

Table S1:List of ligands and elution reagents used in biopanning

S.No.	Ligand	Elution reagent
1	Mucin from porcine stomach (Sigma)	· 100 mM of sialic acid in water, pH 5 (adjusted with --) · 100 mM of L-fucose in water · 100 mM of D-galactose in water · 100 mM of N-acetyl-D-glucosamine in water · 100 mM of N-acetyl-D-galactosamine in water · 100 mM of D-mannose in water
2	PAA-β-D-Galactose (Glycotech)	· D-Galactose (100 mM in water)
3	PAA-β-D-GlcNAc (Glycotech)	· N-Acetyl-D-glucosamine (100 mM in water)
4	Amylose from Potato (Sigma)	· Amylose (1 µl of 10 mg/ml ligand in DMSO + 99 µl water) · D-Glucose (100 mM in water)
5	Amylopectin from Maize (Sigma)	· Amylopectin (1 mg/ml in water) · D-Glucose (100 mM in water)
6	Starch from Rice (Sigma)	· Starch (1 µl of 10 mg/ml ligand in DMSO + 99 µl water) · D-Glucose (100 mM in water)
7	β-D-Glucan from Barley (Sigma)	· β-D-Glucan (1 µl of 10 mg/ml ligand in DMSO + 99 µl water) · D-Glucose (100 mM in water)
8	Dextran from <i>Leuconostoc mesenteroides</i> (Sigma)	· Dextran (1 mg/ml in water) · D-Glucose (100 mM in water)
9	Laminarin from <i>Laminaria digitata</i> (Sigma)	· Laminarin (1 mg/ml in water) · D-Glucose (100 mM in water)
10	Arabinogalactan from Larch wood (Sigma)	· Arabinogalactan (1 mg/ml in water) · L-Arabinose (100 mM in water) · D-Galactose (100 mM in water)
11	Inulin from Chicory (Sigma)	· Inulin (1 mg/ml in water) · D-Fructose (100 mM in water) · D-Glucose (100 mM in water)
12	Levan from <i>Erwinia herbicola</i> (Sigma)	· Levan (1 µl of 10 mg/ml ligand in DMSO + 99 µl water) · D-Fructose (100 mM in water)
13	Pectin from Apple (Sigma)	· Pectin (1 mg/ml in water) · D-Galacturonic acid (100 mM in water, pH ~5)
14	Xylan from Beechwood (Sigma)	· Xylan (1 mg/ml in water) · D-Xylose (100 mM in water)
15	Peptidoglycan from <i>Methanobacterium sp</i> (Sigma)	· Peptidoglycan <i>Metanobacterium</i> sp (1 mg/ml in water) · N-Acetyl-D-glucosamine (100 mM in water)
16	Peptidoglycan from <i>Staphylococcus aureus</i> (Sigma)	· Peptidoglycan <i>Staphylococcus aureus</i> (1 mg/ml in water) · N-Acetyl-D-glucosamine (100 mM in water)

Table S2: Titer of the eluate containing phages in various rounds of biopanning using 1×10^3 : 1×10^{11} ratio of SrNaFLD-T7 phage: T7 10-3b (non-recombinant) phage

S.No.	Titer
1 st	4×10^4
2 nd	2×10^4
3 rd	4×10^3
4 th	3.4×10^3
5 th	1.5×10^4
6 th	2×10^5

Table S3: List of the titers of the eluates obtained after screening against various glycans/glycoconjugates and eluting with different reagents from the 8th round of biopanning

Ligand	Eluate	Titer
Mucin from porcine stomach, Type II	L-Fucose	1x10 ⁶
	D-Galactose	2.6x10 ⁷
	N-Acetyl-D- galactosamine	2.8x10 ⁷
	N-Acetyl-D- glucosamine	2.5x10 ⁷
	D-Mannose	8x10 ⁶
	D-Sialic Acid	6x10 ⁶
Amylose from Potato	Amylose	3x10 ⁶
	D-Glucose	2x10 ⁸
Amylopectin from Maize	Amylopectin	1x10 ⁸
	D-Glucose	1x10 ⁶
Starch from Rice	Starch	1.4x10 ⁷
	D-Glucose	2x10 ⁷
PAA-β-D-Galactose	D-Galactose	2.3x10 ⁵
PAA-β-D-GlucNAc	N-Acetyl-D-glucosamine	2.0x10 ⁵
β-D-Glucan from Barley	β-D-Glucan	1x10 ⁸
	D-Glucose	1.2x10 ⁸
Dextran from Leuconostocmesenteroides	Dextran	3x10 ⁴
	D-Glucose	1x10 ⁶
Laminarin from Laminariadigitata	Laminarin	1.8x10 ⁵
	D-Glucose	6x10 ⁴
Arabinogalactan from Larch wood	Arabinogalactan	2x10 ⁷
	L-Arabinose	2x10 ⁵
	D-Galactose	6x10 ⁵
Inulin from Chicory	Inulin	1x10 ⁵
	D-Fructose	13x10 ⁵
	D-Glucose	7x10 ⁵
Levan from <i>Erwiniaherbicola</i>	Levan	3x10 ⁷
	D-Fructose	7x10 ⁵
Pectin from Apple	Pectin	1x10 ⁷
	D-Galacturonic acid	2x10 ⁷

Xylan from Beechwood	Xylan	1.6×10^6
	D-Xylose	1.2×10^6
Peptidoglycan Metanobacteriumsp	Peptidoglycan Metanobacteriumsp	4×10^7
	N-Acetyl-D-glucosamine	1.4×10^6
Peptidoglycan Staphylococcus aureus	Peptidoglycan Staphylococcus aureus	5×10^7
	N-Acetyl-D-glucosamine	2×10^7

