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Supplementary Information Appendix

UDP-glucose pyrophosphorylase 2, a regulator of glycogen synthesis and glycosylation, is critical for pancreatic cancer growth

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This file includes Supplementary Figures S1-S5, Table S1, and legends.

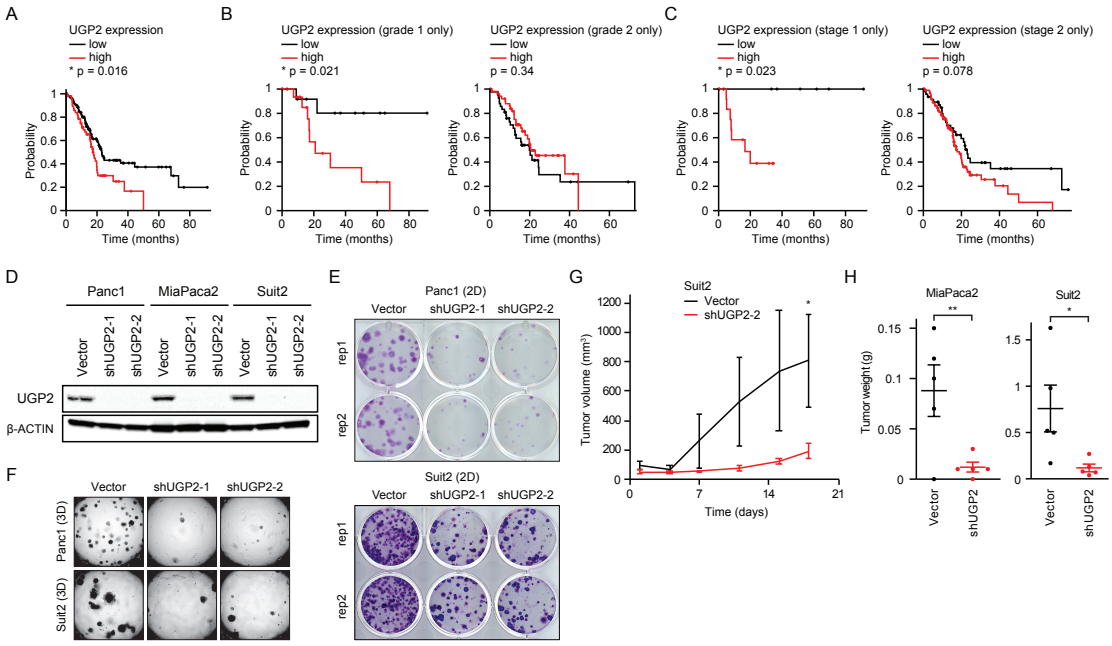

Figure S1. A-C, Cumulative probability of survival of 177 patients with pancreatic ductal adenocarcinoma based on expression level of UGP2 for all patients (A), grade 1 (B, left), grade 2 (B, right), stage 1 (C, left), and stage 2 (C, right). Data adapted from cBioPortal and KM Plotter (12). **D**, Immunoblots for shRNAs knocking down UGP2 in Panc1, MiaPaca2, and Suit2 cells, probed as indicated. **E**, Representative crystal violet staining of Panc1 and Suit2 cells with two independent shRNAs against UGP2 or empty vector control grown in two-dimensional culture for 10 days. **F**, Representative images of Panc1 and Suit2 cells stably expressing shUGP2 or empty vector control grown in three-dimensional matrigel for 14 days. **G,** Tumor volumes of Suit2 cells with a second shRNA against UGP2 or empty vector control xenografted on opposite flanks of nude mice, n = 5, * $p < 0.05$. Error bars represent SEM. **H**, Tumor weights at endpoint of MiaPaca2 and Suit2 cells with shUGP2 or empty vector control xenografted on opposite flanks of nude mice, n = 4, * $p < 0.05$, ** $p < 0.01$.

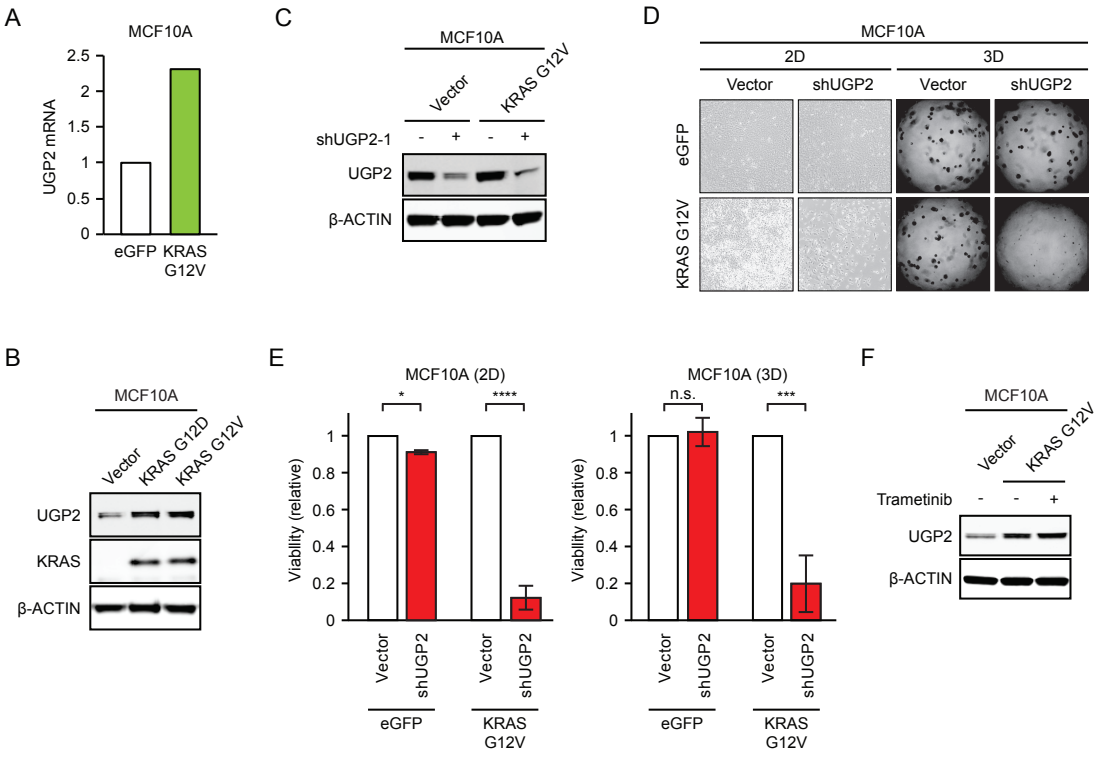

Figure S2. A, mRNA expression of UGP2 from RNAseq on MCF10A cells stably expressing KRAS G12V or empty vector. **B**, Immunoblot of lysates from MCF10A cells stably expressing KRAS G12D, KRAS G12V, or empty vector. **C**, Immunoblot of lysates from MCF10A cells expressing KRAS G12V or empty vector with or without knockdown of UGP2. **D-E**, Representative images (D) and relative viability (E) of MCF10A cells expressing KRAS G12V or empty vector with or without UGP2 knockdown grown in 2D or 3D matrigel for 14 days, n = 3. Error bars represent SEM, n = 3. * $p < 0.05$, *** $p < 0.001$, **** $p < 0.0001$. **F**, Immunoblot of lysates from MCF10A cells stably expressing KRAS G12V or empty vector treated with 100 nM trametinib for 48 hours, probed as indicated.

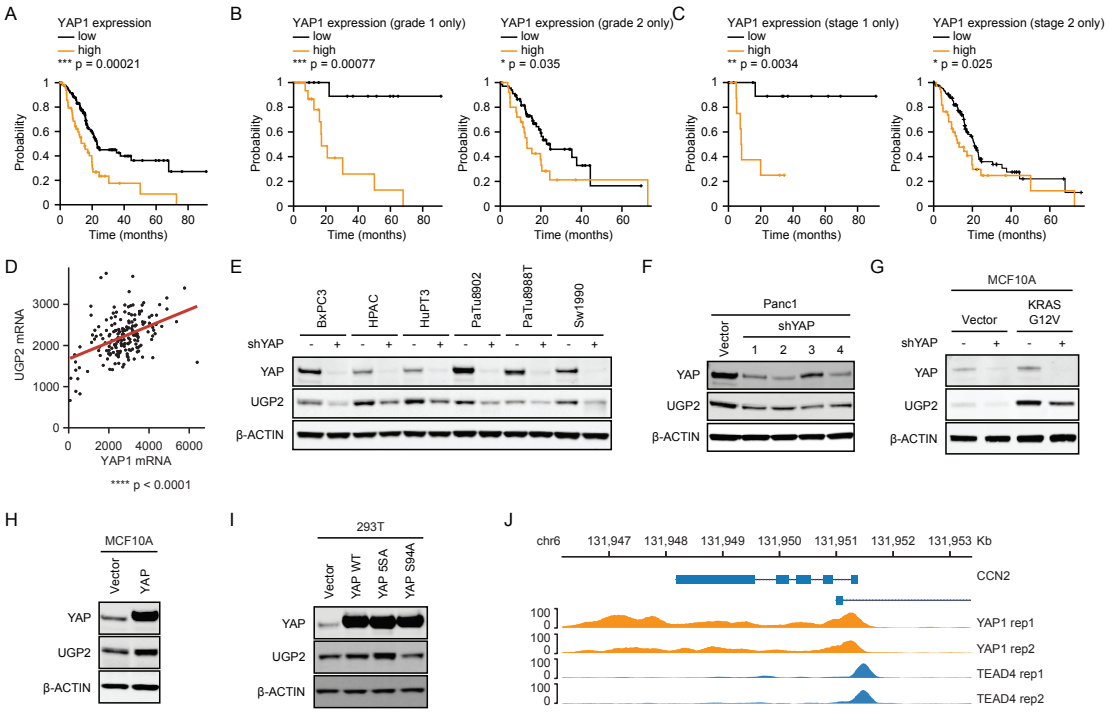

Figure S3. A-C, Cumulative probability of survival of 177 patients with pancreatic ductal adenocarcinoma based on expression level of YAP1 for all patients (A), grade 1 (B, left), grade 2 (B, right), stage 1 (C, left), and stage 2 (C, right). Data adapted from cBioPortal and KM Plotter (12). **D**, Correlation between UGP2 and YAP1 mRNA level in PDAC patient samples. Analysis performed using cBioPortal, n = 178, R^2 = 0.18, Pearson = 0.43, p = 3*10-9. **E**, Immunoblots on a panel of PDAC cell lines cells with shRNAs against YAP or vector control, probed as indicated. **F**, Immunoblots of Panc1 with four different YAP shRNAs, probed as indicated. **G**, Immunoblots of MCF10A stably expressing KRAS G12V or control vector with knockdown of YAP, probed as indicated. **H-I**, Immunoblots on lysates from MCF10A (H) and 293T (I) cells stably expressing wild-type YAP, YAP 5SA, YAP S94A, or empty vector, probed as indicated. **J**, ChIP-seq for the control YAP1/TEAD4 binding site in the CCN2 genomic region.

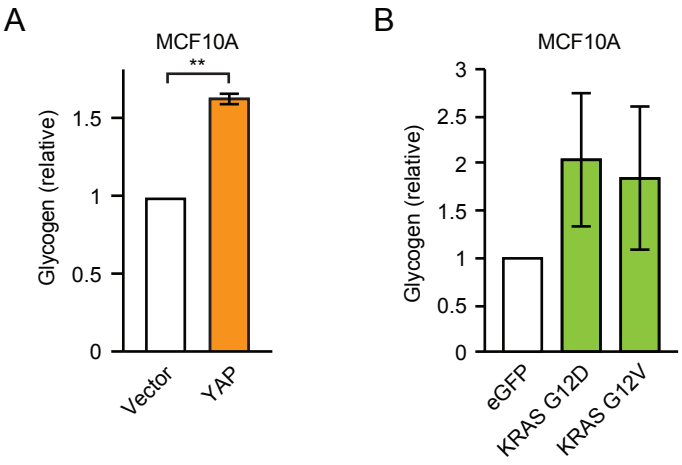

Figure S4. A, Relative glycogen levels in MCF10A cells expressing YAP or empty vector control, ** $p < 0.01$. **B**, Relative glycogen levels in MCF10A cells expressing KRAS G12D or G12V or empty vector control.

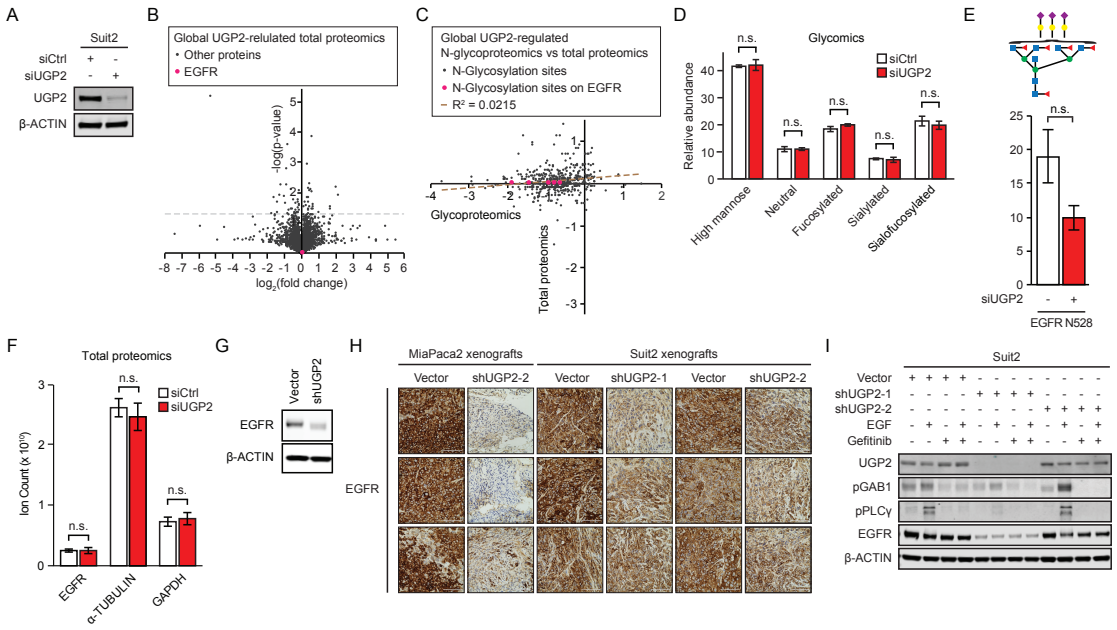

Figure S5. A, Immunoblots on lysates of Suit2 cells transfected with siUGP2 or non-targeting control siRNAs for 48 hours, probed as indicated. **B**, Global total proteomic analysis in Suit2 cells upon knockdown of UGP2 relative to non-targeting control siRNAs after 48 hours, red dots represent total EGFR. **C**, Shown are $\log_2$ of the fold change in specific modifications plotted against $\log_2$ of the fold change in total protein upon knockdown of UGP2 in Suit2 cells. $R^2 = 0.0215$, red dots represent EGFR modifications. **D**, Global glycomic comparison in Suit2 cells with siUGP2 of non-targeting control siRNAs at 48 hours, n.s. not significant at a threshold of $p < 0.05$. **E**, Quantification of glycan modifications on EGFR N528 in Suit2 cells with siUGP2 or non-targeting control siRNAs at 48 hours. n.s. not significant at a threshold of $p < 0.05$, blue squares represent N-acetylglucosamines, green circles represent mannoses, yellow circles represent galactoses, red triangles represent fucoses, and purple diamonds represent N-acetylneuraminic acid. **F**, Quantification of total EGFR, α-TUBULIN, and GAPDH proteins by mass spectrometry in Suit2 cells upon knockdown of UGP2 or non-targeting control siRNAs. n.s. not significant at a threshold of $p < 0.05$. **G**, Immunoblot of lysates from Panc1 cells stably expressing shUGP2 or empty vector, probed as indicated. **H**, Representative immunohistochemical staining of EGFR in three opposite-flank pairs of MiaPaca2 and Suit2 tumors with shUGP2-1, shUGP2-2, or vector control at endpoint. Scale bars represent 100 μm. **I**, Immunoblot of Suit2 cells stably expressing shUGP2-1, shUGP2-2, or empty vector, pretreated with 10 μM gefitinib for 1 hour and/or stimulated with 100 ng/mL EGF for 10 minutes, probed as indicated.

Table S1. N-glycoproteomics and total proteomics. A-B, Changes in N-glycan modifications (A) and total protein (B) in Suit2 cells treated with siUGP2 or siCtrl pools for 48 hours, n = 3.

Table S1. N-glycoproteomics and total proteomics. A-B, Changes in N-glycan modifications (A) and total protein (B) in Suit2 cells treated with siUGP2 or siCtrl pools for 48 hours, n = 3.

