(1)					
O60637	152	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1403.5073	HexNAc(3)Hex(4)Fuc(1)					

O60637	152	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1768.6395	HexNAc(4)Hex(5)Fuc(1)
O60637	152	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	2498.9039	HexNAc(6)Hex(7)Fuc(1)
O60637	152	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	2791.0197	HexNAc(6)Hex(7)Fuc(3)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1038.3751	HexNAc(2)Hex(3)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1054.37	HexNAc(2)Hex(4)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1095.3966	HexNAc(3)Hex(3)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1200.4279	HexNAc(2)Hex(4)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1216.4228	HexNAc(2)Hex(5)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1241.4545	HexNAc(3)Hex(3)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1257.4494	HexNAc(3)Hex(4)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1362.4807	HexNAc(2)Hex(5)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1378.4757	HexNAc(2)Hex(6)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1403.5073	HexNAc(3)Hex(4)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1419.5022	HexNAc(3)Hex(5)

O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1540.5285	HexNAc(2)Hex(7)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1565.5601	HexNAc(3)Hex(5)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1581.555	HexNAc(3)Hex(6)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1606.5867	HexNAc(4)Hex(4)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1702.5813	HexNAc(2)Hex(8)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1727.6129	HexNAc(3)Hex(6)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1768.6395	HexNAc(4)Hex(5)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1914.6974	HexNAc(4)Hex(5)Fuc(2)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	2117.7768	HexNAc(5)Hex(5)Fuc(2)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	2133.7717	HexNAc(5)Hex(6)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	2498.9039	HexNAc(6)Hex(7)Fuc(1)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	2644.9618	HexNAc(6)Hex(7)Fuc(2)
O60637	167	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	892.3172	HexNAc(2)Hex(3)
O60637	183	N	Tetraspanin-3 OS=Homo sapiens OX=9606 GN=TSPAN3 PE=2 SV=1	TSPAN3	1038.3751	HexNAc(2)Hex(3)Fuc(1)

O75417	1232	N	DNA polymerase theta OS=Homo sapiens OX=9606 GN=POLQ PE=1 SV=2	POLQ	1590.5918	HexNAc(4)Hex(3)Fuc(2)					
O75477	108	N	Erlin-1 OS=Homo sapiens OX=9606 GN=ERLIN1 PE=1 SV=2	ERLIN1	1378.4757	HexNAc(2)Hex(6)	0.973010552	1.026989448	1.460780761	0.563438024	0.386
O75477	108	N	Erlin-1 OS=Homo sapiens OX=9606 GN=ERLIN1 PE=1 SV=2	ERLIN1	1540.5285	HexNAc(2)Hex(7)	0.973010552	1.026989448	1.339241948	0.678588718	0.507
O75477	108	N	Erlin-1 OS=Homo sapiens OX=9606 GN=ERLIN1 PE=1 SV=2	ERLIN1	1702.5813	HexNAc(2)Hex(8)	0.973010552	1.026989448	1.182390868	0.827195655	0.7
O75477	108	N	Erlin-1 OS=Homo sapiens OX=9606 GN=ERLIN1 PE=1 SV=2	ERLIN1	1864.6341	HexNAc(2)Hex(9)	0.973010552	1.026989448	0.735604655	1.250498641	1.7
O75503	255	N	Ceroid-lipofuscinosis neuronal protein 5 OS=Homo sapiens OX=9606 GN=CLN5 PE=1 SV=2	CLN5	1257.4494	HexNAc(3)Hex(4)					
O75629	160	N	Protein CREG1 OS=Homo sapiens OX=9606 GN=CREG1 PE=1 SV=1	CREG1	1038.3751	HexNAc(2)Hex(3)Fuc(1)	1.194796864	0.805203136	0.836962358		
O75629	160	N	Protein CREG1 OS=Homo sapiens OX=9606 GN=CREG1 PE=1 SV=1	CREG1	1216.4228	HexNAc(2)Hex(5)	1.194796864	0.805203136	0.803356878	1.291787966	1.608
O75629	160	N	Protein CREG1 OS=Homo sapiens OX=9606 GN=CREG1 PE=1 SV=1	CREG1	1378.4757	HexNAc(2)Hex(6)	1.194796864	0.805203136	0.836962358		
O75629	160	N	Protein CREG1 OS=Homo sapiens OX=9606 GN=CREG1 PE=1 SV=1	CREG1	1458.442	HexNAc(2)Hex(6)Phospho(1)	1.194796864	0.805203136	0.67102718	1.488144762	2.218
O75629	160	N	Protein CREG1 OS=Homo sapiens OX=9606 GN=CREG1 PE=1 SV=1	CREG1	1540.5285	HexNAc(2)Hex(7)	1.194796864	0.805203136	0.836962358		
O75718	87	N	Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1	CRTAP	1540.5285	HexNAc(2)Hex(7)	1.137895336	0.862104664			
O75718	87	N	Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1	CRTAP	1702.5813	HexNAc(2)Hex(8)	1.137895336	0.862104664	0.959097275	1.053987668	1.099
O75718	87	N	Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1	CRTAP	2028.7403	HexNAc(6)Hex(5)	1.137895336	0.862104664	0.878815448		