Table S4: Sequences of metagenomic inserts in screened phages

Final Clone ID	Accession Number	Old Clone ID	Ligand used for biopanning	Elution agent	Nucleic Acid Sequence (5'-3')	Amino Acid Sequence
Am-Glc2	ON711254	AmG2 or Am2	Amylose	Glucose	CTTTTCAATCCAGCTAATGGTACAGCCTTCTCTGATGAGTCTCTCACTGCTGACTGCTAC TCCTTTGAATGCTGTTTTCTGCCCTGGATTTCAGGTGAATGATGGTGCTAAGCAGGATTTTA CTGCTGACAAGCAGTTTACTGTAGGTGCTGATGTTGCCATTGGTAAGAAATGTTACTATC ACTTGGGGTGCAACTGACACAGGAAGGCAATACAGAAACAGGTTCCGGTAACCTTACAAGA AGGTGAAGGCTTACGTTCCAGAAATTGGGCAAGGCTGACGAAATCTCCTGTTTCTTGGG GACATCCAATGCGGCAGCAGCCGTATATGTATGGAATAACAAGGTTAAGCCTGTAATT AAGTATGCTGGTGAATGGAATGATGCTATCAATAAAAAGTTGCCCTCTGTAGTAAGAG TGTTTCTGGAAGAAATGTCTTCAAGTGGACTTATGATGGCACCAGACAACTGTTCCCTA CTCAACTCATTTTCTTGGATGGTAATGGAATAAGTTAACTAATAACGTGGACTTTGTCA ACCACGGCTACTATGTTGACGGAACATACAGCACTACTGTGACCAAGGTACATGAAGA TGGGG	LFPNANGTAFSDSLTVTATPLNAVSAWIVQVNDGAKQDFTADKQFTVGADVAYGKNVITWGTAD KEGNTETGSVYTKVKVAYVPELGKADEISCFLETSNAAAAVYVWNNKVPVYKAGEWNDAINKK LPLVGKSVSGKNVFKWTYDGTETTTPVTQLIFLDGNGNKLNNVDFVNHGYDGTSTVTVTKVHE DG
Am-Am1	ON711255	AmAm1	Amylose	Amylose	CTTCTACTCCAACAGGTATCTACGCTTACTTCTCGCTCCTTCAGACTGGAATCAGGT TGACTGCTGGGCTTGGACTGAAACAGACAACTTTACCGGTGGTACCTGGCCAGGTGTA GCATGTACCAAGATTGGTGGAAGAAGAAATGGTTGGATGCTCGATGTGGAAGTATG ATGGCGATTGACAACTGCTCTACTAAGATCATCTTCAACAACGGTGGTAATGGTCAG CAGACAGCCAACTTGGATTTCGTCAACGGTGCGATTTATGACCGCAACGGTAAGACCA ATGAGTCTGTCTCAACAGGCATCAACCAGACTGTAGCAGCTCAGAAGGCAGGCGCAGT GAAGATCTACACCCTCACAGGTGTGAAGTTGCCGAGGTAAGAAACGTTACGAGTGTCT GAATACCTCTTGGCTCCAGGTGCCTACATCTGCAATTGGCAAGAAAGTTTGTATCAAGTA ATATTGAAATTTAGTAACCTCATCAATAGTAATAAGTTTTTTAGCCCGATTCTGCTTCGT GAGAAGCGGTATCGGGCCTTTTTATGTCCAAAAGGATAAATATTTATGTTCAAAAGGA TAAATAAAGTAAATAATTTCTCATATTGCGATAACTTTGTGTAACCTTGTAGCGAAAAATA AAAAAGGG	LPTPTGIYAYFLAPSDWNQVDCWAWTETDNFTGGTWPVACTKIGVKKNGLDVVMWKYDGL TTAPTIIFNNGGNGQQTANLDFVNGAVYDRNGKTNESVSTGINQTVAQKAGAVKIYTLTGVKVA EVRNVQDAEYLLAPGAYICNGKKFVIK
Ap-Ap2	ON711256	ApAp2	Amylopectin	Amylopectin	CCTTGGCAACAGGTTGTTGCGGCAAGAATCTGACAGGTGCATGGCCTGGTAAGGTG ATGAAGGGTCTGAGGAGATTGAGTGTAAATCTGGAATGACTTATGATTCGATAACG TTGAGAGCTTCAATGATAATATTGAAATGGTAGCGGTGATCAGTCTGGTGACATCAC GGTATTACAAGTGATACCTACTTGGAGTATGACGGTGGTAAAGTGCCAAGAAATTTTC TGCTCCAGCAAATTCGACAGCTGCTGCTAAGGTGGCTTTCAGCCCTAACGGTGGTGAA TTTTGGAAGTCAATCACTGTAACGTGCAACGGCTGAGCAGCAATGCTAAGAGCGGTGGT ATAAGATTGGTGATGGTGCGCAGGTAAATCTGACTCCTGGTAAGGCTGCTACATCAC ACTCGGTGCTGACATGATGGAAGGCGAGAGCAAGACTGTAACTTGGAGTGCAACCAAT GCTGATGGTACAAACCAAGACAGGTTCTTCAACCTTCAACAAGATTAAAGAGGTAGTTAT TTCTACTCCAACAGGTATCTTGGCTTACTTCTCGCTCCTTCAGACTGGAGTCAAGGTAG ATTGCTGGGCTTGGACTGATTCTGAGAAAGTGAACTTTACCGGTGGTAAATGGCCAGG TGTAGCTTGTGTAAGACTGGTGTGAAGAAAGTGGTCTGGATGTCTGGATGTGGAAG TATGATGGCGATTGACAACCTGCTCCTACTATGATCATCTTCAACAACGGCGGTGGTCA GCAGACAAAGGATTGAAATTCGAAAACGGTGCACTTTATAACCTTCCCGGTAAAGACC AATGAGTCTGTCTCAACAGGTATCAATCAGGTAGGTAGCAAGAAGGCTCTGCTAAGT TGAAGATTACTCTATTATGGTCAGAAGGGGG	PWTTGVGGKNTGAWPGKVMKGPEEIDGAKYWTYDFDNVESFNVLNNGSGDQSGDITGITS YLEYDGGKSARKKISAPANSTAAKAVFSPNGGEFEKSITVTATLSSNAKSGWYKIDGAQVNLTP GKAATFTLADMMEGESKTVWTSATNADGTTKTGSSFTNKIEVPIPTPTGIFAYFLAPSDWSQV DCWAWTDSEKVNFTGGKWPVGVACVKTGVYKKNGLDVMWYKDGDLTAPTMIIFNNGGQQTK DLKFENGAVYNLAGKTNEVSTGINQVGSKKAPAKLIYSINGQKG
Ap-Ap5	ON711257	ApAp5	Amylopectin	Amylopectin	CCTTATGATGTCGATAACGTTGAGAGCTTCAATGTAATATTGAATAATGGTAGCGGTGA TCAGTCTGGTAACATCACTGGTATTACAAGTGATACCTACTTGGAAATGACGGTTCGTA AAAGTGCCAAGAAAGATTTCTGCTCCAGCAAAATTCGACAGCTGCTGCTAAGGTGGCTTT CAGCCCTAACGGTGGTGAATTTGAGAAGTCAATCACTGTAACGTCAACCGTGAGCAGC AATGCTAAGAGCGGTTGGTAAAGATTGGTGGTGGTGCGCAGGTAAATCTGACCCCTG GTCAGGCTGCTACATTCACTCGGTGCTGACATGATGGAAGGCGAGAGCAAGACTG TAACCTGGAGCGCAACCAATGCTGATGCTACAACCAAGACAGGTTCTTCAACCTTCAAC AAGATTAAAGAGGTAGTTATTCTACTCCGACAGGTATCTTCGCTTACTTCTCGCTCC TTCAGATTGGAATCAGGTAGATTGCTGGGCTTGGACTGAAACAGACAACTTTACTGGT GGTAACTGGCCAGGTGATGATGATACCAAGACCGGTGTGAAGAAAGTGGTCTGGAT GTCTGGATGTGGAAGTATGATGGCGATTGACAACCTGCTCCTACTATGATCATCTTCAA CAACGGCGGTGGTACGACAGCAAGGATTGAAATTCGAAAACGGTGCACTTTATAAC CTTGGGG	PYDNDVNESFNVLNNGSGDQSGNITGITSYTYLEYDGRKSARKKISAPANSTAAKAVFSPNGGEF EKSITVTATLSSNAKSGWYKIDGAQVNLTPGQAATFTLADMMEGESKTVWTSATNADGTTKT GSSFTNKIEVPIPTPTGIFAYFLAPSDWNQVDCWAWTETDNFTGGNWPVGVACTKTGVYKKNGLD VWMWYKDGDLTAPTMIIFNNGGQTQKDLKFENGAVYNLNG
BDG-Glc5	ON711258	BdG5; 1kb band	Beta-D-Glucan	Glucose	CATTGAGGAGAGGAGCCTGATGGTGGAAGAGCCTGATGGTGGCGAAGAGCCAGGT GGCGGATCATCAGCAACAGGAAATGTGACAGGTGTGGCAGCAGCTTCGATCAGACAC AATACAGTATGGAGCAGTTGAGTGCAGTTCTCACATTTGACGCTACTTCAGATACGAC ATGGAAGGATAAAGCGTACCGCAGCAATGACAGCGATACATATGCTGATATGGCGAGA ATAGGGGTGCAACTGTAGGTGAAAAGGCAAGCTCACAGCTATGGTTTCACTTGTG GCGATATATCAGGCTTGACGGCGCTGAGGCATCAGACGGATCATCAATGGATGCCA GCTTGCCTGTGCCATGAAGACAGGAGACAGCTGGGATTACGTCAAGTCAGGCGACTA TCCGTTTATCAAGGCTGAGAATTTGTGATGGCAAGTGCGATATATCATTTGCATTTG ATGATCAGAGGTGGGAAATGTACAGGAGATCGTATTCCAGTACAATTCACACTCAGC ATATGCTGGCAAGTACAATAAGCAACGTTAAGGTACTTGATGTTAAGGAGAGCAGC GGCGGACTTGAGCAGAGAGATCCTGCTGTGATCTCAGATCTCTCATCGGCTGAGGATT ATGACAAGTGGAGCAGAGAGGCGCGATATGCATACAAGCAGCGGATGACGCCAACA AGGCCGCAATGCCACACCTGACATATCATATGACAGTGCAAAATGAGAGACTTAAGGT TTCTGTGACTACTCAGCAGATTCAACTTCCTCATGGAGTGAGGCAAGGTTAAGTGTG TTCTACAGAGGCTATGATGTGAGGGG	HSGEEDPGGKEPDGGEPPGGSSATGNVTGVAAPSITDNTVSSSDAVLTFDATSDTTWKDKA YASNDSYDYMAREIAGTVGEKAKLTAMVSLDGDISGLDGAESDGSYNAILACAMKTGDSW DYVKSGDYPFIKAENFVDGKCDISFAFDVSEVGNVQEIYVQYNSNSAYAGKITISNVKVLVDKES GGLEQRDPAVISDLSSAEDYDKWSTEAGYAYKHGDAANKAGNATPDISYSANERLKVSVDYSA DSTSSWSEAKV/KCVPTAEMDVR