Protein symbol	Protein\nname	Sequence	Glycans	N-Glycosylation Site	siCtrl repA	siCtrl repB	siCtrl repC	siUGP2 repA	siUGP2 repB	siUGP2 repC	siCtrl AVG	siUGP2 AVG	siCtrl STD	siUGP2 STD	Fold change
COPE	sp|O14579|COPE_HUMAN Coatomer subunit epsilon OS=Homo sapiens GN=COPE PE=1 SV=3	RSVDVTnTTFLLMAASIYLHDQNPDAALRA	HexNAc(2)Hex(7)	116	90900	354000	240000	25100	15100	11800	228300	17333.33	131939.6	6925.557	0.075923
CDCP1	sp|Q9H5V8|CDCP1_HUMAN CUB domain-containing protein 1 OS=Homo sapiens GN=CDCP1 PE=1 SV=3	RTCSSnLTLTSGSKH	HexNAc(4)Hex(5)Fuc(1)	386	494000	593000	566000	21900	16000	178000	551000	71966.67	51176.17	91874.93	0.130611
TAGL2	sp|P37802|TAGL2_HUMAN Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	RnFSDNQLQEGKN	HexNAc(6)Hex(7)Fuc(3)	161	2040000	2030000	678000	39700	158000	428000	1582667	208566.7	783480.3	199027.5	0.131782
MPRD	sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	REAGnHTSGAGLVQINKS	HexNAc(4)Hex(5)Fuc(3)	83	845000	627000	50600	168000	8110	28700	507533.3	68270	410453.5	86980.12	0.134513
FLNA	sp|P21333|FLNA_HUMAN Filamin-A OS=Homo sapiens GN=FLNA PE=1 SV=4	KASGPGLnTTGVPASLPVEFTIDAKD	HexNAc(2)Hex(3)	1556	22600	770000	1170000	283000	44000	1710	654200	109570	582399.3	151675.9	0.167487
HYOU1	sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	RVFGSQnLTTVKL	HexNAc(2)Hex(9)	515	440000	303000	391000	1910	189000	8140	378000	66350	69419.02	106263.7	0.175529
MRP1	sp|P33527|MRP1_HUMAN Multidrug resistance-associated protein 1 OS=Homo sapiens GN=ABCC1 PE=1 SV=3	RnATFTWARS	HexNAc(4)Hex(6)Fuc(2)Ne	648	835000	1440000	1460000	98300	10700	604000	1245000	237666.7	355211.2	320263.2	0.190897
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KGEYFVnVTTRI	HexNAc(3)Hex(6)	1074	3440000	1930000	1580000	242000	48200	1040000	2316667	443400	988450	525678.9	0.191396
CD63	sp|P08962|CD63_HUMAN CD63 antigen OS=Homo sapiens GN=CD63 PE=1 SV=2	KCCGAAnYTDWEKI	HexNAc(7)Hex(6)Fuc(3)	150	2670000	582000	1150000	195000	79700	617000	1467333	297233.3	1079565	282863.2	0.202567
MPRD	sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	RLKPLFnKS	HexNAc(2)Hex(5)	57	1230000	1780000	958000	91800	207000	534000	1322667	277600	418761.7	229398.1	0.209879
DJC11	sp|Q9NVH1|DJC11_HUMAN DnaJ homolog subfamily C member 11 OS=Homo sapiens GN=DNAJC11 PE=1 SV=2	RnLTPRC	HexNAc(3)Hex(4)Fuc(2)	230	296000	1340000	1040000	327000	33500	266000	892000	208833.3	537505.3	154876	0.234118
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RAHCVWLECPIPDAPVVTnVTVKA	HexNAc(5)Hex(6)	926	826000	918000	1540000	118000	169000	483000	1094667	256666.7	388403.6	197662.2	0.23447
CERS2	sp|Q96G23|CERS2_HUMAN Ceramide synthase 2 OS=Homo sapiens GN=CERS2 PE=1 SV=1	RLWLPVnLTWADLEDRDGRV	HexNAc(2)Hex(8)	19	415000	352000	695000	80600	180000	86700	487333.3	115766.7	182582.4	55711.25	0.237551
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RKLLLSInVTNTRT	HexNAc(2)Hex(6)	656	2310000	1780000	937000	4020	660000	538000	1675667	400673.3	692420.6	348885.9	0.239113
ASPH	sp|Q12797|ASPH_HUMAN Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	RCAnETKTWEEGKV	HexNAc(2)Hex(8)	706	458000	349000	341000	131000	114000	34800	382666.7	93266.67	65363.09	51342.12	0.243728
COPB	sp|P53618|COPB_HUMAN Coatomer subunit beta OS=Homo sapiens GN=COPB1 PE=1 SV=3	KALSGYCGFMAANLYARSIFGEDALAnVSIEKP	HexNAc(2)Hex(3)Fuc(1)	908	1210000	286000	902000	293000	198000	102000	799333.3	197666.7	470477.8	95500.44	0.247289
ZC3HF	sp|Q8WU90|ZC3HF_HUMAN Zinc finger CCCH domain-containing protein 15 OS=Homo sapiens GN=ZC3H15 PE=1 SV=1	RSALGPnVTKITLESFLAWKKR	HexNAc(7)Hex(7)Fuc(4)	246	7460000	6460000	4430000	1360000	1380000	1930000	6116667	1556667	1543902	323470.8	0.254496
DNJA3	sp|Q96EY1|DNJA3_HUMAN DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens GN=DNAJA3 PE=1 SV=2	RnASQKE	HexNAc(4)Hex(5)Fuc(3)	103	187000	429000	397000	168000	77500	19700	337666.7	88400	131458.5	74748.44	0.261797
NPTN	sp|Q9Y639|NPTN_HUMAN Neuroplastin OS=Homo sapiens GN=NPTN PE=1 SV=2	KAnATIEVKA	HexNAc(2)Hex(8)	229	538000	610000	198000	90700	193000	78800	448666.7	120833.3	220048.5	62780.76	0.269316
EGFR	sp|P00533|EGFR_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2	KnCTSISGDLHILPVAFRG	HexNAc(2)Hex(8)	361	804000	847000	1230000	73500	70600	634000	960333.3	259366.7	234525.8	324445.2	0.27008
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	KQLSCVANQnGSQADCELGNPFKRN	HexNAc(4)Hex(5)	770	2530000	1210000	982000	181000	415000	713000	1574000	436333.3	835732	266640.8	0.277213
EXOC1	sp|Q9NV70|EXOC1_HUMAN Exocyst complex component 1 OS=Homo sapiens GN=EXOC1 PE=1 SV=4	RGVFVNVEKVAnESQKT	HexNAc(3)Hex(4)Fuc(2)	718	1010000	703000	481000	279000	210000	121000	731333.3	203333.3	265635.7	79210.69	0.278031
FKBP8	sp|Q14318|FKBP8_HUMAN Peptidyl-prolyl cis-trans isomerase FKBP8 OS=Homo sapiens GN=FKBP8 PE=1 SV=2	KLEPSnKT	HexNAc(3)Hex(3)	339	731000	686000	670000	247000	132000	242000	695666.7	207000	31628.05	65000	0.297556
BASI	sp|P35613|BASI_HUMAN Basigin OS=Homo sapiens GN=BSG PE=1 SV=2	KSESVPPVTDWAWYKITDSEDKALMnGSESRF	HexNAc(7)Hex(4)NeuAc(1)	268	137000	80600	38700	15600	59100	2030	85433.33	25576.67	49327.92	29814.37	0.299376
SMRC2	sp|Q8TAQ2|SMRC2_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1	KDEDEnSTGNKG	HexNAc(6)Hex(5)Fuc(4)Ne	398	4780000	3010000	2980000	1390000	720000	1140000	3590000	1083333	1030679	338575.4	0.301764
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RTASCSnVTCWLKD	HexNAc(4)Hex(5)Fuc(2)	1057	1480000	470000	1590000	115000	62800	894000	1180000	357266.7	617333	465556.9	0.302768
EXOC6	sp|Q8TAG9|EXOC6_HUMAN Exocyst complex component 6 OS=Homo sapiens GN=EXOC6 PE=1 SV=3	RnETVLKH	HexNAc(6)Hex(5)Fuc(4)Ne	256	2570000	2120000	1630000	1210000	351000	361000	2106667	640666.7	470141.8	493082.5	0.304114
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KenSSEICSNNGECVCGQCVCRK	HexNAc(6)Hex(3)Fuc(1)	520	1070000	1120000	1150000	72400	157000	803000	1113333	344133.3	40414.52	399635.2	0.309102
MDN1	sp|Q9NU22|MDN1_HUMAN Midasin OS=Homo sapiens GN=MDN1 PE=1 SV=2	KKQnFTFLGHIQTCYRQKR	HexNAc(2)Hex(7)	745	412000	855000	662000	148000	266000	190000	643000	201333.3	222110.3	59810.81	0.313116
AMPN	sp|P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	KAEFnITLIHPKD	HexNAc(4)Hex(5)NeuAc(1)	234	791000	842000	283000	10800	191000	399000	638666.7	200266.7	309070.1	194265.8	0.31357
EXOC4	sp|Q96A65|EXOC4_HUMAN Exocyst complex component 4 OS=Homo sapiens GN=EXOC4 PE=1 SV=1	RnITVIFHPLLRF	HexNAc(5)Hex(6)Fuc(1)Ne	495	711000	573000	1570000	624000	110000	164000	951333.3	299333.3	540205.8	282463	0.314646
ARHGC	sp|Q9NZN5|ARHGC_HUMAN Rho guanine nucleotide exchange factor 12 OS=Homo sapiens GN=ARHGEF12 PE=1 SV=1	KeQERLQLLQEDYnRTPAQRL	HexNAc(3)Hex(3)	228	1640000	1080000	1270000	504000	137000	632000	1330000	424333.3	284780.6	256936.4	0.319048
RTN4	sp|Q9NQC3|RTN4_HUMAN Reticulon-4 OS=Homo sapiens GN=RTN4 PE=1 SV=2	KnTSTKT	HexNAc(6)Hex(6)Fuc(3)Ne	509	3070000	499000	524000	241000	587000	502000	1364333	443333.3	1477204	180306.2	0.324945
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RSLDAYPILNQAQALEnHTEVQFQKE	HexNAc(3)Hex(3)	605	1440000	2500000	1280000	1020000	65700	611000	1740000	565566.7	663023.4	478769.5	0.325038
TM87A	sp|Q8NBN3|TM87A_HUMAN Transmembrane protein 87A OS=Homo sapiens GN=TMEM87A PE=1 SV=3	RnTTIFLKF	HexNAc(6)Hex(3)Fuc(3)	62	7230000	6380000	2070000	239	3650000	1500000	5226667	1716746	2766592	1834509	0.328459
ITB4	sp|P16144|ITB4_HUMAN Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=5	RDEDDDCTYSYTMEGDGAPGPnSTVLVHKK	HexNAc(4)Hex(4)	695	917000	515000	122000	70100	252000	200000	518000	174033.3	397508.5	93688.86	0.335972
ABHDA	sp|Q9NUJ1|ABHDA_HUMAN Mycophenolic acid acyl-glucuronide esterase, mitochondrial OS=Homo sapiens GN=ABHD10 PE=1 SV=1	KSPGIIFIPGYLSYMnGTKALAIEEFCKS	HexNAc(3)Hex(3)Fuc(1)	89	1280000	428000	652000	491000	130000	175000	786666.7	265333.3	441675.6	196724	0.337288
AMPN	sp|P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	KKLnYTLSQGHRV	HexNAc(2)Hex(6)	128	289000	254000	312000	50700	83600	159000	285000	97766.67	29206.16	55522.46	0.343041
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RYFFnVSDEAALLEKA	HexNAc(4)Hex(5)	343	3020000	2830000	2290000	1310000	634000	870000	2713333	938000	378725.9	343091.8	0.3457
RL4	sp|P36578|RL4_HUMAN 60S ribosomal protein L4 OS=Homo sapiens GN=RPL4 PE=1 SV=5	KnVTLPAVFKA	HexNAc(4)Hex(6)NeuAc(1)	21	1820000	826000	396000	86700	248000	721000	1014000	351900	730378	329667.3	0.347041
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KNKnVTNRS	HexNAc(2)Hex(9)	94	125000	422000	203000	63700	48100	150000	250000	87266.67	153977.3	54885.73	0.349067
PO210	sp|Q8TEM1|PO210_HUMAN Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3	RIREGSGYFFLnTSTADVVKV	HexNAc(2)Hex(6)	926	1140000	1700000	1390000	54400	568000	863000	1410000	495133.3	280535.2	409195.1	0.351158
VDAC1	sp|P21796|VDAC1_HUMAN Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	KVNnSSLIGLGYTQTLKPGIKL	HexNAc(7)Hex(6)Fuc(2)Ne	239	799000	1040000	406000	397000	130000	262000	748333.3	263000	320022.4	133502.8	0.351448
ALG2	sp|Q9H553|ALG2_HUMAN Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Homo sapiens GN=ALG2 PE=1 SV=1	KnLTLALEALVQLRG	HexNAc(4)Hex(5)Fuc(3)	239	269000	779000	335000	96600	57300	333000	461000	162300	277366.2	149130.8	0.352061
MRP4	sp|O15439|MRP4_HUMAN Multidrug resistance-associated protein 4 OS=Homo sapiens GN=ABCC4 PE=1 SV=3	RSLLVFYVLVnSSQTLHNKM	HexNAc(6)Hex(4)	792	11400000	9630000	8110000	5440000	1470000	3420000	9713333	3443333	1646582	1985103	0.354496
KIRR1	sp|Q96J84|KIRR1_HUMAN Kin of IRRE-like protein 1 OS=Homo sapiens GN=KIRREL PE=1 SV=2	RAVLPCVLLnYSGIVQWTKDGLALGMGQGLKA	HexNAc(6)Hex(3)Fuc(1)	46	5010000	4670000	5200000	2360000	1300000	1630000	4960000	1763333	268514.4	542432.8	0.355511
MPPB	sp|O75439|MPPB_HUMAN Mitochondrial-processing peptidase subunit beta OS=Homo sapiens GN=PMPCB PE=1 SV=2	KYIYnRS	HexNAc(4)Hex(3)	460	998000	635000	779000	379000	60300	428000	804000	289100	182786.8	199655.5	0.359577
IF2G	sp|P41091|IF2G_HUMAN Eukaryotic translation initiation factor 2 subunit 3 OS=Homo sapiens GN=EIF2S3 PE=1 SV=3	RnITIKL	HexNAc(2)Hex(4)Fuc(1)	76	2300000	2800000	1900000	917000	750000	853000	2333333	840000	450925	84255.56	0.36
AT1B3	sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	KFLKPYTLEEQKnLTVCPDGALFEQKG	HexNAc(2)Hex(5)Fuc(1)	124	2640000	2210000	1160000	969000	620000	582000	2003333	723666.7	761336.5	213312.8	0.361231
SMHD1	sp|A6NHR9|SMHD1_HUMAN Structural maintenance of chromosomes flexible hinge domain-containing protein 1 OS=Homo sapiens GN=SMC	KAIYnKS	HexNAc(5)Hex(7)Fuc(1)Ne	1348	2280000	862000	1290000	593000	78000	931000	1477333	534000	727324.8	429549.8	0.361462
AT1B3	sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	KFLKPYTLEEQKnLTVCPDGALFEQKG	HexNAc(4)Hex(5)Fuc(1)Ne	124	2810000	2210000	1350000	1020000	463000	832000	2123333	771666.7	733848.3	283359	0.363422
EGFR	sp|P00533|EGFR_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2	KHFKnCTSISGDLHILPVAFRG	HexNAc(2)Hex(7)	361	2470000	3500000	2000000	720000	1530000	663000	2656667	971000	767224.4	484946.4	0.365496
ERP29	sp|P30040|ERP29_HUMAN Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	KQGQDnLSSVKE	HexNAc(4)Hex(3)Fuc(2)	187	653000	170000	531000	410000	6110	79900	451333.3	165336.7	251162	215072.9	0.366329
DESP	sp|P15924|DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	KnATILELRS	HexNAc(6)Hex(5)Fuc(3)	1746	1940000	1200000	2710000	649000	435000	1060000	1950000	714666.7	755049.7	317632.4	0.366496
IMA5	sp|P52294|IMA5_HUMAN Importin subunit alpha-5 OS=Homo sapiens GN=KPNA1 PE=1 SV=3	RKEAAWAITnATSGGSAEQIKY	HexNAc(4)Hex(4)	406	2090000	834000	1150000	260000	753000	491000	1358000	501333.3	653323.8	246662.4	0.36917
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RLnGTKD	HexNAc(2)Hex(8)	409	425000	545000	304000	149000	167000	156000	424666.7	157333.3	120500.3	9073.772	0.370487
TBL2	sp|Q9Y4P3|TBL2_HUMAN Transducin beta-like protein 2 OS=Homo sapiens GN=TBL2 PE=1 SV=1	KEKPQQHnFTHRLLAAALKS	HexNAc(5)Hex(4)Fuc(3)	76	2400000	1970000	2280000	1140000	361000	981000	2216667	827333.3	221885.9	411607	0.373233
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(4)Hex(5)Fuc(1)Ne	212	3150000	2040000	2340000	865000	1440000	514000	2510000	939666.7	574195.1	467493.7	0.374369
ALG2	sp|Q9H553|ALG2_HUMAN Alpha-1,3/1,6-mannosyltransferase ALG2 OS=Homo sapiens GN=ALG2 PE=1 SV=1	KETFKSLSHIDPDVLYPSLnVTSFDSVVPEKL	HexNAc(3)Hex(4)Fuc(2)	204	3590000	1920000	1220000	347000	1340000	870000	2243333	852333.3	1217634	496735.7	0.379941
TFR1	sp|P02786|TFR1_HUMAN Transferrin receptor protein 1 OS=Homo sapiens GN=TFRC PE=1 SV=2	RKQNNGAFnETLFRN	HexNAc(2)Hex(8)	727	1520000	3700000	1870000	1060000	606000	1050000	2363333	905333.3	1170741	259278.5	0.383075
CLP1L	sp|Q96KA5|CLP1L_HUMAN Cleft lip and palate transmembrane protein 1-like protein OS=Homo sapiens GN=CLPTM1L PE=1 SV=1	RTVnVSVPKK	HexNAc(2)Hex(6)	91	706000	285000	358000	193000	58000	271000	449666.7	174000	224971.9	107763.6	0.386953
TF3C1	sp|Q12789|TF3C1_HUMAN General transcription factor 3C polypeptide 1 OS=Homo sapiens GN=GTF3C1 PE=1 SV=4	KnITNDIRT	HexNAc(7)Hex(6)Fuc(5)Ne	122	2670000	2430000	1370000	764000	563000	1180000	2156667	835666.7	691761	314681.3	0.387481
DYN2	sp|P50570|DYN2_HUMAN Dynamin-2 OS=Homo sapiens GN=DNM2 PE=1 SV=2	KGISPVPINLRVYSPHVLnLTLIDLPGITKV	HexNAc(3)Hex(5)Fuc(2)	131	2360000	2030000	991000	288000	1050000	754000	1793667	697333.3	714444.1	384147.5	0.388775
PLRG1	sp|O43660|PLRG1_HUMAN Pleiotropic regulator 1 OS=Homo sapiens GN=PLRG1 PE=1 SV=1	KADAnRT	HexNAc(7)Hex(7)	139	754000	791000	969000	415000	165000	400000	838000	326666.7	114947.8	140208.2	0.389817
INT1	sp|Q8N201|INT1_HUMAN Integrator complex subunit 1 OS=Homo sapiens GN=INTS1 PE=1 SV=2	RPSAAAKPSGHPPPGDFIALGSKGQAnESKT	HexNAc(3)Hex(3)Fuc(2)	37	4250000	3540000	1710000	745000	1280000	1680000	3166667	1235000	1310509	469121.5	0.39
DNJA3	sp|Q96EY1|DNJA3_HUMAN DnaJ homolog subfamily A member 3, mitochondrial OS=Homo sapiens GN=DNAJA3 PE=1 SV=2	RnASQKE	HexNAc(4)Hex(6)Fuc(2)	103	396000	304000	83200	67300	14400	224000	261066.7	101900	160758.9	108999.6	0.390322