O75718	363	N	Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1	CRTAP	1378.4757	HexNAc(2)Hex(6)	1.137895336	0.862104664			
O75718	363	N	Cartilage-associated protein OS=Homo sapiens OX=9606 GN=CRTAP PE=1 SV=1	CRTAP	1702.5813	HexNAc(2)Hex(8)	1.137895336	0.862104664			
O75976	522	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1864.6341	HexNAc(2)Hex(9)	1.0373407	0.9626593	0.964003436		
O75976	811	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1216.4228	HexNAc(2)Hex(5)	1.0373407	0.9626593	0.75123231	1.268066646	1.688
O75976	811	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1403.5073	HexNAc(3)Hex(4)Fuc(1)	1.0373407	0.9626593	0.964003436		
O75976	811	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1727.6129	HexNAc(3)Hex(6)Fuc(1)	1.0373407	0.9626593	0.955969184	1.047446649	1.096
O75976	811	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1768.6395	HexNAc(4)Hex(5)Fuc(1)	1.0373407	0.9626593	0.572792597	1.460349395	2.55
O75976	811	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1864.6341	HexNAc(2)Hex(9)	1.0373407	0.9626593	1.077751485	0.916216693	0.85
O75976	955	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1216.4228	HexNAc(2)Hex(5)	1.0373407	0.9626593	0.835059186	1.17773663	1.41
O75976	955	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1378.4757	HexNAc(2)Hex(6)	1.0373407	0.9626593	0.964003436		
O75976	955	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1864.6341	HexNAc(2)Hex(9)	1.0373407	0.9626593	0.964003436		
O75976	978	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	2117.7768	HexNAc(5)Hex(5)Fuc(2)	1.0373407	0.9626593	0.964003436		
O75976	978	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	2263.8347	HexNAc(5)Hex(5)Fuc(3)	1.0373407	0.9626593	0.964003436		
O75976	978	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	2466.914	HexNAc(6)Hex(5)Fuc(3)	1.0373407	0.9626593			