BDG-BD6	ON711259	Bd6 or Bd6; 1.5 kb band	Beta-D-Glucan	Beta-D-Glucan	CTAAACCGCTATACATCTCGCACCAACACAGAGATTGTATGCCAGGTTCTGCCAATGC AGAAGTTGGTACCTACAAGATCGTGATGGAAGACCCAGACGGCAACAAGATTGAAGGT CCTGAGTTCAAGGTAGTTCCTCGACAAAAGGATATCGCTACTATCACAACCAACATGG CAACAGCGCCATCAAGTATCCATACAACCTTCACTTGGGATGACACCGGTCTGTTCCGC ATCATGAAGCGACGCTCATCAAGTTGGGTGTCAAAGTTGGTTCAAAGATGCTCTTCTA TAAGGAAGCAGGAGCTACCGGTGAGGTACAGATCAACAACGCCAACTGGGGCGGTAT TGATCTCTGCGGACTGGAATGGTGACCAAGCTGCCTTGTGAAGTATTGATGCA GCCATGATGGAAGCAGTAAACAGCATCTCTGACGGTTGGAGCGATACAGCCTTCATT TCCAGGGCGGACCTGAAGAATGTAAACAGATTCGATCTCTCCATAGATAGAAATCTT TAACATAAAAAACGATTTATGTGAAATATAATTCTGTAATTTGTGGCGTAGTTATATCA ACTGCCACCATTTTTAATTAACACCAACATTAACCCGATATGAAGAAATAGCATTA TCCTTACTGATAGCTCTGAGTTTCATCTCAGCCAAAGCTGCAGACGGCAAGTCGCTGT TCGTATCATTCAACGATGGTAGCAAGATAGAGTTTGACCTGAGCACTACCGGGAAGT GACCTTCGGAATGACAAGATGACCGTGACTTCAACTGCCACTACTGCCTGTTACGAA CTGTGGAAGGTTTCTACCTTCACTATGGAACACCAACCGGTATCAACAAGTAGAAAC GAACAACAAGTTTGCCTTGAAGGTGACCGCATCATCTAGACGGCACCCGCAACCG GTGAGTGCCTTTGCTCTCGACGGAAGGCGAGTAAATCTCTCCGGTCACTCGCAGGCG ACAAGACCATCATCCCGCTGGATGAATTGACTCATGGCGTATATATCATCAAGATTAA AACAAATCCATCAAAGTAGCAAGACAATGAAAAGATATTACTCTCACTCTGGCAGTA ATGATTTCACTTCACTGCCTTGGCAGAGCTAAGGGGGACAAGTTGACCATCAACATGA GAAACGGAACATCGCAAGCCTGGGATCTGACAGCAGACGGAAAGACTCCTGTTTCCAA AATCACTCATACAGCAGCGAAAGGTAGGATTGCTGATGACGGGAATGAAAAAGG G	LNRYTSRTNTEIVCQVPANAENVGTIKVIMEDPDGNKIEGPEFKVPAEKDIATITTTMDSNAIKYPY NFTWDDTGRFRIMKADLIKLVKVGSKMLFYKEAGATGGQVQINANNWGGIDTPADWNGDQSCLV KVFDAMMEAVNSIDGWSDTAFILQDGLKNVTKIALP
Dex-Dex7	ON711260	DexDex7 / LamG9 / LamLam9; 800 bp band)	Dextran / Laminarin / Laminarin	Dextran / Glucose / Laminarin	CAGATCACTCTTCTGTCGTTGCAAGCAAACTGCTGGCAAGACTTTCAACAATGAGG CTGCCAAGCTCGTATTTGCAATGAACGACCTCAGTAATGCAAGTGCCAACACAAACAGC TCCTACTGATGCTTTTCAGCACCATTTGCTTTAATTACGGAACAACTTATCTTTGAAAGG AATTCTCGAAATTACCAAGGCGGATGGTACCGCATCAGGTATCAAAAGTCTCAAAATTG GTAATGACTCAGGAAAGAGGAACAGAAATCAACTGGTTTGTTCGCTGCTGTCGAG ACTTACTTTACCCCAACCAAGGTGAGCGGTTATGTAAACCGTTGTGGTACGAATGTA GAAACGGGAATCGTTATCAGCGCCCATAGGCAACGGAGAAGTAGTACTGCTGGGC ACCTATACCGCATGGCGTCAAAGCAAGGCTACATCAGATCAAACCTACGATAACACCG CTATCCATCAGTTTGAATCAGACTGACAGCAGAGCAGCAGCGCCTTGCGTGGTAC CGATGGCTTCTATCTGACATCTACTATCGCGTAGCTAAAAATAAGCAGGCGATTTTCG GTCCTGTTACGATCGAAGGAACCGTCAACGGAACACTCGTTGCGATAAACAATGGG	QITLPVASKPAGKTFNNEAANVVFAMNDLSNASANTPTDAFSTIAFYNTLSLKGILEITKAD GTASGIKGLKIGNDSGKKETEINWVFRPAAGLTFTPTKVSQVYVNRGCTNVENGIVISAHKANGEV ALGTYTAWRQSKATSDQTYDNTAIHQFEITLAEQQAALAGTDGFYLTSTIGVAKNKQAVFGPVTI EGTVNGTLVAVNKKW
AG-Gal2	ON711261	Gal2 or A-Gal2	Arabinogalactan	Galactose	CTCAAGGCCGAACCGAGCTTCAAACCTCAGCGACCAAGCAGTATCAGGCATTGACTAATG CCTTCAGTCATGATAAGGAGGTTCCGATCAGGCCGAGAACTCTTTTCCAAAAAGGG CAAGGATAAGAACGCTGCACAGACGAGCAGGACACCTTCATGCCGAAAACTCGTTGGA GTCAAGCAAGCAGCAGCAGTTCAAGCCGCTCGGTAAAGTTGACTTGGATAGCATCGG CAAGGGAACTCTGCAGAGCTGCTGCTGCCCATAAAGTCAGAGAAACCTAAGCAGCAGACT GCTGCCGTCAGTCACGCGCCAGTAAAGAAAGCTCGTAAGGCTGAGCCAAAAATGATGATC AGAGACCTCATCAACAGGGCTCTCAGCAAAAAACACAGATGAAACAAGAGAATCAGTCA AAAAACACAGCAGCCAAAGATGAATGACTCCAAGGGTCAATAAGAAATGCTGCACAGGGT AAACAGAATGGAACGCTCAGCACCAGAATGCTGAGCAGAAGTACAGCAGAAATACTG CTGCTAGCAGTCAGGCCTCAAGTGATTACACTTAAGAGTGAGAGAAGATTCTCTGC CAATGAGCCTAAGGTGTTGGGTAAGATTGACCTCTCTTCTCAACCCAGAGTACTCGTC CTAAGAAAAAGTCGAAGGAGGAGAGACGCAAGGAGCGTGAGGAGAAATTTGGCTCAGC AGCACAACGATCGCAAGAAAGCGTGTTCGTATCAACAAGGAACGTGTTGACATCAATGC CGAAGCTAAGACAATGGCGACGCTAACGCCCAAGTAATAAAGGGCAATAATGGCAAC AATGGTGGCAACAAGAAACAGAAACAAAGCAAGAAATAATAACAATAATAACAAGGG CAATAACAACAACCGCGGCAACGAGCGCCGATTGAGGTGGACGACGAGGCTGTAGC ACGCCAGGTAAGGAGACTCTTGCTCGCTTGACCAGCAAGAGTCAGAACAGAAGGG TGCTAAGTACCGTAAGGGG	LKAEPFSLSDQOYQALTNAFSHDKEVRDQAEKLFSSKKDKDKKRAEQDDLHAENSLSSKQQQ FKPLGKIDLSIGKNSAESAAHKSSEPKHETAAVSHAPVKEARKEPKHODRPHQOQSQKQO MKOENQOQSQPKMNDKSGHKHNAAGKQNGNAQHONAEQKSOQNTAASSQASSVFTLKSEK KFSANEPKVLKIDLSLNQSTRPKKKSKEERRKEREKLAQQHNDKRRVINKERVVDINAEAKN NGDGNQNNKNGNNGNNGNKNKRNKRNNNNNNNKNNNNNRGNRQRIEVDDEAVARQVKETL ARLTSKSNKKGAKYRKG
Iln-Glc6	ON711262	Igluc6 or I-gluc6	Inulin	Glucose	CTAGTCGGAAGCGTACGGGTGTATCTATAACCTTGGTGACCCTGTGAGAATCCGTG TGAATCTACCAATCTGGAGCAGAACTCCTTGATTGATGAGTTGGTTGAGACGGGTAG AGAAGACCGCATGAGCCATCATGAGGATATCCGGGACAGTACGAAGAGCGCAAAAC TGCTGTAAAAAGTATTTGATAGGACTACCCGCAAGAAAGATTCCGACAGACGTGACGGA AGAAAAACGACAGTTTCGATAAAGGGCGGAAGAAAGAGCTTCGGTGACTCTTCCGAG GTGGCGAAGCTGCGGGATTTCGAGCAAGGATGATAGTACTCTCCAGGCGTGAAC GCTTCAGTATCCAGAGGAACAAGGGGACGCGGCTCCTACCCAGAAAGGAAACACA GTTTTAGGGAAAAATAGTCCGTTTTCTGAAGAAAGTTCCGGGAAGTAGAGCCGAAGATTAC CGTACCTGAGGCACCTGAGGTTTCTCAGCAGATGCCTGAGACCGCTCCAGCCGTAGT GAAGAAGGTAAAGGCTCCGAAACCTGCTGCTGGTGAGGGAGATAAGGCCGACAGTAA GGCCAAGGTGAAACAGGCTATCAAACCTTCCAAAGGCAAGTCTGCGAAGCCTTTCATCC AAAAAGTCAAAGCTGTCGCCGGAAGGCCGCAAACTCGCGGCAAGAAAGCAAGAAAGT CAGAGTAACAAACACTATATTTTTTCGATGAAAAACAGAAAAAGAAATCCATACTGGGCATA GGAACGCAATTGACAGATATCTGGCGGTGCTTCTGACGACTCATTCTGAAAAATGT ACCACCTCCGAAAGGCGAGCATGAGTTCTGGGATATGAGACAGGCAACAGAAATCTT TGAGAGCCTGAAGCCATACGAGCTTCACTATGCGGAGCGGTTGACGAGCGAACAC CATCACCTGTGCAGCCATTTTCGGTATGCGGTCGCTTTCATCGGAAAGTAGGTGGG G	LVGKRTGVIYNLGDPIRVIRKSTNLQKLLDYELVETGREDRMSHEDIPGOYEERKPAVKVFDRT TRKKDSDRDRGRKYDSFDKGGRRKSFDDSSERRGFRSKDVDDSPRRDRFSRSGTRGRGS YPRKENSFRNSPFSEEVREVEPKITVPEAPEVPQOMPETAPAVVKVRAPKPAAGEGDKAARK AKVKQAIKLSAKSAKPSKKSKSPKADKFAARSKKKSE