APLP2	sp|Q06481|APLP2_HUMAN Amyloid-like protein 2 OS=Homo sapiens GN=APLP2 PE=1 SV=2	RRnQSLSLLYKV	HexNAc(2)Hex(8)	541	2030000	1760000	1890000	1300000	450000	480000	1893333	743333.3	135030.9	482320.8	0.392606
ITAV	sp|P06756|ITAV_HUMAN Integrin alpha-V OS=Homo sapiens GN=ITGAV PE=1 SV=2	KSLLWTETFMNKENQnHSYSLKS	HexNAc(5)Hex(4)	945	17500000	11800000	11900000	7020000	3550000	5620000	13733333	5396667	3262412	1745747	0.392961
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KTnMSLGLILTRN	HexNAc(2)Hex(9)	112	15600000	14100000	13200000	5350000	5280000	6250000	14300000	5626667	1212436	540955.9	0.393473
APMAP	sp|Q9HDC9|APMAP_HUMAN Adipocyte plasma membrane-associated protein OS=Homo sapiens GN=APMAP PE=1 SV=2	RAGPnGTLFVADAYKG	HexNAc(2)Hex(6)	160	3320000	4370000	4230000	1690000	1250000	1770000	3973333	1570000	570116.9	280000	0.395134
CIR1A	sp|Q969X6|CIR1A_HUMAN Cirhin OS=Homo sapiens GN=CIRH1A PE=1 SV=1	RLAVSRTDGTVEIYnLSANYFQEKF	HexNAc(2)Hex(7)Fuc(1)	44	1390000	97600	296000	123000	339000	243000	594533.3	235000	696000	108222	0.395268
PDCD6	sp|O75340|PDCD6_HUMAN Programmed cell death protein 6 OS=Homo sapiens GN=PDCD6 PE=1 SV=1	RENKAGVnFSEFTGVWKY	HexNAc(2)Hex(4)	81	2960000	2680000	3920000	1610000	1050000	1120000	3186667	1260000	650333.2	305122.9	0.395397
SPS2L	sp|Q9NUQ6|SPS2L_HUMAN SPATS2-like protein OS=Homo sapiens GN=SPATS2L PE=1 SV=2	KAQIMLCGEITHPKNnYSSRT	HexNAc(7)Hex(4)	360	6750000	3690000	5200000	3530000	487000	2180000	5213333	2065667	1530044	1524718	0.396228
SUN2	sp|Q9UH99|SUN2_HUMAN SUN domain-containing protein 2 OS=Homo sapiens GN=SUN2 PE=1 SV=3	KALSPnSTISSAPKD	HexNAc(2)Hex(6)	636	2940000	2790000	2840000	1110000	1010000	1280000	2856667	1133333	76376.26	136504	0.396733
MRP3	sp|O15438|MRP3_HUMAN Canalicular multispecific organic anion transporter 2 OS=Homo sapiens GN=ABCC3 PE=1 SV=3	KGSVAYVPQQAWIQnCTLQENVLFGKA	HexNAc(2)Hex(3)	702	1560000	934000	450000	167000	230000	781000	981333.3	392666.7	556511.8	337778.5	0.400136
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RYFFnVSDEAALLEKA	HexNAc(5)Hex(5)	343	2060000	2040000	1370000	841000	531000	820000	1823333	730666.7	392725.5	173234.9	0.400731
GT251	sp|Q8NBJ5|GT251_HUMAN Procollagen galactosyltransferase 1 OS=Homo sapiens GN=COLGALT1 PE=1 SV=1	RTALWVATDHNMDnTSTVLREWLVAVKSLYHSVEWRP	HexNAc(4)Hex(4)Fuc(1)	96	5120000	5850000	5450000	3650000	2020000	1010000	5473333	2226667	365558.9	1332079	0.406821
ADA10	sp|O14672|ADA10_HUMAN Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1	RInTTADEKDPTNPFRFPNIGVEKF	HexNAc(6)Hex(4)	278	667000	257000	513000	111000	171000	304000	479000	195333.3	207103.8	98774.15	0.407794
SPB5	sp|P36952|SPB5_HUMAN Serpin B5 OS=Homo sapiens GN=SERPINB5 PE=1 SV=2	KSLnLSTEFISSTKRP	HexNAc(4)Hex(3)Fuc(2)	99	5190000	3550000	3660000	2480000	1390000	1190000	4133333	1686667	916751.5	694286.2	0.408065
NDUS2	sp|O75306|NDUS2_HUMAN NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial OS=Homo sapiens GN=NDUFS2 PE=1 SV	RPGGVHQDLPLGLMDDIYQFSKnFSLRL	HexNAc(3)Hex(4)	250	806000	699000	1080000	964000	6260	88400	861666.7	352886.7	196505.3	530830.8	0.40954
MYOF	sp|Q9NZM1|MYOF_HUMAN Myoferlin OS=Homo sapiens GN=MYOF PE=1 SV=1	KSLGPPGPPFnITPRK	HexNAc(4)Hex(3)Fuc(1)	1779	2450000	1730000	2390000	783000	638000	1300000	2190000	907000	399499.7	347984.2	0.414155
SYVC	sp|P26640|SYVC_HUMAN Valine--tRNA ligase OS=Homo sapiens GN=VARS PE=1 SV=4	KPEYGRPnVSAANPRG	HexNAc(2)Hex(3)Fuc(1)	327	1670000	1530000	1970000	920000	587000	642000	1723333	716333.3	224796.2	178511.4	0.415667
MRE11	sp|P49959|MRE11_HUMAN Double-strand break repair protein MRE11A OS=Homo sapiens GN=MRE11A PE=1 SV=3	KEDENSWFNLFVIHQnRS	HexNAc(4)Hex(4)	219	1610000	1380000	985000	722000	445000	487000	1325000	551333.3	316109.2	149286.1	0.416101
PON2	sp|Q15165|PON2_HUMAN Serum paraoxonase/arylesterase 2 OS=Homo sapiens GN=PON2 PE=1 SV=3	KLFVYDPNNPPSSEVLRIQNILCEKPTVTTVYANnGSVLQG	HexNAc(7)Hex(4)Fuc(1)	323	893000	1100000	536000	371000	103000	587000	843000	353666.7	285305.1	242465.1	0.419533
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RTASCSnVTCWLKD	HexNAc(4)Hex(5)Fuc(1)	1057	2980000	1600000	2280000	1880000	210000	790000	2286667	960000	690024.2	847879.7	0.419825
PIGT	sp|Q969N2|PIGT_HUMAN GPI transamidase component PIG-T OS=Homo sapiens GN=PIGT PE=1 SV=1	KPLGLAnDTDHYFLRY	HexNAc(5)Hex(5)	164	3210000	2700000	1210000	1110000	974000	932000	2373333	1005333	1039247	93044.79	0.423596
AMPN	sp|P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	KAEFnITLIHPKD	HexNAc(4)Hex(5)	234	2880000	2380000	2450000	1400000	685000	1190000	2570000	1091667	270739.7	367502.8	0.424773
NU153	sp|P49790|NU153_HUMAN Nuclear pore complex protein Nup153 OS=Homo sapiens GN=NUP153 PE=1 SV=2	REQRESGFSYPnFSLPAANGLSSGVGGGGGKM	HexNAc(3)Hex(4)	429	4090000	2610000	3150000	1080000	1710000	1400000	3283333	1396667	748954.8	315013.2	0.425381
GCP3	sp|Q96CW5|GCP3_HUMAN Gamma-tubulin complex component 3 OS=Homo sapiens GN=TUBGCP3 PE=1 SV=2	RHLMDLLKPELVRPATTLYQHnLTGILETAVRA	HexNAc(3)Hex(3)	596	6500000	5170000	4190000	1110000	2700000	2960000	5286667	2256667	1159411	1001516	0.42686
FAT1	sp|Q14517|FAT1_HUMAN Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2	RIVQQLDFEKKQVYnLTVRA	HexNAc(6)Hex(3)Fuc(3)	998	439000	424000	379000	322000	59900	149000	414000	176966.7	31224.99	133269.3	0.427456
LAMA5	sp|O15230|LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	RTEVKTQAGFADGAPHYVAFYSnATGVWLYVDDQLQQMK	HexNAc(5)Hex(3)Fuc(2)	3209	2510000	3220000	2310000	880000	689000	1880000	2680000	1149667	478225.9	639656.4	0.42898
MY18A	sp|Q92614|MY18A_HUMAN Unconventional myosin-XVIIIa OS=Homo sapiens GN=MYO18A PE=1 SV=3	RnLTLFQAACRGYLARQ	HexNAc(4)Hex(3)	1191	4780000	2330000	1300000	406000	1610000	1600000	2803333	1205333	1787633	692261	0.429964
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KQAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(6)Hex(3)	432	7410000	5350000	5110000	2280000	2760000	2650000	5956667	2563333	1264331	251462.4	0.43033
RRP1B	sp|Q14684|RRP1B_HUMAN Ribosomal RNA processing protein 1 homolog B OS=Homo sapiens GN=RRP1B PE=1 SV=3	KnHSRK	HexNAc(5)Hex(4)Fuc(1)	270	3310000	3250000	2400000	2200000	312000	1380000	2986667	1297333	508953.2	946710.8	0.434375
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KKDTCTQECSYFnITKV	HexNAc(4)Hex(5)Fuc(1)Ne	669	3220000	2270000	2640000	1900000	451000	1190000	2710000	1180333	478852.8	724548.4	0.435547
DDX3X	sp|O00571|DDX3X_HUMAN ATP-dependent RNA helicase DDX3X OS=Homo sapiens GN=DDX3X PE=1 SV=3	RVGNLGLATSFFNERNInITKD	HexNAc(4)Hex(3)	551	4520000	6940000	5390000	3180000	1430000	2740000	5616667	2450000	1225819	910329.6	0.436202
LAMA5	sp|O15230|LAMA5_HUMAN Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	RPnVTGRR	HexNAc(3)Hex(4)NeuAc(1)	1555	5980000	1870000	669000	151000	1700000	1880000	2839667	1243667	2785116	950547.4	0.437962
AT1B3	sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	KFLKPYTLEEQKnLTVCPDGALFEQKG	HexNAc(4)Hex(5)Fuc(3)	124	1930000	1280000	1120000	831000	481000	589000	1443333	633666.7	428991.1	179224.3	0.43903
QCR2	sp|P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	KTIAQGnLSNTDVQAAKN	HexNAc(3)Hex(5)Fuc(1)	365	3670000	3220000	3800000	2830000	628000	1240000	3563333	1566000	304357.2	1136621	0.439476
ITFG3	sp|Q9H0X4|ITFG3_HUMAN Protein ITFG3 OS=Homo sapiens GN=ITFG3 PE=1 SV=1	KVTGSGGPFKSDPHWESMLnATTRR	HexNAc(3)Hex(5)	314	2330000	2500000	2240000	1270000	684000	1170000	2356667	1041333	132035.3	313473	0.441867
SF3A3	sp|Q12874|SF3A3_HUMAN Splicing factor 3A subunit 3 OS=Homo sapiens GN=SF3A3 PE=1 SV=1	KIQAEFEKKWEnGTFPGWPKE	HexNAc(2)Hex(3)	223	14300000	14500000	15000000	9540000	4170000	5660000	14600000	6456667	360555.1	2772225	0.442237
GCP3	sp|Q96CW5|GCP3_HUMAN Gamma-tubulin complex component 3 OS=Homo sapiens GN=TUBGCP3 PE=1 SV=2	RPATTLYQHnLTGILETAVRA	HexNAc(3)Hex(3)	596	335000	398000	324000	216000	153000	98500	352333.3	155833.3	39929.1	58801.22	0.442289
SMRC2	sp|Q8TAQ2|SMRC2_HUMAN SWI/SNF complex subunit SMARCC2 OS=Homo sapiens GN=SMARCC2 PE=1 SV=1	KDEDEnSTGNKG	HexNAc(7)Hex(7)Fuc(2)Ne	398	30600000	21500000	20500000	11800000	6800000	13700000	24200000	10766667	5565070	3564174	0.444904
GALT5	sp|Q7Z7M9|GALT5_HUMAN Polypeptide N-acetylgalactosaminyltransferase 5 OS=Homo sapiens GN=GALNT5 PE=1 SV=1	KELQQFnYTWLRL	HexNAc(4)Hex(4)Fuc(3)	845	16200000	17300000	17100000	10600000	4460000	7480000	16866667	7513333	585946.5	3070136	0.445455
RAB6C	sp|Q9H0N0|RAB6C_HUMAN Ras-related protein Rab-6C OS=Homo sapiens GN=RAB6C PE=1 SV=2	KGLnVTFIETRAKA	HexNAc(7)Hex(3)Fuc(1)	149	1800000	1120000	1800000	1120000	207000	778000	1573333	701666.7	392598.2	461261.7	0.445975
TMEM2	sp|Q9UHN6|TMEM2_HUMAN Transmembrane protein 2 OS=Homo sapiens GN=TMEM2 PE=1 SV=1	RNnISLVKF	HexNAc(2)Hex(9)	914	955000	1100000	642000	721000	186000	301000	899000	402666.7	234079	281617.4	0.447905
CLP1L	sp|Q96KA5|CLP1L_HUMAN Cleft lip and palate transmembrane protein 1-like protein OS=Homo sapiens GN=CLPTM1L PE=1 SV=1	RTVnVSVPKKT	HexNAc(2)Hex(5)	91	204000	155000	276000	51100	81600	153000	211666.7	95233.33	60863.23	52300.13	0.449921
NICA	sp|Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2	RKIYIPLnKT	HexNAc(2)Hex(8)	45	1390000	755000	1070000	834000	123000	492000	1071667	483000	317503.3	355585.4	0.4507
UBP10	sp|Q14694|UBP10_HUMAN Ubiquitin carboxyl-terminal hydrolase 10 OS=Homo sapiens GN=USP10 PE=1 SV=2	RPGAAFEPTYIYRLLTVnKS	HexNAc(5)Hex(6)Fuc(3)Ne	511	5860000	4380000	5820000	3250000	1510000	2490000	5353333	2416667	843168.6	872314.9	0.451432
ADA10	sp|O14672|ADA10_HUMAN Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1	KAIDTIYQTTDFSGIRnISFMVKR	HexNAc(2)Hex(3)	267	5160000	6500000	7770000	4200000	2420000	2160000	6476667	2926667	1305156	1110375	0.451879
CD151	sp|P48509|CD151_HUMAN CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3	RYHQPGHEAVTSAVDQLQQEFHCCGSnNSQDWRD	HexNAc(5)Hex(6)NeuAc(1)	159	2220000	1420000	1080000	485000	719000	933000	1573333	712333.3	585263.5	224074.4	0.452754
RHDF2	sp|Q6PJF5|RHDF2_HUMAN Inactive rhomboid protein 2 OS=Homo sapiens GN=RHBDF2 PE=1 SV=2	KPPnLSITIPPPEKE	HexNAc(6)Hex(4)Fuc(3)	26	732000	3640000	2570000	1170000	1390000	589000	2314000	1049667	1470805	413836.1	0.453616
UTP11	sp|Q9Y3A2|UTP11_HUMAN Probable U3 small nucleolar RNA-associated protein 11 OS=Homo sapiens GN=UTP11L PE=1 SV=2	KGVTnQTGLKR	HexNAc(5)Hex(3)Fuc(1)	184	2880000	4260000	2770000	2230000	339000	1940000	3303333	1503000	830321.2	1018429	0.454995
AMPN	sp|P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	KKLnYTLSQGHRV	HexNAc(4)Hex(5)	128	3350000	4250000	4260000	2170000	1110000	2130000	3953333	1803333	522525.9	600777.3	0.456155
PI3R4	sp|Q99570|PI3R4_HUMAN Phosphoinositide 3-kinase regulatory subunit 4 OS=Homo sapiens GN=PIK3R4 PE=1 SV=3	RITPYLLHFSnDSVPRV	HexNAc(4)Hex(4)Fuc(2)	427	817000	1040000	469000	368000	461000	234000	775333.3	354333.3	287771.3	114115.4	0.457008
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RSGEDAHEALLTLVVPPALLLSSVRPPGACQAnETIFCELQ	HexNAc(4)Hex(5)	697	946000	1050000	721000	570000	343000	343000	905666.7	418666.7	168167.6	131058.5	0.462275
TMED9	sp|Q9BVK6|TMED9_HUMAN Transmembrane emp24 domain-containing protein 9 OS=Homo sapiens GN=TMED9 PE=1 SV=2	RFTFTSHTPGEHQICLHSnSTKF	HexNAc(2)Hex(8)	125	1540000	209000	243000	222000	249000	454000	664000	308333.3	758828.7	126871.3	0.464357
MAGD2	sp|Q9UNF1|MAGD2_HUMAN Melanoma-associated antigen D2 OS=Homo sapiens GN=MAGED2 PE=1 SV=2	KLGLLMVLLSIIFMNGnRSSEAVIWEVLRK	HexNAc(2)Hex(6)	384	113000	280000	261000	105000	137000	63000	218000	101666.7	91427.57	37112.44	0.466361
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KKDTCTQECSYFnITKV	HexNAc(4)Hex(5)Fuc(1)	669	2620000	1600000	2560000	1400000	701000	1070000	2260000	1057000	572363.5	349681.3	0.467699
ODP2	sp|P10515|ODP2_HUMAN Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial OS=H	KASALACLKVPEAnSSWMDTVIRQ	HexNAc(3)Hex(3)	495	1420000	45100	61000	12000	145000	564000	508700	240333.3	789249	288083.9	0.472446
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KGEYFVnVTTRI	HexNAc(2)Hex(7)	1074	11500000	7610000	11500000	6840000	2640000	5000000	10203333	4826667	2245893	2105358	0.473048
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	RGHTLTLnFTRN	HexNAc(3)Hex(5)NeuAc(1)	103	2450000	3000000	1830000	793000	1310000	1350000	2426667	1151000	585348.9	310681.5	0.474313
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KqAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(7)	432	5660000	5500000	4920000	2810000	2330000	2490000	5360000	2543333	389358.4	244404	0.474502
BMS1	sp|Q14692|BMS1_HUMAN Ribosome biogenesis protein BMS1 homolog OS=Homo sapiens GN=BMS1 PE=1 SV=1	KLTGFPYKIFKnTSFIKG	HexNAc(2)Hex(4)Fuc(1)	1039	4450000	3160000	3860000	2520000	1090000	1840000	3823333	1816667	645781.2	715285.5	0.475153
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RAHCVWLECPIPDAPVVTnVTVKA	HexNAc(5)Hex(6)Fuc(2)	926	1480000	1650000	1420000	963000	507000	702000	1516667	724000	119303.5	228794.7	0.477363
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KQAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(7)Fuc(1)	432	6520000	6640000	4910000	3060000	2610000	2970000	6023333	2880000	966040	238117.6	0.478141
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RnVTRL	HexNAc(4)Hex(5)	269	2100000	1970000	1730000	939000	1010000	836000	1933333	928333.3	187705.4	87489.05	0.480172
DESP	sp|P15924|DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	RnLTIRS	HexNAc(7)Hex(6)Fuc(2)	2601	1400000	1900000	1930000	890000	1250000	376000	1743333	838666.7	297713.5	439255.4	0.481071
MK01	sp|P28482|MK01_HUMAN Mitogen-activated protein kinase 1 OS=Homo sapiens GN=MAPK1 PE=1 SV=3	KPSNLLLnTTCDLKICDFGLARV	HexNAc(4)Hex(4)Fuc(3)	158	2750000	2320000	1970000	1130000	720000	1540000	2346667	1130000	390683.2	410000	0.481534
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KKDTCTQECSYFnITKV	HexNAc(2)Hex(8)	669	4520000	4060000	4040000	1460000	1670000	2970000	4206667	2033333	271538.8	817944.6	0.48336
AT1B3	sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	KFLKPYTLEEQKnLTVCPDGALFEQKG	HexNAc(4)Hex(5)Fuc(1)Ne	124	2170000	1720000	1610000	919000	770000	970000	1833333	886333.3	296704.1	103924.7	0.483455