O75976	978	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	2612.972	HexNAc(6)Hex(5)Fuc(4)	1.0373407	0.9626593			
O75976	1070	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1864.6341	HexNAc(2)Hex(9)	1.0373407	0.9626593	0.937244412	1.067624055	1.139
O75976	1070	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	1873.6708	HexNAc(3)Hex(6)Fuc(2)	1.0373407	0.9626593	0.964003436		
O75976	1070	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	2263.8347	HexNAc(5)Hex(5)Fuc(3)	1.0373407	0.9626593	0.964003436		
O75976	1070	N	Carboxypeptidase D OS=Homo sapiens OX=9606 GN=CPD PE=1 SV=2	CPD	2466.914	HexNAc(6)Hex(5)Fuc(3)	1.0373407	0.9626593	0.964003436		
O94901	561	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1054.37	HexNAc(2)Hex(4)	1.563079611	0.436920389	0.639762679		
O94901	561	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1216.4228	HexNAc(2)Hex(5)	1.563079611	0.436920389	1.033758786	0.879228183	0.851
O94901	561	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1378.4757	HexNAc(2)Hex(6)	1.563079611	0.436920389	0.93934822	1.216981316	1.296
O94901	561	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1540.5285	HexNAc(2)Hex(7)	1.563079611	0.436920389	0.985817377	1.050738235	1.066
O94901	561	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1702.5813	HexNAc(2)Hex(8)	1.563079611	0.436920389	0.984785797	1.054428702	1.071
O94901	561	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1864.6341	HexNAc(2)Hex(9)	1.563079611	0.436920389	0.715696562	2.017093545	2.818
O94901	561	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	406.1587	HexNAc(2)	1.563079611	0.436920389	0.639762679		
O94901	561	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	730.2644	HexNAc(2)Hex(2)	1.563079611	0.436920389	0.639762679		
O94901	705	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1216.4228	HexNAc(2)Hex(5)	1.563079611	0.436920389	0.639762679		

O94901	705	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1378.4757	HexNAc(2)Hex(6)	1.563079611	0.436920389	0.948490867	1.184273559	1.249
O94901	705	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1540.5285	HexNAc(2)Hex(7)	1.563079611	0.436920389	0.967893835	1.114859578	1.152
O94901	705	N	SUN domain-containing protein 1 OS=Homo sapiens OX=9606 GN=SUN1 PE=1 SV=4	SUN1	1702.5813	HexNAc(2)Hex(8)	1.563079611	0.436920389	0.853098703	1.525538354	1.788
O94923	225	N	D-glucuronyl C5-epimerase OS=Homo sapiens OX=9606 GN=GLCE PE=1 SV=3	GLCE	1606.5867	HexNAc(4)Hex(4)Fuc(1)					
O94923	225	N	D-glucuronyl C5-epimerase OS=Homo sapiens OX=9606 GN=GLCE PE=1 SV=3	GLCE	1768.6395	HexNAc(4)Hex(5)Fuc(1)					
O95158	72	N	Neurexophilin-4 OS=Homo sapiens OX=9606 GN=NXPH4 PE=2 SV=3	NXPH4	1702.5813	HexNAc(2)Hex(8)					
O95297	50	N	Myelin protein zero-like protein 1 OS=Homo sapiens OX=9606 GN=MPZL1 PE=1 SV=1	MPZL1	2482.909	HexNAc(6)Hex(6)Fuc(2)	1.251665534	0.748334466	0.798935477		
O95302	174	N	Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens OX=9606 GN=FKBP9 PE=1 SV=2	FKBP9	1378.4757	HexNAc(2)Hex(6)	1.309258306	0.690741694	0.945522757	1.103258256	1.167
O95302	174	N	Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens OX=9606 GN=FKBP9 PE=1 SV=2	FKBP9	1540.5285	HexNAc(2)Hex(7)	1.309258306	0.690741694	0.992541668	1.014136809	1.022
O95302	174	N	Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens OX=9606 GN=FKBP9 PE=1 SV=2	FKBP9	1702.5813	HexNAc(2)Hex(8)	1.309258306	0.690741694	0.911263099	1.168195327	1.282
O95302	174	N	Peptidyl-prolyl cis-trans isomerase FKBP9 OS=Homo sapiens OX=9606 GN=FKBP9 PE=1 SV=2	FKBP9	1864.6341	HexNAc(2)Hex(9)	1.309258306	0.690741694	0.752753844	1.468639849	1.951