Lev-Lev5	ON711263	Lev-Fru3 or Lev3 or L-Lev5 or L-Fruc3	Levan / Levan	Levan / Fructose	CCGGGTGCACCAAGTCGACTTCACGAATCCTGTGGCCCTATACCGTAACCAACAATACGGCTACAAGCACCTACACTGTAAACCGTCAATCAGATAGGCCAAGCCTACTGCTGTATTCGCAAGCTTGGCTCTGACGATGGACGAGCTGGTGCTGAGGAGAAGCGTCGCTGGAGTGGATGCTCGCGAATGTGGACAACCTCTATCTATGCTTCGTTACTGATATCAAGAATGGCAATGTAGACTTGACCGAGTGTAAAGTGATATGGTGGCACTTCCACAAGAAGCGGTGGAGTGGACGGTAAGGCGAAATTCGAGCAGGCTGCTCCTGAGGCTATTGCCGCACAGGCTGTCTGTAGAGACTACTACAAAGCTGGTGGCTCCTTCCTCTCACACGTTACGCTACCAATATGCCAGGCGAGTTGGGTATCGACAATAAGGATTGGTACCACAACACTGCTGGGGACAGGTGGAGAATGACGCCGAAACTTGTGGAGGTCTTGGGACTTCAAAATGGGCAATGATGCCGCAGGTTCATTCCGACCAAGCCCTCTATCAGGGCACTGGTGAAGGTGATGACGCCAACAGTGTATACACTACTGATGCCAACTACCCGATCACCAACTCTACTGCTCAATGCGATATTGGAGTCGACTGGGGTGGTTTTGACAATTATGCCGTATGGAGAGAGAAGACTGGTGCCATCGACCTGGGTTACGGTGGTGACGGTGGTCTGCTGGTATGGAGATACCTGCCAAAGAGAATTACGGTAAGACCCCTCTGTATAGGTTCTGGTGGTACGACTGGTACACGCTAGGTCTTTACAGAGAAGTTCATGCTCAATGTGGCCATCATGACCAAGAATGCATTTAATTATCTTATGAACCATTAACAATAAACAAAAATGAAGACAATGATAAATCTATAATATTGGCGCTATGCTCGCTTTCCTCTCGCTTCAATGCAGCGACAGCGATGCTGCCCCGAGCAGAAGGACTGGTCTACCACTACTTATTTCAACTCATCCGATGCTGCAGCACAGGATACTTATACAAGCCTGCTGTGGGCTATGTAGCGCAGCCCTATGCCTTTCTTCGATCCAGTGGCTGGCGATTTCAAGGTGTTGATCTGCAGGACTTCGCTCCTAATCCTGAAGGAACCTACCACCCCATCTGGGGTGTAAAGTACCAAGGATGCTGCCCACTATACCTGTTGGTGAACCTGGTTCTGTGGCACCCCTGAAGTCGACAGGATGCTGCCATCGGTACTGGTTCTACCATCTACGATGAGGCAAGTAAGCTTTACTATACATGCG	PGAPVDFTNPVAYVTNNATSTYTVTVNQIKPTAVFASLALTMDELVPEEKAAACEWMLANVDN SIYASFDTIKNGNVDLSECKVIWWHFHKDGGVDGKAKEFEQAAPAIQAALVRDYYKAGGSLFT RYATNMPGELGIDNNGLVPNNCWGOVENDAEETCGGPWDFKMGNDAGGSHSDHALYQGLVKGD DANSVYTTDANYRITNSTAQWHIGVDWGGFDNYAVWREKTAIDLGYGGDGAUVVWEYPAKEN SGKTLICSGSCYDWYVSGPFTEKFHANVAIMTKNAFYLMNH
Pec-Pec1	ON711264	PecPec1/ PecGalU9 or Pec9	Pectin / Pectin	Pectin / Galacturonic acid	CCAGTCGTTACAAAAGCAAGTGACATTACCCCTCACTTACTCTTTAGGAACGACGACAGCAGAGAGAACACTCCCTGCAAGCGCAAAGGTAGAAGTGGGAAGCAGCTATACGTTTCCTGTCAATACCACTCTCTACTTAGCAGGCGACACTTTGACAGGCTGGACAGATGGCACCACAACACCTATAAACCAAGGTGAAACCATCACTGCTCCAAGCGCAAGCGCTACGTTGACTCCGTCTTTAAAGCCAACACCAAGTCGCTTGCCGACCGCACAGAGGCAACCAACCCCTCACCTATTACTTCGGTCACAAAAATGGTGCGCAGGATATCAACTATCAAGGAAGAAAGGCGATTTTGGTAACCCAGGCGACTGCGATGGTGAACCATTGATGTAAGATTGACCTCGACGGAAACCAACGCGGAGCTAAGTTCAACAATGCAGGTGCTGCAGACGAATGGGCACAGATGAATGCAACCGCATCATCACCGTTCCCTTCTTCAAGGGTGCAACCATGAAATGGCTGCATACGGCAATATCACAAACGACAACAATTTGATGGACAGGCAGAATACTTCAGGTAAAGTCATCAGCCAGACCATCGCGTCAAGTCAGAAACAGTGAACATCGTCATTGGCGATGGTTCATACATAGCTATTTGAAGATTACCCCTCCTGCTGCTTGAAGCAACACCTGCTGGCAAGACTTTCAACGGG	PVVTKASDITLYSLGTTTAEGLPASAKVEVGSSYTFPVNTTLYLAGSTLTGWDGTNTYKPGETI TAPSASATLTPVFKANTKSLADRTAATLTYFVGHKNGAQDINYQGGKILVTQATVDGETIDVKID LDGTPSGAKFNNAGRADEWAQMNANGIITVPSCKGATIEMAAYGNITTTIDGQAEYTSKGVISQT IASSAETVNIVIGDGSYSYLKITLPVVASKPAGKTFNG
St-Glc1	ON711265	St1 or StG1	Starch	Glucose	CGTTCTGACCGTGACGTGACTGTAGCCAAATGGTGCTGGCGACGGCCAGTGGCTCAAGTCTGGTACTTATAAGGATATGTTAGGCGGTGGCGCTTTTACCCTGCGATGCTTCTACAATCTCTGGTCAATGTGGCAAGTCAAGGTATTTGCTGCTCATCTATAAAGTGGTTCATTGTGCTGCTCCTGAGGTTGTTTTCAATCCAGCTAATGGTACAGCCTTCTCTGATGAGTCTCTCACTGTGACTGCTACTCCTTTGAATGCTGTTTCTGCCTGGATTCAAGTGAATGATGGTGTAAGCAGGATTTTACTGCTGACAAGCAGTTTACTGTAGGTGCTGATGTTGCCATATGTTAGAATGTTACTATCACTTGGGGTGCAACTGACAAGGAAGGCAATACAGAAACAGGTTCCGTAACCTTACAAGAAGGTGAAGGCTTACGTTCCAGAAATGGGCAAGGCTGACGAAATCTCCTGTTTCTTGGAGACATCCAATGCGGCAGCAGCCGTATATGATGGAATAACAAGGTTAAGCCTGTAATTAAGTATGCTGGTGAATGGAATGATGCTATCAATAAAAAAGTTGCCTCTTGTAGGTAAGAGTGTCTTGGAAGAAATGTCTTCAAGTGGACTTATGATGGCACCGAGACAAGTGTCTTACTCAACTCACTTTTCTTGGATGGTAATGGAAATAAGTTAACTAATAACGTGGACTTTGTCAACCAAGGCTACTATGTTGACGGAAACATACAGCACTACTGTGACCAAGGTACATGAAGATGAGACCGTTGATCCAGAGTATGTTTACTTCGATAACGCTTCCAAGTGGGAGAATGTTTATTGCTACTTCTATAATGGTAAAAACATCTTCAACCGCATGGCCGAGGATCAAGATGACTTTGATGCTATGCTTCTCATAATGGTAAGACTGGTTGGTATAAGGTTCAAGTCTTCAAGGCTATCTCAAGGCTAAGTCTTATCAACGATGGTACTGCGCGTACTCCTATCAATGGTGCAAAATGCTTCTGCTGAAAAGGTAGTAAACGAAGGTGTTGTAAGTGGCACCAACTCCAACCCCTACCCTAATCCACAGAATTTGGATGTCAGTATTAGACCAATCCAATGGTGACGGTGAAGAAAACCACTACTGTAGATGGTGATATCAGCGATTGGGATGAGAGTATGATTATGGG	RSRDRDVTVANGAGDQWLKSGTYKDMVGGGVFTVDASTISGHVKGSGIAVIYNAGSIVLPPEVVF NPANGTAFSDSLTATPLNNAVSAWIQVNDGAKQDFADKQFTVGADEVYKKNVTITWGATDK EGNTEGTSVITYKKVAYVPELGADEISCFLETSSNAAAAYVWNKKVPKVIKAGEWNDAINKKL PLVGKSVSGKNVFKWTYDGTETTVPTQLIFLDGNGKNLTNNVDFVNHGYVVDGTYSTVTVKVHE DETVDPEYVYVFNASNWENVYCYFYNGKTSSTAWPVGKMTFDASASHNGKGTGWYKQIPTAYL KAKFFINDGTAGTPINGANASAEKVVNVEGVVAPTPNPPTPNQNLNDVQY
St-Glc2	ON711266	St2 or StG2	Starch	Glucose	CCCCCTGGTAAGCGCTGTTACCTTCACTATCGGTGAAGACATGAACCTCAAGGATACCAAGACAGTGACTTGGAGTGTAAACAGCTCTGAAGGCAAGGAGAAGACTGGTAAGGTTACATATAAGGTTGATCCTAACGCATCTATCGTGGTCATGGTGAAGGCTGACAAGGCTCTTACATCCACGCTTGACACAAGGCTGTTGGCGGCAAGAACTGACAGGTGCATGGCTGCTGAAGGTGATGAAGGCTCTGAGGAGATTGATGGTGCTAAATACTGGACTTATGATTTTGATAACGTTGAGAGCTTCAATGTAATTAATAATGGTAGCGGTGCTCAGTCTGTGACATCACTGGTATTACAAGTGATACTACTTGGAGTATGACGGTGGTAAAAAGTGCACAAGAAGATTCTGCTCCAGCAAAATCGCAGCTGCTGCTAAGGTGGCTTTCAGCCCTAACGGTGGTGAATTTGAGAAGACAATCACTGTAACGTCAACGCTGAGCAGCAATGCTAAGAGCGGTGATATAAGATTGGTGGTGGCGCAGGTAATCTGACTCTGGTCAGGCTCTACTCTTACCGCTCGGTGCTGACATGATGGAAGGCGAGAGCAAGACTGTAACCTTGAGTGCAACCAATGCTGATGGTACAACCAAGCAGGTTCTTCAACCTTCAACAAGAGGG	PPGKPVTFITIGEDMNFKDKTVTWSVTSSEGEKEKTGKVITYKVDPNASIVVMVKADKAPYIHAWT TGVGGKNLTGAWPVKVMKGP EEDGAKYWTYDFDNVESFNILNNGSGAQSBDITGITSDTYLE YDGGKSAKKISAPANSTAAAKVAFSPNGGEFEKITITVATLSSNAKSGWYKIGDGAQVNLTPGQA ATFTLGADMMEGESKTVTWSATNADGTTKTSSTFNKR

St-Glc5V1	ON711267	St5 or StG5	Starch	Glucose	CAGTTTGTGTTGGTGCTGATGTTGCCTATGGTAAGAATGTTACTACTCACTTGGGGTGCAACCGACAAGGATGGCGAAGCGGAAACAGGTTCCGGTCACTTACAAGAAGGTAAGGCCTACGTTCCAGAATTGGGCAAGGCTGATGAAATCTCCTGTTCTTGGAGACATCCAATA CGGCAACAGCCGTATATGTATGGAATAACAAGGTTAGTCCTGTAATTAAAGTATGCTGGTGAATGGAATGATGCTATCAATAAAAAAGTTGCCTCTTGTAGGTAAGTGTGTTTCTGAAA GAATGTCTTCAAGTGGACTTATGATGGCACCGAGACAACCTGCTCCTGCTCAACTCAATT TCTTGGATGGTAATGAAAATAAGTTAACTGCTGACGTGGACTTTGTCAACCACGGCTA CTATGTTGACGGAGCATACAGCACTACTGTGACCAAGGTACATGAAGATGAGACCGTT GATCCAGAGTATGTTTACTTCGATAACGCTTCTAAGTGGGAGAATGGGG	QFVVGVADVAYGKNVTITWGATDKDGKTETGVSVTYKVKYAVVPELGADEISCFLETSNTATAVYV WNNKVSPIKYAGEWNDAINKKLPLVGKCVSGKNVFKWTYDGTETTAPAQILFDGNGNKLTDV DFNHNGYYVDGAYSTTVTKVHEDETVDPVEYVYFDNASKWENG
St-Glc5V2	ON711268	St5 or StG5	Starch	Glucose	CAGTTTGTGTTGGTGCTGATGTTGCCTATGGTAAGAATGTTACTACTCACTTGGGGTGCAACCGACAAGGATGGCAAGCGGAAACAGGTTCCGGTCACTTACAAGAAGGTAAGGC TTACGTTCCAGAATTGGGCAAGGCTGATGAAATCTCCTGTTCTTGGAGACATCCAATA CGGCGACAGCCGTATATGTATGGAATAACAAGGTTAGTCCTGTAATTAAAGTATGCTGG TGAATGGAATGATGCTATCAATAAAAAAGTTGCCTCTTGTAGGTAAGAGTGTGTTCTGGAA AGAATGCTTCAAGTGGACTTATGATGGCACCGAGACAACCTGCTCCTGCTCAACTCATT TTCTTGGATGGTAATGAAAATAAGTTAACTGCTGACGTGGACTTTGTCAACCACGGCTA CTATGTTGACGGAGCATACAGCACTACTGTGACCAAGGTACATGAAGATGAGACCGTT GATCCAGAGTATGTTTACTTCGATAACGCTTCTAAGTGGGAGAATGGGG	QFVVGVADVAYGKNVTITWGATDKDGKTETGVSVTYKVKYAVVPELGADEISCFLETSNTAAVVVWNNKVSPIKYAGEW NDAINKKLPLVGKVSNGKNVFKWTYDGTETTAPAQILFDGNGNKLTDVDFNVHGYVDGAYSTTVTKVHEDETVDPVEY VYFDNASKWENG
St-Glc8	ON711269	St8 or StG8	Starch	Glucose	CTCCAGGAGCCTTGGAAAGAGCTGGAAGCCAGTGGCTCCTGTATATGGTATGGCAGGC AACCTATACACCATGGTTATGTGTTCCAGATGGCGGTTCACTCAAGTGGGCTACATACGA GAACGACTGGCGTGGCTATAGCCGCTGGCTGCTATCAACGATAATGCTGGCGCTGA ATTCTCAGAGGATGGCGACGCGAAACCTGAAGGTTGCTCATGGCGGCTGGTTCGTTCT CCACCTTCGTTGGTGAATGTCAGCAGACAAGAAGAACATCAACTACTCACTGAATGTTT ATCCTGGTGCAAGCTTACATCATCGGTGCTTCAGCTGGTGGCAATTGGGACGACGCTTC TGCCGCTTGGGCTATGACAGCTCCTGCGACACGACAGCGGAATGGGTATCTCCAGC CTTCGGTGGTATGGCGAGCTCCGCGCATATATCAAGATTCCAGGACTCGACTGGTG GCGTACAGAGTTTACTATCTTCAAGGGCAACTGCTTCTGGAGAAACGATAACATTTGATG ACTCTTGGACTGAGATTGGCGAAGGTTACGCTGTATCTTGCTCAACTGGACAAAACCT CTATGTCAACTTCGACAAGAACACAGCAAAAGTTGAATAATTAACAAACATGAACACAAT GAAAAGACATTATTATATAGCTTAGCAGCAATGGCAAGCTCGCACTTGCCAGCTGC GCTGGCGACTACGAGACTGGGCTAACCACACAGGCCAACGAGCAGGAAGCATCTGCA GCCAATATGGGGTAACCTTTGCCAACGGTTCTGAGGCAGAAAGCAGCATGGCTGAT GAAGATGGTATCATCAATCTCGTAACAGTCAATTCTACTGATGCCAATGTCTCTGGTT CACACTCAAAGACCTTAAGGTGAACGGAGTAGCCGCTCAATGGAACAATGATTGGCAAC AGCGTTCAAGTAAGTGCTTCTGAATGGG	LOEAWKSWKPVAPVYVGMAGNYTMYVYPDGGSFKWGTYENDWRGYSRLAINDNAGAEFSED GDGNLKVAHGGWVFLHFVGEMSADKKNINYSLVYPGAAYIIGASAGGNWDDASAAWAMTAPA DQTGEWVSPAFGGDGLRAYIKIPLDWWRTEFTIFKNCFRWRNDIVDSWTEIGEYAVSCST GQKLYVNFDKNTAKVE
St-St4	ON711270	StSt4	Starch	Starch	CATCAGGCTCCTGATGCGAAGTTCAACGATAATCTCTACTTGATAGGTAGCTCTATCCA GACTCCATGGCAGAGTTGGAAGCCTATTCCACAGGTACAAGGTGTAGCTGGCAACTAC TATGGTATGCTCTACTTGCTGCGAGGTGGTGAGTTCAAGTGGGGTACAGAAACAAATG ACTATCGCGGCATCAACCGCTCTTAAGGAAATCAACGATGAAGCCGGTGCGAATACTC TGCAGGTGAGGAACAAAACATCAAGGTAGCCAACGCTGGCTGGTACACTCTCCACTTC AAGGGTAAGATTACCGAAGACAAGAAGAACATCGACTGGACACTGACTGTTTACAAGA CTCAGGTATACCTGATTGGTGCTTGATTGGTCAAAGCACTTGGGGCTTTGCTGATGA TACAGCTCTGACACCTCCAGACGATCCAAATGGCGAATGGGTTTCTCCTGCAATCACT GCCAGCACAGAGCTCCGTGTATCTGCAAGTCCGTAGCCTCGACTGGTATAGTACAG AGTTCAGTGTTCACAATGGCGAAGTGTCTGGCGTAAATGATATGCCAAACCACTGG GCTGAGACTATGGGTGCAGATTACTCTGTAACCTACCGCCCCTGGCAAGAAGTTGTATG TCAACTTTGATACAAATAAAGCAGAAGTTAGATAATTATAGGG	HQAPDAKFTDNLYLIGSSIQTPWQSWKPIPVQGVAGNYGIVYLPAGGEFKWGTENNDYRGIN RLKEINDEAGAEISAGEEQNIKVANAGWYTLHFKGKITEDKKNIWDVTLTYKTKQVYLIGACIGQSTW GFADDALTTPDDPNGEWVSPAFTASTELRVSVKVGSLDWYSTEFTVHNGEVFWRKYDMPNN WAETMGADYSVTTAPGKKLYVNFDTNKAERV
St-St5	ON711271	StSt5	Starch	Starch	CATGATGGGTTTGCAAGTGTGTTAGACAATCAGACCCTTGGGATGCATCTGCTCTCTA TATGTGGGGCGATGTAAGCGACCTGAATGGTGGATGGCGAGGCATGCAGCCTACAGG CACACAGGTTATCAATGGCGTGACCTATACCTACTTTGATTTCGGAGAAGGTAACCTCG GATTGGCAGAGAATCTCATCTTCAATAACAATGGTGGTGGCTTGCAAGTTGGCTGATCA CGCCTTCACTATCAACGAAACCTTTATGTCCGCATTACCGATAGCGGTGTAGAGGTCAT CGATCCTTATGCAAGTGAGGCGAAGAAACATCCTGCAGGTATTCTTTCAATAATTG ATTTGATTAGGTTAAATTAAGTGTATGAAAGAGCTAATGACAAAATGGCTCCTTATTGT AGCTGTGTTGCTGCTCCTTTTGGGGCGAGCAACATGGTGAAGGCCAGCGGCGTACG CAATGTCTTAGGAGCGACAGCCGCTGGCAGACATTATGTGTCGGTTATCAATGCCAAG ACTTATGGCTCTGGGCATCAAGTGATTATGAGATGAATGAGGCTCGTTCTCCTTGGA AGGAACITTTGTGGCAGCTCAGCAAAAGCTCAGCCAACCTCAAAATGGTAGGCATTGAC ATCATTGGCTCATGCCTGTTTATCCGCGTGATGGTGGACTGAACAGTCCGTATGCTG CTGTTGATTCAAGCAGGTGAATCCTTCTTATGGAACATTGACGATTTCAGAACTTT GTTGGCGCTGCCATCGTCTGGGTATGAAGGTATGGCTCGACTGGGTGCCTAATCATA CTGCCAGGAATGCCACATGGGTGACAACCTATCCAGAGTATTACAAGAAGACTAATGG AGCTATGATTATCCTCAACAATTACGGCGATGCTTTCACTCGATTACTCTAATTCAGG GCTTGTGAGGCAATGAACGATTGCCTGAAGTTCTGGATTGATCAGGTAGATATCGAT GGTATCGTTGGCGACTATATCAGCAGCTCGTGAATTCAGCGAGTTATTGGACGAGCA CCATTCTATGCTCAAGAGTTACAAGGCTGTGAAGGAAATTTGATGCTTGGCGAATC TGATTTACAGATAAAGACAACGAGGG	HDFGAVFVDNQTTWDALALYMWGDVSLNNGWPGMQPTGTQVINGVTYTYFDFGEGNSGLAE NLIFNNNGGLQLADHAFTINENLYVRITDSGVEIDPYASEAKHPAGIPFK