RBM28	sp|Q9NW13|RBM28_HUMAN RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3	RnLSFKC	HexNAc(5)Hex(5)Fuc(2)	120	2360000	1500000	2330000	1460000	121000	1430000	2063333	1003667	488091.5	764558.9	0.48643
LDLR	sp|P01130|LDLR_HUMAN Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR PE=1 SV=1	RLTGSDVNLLAENLLSPEDMVLFHnLTQPRG	HexNAc(5)Hex(5)Fuc(2)	657	959000	1000000	1030000	711000	249000	506000	996333.3	488666.7	35641.74	231487.2	0.490465
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RKYQTLnCSVNVNCVNIRC	HexNAc(2)Hex(6)	966	3900000	2170000	2300000	1830000	971000	1310000	2790000	1370333	963483.3	432666.5	0.491159
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KQAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(5)Fuc(1)	432	426000	883000	486000	568000	98300	216000	598333.3	294100	248347.2	244395.6	0.491532
FLNB	sp|O75369|FLNB_HUMAN Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	RAPSVATVGSICDLNLKIPEInSSDMSAHVTSPSGRV	HexNAc(4)Hex(3)	2125	4060000	2720000	3300000	2090000	1460000	1420000	3360000	1656667	672011.9	375810.2	0.493056
PO210	sp|Q8TEM1|PO210_HUMAN Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3	RIETVLPAEFFEVLSSSQnGSYHRI	HexNAc(2)Hex(9)	405	416000	987000	274000	268000	323000	236000	559000	275666.7	377397.7	44003.79	0.493143
FUMH	sp|P07954|FUMH_HUMAN Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3	RINKLMnESLMLVTALNPHIGYDKA	HexNAc(6)Hex(3)Fuc(2)	450	3090000	2920000	1720000	1330000	1860000	623000	2576667	1271000	746748.5	620607	0.493273
NDUA2	sp|O43678|NDUA2_HUMAN NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 2 OS=Homo sapiens GN=NDUFA2 PE=1 SV=3	KLWARYAFGQETNVPLNnFSADQVTRA	HexNAc(5)Hex(5)Fuc(1)Ne	81	2330000	1640000	828000	556000	1170000	674000	1599333	800000	751825.3	325815.9	0.500208
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(4)Hex(5)Fuc(1)	212	7220000	6080000	3940000	3640000	2710000	2290000	5746667	2880000	1665213	690869	0.50116
PON2	sp|Q15165|PON2_HUMAN Serum paraoxonase/arylesterase 2 OS=Homo sapiens GN=PON2 PE=1 SV=3	KHTNMnLTQLKV	HexNAc(2)Hex(7)	254	105000	433000	265000	170000	13600	219000	267666.7	134200	164016.3	107277.8	0.50137
PO210	sp|Q8TEM1|PO210_HUMAN Nuclear pore membrane glycoprotein 210 OS=Homo sapiens GN=NUP210 PE=1 SV=3	RFDnFSSLSIQWESTRPVLASIEPELPMQLVSQDDESGQK	HexNAc(4)Hex(6)Fuc(2)	801	738000	864000	694000	852000	76400	226000	765333.3	384800	88234.54	411463.1	0.502787
IMA1	sp|P52292|IMA1_HUMAN Importin subunit alpha-1 OS=Homo sapiens GN=KPNA2 PE=1 SV=1	RnLTWTLSNLCRN	HexNAc(4)Hex(6)Fuc(2)	228	5790000	6660000	6670000	5730000	1330000	2560000	6373333	3206667	505206.2	2270162	0.503138
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KqAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(8)	432	10100000	11100000	9280000	6300000	4180000	4890000	10160000	5123333	911482.3	1079089	0.504265
UTP20	sp|O75691|UTP20_HUMAN Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3	KnLSQEIIELLKK	HexNAc(3)Hex(4)Fuc(2)	2691	7920000	5760000	5420000	4580000	2450000	2620000	6366667	3216667	1355925	1183737	0.505236
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RVWnSTFIEDYRDFDRV	HexNAc(2)Hex(9)	935	3780000	3700000	2890000	2460000	1110000	1670000	3456667	1746667	492375.2	678257.6	0.505304
LIMA1	sp|Q9UHB6|LIMA1_HUMAN LIM domain and actin-binding protein 1 OS=Homo sapiens GN=LIMA1 PE=1 SV=1	KSLnWSSFVDNTFAEEFTTQNQKS	HexNAc(2)Hex(6)	706	10800000	10600000	11000000	8570000	3030000	4790000	10800000	5463333	200000	2830713	0.505864
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KQAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(9)	432	912000	1110000	951000	447000	415000	645000	991000	502333.3	104885.7	124584.6	0.506895
SMC2	sp|O95347|SMC2_HUMAN Structural maintenance of chromosomes protein 2 OS=Homo sapiens GN=SMC2 PE=1 SV=2	KEQNnDSQLKI	HexNAc(3)Hex(3)Fuc(1)	904	12800000	10100000	10600000	6470000	3090000	7550000	11166667	5703333	1436431	2326743	0.510746
HEAT1	sp|Q9H583|HEAT1_HUMAN HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3	KAVSFnKS	HexNAc(3)Hex(4)Fuc(1)Ne	1488	1770000	1740000	2170000	1520000	586000	808000	1893333	971333.3	240069.4	487952.2	0.513028
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RSRLWnSTFLEEYSKL	HexNAc(2)Hex(9)	997	2960000	2870000	2500000	1760000	1050000	1470000	2776667	1426667	243789.5	356978.1	0.513806
FAT1	sp|Q14517|FAT1_HUMAN Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2	KKQVYnLTVRAKD	HexNAc(3)Hex(5)NeuAc(1)	998	264000	211000	161000	128000	80300	119000	212000	109100	51507.28	25344.23	0.514623
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KQAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(7)	432	9810000	8330000	6880000	5650000	3320000	3910000	8340000	4293333	1465026	1211377	0.514788
ASPH	sp|Q12797|ASPH_HUMAN Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	RLVQLFPnDTSLKNDLGVGYLLIGDNDNAKK	HexNAc(2)Hex(8)	452	535000	673000	785000	344000	238000	444000	664333.3	342000	125225.1	103014.6	0.514802
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RKEnSSEICSNNGECVCGQCVCRK	HexNAc(2)Hex(7)	520	348000	620000	556000	488000	71700	231000	508000	263566.7	142211.1	210052	0.518832
SAC1	sp|Q9NTJ5|SAC1_HUMAN Phosphatidylinositide phosphatase SAC1 OS=Homo sapiens GN=SACM1L PE=1 SV=2	RQDSIDLFLGnYSVDELESHSPLSVPRD	HexNAc(4)Hex(4)	501	476000	773000	1210000	1190000	17600	70100	819666.7	425900	369218.5	662250.5	0.519601
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KQAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(6)	432	1980000	1850000	1890000	1040000	879000	1060000	1906667	993000	66583.28	99232.05	0.520804
ATM	sp|Q13315|ATM_HUMAN Serine-protein kinase ATM OS=Homo sapiens GN=ATM PE=1 SV=4	KeLQWTFIMLTYLnNTLVEDCVKVRS	HexNAc(4)Hex(5)Fuc(1)Ne	1719	2420000	1760000	1160000	849000	824000	1110000	1780000	927666.7	630238.1	158399.3	0.521161
DESP	sp|P15924|DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	RnLTIRS	HexNAc(7)Hex(4)Fuc(4)Ne	2601	2630000	2050000	2690000	1190000	1220000	1440000	2456667	1283333	353459.1	136504	0.522388
S23IP	sp|Q9Y6Y8|S23IP_HUMAN SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1	KITLPSIGRFRHFTnETLLDILFYNSPTYCQTIVEKV	HexNAc(3)Hex(4)Fuc(2)	533	1150000	1880000	1090000	999000	480000	674000	1373333	717666.7	439810.6	262241	0.522573
EGFR	sp|P00533|EGFR_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2	RnVSRG	HexNAc(7)Hex(6)Fuc(5)Ne	528	26600000	16800000	13600000	8160000	8070000	13600000	19000000	9943333	6773478	3167086	0.523333
ASPH	sp|Q12797|ASPH_HUMAN Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	RLVQLFPnDTSLKNDLGVGYLLIGDNDNAKKV	HexNAc(2)Hex(6)	452	4350000	3800000	3520000	2450000	1370000	2310000	3890000	2043333	422255.8	587310.3	0.525278
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KGEYFVnVTTRI	HexNAc(2)Hex(5)	1074	2620000	877000	1400000	1420000	230000	929000	1632333	859666.7	894425.1	598022	0.526649
AMPN	sp|P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	KAEFnITLIHPKD	HexNAc(2)Hex(7)	234	2800000	2950000	3360000	1570000	1260000	1970000	3036667	1600000	289885	355949.4	0.526894
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RTASCSnVTCWLKD	HexNAc(4)Hex(5)Fuc(1)Ne	1057	3010000	2480000	2050000	2010000	274000	1690000	2513333	1324667	480867.3	923864.3	0.527056
ENPL	sp|P14625|ENPL_HUMAN Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	KHNnDTQHIWESDSNEFSVIADPRG	HexNAc(2)Hex(5)	217	1060000	243000	538000	114000	309000	550000	613666.7	324333.3	413722.5	218404.1	0.528517
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KQAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(5)	432	1480000	842000	897000	819000	432000	451000	1073000	567333.3	353543.5	218156.7	0.528736
NCEH1	sp|Q6PIU2|NCEH1_HUMAN Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3	KGNYDFVQAMIVNnHTSLDVEEAAAVRA	HexNAc(2)Hex(8)	270	1020000	801000	644000	188000	699000	417000	821666.7	434666.7	188850	255957.7	0.529006
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RVWnSTFIEDYRDFDRV	HexNAc(6)Hex(4)	935	750000	93600	141000	413	316000	205000	328200	173804.3	366057.5	160089.6	0.529568
PLXB2	sp|O15031|PLXB2_HUMAN Plexin-B2 OS=Homo sapiens GN=PLXNB2 PE=1 SV=3	RISVAGRnCSFQPERY	HexNAc(3)Hex(5)	844	1420000	757000	388000	230000	533000	602000	855000	455000	522933.1	197886.3	0.532164
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KCHEGnGTFECGACRC	HexNAc(2)Hex(8)Fuc(1)	481	311000	1400000	596000	734000	110000	387000	769000	410333.3	564736.2	312653.7	0.533593
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(4)Hex(5)Fuc(3)	212	4980000	2770000	1640000	1970000	2520000	540000	3130000	1676667	1698853	1022073	0.535676
HYOU1	sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	RLSALDNLLnHSSMFLKG	HexNAc(2)Hex(6)	830	1960000	1310000	333000	259000	806000	868000	1201000	644333.3	818958.5	335145.2	0.536497
STT3A	sp|P46977|STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE	RTILVDNNTWnNTHISRV	HexNAc(2)Hex(5)	548	3190000	3260000	2550000	2120000	1060000	1660000	3000000	1613333	391280	531538.6	0.537778
FAT1	sp|Q14517|FAT1_HUMAN Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2	KKLDIGQYLLnVSVTDGKF	HexNAc(2)Hex(5)	3613	5900000	4850000	2590000	987000	2590000	3620000	4446667	2399000	1691459	1326851	0.539505
CALX	sp|P27824|CALX_HUMAN Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	KPKAEEDEILnRSPRN	HexNAc(7)Hex(4)NeuAc(1)	581	2290000	3320000	4240000	3680000	457000	1190000	3283333	1775667	975517	1689434	0.540812
CD47	sp|Q08722|CD47_HUMAN Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1	RDIYTFDGALnKS	HexNAc(2)Hex(7)	73	1310000	1210000	1360000	801000	433000	869000	1293333	701000	76376.26	234572	0.54201
PLSI	sp|Q14651|PLSI_HUMAN Plastin-1 OS=Homo sapiens GN=PLS1 PE=1 SV=2	RVPVnWSHVNKPPYPALGGNMKK	HexNAc(3)Hex(4)Fuc(1)	439	7470000	4870000	6150000	3870000	2790000	3400000	6163333	3353333	1300051	541510.2	0.544078
PB1	sp|Q86U86|PB1_HUMAN Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1	RIQnGSYKS	HexNAc(6)Hex(7)Fuc(5)	239	8210000	5440000	8650000	6380000	2670000	3140000	7433333	4063333	1740239	2020008	0.546637
HYOU1	sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	RAEPPLnASASDQGEKV	HexNAc(2)Hex(6)	931	419000	436000	200000	297000	112000	169000	351666.7	192666.7	131621.9	94743.51	0.547867
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RAnHSGAVVLLKR	HexNAc(2)Hex(5)	323	3530000	3320000	3320000	2940000	772000	1860000	3390000	1857333	121243.6	1084002	0.547886
SERPH	sp|P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	RnVTWKL	HexNAc(2)Hex(6)	125	1690000	1350000	1280000	1050000	863000	456000	1440000	789666.7	219317.1	303714.2	0.54838
ADA10	sp|O14672|ADA10_HUMAN Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1	RInTTADEKDPTNPFRFPNIGVEKF	HexNAc(2)Hex(9)	278	2420000	3200000	2560000	2040000	987000	1460000	2726667	1495667	415852.5	527405.3	0.548533
PYRD	sp|Q02127|PYRD_HUMAN Dihydroorotate dehydrogenase (quinone), mitochondrial OS=Homo sapiens GN=DHODH PE=1 SV=3	RVLGPLADYLVVnVSSPNTAGLRS	HexNAc(3)Hex(3)	211	3330000	1900000	3380000	1630000	1280000	1840000	2870000	1583333	840416.6	282901.6	0.551684
NU214	sp|P35658|NU214_HUMAN Nuclear pore complex protein Nup214 OS=Homo sapiens GN=NUP214 PE=1 SV=2	KPSFPPSTSAVKVnLSEKF	HexNAc(2)Hex(7)	586	2520000	1470000	1080000	1590000	670000	545000	1690000	935000	744781.8	570679.4	0.553254
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RAnHSGAVVLLKRD	HexNAc(2)Hex(8)	323	3120000	2750000	2330000	2330000	648000	1560000	2733333	1512667	395263.6	841998.4	0.553415
MET	sp|P08581|MET_HUMAN Hepatocyte growth factor receptor OS=Homo sapiens GN=MET PE=1 SV=4	RPSFSELVSRISAIFSTFIGEHYVHVnATYVNVKC	HexNAc(3)Hex(4)Fuc(1)	1353	1200000	1360000	1240000	959000	648000	497000	1266667	701333.3	83266.64	235572.4	0.553684
STRBP	sp|Q96SI9|STRBP_HUMAN Spermatid perinuclear RNA-binding protein OS=Homo sapiens GN=STRBP PE=1 SV=1	KKDGEnVSMKDPPDLLDRQ	HexNAc(5)Hex(3)Fuc(4)	180	3910000	3740000	4410000	3330000	1630000	1720000	4020000	2226667	348281.5	956573.7	0.553897
MFTC	sp|Q9H2D1|MFTC_HUMAN Mitochondrial folate transporter/carrier OS=Homo sapiens GN=SLC25A32 PE=2 SV=2	KGIAPNLIRVTPACCITFVVYEnVSHFLLDLRE	HexNAc(3)Hex(3)	302	19000000	19600000	18100000	12600000	10200000	8650000	18900000	10483333	754983.4	1990184	0.554674
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KCHEGnGTFECGACRC	HexNAc(2)Hex(6)	481	1190000	1060000	891000	782000	694000	270000	1047000	582000	149923.3	273759	0.555874
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RVWnSTFIEDYRDFDRVRV	HexNAc(2)Hex(9)	935	2870000	2790000	2180000	1670000	1200000	1490000	2613333	1453333	377403.4	237135.7	0.556122
DESP	sp|P15924|DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	RIKDFLQGSSCIAGIYnETTKQKL	HexNAc(2)Hex(3)	2265	13900000	20300000	14000000	10600000	6300000	9960000	16066667	8953333	3666515	2320029	0.557261
PRKDC	sp|P78527|PRKDC_HUMAN DNA-dependent protein kinase catalytic subunit OS=Homo sapiens GN=PRKDC PE=1 SV=3	KGAnRTETVTSFRK	HexNAc(5)Hex(6)Fuc(3)	3863	1810000	1010000	964000	644000	545000	921000	1261333	703333.3	475715.6	194895.7	0.557611
HMGB1	sp|P09429|HMGB1_HUMAN High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	KKLGEMWnNTAADDKQ	HexNAc(3)Hex(3)Fuc(1)	134	5610000	3830000	4080000	723000	2190000	4630000	4506667	2514333	963656.2	1973590	0.557914
MYO1C	sp|O00159|MYO1C_HUMAN Unconventional myosin-Ic OS=Homo sapiens GN=MYO1C PE=1 SV=4	RVGVQDFVLLEnFTSEAAFIENLRR	HexNAc(2)Hex(4)	56	4150000	4550000	4220000	3810000	1220000	2190000	4306667	2406667	213619.6	1308523	0.558824
CDC5L	sp|Q99459|CDC5L_HUMAN Cell division cycle 5-like protein OS=Homo sapiens GN=CDC5L PE=1 SV=2	KPVInSTPGRTPLRDKL	HexNAc(5)Hex(5)Fuc(2)Ne	436	18500000	13700000	9010000	9050000	9000000	4980000	13736667	7676667	4745106	2335516	0.558845
MAP1B	sp|P46821|MAP1B_HUMAN Microtubule-associated protein 1B OS=Homo sapiens GN=MAP1B PE=1 SV=2	KIIRVLFPGnSTQYNILEGLEKL	HexNAc(2)Hex(5)	492	2100000	4240000	1270000	2410000	1090000	766000	2536667	1422000	1532395	870834.1	0.560578
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(2)Hex(9)	212	6160000	4990000	4720000	3360000	2440000	3100000	5290000	2966667	765441	474271.4	0.560807