Xln-Xyl8	ON711272	Xose8 or XylXose8	Xylan	Xylose	CGCGAGGGTGACCTTGTCAATGCCAACTACCAGATGTTCAACCCTGGCAACGCTATGAAGAGCGATGCCGATGCTTGGTAATAGCGGAACCATCAACTTCGCTACTGTGATGAAGCTGATTGCTGCCATGCCAGAGGGGAATGAACTCTATGGTCACAACTTCTTCTGGCATACCCAGCAGAACCAAGAGCTATCTCAAGTCGCTCATCGCTCCTACCCTCGTGGTGGAAAGCA GCAGCGACATTCAAACCATCATCAAGAATGGTGACTTCGAGAAAGCGACAAAGAGCAG TTGGAGTTCTTGGGGAATAATAGTACTACAGAAGCTTCGGCAGAGGCTGCCAAAGAA GGAAGTTATGGCGTGAACCTCGTCAACCCTAAAGATGGCGACGACTTTTACAAGGCAC AGTTCGTACAAGCTCTCGATAATGTTTTGGAAGTCGGCAAGACATACACCATTCGCTTC CAGGCTAAGTCATCTGTGGCAGGTGAAGTTCCTCAATTTGCTACGCAGAAACAACAAGA CCAATGCGAGGAGAGGCTATCACGGCTTCACAGTTGGTACAGATTGGACAACATCGA ATACGACTACACTTGCACAAAGAGGACATGAATCGTATCTGTATCAACTTCGAAAAAG TTGCCAGCACCATCTACCTTGACAATATTGAGTTTCGGTATCAAGGAAGTTGACCCATG GACAATGTATTAGCTGGTGACGACTATGACTTCGAAGGTGGAACCAAGGAAGTTGGA TGCTTTGGGGCAGCAACAAGGAAGGTGTGACAGCCGAGAAAGGAATGGGATACAAAG AAAGTGTGGAGTTGTCTCAAGACAAAGAAAGACGGAGGACGCGGCATAGCTGGA AAGCCCAACTTTGTAAAGAATTGACGACCCACTCGTAACTGGCAAGAATTATATTCTC CAATTCTATGCCAAGTCGAACATTGCCGACGGCAAGCTTCAGATTATCTATCAGAACAA GAGTTCAGGCAACCAAGGTCTCTACAAGGACCTCGTAGTCGGCAAGGACTGGGCTAA ATATGAAGTTGAATTTCTTACCCCAAATGATGATAGCTACCGAGTTGTATCAACTTCG GAGAGAAGGAAGCTACCTATTGCGTGGACAAACATCAAGTTTCGGTCTCGCCAAAGACCA AGGCGCTGCAGCAGGAGCTAAGCAAACGATATCCGTGCTCGTGGCAAGCAACATCG TGCAAGCTAGCAAGAGCTACTATGTATTGAAGACTCCTGCAGAAAGCAGGCTGCCCTT GAGGGAGCCATGGAAGCATGGGTAAAGCGGTGTGGCAAACTTGAAGGAAAAGGGT GTTACTCCTTACGGCTATGATGTAGTCAATGAACCTATCGCTGATGGCAGCAACAAGTT CCGTGTCTCGACGAAGGCATCTTCGGTACCGGG	REGDLVNANYQMFTPGNAMKSDAMLGNSGTINFATVDKLIAMPEGMKLYGHNFVHTQONQS YLKSIAPTLVVSSSDIQTIIKNGDFEKGDKSSWSSWGNNSTTEACAEAAKEGSYGVLVNPDKG DDFYKAQFVQALDNVLEVGKTYTIRFOAKSSVAGEVLQFATQNNKTNAGEGYHAFTVGTDWTTIE YDYTCNKEDMNRICINFVKASTIYLDNIEFGIKEVDPMNDVLNLAGDDYDFEGGTTGFSWMSWGSNK ESVTAEMKMGYKESVGVVLKTKEDGSGNSWKAOLVKEFDDPLVTGKNYILQFYAKSNADGKL QIYYQNKSSGNQGLYKDLVVGKDWAKYVEFSTPNDDSYRVVINFGEKEATCYVDNIKFLAKDQ GAAAGAKQITFRARGKQHRASKSYVVLKTPAEKQAALEGAMEAWVSGVANHLKEKVTPYGY DUVNEPIADGSGNKFRLDEGIFGTG
PBGal-Gal8	ON711273	PBG8 or PBGal8	PAA-beta-D-Galactose	Galactose	CTTTTCATTGTAGGTTCTAAAGAACTATGCCCTCAGAAAAGCAACAGCCATAACGA TAGTATCATCAGACATGCCACGCGACAAAGCGCAGGCTATTATGACGAAGGACTTCAG TCAGCGCAAGTATTGCGCTTTGACCCCAATACGGCAAGCCAATCTGATTTCCAAGCGC TGGGACTGGAATCATGGCAAGCCAGAAACATCATCAAATATCGAAATAAGGAGGATT CTTCAGGACACCTAGAGACTTTGCACGGGTTTACGGACTAACCAAGAAGCAATTCGAA AAAGTGTGCGCTTTATCAGAAATGGTAAAGACTACCGCGGCTGCCAAGTTTATACCC AAGAGAAAGATACAACCTACGGCTATCAAGAGACGGCTATAAGAACTAGAGAAGAAAGG AAGAAAGACACTACCCAAATACAGTTATCCACGAAAACGTAAGAAAGGTGAGTATATCAA CATCAATTTGCTGATACGACCGAAGTGCAGAAAATTCGCCGCATAGGCTCTTACTATG CCAGAAGCATCATCGTTACAGAGAGCGGTTAGGCGGTTTCGTTTCCATGAGCGAGAT ACAAGAAGTGGAAAGGCGTGCCTGAGACAGCCCTCCACTATATGAATATTGATGCAAAA CATATCGGAAAATGAATGTCAACCAAGCTCAGTTTAGCCGAACTGGCAGAAACATCCTTA CCTGGACTTTTACCAGGCAAGGAAATCGTAAACTACCGAGAACCCATGGTCCGCTG AAAAGTGTCTGAAGAGCTGCGTCTCCTCAAAGACTTTCCACCTGCCGAAATAGAAAGAA TCAAGCCTTATCTTGCCTACTAGGGGAAAGACAAAGCTAGCTTGCCTGTCTGCAAGTTT GCCGGTTTTGCTAAATGACACCAAACTGGTGAGGAAGATAAGGAAAATACAGACTGG ACAGATGAAACGGATGGTGAACAGGAAGACTGGGAAGAGAGTTCCTTCAGGGTTCC CCAGTTGGTAACTCGGG	LFVGSKETMPSEKQQAHNDSIIRHATRQQPGYYDEGLQSSEVAFDPNTASQSDFORLGLSEW QARNIIKYRNKGIFRTPRDFARVYGLTKQFELKLPFIRIGKDYQPAANFYPRERYNYGYOETAIR TREERKDDTTQYSYPRKLKEGQYININSADTTELQKPGISYYARSIIYRERLGGFVMSQIQEV EGVPE TALHYMNDIAKHIRKMNVNQLSLAELRKHPLYDFYQAKEIVNRYRTHGPLKSAEELRLKLD FPPAEIERIKPYLAY
PBGlcNac-GlcNac4F1		PGlc4 or P-Gluc4	PAA-beta-D-GlcNac	GlcNac	CGCGCTCGAGCGCAAGGTGCTCGCCGAGAACCTCACGAAGGTGCTCTACCCGAACGA CAACACGATGGCCGGCAAGGAGCTCGCGCTCCGCCAGCAGTACTTCTTCTGTGTGCTG TTCGCTGGCGGACATCTCGCGCGCTTCCGCGAGGACGGCAACGACTGGTCGCACTG GCCCGAGAAAGCGTTTATCCACCTCAACGAGACGACCCCGCTCGTGATCCCGGA ACTCATCGCATCTCTGTCGACGAGGAGGCGATCGGCTGGAGGCGGCGCTGGGACC TGACGTGCGCGCAGCAGCGGCTACACGAACACACGATCCTCCCGAGGCGCTGGAGA AGTGTGCCGTCCGATGATGGAGCGTCTGCTCGCGCGCATCTGCGAGATTATCTACG AGATCAACGGGCGCTTCTCAGCGCGTCTCGGCGATCTACCCGGCGACCAAGACC GCCTCGCGCGGATGTCCCTCATCGACGAGGGCGGCGAGCGCTACGTGCGCATGCGG AACCCTCGCGATCATCGGTTCTCAGCGTCAACGGCGTCCCGGAGCTCCACACGGAA ATCCTCAAGGCGTCCCTTTCAGGGACTTCTACGAGCTGATGCCGGAACCACTTCCACA ACGTGACGAACGGCATCACGCCGCGCGGTGGCTTCTGAAGCGGAACCCGCGCTC CGCGCAGCTCATACCGAGAAGATCGGCAACGCGCTGGATCACCCACCTCGACGAAGTC AAGAAGCTCGAACGTGAGGCGGGGACGCGGTGTTCCTCGAATGCCTTGGCAAGATC AAGCGCTCCAACAAGCGCATCTCTCGGGG	RRRAQGARREPHEGALPERQHDGROGAAPPAVLRLVLFAGGHPAPLPRGRQRLVAAAREGVH PPRQDAPRARDPGTHAHPRGRGGHRLGGGLGPDVPHDGLHEPHDPPRGAGEVVRPDDGASAA APSADYLRDORALPQRLRLPRRPGPBRADVPHRRGRALRAHGEPRDRFLRQRRRRAPH GNPQGVPLQGLLRADAGPLPORDERHHAAPVASEGEPAARAHAHREDRHALDHPPRRTEART
PBGlcNac-GlcNac4F2	ON711274	PGlc4 or P-Gluc4	PAA-beta-D-GlcNac	GlcNac	CGCGCTCGAGCGCAAGGTGCTCGCCGAGAACCTCACGAAGGTGCTCTACCCGAACGA CAACACGATGGCCGGCAAGGAGCTCGCGCTCCGCCAGCAGTACTTCTTCTGTGTGCTG TTCGCTGGCGGACATCTCGCGCGCTTCCGCGAGGACGGCAACGACTGGTCGCACTG GCCCGAGAAGCGTTTATCCACCTCAACGAGACGACCCCGCTCGTGATCCCGGA ACTCATCGCATCTCTGTCGACGAGGAGGCGATCGGCTGGAGGCGGCGCTGGGACC TGACGTGCGCGCAGCAGCGGCTACACGAACACACGATCCTCCCGAGGCGCTGGAGA AGTGTGCCGTCCGATGATGGAGCGTCTGCTCGCGCGCATCTGCGAGATTATCTACG AGATCAACGGGCGCTTCTCAGCGCGTCTCGGCGATCTACCCGGCGACCAAGACC GCCTCGCGCGGATGTCCCTCATCGACGAGGGCGGCGAGCGCTACGTGCGCATGCGG AACCCTCGCGATCATCGGTTCTCAGCGTCAACGGCGTCCCGGAGCTCCACACGGAA ATCCTCAAGGCGTCCCTTTCAGGGACTTCTACGAGCTGATGCCGGAACCACTTCCACA ACGTGACGAACGGCATCACGCCGCGCGGTGGCTTCTGAAGCGGAACCCGCGCTC CGCGCAGCTCATACCGAGAAGATCGGCAACGCGCTGGATCACCCACCTCGACGAAGTC AAGAAGCTCGAACGTGAGGCGGGGACGCGGTGTTCCTCGAATGCCTTGGCAAGATC AAGCGCTCCAACAAGCGCATCTCTCGGGG	AVERKVLAEHLTKVLPNDNTMAGKELRLRQYFFVCCSLADILRRFREDGNDWSQLPEKAFIHL NETHPALVIPELMRLVDEEGIGWEAAWDLTRTGTYNHTLPEALEKWSVPMMERLLPRHLQIY IEINGRFLSRVSGIYPGDQDRLARMSLIDEGGERYVRMANAIIGSSSVNGVAELHTEILKASLFRDF YELMPDHFHNVTNGITPRRWLLKANPLAQLITEKIGTRWITHLDELKLEREAGDAVLEFLAKIK RSNKRILSG

PBGlcNAc-GlcNAc8	ON743769	PGluc8 or P-Gluc8	PAA-beta-D-GlcNAc	GlcNAc	CGAATAATTCTAATCGGCGCAGCCGACAATTCAAACCTCAAATTCAAAACCTCAAAATTCGCGCAGGCAACACTCAAACTCAAACTCAAAATTCATATAGAAATAACAATCATCAACGACCGCAACCTCAACATGCTTGGCACACGCGAGCCGAGCATCTACGGCAACACTCTTTCGAACAGTATCTCAACACGCTCTGCCGTGATATCCAGACGTGGATATCGACTACTATCAGACCAACATCGAGGGG	RIIPNRRSRQFKTONSKLKIAGNNSKLTQNSKLIYENNHNHQRTEPQHAWHTRAEHLRQHLFRTV SQPALPSVSRRGYRLLESEQHRG
PBGlcNAc-GlcNAc9F1		PGlu9 or P-Gluc9	PAA-beta-D-GlcNAc	GlcNAc	CCACCGCTTCGACGCGACGCCAATGGGTGCGCGCCATCAAGGCCGCGAGGAGCCAAATACTCTGCTTCACACACGCGCCACGACGCGGATCTCCATGTGGGACACGACGAAAGCGACTACAACATCGTGAAGCGACACCCCTTCAAGCGCGACATCTGAAGGAGCTGGCCGACGCATGCCACGAGGAAGGCATACGATTGCACCTCTATTATAGCCACGGG	PPLRRTPMGARHQGRRSQIHLHHTPPRILHVGHAAKRLQHRESLDLARHREGAGRRMPRGR HTIAPLL
PBGlcNAc-GlcNAc9F2	ON711275	PGlu9 or P-Gluc9	PAA-beta-D-GlcNAc	GlcNAc	CCACCGCTTCGACGCGACGCCAATGGGTGCGCGCCATCAAGGCCGCGAGGAGCCAAATACTCTGCTTCACACACGCGCCACGACGCGATTCTCCATGTGGGACACGACGAAAGCGACTACAACATCGTGAAGCGACACCCCTTCAAGCGCGACATCTGAAGGAGCTGGCCGACGCATGCCACGAGGAAGGCATACGATTGCACCTCTATTATAGCCACGGG	HRFDARQWVRAIKAAGAKYICFTTRHHDGFSMWDTQQSDYNIVKATPFKRDIVKELADACHEEGI RLHLYYSHG
PBGlcNAc-GlcNAc17F1		PGluc17 or P-Gluc17	PAA-beta-D-GlcNAc	GlcNAc	CACAAACAAGCTACAGATGGCGCAAGTGGCACATCCGGAAGCCTTAAAGCCGACCTCGGGCTCAAGCTTATCAGGAGGGCCAAACGCCAAGGCCATCATTATTTATAGCCAACCTATCGGACACGACGCTGGAATCTACGGTTGCCCTGGCCGTTCCGTTCCAAAAAGCGTTATGTTTCGACCCCTATGACAGGCCAGCGTTTCCAAGCCGAAACACACAGCGACTCATTGCACATCTGCCCTACGTTCCGGCGAATCGCTTATCCTACAAACTTTCAAAGAGGCGCTCTGAGGCAATCTTAAGGAGTTGGGCGGCCCTACCGTACGCAACAACAACAGATCAAAACACCCGCAAGGTGCTGGATAAAGGATGGACCCTTTCGTTCAAAGACTGCTCACCACCTACGACAAGCTATTAAAGCAGGG	HKQATDGASGTSGLKSRPRAQAYQEQQRPRPSLFHSQPIGPRRGYICGPRSVPKSMVVRPY DRPAFPSRNTQRLIAHLPTFGRIAYPTNFQRL
PBGlcNAc-GlcNAc17F2	ON711276	PGluc17 or P-Gluc17	PAA-beta-D-GlcNAc	GlcNAc	CACAAACAAGCTACAGATGGCGCAAGTGGCACATCCGGAAGCCTTAAAGCCGACCTCGGGCTCAAGCTTATCAGGAGGGCCAAACGCCAAGGCCATCATTATTTATAGCCAACCTATCGGACACGACGCTGGAATCTACGGTTGCCCTGGCCGTTCCGTTCCAAAAAGCGTTATGTTTCGACCCCTATGACAGGCCAGCGTTTCCAAGCCGAAACACACAGCGACTCATTGCACATCTGCCCTACGTTCCGGCGAATCGCTTATCCTACAAACTTTCAAAGAGGCGCTCTGAGGCAATCTTAAGGAGTTGGGCGGCCCTACCGTACGCAACAACAACAGATCAAAACACCCGCAAGGTGCTGGATAAAGGATGGACCCTTTCGTTCAAAGACTGCTCACCACCTACGACAAGCTATTAAAGCAGGG	TNKLQMAQVAHPEALKADLGLKIRRANAQGHYFIANLSDHDESTVALAVPFQKALWDFDPMTG QRFAETHSDSLHICLRSGESLILQTFKEASEAISKELGGLPVRTTQIKNTRKVLDKGWLTSFKDC SPTYDKLLSR
MethPG-MethPG8	ON711277	PG8 or Meth-PG8	Methanobacterium sp. peptidoglycan	Methanobacterium sp. peptidoglycan	CAAAATCGGCAAGGCAAAATGCTGCTCAGTCTGCTGCTCCTAAAAAGACAGAGGCGAAGGAAACAGAGACTGCTGCCGTGAGTCTCGGCGACGATGAACAACTGCTCTAAGAGGAGGAGAAAGCCGTGTGAGACAGCTCCTGTAGTAGAAAAAAGCTCAGAAAGTCTGTATGTAGAGTCTGTTGCCAAGCAGCCAGAAAGTTAAGGCGGAAAAATAAGTCTGAAAAAGGTGGAAGTCAAGCCTGTCAATAAGCCAGAAAGCTAAGGAAAGTAAAGCCGTGAGGTGAAGGAAAGCAAGCCTGAAGCTAAGGAAGAAAAGGCTGCCAGTCAAGCCTGTAGCAGCTCAGCCAGCTGCAACCAATACGGTCTTACACTGAAGAGCGAGCAGAAAGTTTGTGCTCCAATGAGCCTAAGGTGCTGGAAAGATAGACCTTTTACCCCTTAATCAGAGCACTCGTCTAAGAAGAAAGACCAAGGAGGAGCGCCGTAAAGGAGCGGTGAGGACAAGTTTCCCGCAGCAGCATAGCGAGCGTAAGAAGCGTGTGCGCATCAATAAGGAGCGGTGAGACATCAATGCCGAGTCTTCGACGGGCAATAACGGCAAGAAACAATAAATAATGCGCGCAACCAAGCAATAACAATAATGTTGCGGCAAGAAAAAGAAATAAAAAACAAGAAATAAGAACATAACAACAAGGGCAATAACCAGCGTCAGATAGAGGTGATGACGAGGCTGTAGCAGCGCCAGGTAAGGAAACCCCTTGCCCCTTACAAGCAAGAGCCAGAACAAGAGGGTGCTAAGTACCCTAAGGAAAGCGCGAGGCTGTGAGGAGAAACTTACGACGAGGTTGCTGAGGACGAGAAGGAGTAAGAATACGGG	QIGKANAAQSAAPKTEKETETAASVAPVNNAPKKEEKPETAPVVEKTQKSDVESVAKQPEV KAENKSEKVEYKPVNKPPEAKESKPEVKESKPEAKEEKAASQPVAAQPAATNTVFTLSEQKFAAN EPKVLKIDILSLNQSTRPKKTKKEERRKEREKFAQQHSEKRRVRINKERVINDIAESSQGNNG KNNNNNGNNGNNGGKKNNKNNKNNNNKNNNNQNRQIEVDDEAVARQVETLARLTSKSQ NKKGAKYRKEKREAVQEKLDQVVRQEQKESKIR
StapPG-GlcNAc6	ON711278	StapGluc6 or Stap-Gluc6	Staphylococcus aureus peptidoglycan	GlcNAc	CAGTATAAGCCGTTGGGTAAGATTGACTTGGATAGCATCGGAAAGGGGAAGTCTGTAGAGTCTGCTGCTAAAAAGTCGGAGGCACCGAAGCATGAGACTGCTCCGTCACTCATGCGCCAGTGAAGATGCTCATCTGTAATGAGCCAAACATGACCAGAGATCTACCCATGGATCTCACCACAAAACAGAGATGAACAAGAGAATCAGCAAAAAGTCAAGCAGCAGCCAAAGATGAACGACTTTAAGGGTCAAGAGAAATGCTGCACAAGGTAACAAGAAATGAGAGGCTAGCAGCAGAAATGCTGAGCAGAAAGGCTGCTGACAAACAGCCAGCCCTTAGCGTGTTCACATTGAAGAGTGAGAAGAAATATACCTCAAATGAACCTAAGGTGTTGGGTAAGATTGATCTTTCTTCTCTCAATCAGAGCACTCGTCTAAGAAGAAAGTCTAAGGAGGAGCGCCGCAAGGAGCGTGAAGAGAAGTTGGCGCAGCAGCACAATGATCGCAAGAAGCGTGTTCGTAACAACAAGGAGCGTGTGACATCAATGCCGAGGCTAAGAACACAAGTCCCGATGGTAAATGTTGAGTAAAGGGCAACAATGGTGGCAACAACAAGAAATAGAAACAAGAAATAGAAATAATAACAATAAACAACCGCGGCAATAACAATAACAACCGCGGCAACAGCGTCAAGTCAAGGTGGATGACGAGGCTGTAGCACGCCAGGTAAGAGGAGACTCTCGCTCGCTTGACCAGCAAGGCCAGAACAGAGGGG	QYKPLGKIDLSIGKGSVESAAKKSEAPKHETAASVSHAPVKDAHRNEPKHQDRSTHSHQKQE MKQENQQKSQPKMNDFKGQKNAAGNKNVEAQQQNAEQAAADNSQSSVFTLKSEKYSN EPKVLKIDILSLNQSTRPKKSKKEERRKEREKLAQQHNDRKKVRINKERVINDIAEAKNSAD GNGQNKNGNNGNKNRKNRNNNNNNNNRGNNNNNRGNRQIEVDDEAVARQVETLARLT SKSQNKKG
StapPG-StapPG6	ON711279	StapStap6	Staphylococcus aureus peptidoglycan	Staphylococcus aureus peptidoglycan	CCGGATATCGTGGCTCGTGGAAATCGATATTGATGATATCAGATGGTGCATCAATTATGACGTTCTCACGATACTGAGGATTATGTTCAACCGCATCGGCCGTACAGCCCGTGCCAACCGGATGGTAGAGCCATCACCTTCGTCAACGAGGAAGACAGTACTGTTCCAGCAGATTGAGAAGTTCTCGGAGAAGGTGGTAGAGAAGTGCCTCTGCCGGAAGATTGCGGCCGAAGGCCCTGAATACATCAAGCTCAACAAGCCTTCAAACCGCAACAATGCTGCTAAGGCAAGGGCGGAAGCAGGCGGAAACACCCGCAACGGCAACCGCGCGGCAACAATAACAGCAACGCGGAGGCAAGAGCAAGACCAAGCGCAAGAGCGCAGACAGAAAGCCGACAGACTTCACACAAGCGCAAGCCAAACAGCCAAACGAGCGTCAGGAAAACTCTCAGAACAAATGTTGAGAATGGCGCAGAGAAGAAATCAGGAAACGGCGAGCAAGAATCGCGAGTTCAAGAACAAATGAACAGAGAAACGCTGAGCAGGCAACGGCGAGCAGAAGAATCGCAATAACGGG	PDIVARGIDIDDIEMVINYDVPHTEDYVHRIGRTARANRDRGRAITFVNEEDQYWFQIEKLEKVV EKMLPLEDCGEGPEYIKLNKPSKRNNGRKGKGGKQGGNNRNGNNGNNSNGEKSSTSAKS RRQKDRQOTSHKRKPNKPNRQEKTPQNNGENGAQKNHENGEQKNREFKNNEQRNAEQRNG EQKNRNNNG