ERBB2	sp|P04626|ERBB2_HUMAN Receptor tyrosine-protein kinase erbB-2 OS=Homo sapiens GN=ERBB2 PE=1 SV=1	REnTSPKA	HexNAc(5)Hex(6)	758	1480000	993000	1080000	998000	345000	655000	1184333	666000	259723.6	326638.9	0.562342
ERLN1	sp|O75477|ERLN1_HUMAN Erlin-1 OS=Homo sapiens GN=ERLIN1 PE=1 SV=1	RnYTADYDKTLIFNKI	HexNAc(2)Hex(9)	106	1920000	2860000	2550000	1780000	1070000	1290000	2443333	1380000	478992	363455.6	0.564802
TOR4A	sp|Q9NXH8|TOR4A_HUMAN Torsin-4A OS=Homo sapiens GN=TOR4A PE=1 SV=2	RFVLQnASRA	HexNAc(2)Hex(8)	314	4410000	3710000	3030000	3090000	1090000	2120000	3716667	2100000	690024.2	1000150	0.565022
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	KQAFDQILQDRnHSSYLGYSVAAISTGESTHFVAGAPRA	HexNAc(2)Hex(8)	432	13300000	12400000	10100000	9370000	4890000	6020000	11933333	6760000	1650253	2329871	0.56648
CNOT1	sp|A5YKK6|CNOT1_HUMAN CCR4-NOT transcription complex subunit 1 OS=Homo sapiens GN=CNOT1 PE=1 SV=2	KVQEVIFGLALLnSSSSDLRG	HexNAc(2)Hex(3)Fuc(1)	135	566000	1030000	994000	699000	263000	508000	863333.3	490000	258126.6	218556.6	0.567568
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KDTCTQECSYFnITKV	HexNAc(2)Hex(6)	669	961000	1290000	1480000	385000	532000	1210000	1243667	709000	262584	440060.2	0.570088
RPN1	sp|P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	KTILPAAAQDVYYRDEIGnVSTSHLLILDDSVEMEIRPRF	HexNAc(2)Hex(6)	299	5230000	7410000	3630000	3080000	3530000	2680000	5423333	3096667	1897402	425245	0.57099
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RNPCTSEQnCTSPFSYKN	HexNAc(2)Hex(7)	212	724000	919000	1390000	824000	263000	645000	1011000	577333.3	342398.9	286556	0.571052
SETLP	sp|P0DME0|SETLP_HUMAN Protein SETSIP OS=Homo sapiens GN=SETSIP PE=1 SV=1	KEFHLnESGDPSSKS	HexNAc(4)Hex(3)Fuc(1)	169	3990000	2460000	2490000	2480000	669000	1960000	2980000	1703000	874814.3	932452.1	0.571477
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RPIIISMnYSLPLRMPDRPRLGLRS	HexNAc(2)Hex(5)	573	995000	1130000	869000	644000	682000	390000	998000	572000	130525.9	158757.7	0.573146
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RYFFnVSDEAALLEKA	HexNAc(4)Hex(5)NeuAc(1)	343	11000000	9710000	9250000	7330000	4600000	5280000	9986667	5736667	907211.8	1421138	0.574433
CLP1L	sp|Q96KA5|CLP1L_HUMAN Cleft lip and palate transmembrane protein 1-like protein OS=Homo sapiens GN=CLPTM1L PE=1 SV=1	RTVnVSVPKKT	HexNAc(2)Hex(6)	91	718000	836000	377000	453000	160000	501000	643666.7	371333.3	238357.6	184586.9	0.576903
ACOC	sp|P21399|ACOC_HUMAN Cytoplasmic aconitate hydratase OS=Homo sapiens GN=ACO1 PE=1 SV=3	KQDIENILHWnVTQHKNIEVPFKP	HexNAc(4)Hex(3)Fuc(1)	67	7120000	5800000	5050000	4230000	2480000	3660000	5990000	3456667	1047998	892543.2	0.577073
TMX3	sp|Q96JJ7|TMX3_HUMAN Protein disulfide-isomerase TMX3 OS=Homo sapiens GN=TMX3 PE=1 SV=2	KLVALAVIDEKnTSVEHTRL	HexNAc(2)Hex(8)	258	6360000	5340000	4320000	3830000	2680000	2740000	5340000	3083333	1020000	647327.8	0.577403
ADA10	sp|O14672|ADA10_HUMAN Disintegrin and metalloproteinase domain-containing protein 10 OS=Homo sapiens GN=ADAM10 PE=1 SV=1	RnISQVLEKK	HexNAc(2)Hex(6)	439	1680000	1530000	375000	1060000	382000	628000	1195000	690000	714090.3	343225.9	0.577406
EGFR	sp|P00533|EGFR_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2	KnCTSISGDLHILPVAFRG	HexNAc(2)Hex(5)	361	3930000	3200000	2730000	2310000	1500000	1910000	3286667	1906667	604676.2	405010.3	0.580122
SEM4B	sp|Q9NPR2|SEM4B_HUMAN Semaphorin-4B OS=Homo sapiens GN=SEMA4B PE=1 SV=3	KInSSLQLPDRVLNFLKD	HexNAc(2)Hex(4)	405	128000	1190000	1110000	770000	163000	478000	809333.3	470333.3	591406.2	303572.6	0.581137
RT29	sp|P51398|RT29_HUMAN 28S ribosomal protein S29, mitochondrial OS=Homo sapiens GN=DAP3 PE=1 SV=1	RKPALELLHYLKnTSFAYPAIRY	HexNAc(6)Hex(3)Fuc(2)	114	1360000	1570000	1100000	779000	495000	1070000	1343333	781333.3	235442.8	287507.1	0.581638
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(2)Hex(8)	212	8290000	6610000	10300000	6650000	3890000	4120000	8400000	4886667	1847458	1531415	0.581746
ERCC2	sp|P18074|ERCC2_HUMAN TFIIH basal transcription factor complex helicase XPD subunit OS=Homo sapiens GN=ERCC2 PE=1 SV=1	KLPRWIQEHLTDANLnLTVDEGVQVAKYFLRQ	HexNAc(2)Hex(4)Fuc(1)	707	1570000	1210000	1500000	1320000	401000	773000	1426667	831333.3	190875.2	462268.7	0.58271
HYOU1	sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	RLSALDNLLnHSSMFLKG	HexNAc(2)Hex(8)	830	629000	624000	921000	575000	292000	401000	724666.7	422666.7	170048	142738.7	0.583257
ADA17	sp|P78536|ADA17_HUMAN Disintegrin and metalloproteinase domain-containing protein 17 OS=Homo sapiens GN=ADAM17 PE=1 SV=1	REQQLESCACnETDNSCKVCCRD	HexNAc(2)Hex(7)	594	403000	304000	309000	363000	31000	199000	338666.7	197666.7	55770.36	166004	0.583661
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RAnHSGAVVLLKR	HexNAc(2)Hex(6)	323	11600000	11600000	10400000	9400000	3330000	6970000	11200000	6566667	692820.3	3055034	0.58631
RN213	sp|Q63HN8|RN213_HUMAN E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3	REVAILYRSHnASLHPTPEQCEAVSKF	HexNAc(2)Hex(5)Fuc(1)	4387	7720000	6370000	5370000	3630000	3250000	4560000	6486667	3813333	1179336	673968.3	0.587873
TM131	sp|Q92545|TM131_HUMAN Transmembrane protein 131 OS=Homo sapiens GN=TMEM131 PE=1 SV=3	READnHTAFIRI	HexNAc(2)Hex(6)	290	743000	1290000	1080000	1020000	40400	777000	1037667	612466.7	275946.3	510105.3	0.590235
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RAnHSGAVVLLKRD	HexNAc(2)Hex(6)	323	10800000	10200000	6800000	6810000	4180000	5440000	9266667	5476667	2157159	1315383	0.591007
RBM26	sp|Q5T8P6|RBM26_HUMAN RNA-binding protein 26 OS=Homo sapiens GN=RBM26 PE=1 SV=3	KTLEVLTKnITKL	HexNAc(3)Hex(5)	783	9450000	7850000	5170000	2760000	5370000	5150000	7490000	4426667	2162591	1447561	0.59101
MPRD	sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	REAGnHTSGAGLVQINKS	HexNAc(4)Hex(5)Fuc(1)	83	1340000	950000	1080000	972000	281000	739000	1123333	664000	198578.3	351552.3	0.591098
RM03	sp|P09001|RM03_HUMAN 39S ribosomal protein L3, mitochondrial OS=Homo sapiens GN=MRPL3 PE=1 SV=1	KHNIIYVnGSVPGHKN	HexNAc(7)Hex(4)Fuc(2)Ne	286	325000	1550000	286000	270000	386000	623000	720333.3	426333.3	718777	179923.1	0.591856
MPRD	sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	RLKPLFnKS	HexNAc(2)Hex(6)	57	17000000	17100000	16800000	14100000	4230000	11800000	16966667	10043333	152752.5	5164168	0.591945
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RPTKQNNQVAIVYnITLDADGFSSRV	HexNAc(3)Hex(3)	699	4660000	4630000	4260000	2240000	3250000	2570000	4516667	2686667	222785.4	515008.1	0.594834
TM87A	sp|Q8NBN3|TM87A_HUMAN Transmembrane protein 87A OS=Homo sapiens GN=TMEM87A PE=1 SV=3	RnTTIFLKF	HexNAc(6)Hex(4)Fuc(3)	62	25200000	25500000	32900000	22800000	14300000	12700000	27866667	16600000	4361575	5428628	0.595694
LMAN2	sp|Q12907|LMAN2_HUMAN Vesicular integral-membrane protein VIP36 OS=Homo sapiens GN=LMAN2 PE=1 SV=1	RVFPYISVMVNnGSLSYDHSKD	HexNAc(4)Hex(3)Fuc(1)	183	989000	1430000	1050000	329000	916000	824000	1156333	689666.7	238956.8	315715.6	0.596425
MPRD	sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	RLKPLFnKS	HexNAc(2)Hex(7)	57	18500000	19300000	19100000	15500000	5270000	13300000	18966667	11356667	416333.2	5384759	0.59877
KI20B	sp|Q96Q89|KI20B_HUMAN Kinesin-like protein KIF20B OS=Homo sapiens GN=KIF20B PE=1 SV=3	RTNLKFPISDDRnSSVKK	HexNAc(2)Hex(4)Fuc(1)	1689	1880000	1130000	1360000	1600000	477000	541000	1456667	872666.7	384230.8	630701.5	0.599085
RPN1	sp|P04843|RPN1_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1 OS=Homo sapiens GN=RPN1 PE=1 SV=1	KTILPAAAQDVYYRDEIGnVSTSHLLILDDSVEMEIRPRF	HexNAc(2)Hex(7)	299	3380000	4070000	2640000	1950000	1940000	2160000	3363333	2016667	715145.7	124231	0.599604
AT1B3	sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	KKFLKPYTLEEQKnLTVCPDGALFEQKG	HexNAc(4)Hex(6)Fuc(1)Ne	124	2420000	1640000	1550000	1340000	834000	1190000	1870000	1121333	478434.9	259894.9	0.599643
RECQ1	sp|P46063|RECQ1_HUMAN ATP-dependent DNA helicase Q1 OS=Homo sapiens GN=RECQL PE=1 SV=3	KnITEYCRD	HexNAc(5)Hex(7)Fuc(2)	488	1090000	507000	812000	525000	427000	493000	803000	481666.7	291604.2	49973.33	0.599834
PSA1	sp|P25786|PSA1_HUMAN Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	KnVSIGIVGKDLEFTIYDDDDVSPFLEGLEERPQRK	HexNAc(5)Hex(6)Fuc(1)	209	494000	727000	765000	590000	280000	324000	662000	398000	146727.6	167726	0.601208
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	KnITIVTGAPRH	HexNAc(5)Hex(5)	265	81600000	67900000	80500000	69100000	30600000	38900000	76666667	46200000	7612052	20261540	0.602609
ITB4	sp|P16144|ITB4_HUMAN Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=5	KHNIIPIFAVTnYSYSYYEKL	HexNAc(2)Hex(9)	327	1090000	1890000	981000	983000	552000	858000	1320333	797666.7	496347	221743.8	0.60414
DESP	sp|P15924|DESP_HUMAN Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	RnLTIRS	HexNAc(7)Hex(5)Fuc(2)	2601	41100000	40300000	23400000	33600000	17300000	12600000	34933333	21166667	9996166	11021040	0.605916
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RSLDAYPILNQAQALEnHTEVQFQKE	HexNAc(2)Hex(8)	605	6060000	6590000	4620000	4210000	2420000	3880000	5756667	3503333	1019428	952593	0.60857
GPAT4	sp|Q86UL3|GPAT4_HUMAN Glycerol-3-phosphate acyltransferase 4 OS=Homo sapiens GN=AGPAT6 PE=1 SV=1	KLPILIFPEGTCInNTSVMMFKK	HexNAc(2)Hex(4)Fuc(1)	327	2320000	3650000	2110000	1770000	1640000	1510000	2693333	1640000	835124.7	130000	0.608911
SERPH	sp|P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	RnVTWKL	HexNAc(2)Hex(7)	125	968000	666000	630000	384000	558000	437000	754666.7	459666.7	185626.9	89187.07	0.609099
PB1	sp|Q86U86|PB1_HUMAN Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1	RIQnGSYKS	HexNAc(6)Hex(5)Fuc(5)	239	2690000	1960000	1950000	1410000	1130000	1490000	2200000	1343333	424381.9	189032.6	0.610606
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	RSSCGKEnTSDPSLVIAFGRG	HexNAc(2)Hex(3)Fuc(1)	84	2880000	2580000	2500000	2430000	826000	1610000	2653333	1622000	200333.1	802067.3	0.611307
STT3B	sp|Q8TCJ2|STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE	RTTLVDNNTWnNSHIALVGKA	HexNAc(6)Hex(4)	627	2810000	1370000	744000	461000	1480000	1070000	1641333	1003667	1059389	512728.3	0.611495
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RVWnSTFIEDYRDFDRV	HexNAc(2)Hex(8)	935	2080000	1860000	699000	1260000	475000	1110000	1546333	948333.3	742011	416723.3	0.613279
RIF1	sp|Q5UIP0|RIF1_HUMAN Telomere-associated protein RIF1 OS=Homo sapiens GN=RIF1 PE=1 SV=2	KnETYVLKLWPLFVKL	HexNAc(7)Hex(5)Fuc(3)Ne	245	1770000	1420000	1290000	853000	759000	1140000	1493333	917333.3	248260.6	198480.1	0.614286
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RnVTRL	HexNAc(4)Hex(5)NeuAc(1)	269	3780000	3310000	2550000	2400000	2310000	1220000	3213333	1976667	620671.7	656835.8	0.615145
RBM28	sp|Q9NW13|RBM28_HUMAN RNA-binding protein 28 OS=Homo sapiens GN=RBM28 PE=1 SV=3	RnLSFKC	HexNAc(4)Hex(3)Fuc(1)	120	1280000	1550000	827000	584000	1040000	629000	1219000	751000	365339.6	251290.7	0.616079