StapPG-StapPG7	ON743771	StapStap7	Staphylococcus aureus peptidoglycan	Staphylococcus aureus peptidoglycan	CAGGAGGCTTACTTAACTCTGAACGAGGCACTACCGAACTTAGTCGCAGCATTTACA ATGGTTTTTTAACTATCGACGCATGCACGAGCATGGTGCCAACGACATTCACAAAAT CTGCCCAAAATGCTGAAGCTGAAATAGCTACCCCGGTGGCACGACCTAATGCCGAAC CCAAATACGATAGACGACAAACCACTGTTAACTCTGGCGAAGTGGCTGTGGTCTCCTGT AACAGCAGTGCCTACTGCTCGCAATTATCAAGAGGGAGCAAAATGAGTTGGCAGAG CAAAATGTGCCGAACCATCAGTCCACACGACGTCAGCAAACCGCTCCTGAGTCTAAGC CCAACAGGTTGTTGTACAGAAAGTAGAAACACCGAAGCCTGCTCTACCCCCAAATC TAAGGAGGTGAAGAAAGAGTTGAAAAGCCTAAAGCACCCACTAAAATGTGCACAAAG CCTGTGGCCACTACAAGCAACAAACAACTGCCAAAGACACGACGAAACAAAGCTACTC ATGCTAAAGACAAAGAGCAGTTAACACAAAGGAACTGCCAAAAAGATAAGTCTGTGA ACAAAAGGCAAGAGGCTGATAAAACAAATCAAAACAGTCCGACAAAAATAAAACAAAC ATCGTCTGACAAGAACAAAGGCAACGCAACCAAGCAAAAGGTTAACGATGCCAAGGGC AAACAAAGACGACAAAAGAAACAAACACTGCCAATAAAAGTCTGCCACCAACCCGCA AAGGTCAAAGTAACCTATCGCATTCAAGTGGGTGCAGGCAAAAGCACAAATCGACACGA AGGACGCACAGTTCAAGGCTCTTAACGTAAAGCCGCGTGAAGAAAGGCAGTATGAACAA ATACTTCTACGGCACATACCGCTCATACGCCGAAGCACAAAAGGCACTCAAAACAGTG AAAACATAAAATAGCGCTGCCTACATCGTTGCTTATGTGGGTGGTAAAGCTGTTTCGGT AGCTGAAGCCCGAAGCAAGAGTAGAAGCAAAAGTACAATTATAAGGCATACATA TCCATAAAATATGAAGAAAGAACTAAAATTGCACTGACCGCTGTTGTGGCTTTGGTGC TACTGTTTGTAGGAATCAATTTCTTGAAGGCATCAATGTCTTCAAGGCTACCAATACCT ACTACGTAAAATTTAAGATGTAGCAGGACTCACGGTCTCGACTCCCGTATATGCCAAT GGTTATCCTGTGGGCATCGGGG	QEAYLNSERGTTELSRSIYNGFLTYYRMHEHGANDIPONLPTNAEEIATPVARPNAEPNNDRAQ TTVNTGEVAVVPVTAVPTARIKEGANNELAEQONVRNHQSTRRQQTAPESKPNRVVVQKVETPKP APTPKSKEVKKVEKPKAPTKVTVPVATTSNKQTAKTOKATHAKDKKAVNTKETAOQDKSVT KGKEADKTKSKQSDKNKNTSSDKNKATATKAKVNDAKGQDDKRNKTLPIKSLPPQQRSK
MG1	MN313892.1	MG1/ MA1/ MM8/ MS12	Mucin	D-Galactose, N-acetyl-D- galactosamine, and sialic acid	CCTGAGTATTATCCCGTTAAATTTAAATCGGGTAACTACTTGAGCGACAAAGCGCAG GCAACAAGATGCAAACTGTAGCTCAAAAAGGTGATGCCACTATGTTCCAATTTATTGGC ACACAGAGCAGTTTCATTATGAAGAGTAAAGCGGCACTACGTAGGCTTTGCCAACG AACGCTTCATTACTACAACCAAGAGAATGCCGTTAAAATGTCTATTGCAATGGTTCA GCTGAAAAATACTACGAACGTCAACCGCTAGGTCAAACAAACGATGAACCAATTTGG TGGTACTGGCGTTGGCGTTCAAGTTGGCGAATGGAATGCTGGAGACAAACAAACCA ACTCTTCTTTGAAGGAGCAATTGATTGGGAAGCCGATTAAACAAGTTGGTAGGTCAAA TCAAAGATGCTCAAACTACCAATTCTCTATCGCGATGCTACTGCTGCCCTCGAAGCT ATTCCAGCAGCAAAACCGACGACAAAGGACGAATACAAAGCTGCTATCGAAAAGCTGC AGGCCGCCATCACTGCTTTGAATACTGGCGAAGTAAAGGGTACTGACATTGACGGCAA ACACGTTTACCTTGGCAACAAGCTCCACTCTTCTTCTTCTCGCTTATGCAAATGGCGACA AGATGGGTTCAAAAACCGCTAGCTATAGTAACGATTGCAATTTGGGTTTTGAAAAGGCT GACAACGGCAATACTACATTAGAATGTGGGCACAGGTCTCTATGTAGGTGCGGTTTC CTGAAAAGAACAAACGAATGCTTTAAATTAGTTGAAAAGGCTGAAGCTGCAACATATGTG GTTGCTGCCGCTGCTACTAACGGATATTGCAACATTTATAGCTCAACAGGCACTGCCAA CCTTGAACCTTGACACATGCTGAATTGGAACGGTGTGGTACGTTGGGACAAGGCTGC CGATGCCCTACAATTTATGTTGATCGATGCTTCTGCATTGAAGCTGCTTACGAAAAGT ACTATACTATCCGCAATGTTAAGGTTGGCTATGTGAGCATAGACGGGG	PEYYPVKFKSGNYLSDKGAGNMQTVAQKGDATMFQFIGTQSSFIMKSKSGNYVGFANERFITT KENAVKMSIVNGSAEKYYELQRVGQTKRMNQFGGTGVGVQLGEWNAAGDNNNQLFFEGAIWE ADYNKLVGQIKDAQNYQFFYRDATAALEAIPSTKPTTDEYKAAIEKLQAAITALNTGEVKGTDIAG KHVYLGKLNKSHSFFAYANGDKMGSKTASYSNDCIWVFEKADNGEYIKNVGTGLYGVAVPEKNN ECFKLVEKAEATYVVAATNNGYCNISYSTGTANLETHLMVNNWNGVVRWDKAADASFMLIDA SAFEAAYEKYYTIRNGKGGVYSIDG
MN3	MN313893.1	MN3	Mucin	L-Fucose and D- Mannose	CCTTTGAATACACATTCCGGCAGACGAAGGCTTCGAGTCTACTGGCGGCGGTTCTA CCGGCGGTGGCGAGACTGGCGCGGAAGTAACAGAGAAGTACACTGTTAACTTCGACA AAACAGCTTACCACTACGTAACGACCGTGTCTCAGCAGTTTCTCTCTCCAGCAGATT GGCAAGGACAAGCAGACTGTAAACGTATTGCTTCGAGAGCAGCTTACGAGGATCACA CATCGTCTGTATTCAATGTAGAGGCAGGCAGCGAGCTGACAGCTTCTTCAACTACTC AGGTCAGTGGATGAATGGTTATATCTACATCGACCCGCGCAACGACGGCGAGTCTCT TACAAGGAAGGCCAGTGGGATCAGGCAGGCACCGACTTGGTAGCCTACAGCTTCTAT ACTACACTTGCTAATCCGAAAGTAAACGATGGCAATGGCTACAACCTTACCGGTGCTTC TGATCTGGTAACGATCGTAGCAACGTTAATCCTCCTTCACTTACAGCTCCTACTAGAC CGGTGATACCCGATCCGCTTCAAGATCGACTGGAATCGCATCCTCCTCGAGGTTTC AAGCGACATCCTCTGACGGTGGTGGCGTTTGGGACGCAACTCTCAATGTTGTAGCA CGAGAGCCTGAGGTTAAGGAAGAGAAAGACTTCACAGACGCTATCTATGTGTTGCTA ACGGTGTGTCTGAACCAAGTGGTCAAGGCTCAGGTTACTATCAAGGAGATGACAGACGA GACAATCAGCATGACACTTGCTATTGTTGGTCAGGAAGATGCTGAGTACACAGCTTCT GGTTTCACCAAGACTGTTGACACAGAGAAGAACCCGCACTACCTACACTGGCGAGTCTCA ACGTTGACGGCGATGACTCGGGG	PFEYTFGTDEGFESTGGSTGGGETGGEVTEKYTVNFDKTAHYHSRNDRLVSSFLQIQIGDKQT VNVFASRAAYEDHTSSVFNVEAGSELTASFNYSQWMMNGYIYIDRNDNDEFSYKEGQWDQAGT DLVAYSFYTTLANPKVNDGNGYNSTGASVSGNDRSNVNPSTAPTPEPTYRIRFKIDWNILPG GSSDILSDGGVWDATLNVVAAEPEVKEEKSFDTDAISMVANGVSEPVGQAQVTIKEMTDETISMT LAIVGQEDAEYTAGSFKTVDEKRNRTTYTGSNLVDGDDFG