ZDHC6	sp|Q9H6R6|ZDHC6_HUMAN Palmitoyltransferase ZDHHC6 OS=Homo sapiens GN=ZDHHC6 PE=1 SV=1	KIILRnKTSIESWIEEKA	HexNAc(7)Hex(4)NeuAc(1)	234	9090000	9090000	10500000	9750000	4310000	3610000	9560000	5890000	814063.9	3361131	0.616109
ADA17	sp|P78536|ADA17_HUMAN Disintegrin and metalloproteinase domain-containing protein 17 OS=Homo sapiens GN=ADAM17 PE=1 SV=1	REQQLESCACnETDNSCKVCCRD	HexNAc(2)Hex(8)	594	1050000	1590000	1400000	1240000	176000	1080000	1346667	832000	273922.1	573717.7	0.617822
PDS5A	sp|Q29RF7|PDS5A_HUMAN Sister chromatid cohesion protein PDS5 homolog A OS=Homo sapiens GN=PDS5A PE=1 SV=1	KnISIRR	HexNAc(6)Hex(3)Fuc(2)	975	975000	1610000	1660000	1710000	485000	429000	1415000	874666.7	381870.4	723961.6	0.618139
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RAnHSGAVVLLKR	HexNAc(2)Hex(8)	323	1560000	1600000	1340000	1490000	272000	1030000	1500000	930666.7	140000	615045.8	0.620444
NCLN	sp|Q969V3|NCLN_HUMAN Nicalin OS=Homo sapiens GN=NCLN PE=1 SV=2	RVIYnLTEKG	HexNAc(2)Hex(6)	428	1420000	1010000	1330000	703000	657000	974000	1253333	778000	215484	171292.1	0.620745
LMF2	sp|Q9BU23|LMF2_HUMAN Lipase maturation factor 2 OS=Homo sapiens GN=LMF2 PE=1 SV=2	RSAnSTLAQALHWTRS	HexNAc(2)Hex(8)	616	1910000	1780000	1140000	63900	1500000	1440000	1610000	1001300	412189.3	812366.3	0.621925
SAP	sp|P07602|SAP_HUMAN Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2	RTnSTFVQALVEHVKEECDRL	HexNAc(2)Hex(3)Fuc(1)	215	16200000	16800000	11200000	9810000	8300000	9440000	14733333	9183333	3074627	787040.9	0.623303
MPRI	sp|P11717|MPRI_HUMAN Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	KTnITLVCKPGDLESAPVLRT	HexNAc(2)Hex(6)	581	1980000	2150000	2290000	1650000	996000	1360000	2140000	1335333	155241.7	327697	0.623988
SAP	sp|P07602|SAP_HUMAN Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2	KSLPCDICKDVVTAAGDMLKDnATEEEILVYLEKT	HexNAc(3)Hex(3)	80	4160000	6020000	4880000	3860000	2870000	2680000	5020000	3136667	937869.9	633587.7	0.624834
CD47	sp|Q08722|CD47_HUMAN Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1	KGRDIYTFDGALnKS	HexNAc(3)Hex(6)	73	2760000	1920000	1650000	1430000	1200000	1330000	2110000	1320000	578878.2	115325.6	0.625592
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RYFFnVSDEAALLEKA	HexNAc(4)Hex(5)Fuc(2)	343	5450000	5950000	5540000	4240000	3370000	2990000	5646667	3533333	266520.8	640806.8	0.625738
ARHG9	sp|O43307|ARHG9_HUMAN Rho guanine nucleotide exchange factor 9 OS=Homo sapiens GN=ARHGEF9 PE=1 SV=3	KRSQSPFWQnFSRL	HexNAc(2)Hex(7)	507	1820000	920000	218000	392	1050000	803000	986000	617797.3	803036.7	548766.1	0.626569
SIA4C	sp|Q11206|SIA4C_HUMAN CMP-N-acetylneuraminate-beta-galactosamide-alpha-2,3-sialyltransferase 4 OS=Homo sapiens GN=ST3GAL4 PE	KLFGnYSRD	HexNAc(2)Hex(4)Fuc(1)	61	2360000	2210000	1240000	1910000	528000	1220000	1936667	1219333	607974.8	691000.2	0.629604
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RnVTRL	HexNAc(2)Hex(8)	269	593000	860000	416000	551000	279000	350000	623000	393333.3	223515.1	141082.7	0.631354
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RYFFnVSDEAALLEKA	HexNAc(4)Hex(5)NeuAc(2)	343	6180000	5860000	5280000	4270000	3240000	3440000	5773333	3650000	456216.3	546168.5	0.632217
TM87A	sp|Q8NBN3|TM87A_HUMAN Transmembrane protein 87A OS=Homo sapiens GN=TMEM87A PE=1 SV=3	RnTTIFLKF	HexNAc(6)Hex(4)Fuc(1)Ne	62	41900000	43800000	39700000	39100000	21600000	18700000	41800000	26466667	2051828	11036455	0.633174
SSRA	sp|P43307|SSRA_HUMAN Translocon-associated protein subunit alpha OS=Homo sapiens GN=SSR1 PE=1 SV=3	RYPQDYQFYIQnFTALPLNTVVPPQRQ	HexNAc(7)Hex(3)	136	251000	264000	162000	170000	179000	79800	225666.7	142933.3	55518.77	54859.94	0.633383
ASPH	sp|Q12797|ASPH_HUMAN Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	RLVQLFPnDTSLKNDLGVGYLLIGDNDNAKK	HexNAc(2)Hex(6)	452	8690000	8080000	6930000	5260000	4250000	5530000	7900000	5013333	893700.2	674709.8	0.634599
LDLR	sp|P01130|LDLR_HUMAN Low-density lipoprotein receptor OS=Homo sapiens GN=LDLR PE=1 SV=1	RLTGSDVNLLAENLLSPEDMVLFHnLTQPRG	HexNAc(5)Hex(6)Fuc(2)	657	678000	1520000	1310000	914000	642000	673000	1169333	743000	438270.8	148899.3	0.635405
ILK	sp|Q13418|ILK_HUMAN Integrin-linked protein kinase OS=Homo sapiens GN=ILK PE=1 SV=2	KLNEnHSGELWKGRW	HexNAc(2)Hex(7)	202	2020000	1100000	1500000	1180000	747000	1010000	1540000	979000	461302.5	218158.2	0.635714
ITA2	sp|P17301|ITA2_HUMAN Integrin alpha-2 OS=Homo sapiens GN=ITGA2 PE=1 SV=1	RTASCSnVTCWLKD	HexNAc(4)Hex(5)Fuc(3)	1057	1600000	1250000	1280000	1700000	91100	846000	1376667	879033.3	193993.1	804958.5	0.638523
S23IP	sp|Q9Y6Y8|S23IP_HUMAN SEC23-interacting protein OS=Homo sapiens GN=SEC23IP PE=1 SV=1	KITLPSIGRFRHFTnETLLDILFYNSPTYCQTIVEKV	HexNAc(3)Hex(4)NeuAc(1)	533	8510000	8700000	6860000	6610000	4200000	4570000	8023333	5126667	1011945	1297857	0.63897
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KKDTCTQECSYFnITKV	HexNAc(2)Hex(9)	669	8040000	5900000	8030000	6610000	3110000	4370000	7323333	4696667	1232653	1772719	0.641329
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RYLLLAGAPRELAVPDGYTnRT	HexNAc(2)Hex(3)Fuc(1)	86	1250000	872000	543000	720000	444000	547000	888333.3	570333.3	353782.9	139471.6	0.642026
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(6)Hex(3)	212	148000	1450000	1150000	226000	558000	984000	916000	589333.3	681812.3	379970.2	0.643377
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KSAVGTLSAnSSNVIQLIIDAYNSLSSEVILENGKL	HexNAc(6)Hex(6)Fuc(2)Ne	363	3360000	4630000	1920000	2280000	1730000	2370000	3303333	2126667	1355888	346458.3	0.643794
CD47	sp|Q08722|CD47_HUMAN Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1	RDIYTFDGALnKS	HexNAc(3)Hex(6)	73	3760000	3650000	3610000	2190000	1270000	3660000	3673333	2373333	77674.53	1205501	0.646098
CD47	sp|Q08722|CD47_HUMAN Leukocyte surface antigen CD47 OS=Homo sapiens GN=CD47 PE=1 SV=1	KGRDIYTFDGALnKSTVPTDFSSAKI	HexNAc(3)Hex(6)	73	1510000	1130000	793000	654000	794000	775000	1144333	741000	358714.8	75940.77	0.647539
RN213	sp|Q63HN8|RN213_HUMAN E3 ubiquitin-protein ligase RNF213 OS=Homo sapiens GN=RNF213 PE=1 SV=3	KqPPSDAALTMLSFIKSnCTLRD	HexNAc(7)Hex(5)Fuc(3)	1735	3980000	2180000	2780000	2650000	1330000	1820000	2980000	1933333	916515.1	667258.1	0.64877
ADA17	sp|P78536|ADA17_HUMAN Disintegrin and metalloproteinase domain-containing protein 17 OS=Homo sapiens GN=ADAM17 PE=1 SV=1	REQQLESCACnETDNSCKVCCRD	HexNAc(2)Hex(6)	594	156000	602000	718000	541000	8630	412000	492000	320543.3	296708.6	277718.7	0.651511
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RAnHSGAVVLLKRD	HexNAc(2)Hex(7)	323	6360000	5300000	5770000	4800000	2620000	3950000	5810000	3790000	531130.9	1098772	0.652324
PAR14	sp|Q460N5|PAR14_HUMAN Poly [ADP-ribose] polymerase 14 OS=Homo sapiens GN=PARP14 PE=1 SV=3	KLNInISLDHKRPLIKVLGISRD	HexNAc(4)Hex(3)Fuc(1)	1485	379000	143000	453000	433000	36500	167000	325000	212166.7	161901.2	202072	0.652821
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RLWnSTFLEEYSKL	HexNAc(2)Hex(9)	997	1540000	565000	311000	435000	422000	725000	805333.3	527333.3	648791.4	171307.7	0.654801
SC24C	sp|P53992|SC24C_HUMAN Protein transport protein Sec24C OS=Homo sapiens GN=SEC24C PE=1 SV=3	RGQVPPLVTTNFLVKDQGnASPRYIRC	HexNAc(2)Hex(5)	368	3800000	3040000	3210000	2370000	1550000	2670000	3350000	2196667	398873.4	579770.1	0.655721
NEST	sp|P48681|NEST_HUMAN Nestin OS=Homo sapiens GN=NES PE=1 SV=2	KSLGEEIQESLKTLEnQSHETLERE	HexNAc(4)Hex(3)Fuc(2)	562	49600000	50000000	50200000	44000000	26600000	27700000	49933333	32766667	305505	9743887	0.656208
CLPT1	sp|O96005|CLPT1_HUMAN Cleft lip and palate transmembrane protein 1 OS=Homo sapiens GN=CLPTM1 PE=1 SV=1	RAEDYGPVEVISHWHPnITINIVDDHTPWVKG	HexNAc(2)Hex(9)	241	1450000	1410000	1250000	1090000	617000	994000	1370000	900333.3	105830.1	250024.7	0.657178
STT3A	sp|P46977|STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE	RTILVDNNTWnNTHISRV	HexNAc(2)Hex(9)	548	13000000	9720000	11200000	9480000	5070000	7820000	11306667	7456667	1642600	2227338	0.659493
QCR2	sp|P22695|QCR2_HUMAN Cytochrome b-c1 complex subunit 2, mitochondrial OS=Homo sapiens GN=UQCRC2 PE=1 SV=3	KATAAPAGAPPQPQDLEFTKLPNGLVIASLEnYSPVSRI	HexNAc(4)Hex(3)Fuc(2)	54	25400000	28300000	22300000	17500000	12700000	20300000	25333333	16833333	3000556	3843609	0.664474
SPTB2	sp|Q01082|SPTB2_HUMAN Spectrin beta chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTBN1 PE=1 SV=2	KSAKDALLLWCQMKTAGYPNVNIHnFTTSWRD	HexNAc(2)Hex(3)Fuc(1)	197	2120000	1460000	1290000	1390000	886000	960000	1623333	1078667	438444.2	272149.5	0.664476
EIF3G	sp|O75821|EIF3G_HUMAN Eukaryotic translation initiation factor 3 subunit G OS=Homo sapiens GN=EIF3G PE=1 SV=2	RVTnLSEDTRETDLQELFRPFGSISRIYLAKD	HexNAc(2)Hex(3)	245	196000	331000	157000	130000	219000	106000	228000	151666.7	91307.17	59534.3	0.665205
PB1	sp|Q86U86|PB1_HUMAN Protein polybromo-1 OS=Homo sapiens GN=PBRM1 PE=1 SV=1	KnYTDKR	HexNAc(7)Hex(7)NeuAc(4)	671	3650000	1420000	3020000	2340000	842000	2200000	2696667	1794000	1149623	827422.5	0.665266
EGFR	sp|P00533|EGFR_HUMAN Epidermal growth factor receptor OS=Homo sapiens GN=EGFR PE=1 SV=2	KnCTSISGDLHILPVAFRG	HexNAc(2)Hex(7)	361	2170000	2350000	2300000	2180000	449000	1910000	2273333	1513000	92915.73	931287.8	0.665543
NPTN	sp|Q9Y639|NPTN_HUMAN Neuroplastin OS=Homo sapiens GN=NPTN PE=1 SV=2	KAnATIEVKA	HexNAc(2)Hex(9)	229	224000	551000	401000	371000	276000	138000	392000	261666.7	163685.7	117159.4	0.667517
MPRD	sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	RLKPLFnKS	HexNAc(2)Hex(8)	57	15500000	16600000	9990000	13700000	4310000	10200000	14030000	9403333	3541709	4745422	0.67023
SRBP1	sp|P36956|SRBP1_HUMAN Sterol regulatory element-binding protein 1 OS=Homo sapiens GN=SREBF1 PE=1 SV=2	KqEnLSLRT	HexNAc(6)Hex(4)Fuc(4)	384	25900000	20300000	24900000	26400000	13100000	8170000	23700000	15890000	2986637	9429809	0.670464
HS105	sp|Q92598|HS105_HUMAN Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	RTIGVAAKNQQITHAnNTVSNFKR	HexNAc(6)Hex(3)	61	733000	1250000	1420000	1260000	413000	609000	1134333	760666.7	357807.7	443400.9	0.670585
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(2)Hex(7)	212	6470000	4950000	6160000	5870000	2920000	3000000	5860000	3930000	803181.2	1680565	0.670648
EXOC6	sp|Q8TAG9|EXOC6_HUMAN Exocyst complex component 6 OS=Homo sapiens GN=EXOC6 PE=1 SV=3	RnETVLKH	HexNAc(6)Hex(4)Fuc(2)Ne	256	1070000	1240000	588000	440000	740000	765000	966000	648333.3	338213	180854.5	0.671153
4F2	sp|P08195|4F2_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3	KSLVTQYLnATGNRW	HexNAc(2)Hex(3)Fuc(1)	424	1000000	1060000	1600000	2050000	120000	293000	1220000	821000	330454.2	1067854	0.672951
NEST	sp|P48681|NEST_HUMAN Nestin OS=Homo sapiens GN=NES PE=1 SV=2	KSLGEEIQESLKTLEnQSHETLERE	HexNAc(5)Hex(3)Fuc(1)	562	18700000	19900000	22400000	22700000	8610000	9810000	20333333	13706667	1887679	7811532	0.674098
LAD1	sp|O00515|LAD1_HUMAN Ladinin-1 OS=Homo sapiens GN=LAD1 PE=1 SV=2	RnSSEKKS	HexNAc(3)Hex(5)NeuAc(1)	225	1280000	1230000	1180000	1080000	1030000	379000	1230000	829666.7	50000	391088.7	0.674526
CDCP1	sp|Q9H5V8|CDCP1_HUMAN CUB domain-containing protein 1 OS=Homo sapiens GN=CDCP1 PE=1 SV=3	RGLPSLTSVSWnISVPRD	HexNAc(2)Hex(9)	577	2000000	2190000	1790000	1760000	1140000	1140000	1993333	1346667	200083.3	357957.2	0.675585
5NTD	sp|P21589|5NTD_HUMAN 5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1	RIKLDnYSTQELGKT	HexNAc(4)Hex(5)Fuc(1)Ne	333	274000	72100	700000	579000	21000	107000	348700	235666.7	320545.9	300428.6	0.675844
ITA6	sp|P23229|ITA6_HUMAN Integrin alpha-6 OS=Homo sapiens GN=ITGA6 PE=1 SV=5	RAnHSGAVVLLKRD	HexNAc(2)Hex(4)	323	2620000	2460000	3120000	2310000	1340000	1900000	2733333	1850000	344286.7	486929.2	0.676829
QCR1	sp|P31930|QCR1_HUMAN Cytochrome b-c1 complex subunit 1, mitochondrial OS=Homo sapiens GN=UQCRC1 PE=1 SV=3	KDLPKAVELLGDIVQnCSLEDSQIEKE	HexNAc(3)Hex(4)NeuAc(1)	153	776000	125000	750000	530000	304000	284000	550333.3	372666.7	368578.8	136621.1	0.677165
UTP20	sp|O75691|UTP20_HUMAN Small subunit processome component 20 homolog OS=Homo sapiens GN=UTP20 PE=1 SV=3	KnISHLISAYLPKI	HexNAc(5)Hex(3)	1107	1670000	1620000	1410000	1600000	696000	887000	1566667	1061000	137961.3	476456.7	0.677234
SCRB2	sp|Q14108|SCRB2_HUMAN Lysosome membrane protein 2 OS=Homo sapiens GN=SCARB2 PE=1 SV=2	RTMVFPVMYLnESVHIDKETASRL	HexNAc(2)Hex(9)	412	2030000	2500000	890000	1350000	748000	1580000	1806667	1226000	827909	429637.1	0.678598
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RSGEDAHEALLTLVVPPALLLSSVRPPGACQAnETIFCELQ	HexNAc(4)Hex(5)Fuc(1)	697	2970000	3340000	3050000	2340000	2020000	2020000	3120000	2126667	194679.2	184752.1	0.681624
DDX27	sp|Q96GQ7|DDX27_HUMAN Probable ATP-dependent RNA helicase DDX27 OS=Homo sapiens GN=DDX27 PE=1 SV=2	RGLDIEGVKTVInFTMPNTIKH	HexNAc(2)Hex(4)	537	20000000	21400000	18700000	16600000	12900000	11500000	20033333	13666667	1350309	2635021	0.682196
ATD3B	sp|Q5T9A4|ATD3B_HUMAN ATPase family AAA domain-containing protein 3B OS=Homo sapiens GN=ATAD3B PE=1 SV=1	KnATAVTGRF	HexNAc(7)Hex(7)Fuc(4)Ne	266	1070000	1160000	1440000	1290000	723000	491000	1223333	834666.7	192959.4	411038.1	0.682289
5NTD	sp|P21589|5NTD_HUMAN 5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1	RSPIDERNnGTITWENLAAVLPFGGTFDLVQLKG	HexNAc(4)Hex(5)Fuc(1)Ne	403	270000	375000	351000	259000	220000	205000	332000	228000	55018.18	27874.72	0.686747
SPTN1	sp|Q13813|SPTN1_HUMAN Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	KVQKHQAFEAELSAnQSRI	HexNAc(4)Hex(3)	624	10600000	7520000	12700000	12300000	2820000	6060000	10273333	7060000	2605405	4818464	0.687216
HEAT1	sp|Q9H583|HEAT1_HUMAN HEAT repeat-containing protein 1 OS=Homo sapiens GN=HEATR1 PE=1 SV=3	RGIPVELWAHYVEELnSTQRV	HexNAc(4)Hex(3)Fuc(1)	776	1370000	1640000	1440000	1340000	867000	859000	1483333	1022000	140119	275425.1	0.688989
PGBM	sp|P98160|PGBM_HUMAN Basement membrane-specific heparan sulfate proteoglycan core protein OS=Homo sapiens GN=HSPG2 PE=1 SV	RALVnFTRS	HexNAc(2)Hex(3)	89	6300000	4790000	5760000	5820000	2080000	3730000	5616667	3876667	765136.2	1874309	0.690208
SYF1	sp|Q9HCS7|SYF1_HUMAN Pre-mRNA-splicing factor SYF1 OS=Homo sapiens GN=XAB2 PE=1 SV=2	RGISLFKWPnVSDIWSTYLTKFIARY	HexNAc(2)Hex(3)	552	1150000	1690000	1220000	779000	574000	1450000	1353333	934333.3	293655.1	458192.5	0.690394
AK17A	sp|Q02040|AK17A_HUMAN A-kinase anchor protein 17A OS=Homo sapiens GN=AKAP17A PE=1 SV=2	RISKSTMDFIRFEGEVEnKS	HexNAc(3)Hex(4)Fuc(1)	85	3820000	2970000	1020000	612000	2140000	2640000	2603333	1797333	1435560	1056533	0.690397
SERPH	sp|P50454|SERPH_HUMAN Serpin H1 OS=Homo sapiens GN=SERPINH1 PE=1 SV=2	RnVTWKL	HexNAc(2)Hex(8)	125	1560000	1540000	1450000	1380000	882000	882000	1516667	1048000	58594.65	287520.4	0.690989
CD151	sp|P48509|CD151_HUMAN CD151 antigen OS=Homo sapiens GN=CD151 PE=1 SV=3	RYHQPGHEAVTSAVDQLQQEFHCCGSnNSQDWRD	HexNAc(5)Hex(6)NeuAc(2)	159	4820000	3810000	3920000	3270000	2400000	3020000	4183333	2896667	554105.9	447921.1	0.69243
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RnVTRL	HexNAc(5)Hex(6)Fuc(1)	269	13800000	14100000	11600000	14300000	1780000	11300000	13166667	9126667	1365040	6536829	0.693165
CERS2	sp|Q96G23|CERS2_HUMAN Ceramide synthase 2 OS=Homo sapiens GN=CERS2 PE=1 SV=1	RLWLPVnLTWADLEDRDGRV	HexNAc(2)Hex(6)	19	5650000	6110000	4090000	4010000	3840000	3140000	5283333	3663333	1058741	461121.8	0.693375
5NTD	sp|P21589|5NTD_HUMAN 5'-nucleotidase OS=Homo sapiens GN=NT5E PE=1 SV=1	RSPIDERNnGTITWENLAAVLPFGGTFDLVQLKG	HexNAc(4)Hex(5)Fuc(1)	403	317000	330000	183000	174000	220000	184000	276666.7	192666.7	81377.72	24193.66	0.696386
AT1B3	sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	KFLKPYTLEEQKnLTVCPDGALFEQKG	HexNAc(2)Hex(8)	124	3360000	2900000	1090000	2080000	1260000	1780000	2450000	1706667	1200042	414889.5	0.696599
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	KAAnGSLRA	HexNAc(2)Hex(8)	322	1670000	1860000	1200000	1540000	946000	828000	1576667	1104667	339754.8	381598.4	0.700634
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KCHEGnGTFECGACRC	HexNAc(2)Hex(8)	481	1880000	1800000	1930000	1830000	999000	1130000	1870000	1319667	65574.39	446788.9	0.705704
ELYS	sp|Q8WYP5|ELYS_HUMAN Protein ELYS OS=Homo sapiens GN=AHCTF1 PE=1 SV=3	KIGEVWASKEPInSTTPFNSSKI	HexNAc(2)Hex(3)Fuc(1)	1073	775000	739000	606000	185000	504000	808000	706666.7	499000	89018.72	311530.1	0.706132
ARHG9	sp|O43307|ARHG9_HUMAN Rho guanine nucleotide exchange factor 9 OS=Homo sapiens GN=ARHGEF9 PE=1 SV=3	KRSQSPFWQnFSRL	HexNAc(2)Hex(8)	507	3330000	2960000	2530000	1870000	2290000	2080000	2940000	2080000	400374.8	210000	0.707483
MPRD	sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	RLKPLFnKS	HexNAc(3)Hex(6)	57	327000	574000	1400000	610000	10200	1010000	767000	543400	561933.3	503216.3	0.708475
PON2	sp|Q15165|PON2_HUMAN Serum paraoxonase/arylesterase 2 OS=Homo sapiens GN=PON2 PE=1 SV=3	KHTNMnLTQLKV	HexNAc(2)Hex(6)	254	9020000	8210000	8350000	7910000	3480000	6740000	8526667	6043333	432935.7	2295699	0.708757
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	KLRPIIISMnYSLPLRM	HexNAc(2)Hex(9)	573	2670000	4660000	2630000	2600000	2430000	2030000	3320000	2353333	1160646	292631.7	0.708835
STT3B	sp|Q8TCJ2|STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE	RTTLVDNNTWnNSHIALVGKA	HexNAc(2)Hex(9)	627	11000000	10500000	11700000	9850000	5500000	8190000	11066667	7846667	602771.4	2195230	0.709036
ODO2	sp|P36957|ODO2_HUMAN Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondria	RSLPGVSLCQGPGYPNSRKVVInNSVFSVRF	HexNAc(2)Hex(4)	51	9110000	8010000	8940000	7230000	5630000	5680000	8686667	6180000	592143	909670.3	0.711435
SSRB	sp|P43308|SSRB_HUMAN Translocon-associated protein subunit beta OS=Homo sapiens GN=SSR2 PE=1 SV=1	RIAPASnVSHTVVLRPLKA	HexNAc(2)Hex(9)	88	48300000	46100000	53600000	51100000	22700000	31800000	49333333	35200000	3855299	14502069	0.713514
NUFP2	sp|Q7Z417|NUFP2_HUMAN Nuclear fragile X mental retardation-interacting protein 2 OS=Homo sapiens GN=NUFIP2 PE=1 SV=1	KSDTIPIPNGVVTnNSGYITNGYMGKG	HexNAc(2)Hex(9)Fuc(1)	193	853000	779000	2770000	2390000	197000	558000	1467333	1048333	1128749	1175854	0.714448
SAMH1	sp|Q9Y3Z3|SAMH1_HUMAN Deoxynucleoside triphosphate triphosphohydrolase SAMHD1 OS=Homo sapiens GN=SAMHD1 PE=1 SV=2	RnFTKPQDGDVIAPLITPQKK	HexNAc(4)Hex(4)Fuc(2)Ne	577	4160000	3380000	2710000	2830000	2390000	2110000	3416667	2443333	725695.1	362950.9	0.715122
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	RGHTLTLnFTRN	HexNAc(3)Hex(5)	103	4480000	3920000	4630000	3740000	2320000	3280000	4343333	3113333	374210.3	724522.8	0.716807
AT1B3	sp|P54709|AT1B3_HUMAN Sodium/potassium-transporting ATPase subunit beta-3 OS=Homo sapiens GN=ATP1B3 PE=1 SV=1	KKFLKPYTLEEQKnLTVCPDGALFEQKG	HexNAc(4)Hex(6)Fuc(1)	124	1060000	1780000	1190000	1360000	548000	987000	1343333	965000	383710	406446.8	0.718362
TRI26	sp|Q12899|TRI26_HUMAN Tripartite motif-containing protein 26 OS=Homo sapiens GN=TRIM26 PE=1 SV=1	RPEDGVWALRLSSSGIWAnTSPEAELFPALRP	HexNAc(6)Hex(3)Fuc(2)	473	2500000	2850000	3010000	2990000	1540000	1500000	2786667	2010000	260832	848940.5	0.721292
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KCHEGnGTFECGACRC	HexNAc(2)Hex(9)	481	4890000	4460000	4690000	4540000	2560000	3070000	4680000	3390000	215174.3	1028056	0.724359
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(2)Hex(6)	212	4250000	2310000	4010000	3450000	1920000	2290000	3523333	2553333	1057607	798269	0.724693
ASPH	sp|Q12797|ASPH_HUMAN Aspartyl/asparaginyl beta-hydroxylase OS=Homo sapiens GN=ASPH PE=1 SV=3	RLVQLFPnDTSLKNDLGVGYLLIGDNDNAKK	HexNAc(2)Hex(5)	452	2990000	2110000	2170000	2500000	1480000	1290000	2423333	1756667	491663.8	650717.6	0.724897
MIRO2	sp|Q8IXI1|MIRO2_HUMAN Mitochondrial Rho GTPase 2 OS=Homo sapiens GN=RHOT2 PE=1 SV=2	KNLRnISELFYYAQKA	HexNAc(2)Hex(3)Fuc(1)	154	10300000	7620000	10200000	5990000	4690000	9770000	9373333	6816667	1519254	2638964	0.72724
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	RGHTLTLnFTRN	HexNAc(3)Hex(6)	103	5650000	6070000	3350000	4320000	2920000	3720000	5023333	3653333	1464286	702376.9	0.727273
TMTC3	sp|Q6ZXV5|TMTC3_HUMAN Transmembrane and TPR repeat-containing protein 3 OS=Homo sapiens GN=TMTC3 PE=1 SV=2	RAnESRLEEADQLYRQ	HexNAc(2)Hex(6)	541	2000000	1480000	29300	993000	593000	973000	1169767	853000	1021322	225388.6	0.729205
P66B	sp|Q8WXI9|P66B_HUMAN Transcriptional repressor p66-beta OS=Homo sapiens GN=GATAD2B PE=1 SV=1	RPGAQGVEPQNLRTLQGHSVIRSATnTTLPHMLMSQRV	HexNAc(5)Hex(5)Fuc(1)	253	3600000	5120000	4170000	4590000	2060000	2780000	4296667	3143333	767875.9	1303546	0.731575
SSRB	sp|P43308|SSRB_HUMAN Translocon-associated protein subunit beta OS=Homo sapiens GN=SSR2 PE=1 SV=1	RIAPASnVSHTVVLRPLKA	HexNAc(2)Hex(8)	88	64300000	57500000	66000000	60700000	31300000	45500000	62600000	45833333	4497777	14702834	0.732162
STT3A	sp|P46977|STT3A_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3A OS=Homo sapiens GN=STT3A PE	RTILVDNNTWnNTHISRV	HexNAc(2)Hex(8)	548	11900000	11400000	10500000	10300000	5760000	8690000	11266667	8250000	709459.9	2301760	0.732249
ITB4	sp|P16144|ITB4_HUMAN Integrin beta-4 OS=Homo sapiens GN=ITGB4 PE=1 SV=5	KHNIIPIFAVTnYSYSYYEKL	HexNAc(5)Hex(6)Fuc(1)Ne	327	1360000	1130000	1000000	1040000	873000	647000	1163333	853333.3	182300.1	197236.7	0.733524
NICA	sp|Q92542|NICA_HUMAN Nicastrin OS=Homo sapiens GN=NCSTN PE=1 SV=2	RKIYIPLnKT	HexNAc(2)Hex(9)	45	2600000	2410000	2230000	2600000	767000	1960000	2413333	1775667	185022.5	930299.1	0.735773
CNDD3	sp|P42695|CNDD3_HUMAN Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=1 SV=2	RqTSnRS	HexNAc(7)Hex(6)	518	386000	273000	562000	371000	387000	142000	407000	300000	145640	137065.7	0.737101
SUN1	sp|O94901|SUN1_HUMAN SUN domain-containing protein 1 OS=Homo sapiens GN=SUN1 PE=1 SV=3	RnVTHHVSVTKQ	HexNAc(2)Hex(6)	588	170000	634000	782000	573000	395000	206000	528666.7	391333.3	319307.6	183527.5	0.740227
GUAD	sp|Q9Y2T3|GUAD_HUMAN Guanine deaminase OS=Homo sapiens GN=GDA PE=1 SV=1	RGASIAHCPNSnLSLSSGFLNVLEVLKHEVKIGLGTDVAGG	HexNAc(2)Hex(5)	305	13900000	18200000	25800000	25800000	8570000	8620000	19300000	14330000	6025778	9933343	0.742487
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	RGHTLTLnFTRN	HexNAc(2)Hex(5)	103	14700000	10600000	13800000	11000000	7340000	10700000	13033333	9680000	2154840	2032043	0.742711
CLH1	sp|Q00610|CLH1_HUMAN Clathrin heavy chain 1 OS=Homo sapiens GN=CLTC PE=1 SV=5	KqLPLVKPYLRSVQNHNnKSVNESLNNLFITEEDYQALRT	HexNAc(6)Hex(5)Fuc(1)	1460	2330000	1780000	2080000	1680000	1490000	1430000	2063333	1533333	275378.5	130511.8	0.743134
PPIL2	sp|Q13356|PPIL2_HUMAN Peptidyl-prolyl cis-trans isomerase-like 2 OS=Homo sapiens GN=PPIL2 PE=1 SV=1	RQDIITLQDPTNLDKFnVSNFYHVKN	HexNAc(3)Hex(3)Fuc(1)	168	2790000	2210000	1150000	976000	1390000	2210000	2050000	1525333	831624.9	628032.9	0.744065
SCMC1	sp|Q6NUK1|SCMC1_HUMAN Calcium-binding mitochondrial carrier protein SCaMC-1 OS=Homo sapiens GN=SLC25A24 PE=1 SV=2	KEGGIRSLWRGnGTNVIKI	HexNAc(2)Hex(3)Fuc(1)	254	1370000	1390000	1420000	1390000	911000	815000	1393333	1038667	25166.11	308026.5	0.745455
SAP	sp|P07602|SAP_HUMAN Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2	KTCDWLPKPnMSASCKE	HexNAc(2)Hex(3)Fuc(1)	101	6130000	6470000	3900000	3610000	3400000	5380000	5500000	4130000	1396030	1087612	0.750909
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RNPCTSEQnCTSPFSYKN	HexNAc(2)Hex(8)	212	1630000	1590000	1630000	1600000	1200000	849000	1616667	1216333	23094.01	375766.3	0.752371
APC1	sp|Q9H1A4|APC1_HUMAN Anaphase-promoting complex subunit 1 OS=Homo sapiens GN=ANAPC1 PE=1 SV=1	KTNnRSIADWLRAPDTMYLLDFVKP	HexNAc(3)Hex(3)Fuc(1)	1380	3770000	5210000	4520000	3620000	3340000	3240000	4500000	3400000	720208.3	196977.2	0.755556
ITA3	sp|P26006|ITA3_HUMAN Integrin alpha-3 OS=Homo sapiens GN=ITGA3 PE=1 SV=5	RAHCVWLECPIPDAPVVTnVTVKA	HexNAc(5)Hex(6)NeuAc(1)	926	1630000	1260000	1190000	1160000	752000	1180000	1360000	1030667	236431.8	241539.5	0.757843
B4GA1	sp|O43505|B4GA1_HUMAN Beta-1,4-glucuronyltransferase 1 OS=Homo sapiens GN=B4GAT1 PE=1 SV=1	RVAQPGINYALGTnVSYPNNLLRN	HexNAc(2)Hex(8)Fuc(1)	204	2530000	3000000	2220000	1960000	2230000	1700000	2583333	1963333	392725.5	265015.7	0.76
TANK	sp|Q92844|TANK_HUMAN TRAF family member-associated NF-kappa-B activator OS=Homo sapiens GN=TANK PE=1 SV=2	RDEEDTSFESLSKFNVKFPPMDnDSTFLHSTPERP	HexNAc(6)Hex(5)NeuAc(1)	241	1680000	2190000	1430000	2220000	619000	1200000	1766667	1346333	387341.4	810469.2	0.762075
SAHH2	sp|O43865|SAHH2_HUMAN Adenosylhomocysteinase 2 OS=Homo sapiens GN=AHCYL1 PE=1 SV=2	KLCVPAMNVnDSVTKQKFDNLYCCRE	HexNAc(3)Hex(3)Fuc(2)	279	1930000	2640000	1420000	1690000	1880000	998000	1996667	1522667	612726.1	464199.7	0.762604
CHK2	sp|O96017|CHK2_HUMAN Serine/threonine-protein kinase Chk2 OS=Homo sapiens GN=CHEK2 PE=1 SV=1	RRPLNnNSEIALSLSRNKVFVFFDLTVDDQSVYPKA	HexNAc(5)Hex(5)Fuc(1)	185	2790000	4640000	3790000	4630000	1600000	2340000	3740000	2856667	926013	1579694	0.763815
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KKDTCTQECSYFnITKV	HexNAc(2)Hex(6)	669	10600000	7880000	10900000	8990000	5750000	7740000	9793333	7493333	1663771	1634024	0.765146
4F2	sp|P08195|4F2_HUMAN 4F2 cell-surface antigen heavy chain OS=Homo sapiens GN=SLC3A2 PE=1 SV=3	RDIENLKDASSFLAEWQnITKG	HexNAc(5)Hex(7)Fuc(2)Ne	365	4200000	3090000	1200000	1960000	2840000	1710000	2830000	2170000	1516806	593548.7	0.766784
DYST	sp|Q03001|DYST_HUMAN Dystonin OS=Homo sapiens GN=DST PE=1 SV=4	KTQVEQnKSFEAELKQNVNKV	HexNAc(5)Hex(5)	4558	1.95E+08	1.81E+08	1.52E+08	1.54E+08	1.33E+08	1.18E+08	1.76E+08	1.35E+08	21931712	18083141	0.767045
AT1B1	sp|P05026|AT1B1_HUMAN Sodium/potassium-transporting ATPase subunit beta-1 OS=Homo sapiens GN=ATP1B1 PE=1 SV=1	KYLQPLLAVQFTnLTMDTEIRI	HexNAc(6)Hex(4)NeuAc(1)	265	2060000	2610000	1980000	1770000	1680000	1660000	2216667	1703333	342977.2	58594.65	0.768421
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RKEnSSEICSNNGECVCGQCVCRK	HexNAc(2)Hex(6)	520	164000	973000	953000	1020000	11400	575000	696666.7	535466.7	461411.2	505460.8	0.768612
CDK13	sp|Q14004|CDK13_HUMAN Cyclin-dependent kinase 13 OS=Homo sapiens GN=CDK13 PE=1 SV=2	KTGPGQHLnHSELAILLNLLQSKT	HexNAc(7)Hex(5)NeuAc(1)	1088	6080000	5800000	4000000	5360000	2890000	3970000	5293333	4073333	1128775	1238238	0.769521
NAT10	sp|Q9H0A0|NAT10_HUMAN N-acetyltransferase 10 OS=Homo sapiens GN=NAT10 PE=1 SV=2	KnGTLNIKQ	HexNAc(5)Hex(5)	82	1830000	1470000	2130000	2470000	476000	1240000	1810000	1395333	330454.2	1006034	0.770902
RS6	sp|P62753|RS6_HUMAN 40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	RGCIVDAnLSVLNLVIVKK	HexNAc(5)Hex(5)	105	1240000	2640000	2060000	1530000	2040000	1010000	1980000	1526667	703420.2	515008.1	0.771044
RL9	sp|P32969|RL9_HUMAN 60S ribosomal protein L9 OS=Homo sapiens GN=RPL9 PE=1 SV=1	MKTILSnQTVDIPENVDITLKG	HexNAc(4)Hex(5)Fuc(3)	7	3970000	2550000	3110000	2030000	3090000	2310000	3210000	2476667	715262.2	549302.6	0.771547
MPRI	sp|P11717|MPRI_HUMAN Cation-independent mannose-6-phosphate receptor OS=Homo sapiens GN=IGF2R PE=1 SV=3	KMnFTGGDTCHKV	HexNAc(2)Hex(8)	1312	570000	779000	573000	433000	519000	548000	640666.7	500000	119809.6	59808.03	0.780437
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RnVTRL	HexNAc(2)Hex(9)	269	3080000	4150000	4070000	3610000	2710000	2520000	3766667	2946667	596014.5	582265.7	0.782301
UD110	sp|Q9HAW8|UD110_HUMAN UDP-glucuronosyltransferase 1-10 OS=Homo sapiens GN=UGT1A10 PE=1 SV=1	RSLnCTVKT	HexNAc(2)Hex(5)	71	2410000	2520000	2360000	2310000	1870000	1530000	2430000	1903333	81853.53	391066.9	0.783265
LYN	sp|P07948|LYN_HUMAN Tyrosine-protein kinase Lyn OS=Homo sapiens GN=LYN PE=1 SV=3	RLGAGQFGEVWMGYYNnSTKVAVKT	HexNAc(3)Hex(3)Fuc(1)	268	895000	1540000	724000	1430000	265000	807000	1053000	834000	430333.6	582969.1	0.792023
HYOU1	sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	RLSALDNLLnHSSMFLKG	HexNAc(6)Hex(6)Fuc(1)	830	1290000	1260000	1110000	1410000	875000	620000	1220000	968333.3	96436.51	403185.2	0.793716
SCYL2	sp|Q6P3W7|SCYL2_HUMAN SCY1-like protein 2 OS=Homo sapiens GN=SCYL2 PE=1 SV=1	KQTKDLTDTLMDnMSSLTSLSVSTPKS	HexNAc(4)Hex(4)	726	3590000	4410000	5030000	5230000	2680000	2590000	4343333	3500000	722311.1	1498900	0.805833
HYOU1	sp|Q9Y4L1|HYOU1_HUMAN Hypoxia up-regulated protein 1 OS=Homo sapiens GN=HYOU1 PE=1 SV=1	RLSALDNLLnHSSMFLKG	HexNAc(4)Hex(3)	830	926000	1240000	1040000	1040000	790000	760000	1068667	863333.3	158950.7	153731.4	0.80786
AMPN	sp|P15144|AMPN_HUMAN Aminopeptidase N OS=Homo sapiens GN=ANPEP PE=1 SV=4	KAEFnITLIHPKD	HexNAc(2)Hex(5)	234	2470000	2080000	1830000	1600000	1520000	2040000	2126667	1720000	322542	280000	0.808777
SAP	sp|P07602|SAP_HUMAN Prosaposin OS=Homo sapiens GN=PSAP PE=1 SV=2	KSLPCDICKDVVTAAGDMLKDnATEEEILVYLEKT	HexNAc(2)Hex(3)Fuc(1)	80	2640000	3170000	2130000	1650000	2440000	2340000	2646667	2143333	520032.1	430155	0.809824
NELFA	sp|Q9H3P2|NELFA_HUMAN Negative elongation factor A OS=Homo sapiens GN=NELFA PE=1 SV=3	RSPTAPSVFSPTGnRTPIPPSRTLLRK	HexNAc(2)Hex(3)	237	1950000	2070000	1550000	1310000	1600000	1630000	1856667	1513333	272274.4	176729.5	0.815081
NCEH1	sp|Q6PIU2|NCEH1_HUMAN Neutral cholesterol ester hydrolase 1 OS=Homo sapiens GN=NCEH1 PE=1 SV=3	RARLnWTSLLPASFTKN	HexNAc(2)Hex(6)	287	5970000	6520000	6360000	6880000	2800000	5740000	6283333	5140000	282901.6	2105137	0.818037
CCD58	sp|Q4VC31|CCD58_HUMAN Coiled-coil domain-containing protein 58 OS=Homo sapiens GN=CCDC58 PE=1 SV=1	RIVHELnTTVPTASFAGKI	HexNAc(3)Hex(4)	35	2580000	1850000	2030000	2450000	1270000	1580000	2153333	1766667	380306.9	611746.1	0.820433
PKP3	sp|Q9Y446|PKP3_HUMAN Plakophilin-3 OS=Homo sapiens GN=PKP3 PE=1 SV=1	RnLSSASQATRQ	HexNAc(3)Hex(4)NeuAc(1)	484	1060000	584000	710000	1190000	45000	700000	784666.7	645000	246627.9	574478	0.822005
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KLRNPCTSEQnCTSPFSYKN	HexNAc(5)Hex(5)Fuc(1)	212	1350000	596000	1110000	541000	897000	1080000	1018667	839333.3	385208.2	274088.2	0.823953
SULF2	sp|Q8IWU5|SULF2_HUMAN Extracellular sulfatase Sulf-2 OS=Homo sapiens GN=SULF2 PE=1 SV=1	KYLNEYnGSYVPPGWKEWVGLLKN	HexNAc(2)Hex(9)Fuc(1)	149	468000	656000	2190000	1950000	223000	558000	1104667	910333.3	944614.9	915825.5	0.82408
SSRB	sp|P43308|SSRB_HUMAN Translocon-associated protein subunit beta OS=Homo sapiens GN=SSR2 PE=1 SV=1	RIAPASnVSHTVVLRPLKA	HexNAc(2)Hex(7)	88	5890000	5610000	3790000	6430000	2720000	3480000	5096667	4210000	1140234	1959770	0.82603
MPRD	sp|P20645|MPRD_HUMAN Cation-dependent mannose-6-phosphate receptor OS=Homo sapiens GN=M6PR PE=1 SV=1	KPLFnKS	HexNAc(6)Hex(6)Fuc(2)Ne	57	542000	297000	156000	48900	271000	505000	331666.7	274966.7	195321.1	228075.9	0.829045
STT3B	sp|Q8TCJ2|STT3B_HUMAN Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B OS=Homo sapiens GN=STT3B PE	RTTLVDNNTWnNSHIALVGKA	HexNAc(2)Hex(8)	627	5150000	4700000	4870000	5090000	2860000	4300000	4906667	4083333	227229.7	1130678	0.832201
CPSF1	sp|Q10570|CPSF1_HUMAN Cleavage and polyadenylation specificity factor subunit 1 OS=Homo sapiens GN=CPSF1 PE=1 SV=2	RQDTCSIVAISLnITQKV	HexNAc(2)Hex(5)	246	2770000	1360000	476000	1880000	502000	1460000	1535333	1280667	1157007	706287	0.834129
CNDD3	sp|P42695|CNDD3_HUMAN Condensin-2 complex subunit D3 OS=Homo sapiens GN=NCAPD3 PE=1 SV=2	RqTSnRS	HexNAc(6)Hex(4)	518	934000	1530000	2120000	2680000	301000	844000	1528000	1275000	593002.5	1246688	0.834424
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	KAAnGSLRA	HexNAc(2)Hex(9)	322	2980000	1750000	2070000	2480000	1810000	1410000	2266667	1900000	638148.4	540647.8	0.838235
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	RGHTLTLnFTRN	HexNAc(2)Hex(7)	103	2050000	1520000	1700000	1640000	1050000	1730000	1756667	1473333	269505.7	369368.8	0.83871
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	RKEnSSEICSNNGECVCGQCVCRK	HexNAc(2)Hex(8)	520	4170000	3280000	2720000	3760000	1600000	3200000	3390000	2853333	731231.8	1120952	0.841691
MIF	sp|P14174|MIF_HUMAN Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	KIGGAQnRSYSKLLCGLLAERL	HexNAc(3)Hex(3)Fuc(1)	73	6390000	7440000	7420000	8210000	5820000	3870000	7083333	5966667	600527.5	2173714	0.842353
VIME	sp|P08670|VIME_HUMAN Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	RQDVDnASLARLDLERK	HexNAc(4)Hex(7)NeuAc(2)	212	1740000	1470000	1750000	1310000	1250000	1620000	1653333	1393333	158850	198578.3	0.842742
FAT1	sp|Q14517|FAT1_HUMAN Protocadherin Fat 1 OS=Homo sapiens GN=FAT1 PE=1 SV=2	KKLDIGQYLLnVSVTDGKF	HexNAc(2)Hex(6)	3613	4330000	5030000	7350000	6340000	1480000	6290000	5570000	4703333	1580759	2791600	0.844405
ITB1	sp|P05556|ITB1_HUMAN Integrin beta-1 OS=Homo sapiens GN=ITGB1 PE=1 SV=2	KnVTNRS	HexNAc(4)Hex(6)Fuc(2)	94	868000	164000	185000	476000	332000	221000	405666.7	343000	400530.1	127855.4	0.845522
CERS2	sp|Q96G23|CERS2_HUMAN Ceramide synthase 2 OS=Homo sapiens GN=CERS2 PE=1 SV=1	RLWLPVnLTWADLEDRDGRV	HexNAc(2)Hex(7)	19	619000	704000	600000	579000	603000	444000	641000	542000	55380.5	85714.64	0.845554
LAMP1	sp|P11279|LAMP1_HUMAN Lysosome-associated membrane glycoprotein 1 OS=Homo sapiens GN=LAMP1 PE=1 SV=3	RGHTLTLnFTRN	HexNAc(2)Hex(6)	103	2010000	1660000	1650000	1870000	1000000	1630000	1773333	1500000	205020.3	449332.8	0.845865