MU1	MN313894.1	MU1	Mucin	N-Acetyl-D-glucosamine	CCTGAAAACGATGCATTGCGCACTCACATTCACATACACAGCAGGTGAGAAGACTCTCG GTGGTGAGTTCAACTACGAGAAGAAGGATCCTGATACTCCAGATCCAGAGCTCTTCTG CAAGGAGAACTACGTAGCTGACGGCACAGGCTTCGAGTGGGATATCAATGTTGATTGG GATACTCAGAAGATCGTTATGCTATCGACCCGCTACATGTACAGGTTCTTGGCAGGGA TGTAATCGGTCTCGGTGCTGTTCCAACAGCATGGGATAACACTCTCCACTTGATCGC ACAAGCGCAGACCAGATGCTTCAGGGATACTTCAATGTACCTGGTGGCAGCAACAACA ACACTGACAAGTTTCGCTGAGACAGCTCCGTTCTGGTAGAGGTTTCTAAGGCTCAGGG CTTTGTTGTTAACAACGAGGTTAAGATTGCTTCAAGCCCAATGAGCTATCTTCACTC TCTCGACCGTTAAGATGGGTACTGGCGAGGGTGCTAACGCAGGTACGCGTGTACATA CAACTACGTTAAGGTTGTTGATAAGGATTGGACAGCACCTAAGGATCCTGACACAGGT ATCAACGCAACAACAGTTGCTGAGGGTGAGGTTGAGTTCTTCACAGTTAACGGCGTTA AGCTTAACAAGCTCCAGAAGGGTCTGAACATCGTTCGCACCGGTGACGGCAAGGTTAA GAAGGTACTCGTTAAGTAATCTTTCAGGGGGTGCACTCAGGGGGTGACAGCTGTCCCA GCTGCCAACAACCAAGTAAACGCGTGACCCACAGAATAAACTCATAAGAGGGCATGGCA TTCCGCCATGCCCTCTTTGCGTTGCTACCCCTCCACGGATCTATCGTAGGAGGGTAT GGCATCCCTGCCATACCCACGCCGCCCTCCACGGGGTGACAGCGGTCTCCGCTGCAC CAACCGAGCAGGG	PENDAFALTFTITAGEKTLGGEFNYEKKDPDTPDPELFCKENYVADGTGFEWDINVDWDTQKIVM SIDPSTCTGSCEDVIGLAVPTAWDNTLHLRYTSADQMLQGYFNVPGGSNNTDKFAETAPFLVE VSKAQGFVNNEVKIASSAMSYLFTLSTVKMGTGEGANDKSRATYNYVKVVDKDWTPAKDPDTG INATTVAEGEVEFFTVMGVKLNKLQKGLNIVRTADGKVKVLVK
MU3	MN313895.1	MU3	Mucin	N-Acetyl-D-glucosamine	CAGACTCCTAAGGATGTAACCGTTGTTGAGAAGTATCAGGCTGACGGCACAGGTTTCT CTCACACAATCAATGTTGATTGGGACAAGCAGAAGATAGTTGCTTCTATCGACTTCTCT AATGGTGGTGACGACAAGGATATCCTTGTCTATGACTACTGGCGACAGCTTCACAGCAT TCCAGACAAGCACATACCGCACAAATGCACTGGTACTGCAATCAGACTGCTAAGCAGAT ATCTGGCTTCTTCGCAAAAGAGCGGCGCTGGTAACAACAACACCCGTCGCTATAGAGCTT GCTGACTGCCTCGCTAAGTTTCAAAATCTCTAAGGCTGAGGGTCTGAAGGTTAATGGTG TCGTTAAGATGACTCCTGATGCTCTTGAAGAACTCCTTACAGGCGATCCTATCATCATC GGTAGCGGTGAGTCTCCAAGTTTCAGCAATGCATTCTACAACATACATCAAGGTTGTTTC TCTCGATTGGAAAGAGACAACAGAGCCAGAGGTAACCGTTAAGGACGAGAAGACCTTC AACGAGGCTCTCTATATGCAGGATCAAAAAGTTGCTGACGCTACGGTTGTAGTTAAGG GG	QTPKDVTVVEKYQADGTGFSHTINVDWKQIVASIDFSNGGDDKILAMTTGDSFTAFQTSTYR TMHWYCNQTAKQISGFFAKSGAGNNNTGRIDVADCLAKFEISKAEGLVNMGVVKMTPDAEELLT GDPHIGSGESPKFSNAFYNYIKVSLDWKETTEPEVTVKDEKTFNEALYMQDQKVADATVVVKG
MF12F1		MF12	Mucin	L-Fucose	CCGTCTCCAAGGGTGTGGAGTCTATCTGGCCACCCGCACAATCTCAAGCTCATCAC CGAGAGCTGCACGAAGACGGATCGCAACGACTCGAAGACCCCTGGCCGGTTATCTCCG TCTCTGGGACAAGCACGAACCTCAACATCTCGATCTCGTTCTGTTGTAGACGGCGACAAC AGATCGGG	PSPRVWSPWPTRTISSSSPRAARRRIATRRPWPVIVSVGTSTNSTSRSRSL
MF12F2	ON743770	MF12	Mucin	L-Fucose	CCGTCTCCAAGGGTGTGGAGTCTATCTGGCCACCCGCACAATCTCAAGCTCATCAC CGAGAGCTGCACGAAGACGGATCGCAACGACTCGAAGACCCCTGGCCGGTTATCTCCG TCTCTGGGACAAGCACGAACCTCAACATCTCGATCTCGTTCTGTTGTAGACGGCGACAAC AGATCGGG	VSKGVESYLAPHNLKLITESCTKTDRNDSKTLAGYLRWLWDKHELNISFVVDGDNRS

Table S8: Search_Result_UniRef100_sensitivity_8.8.ms_processed

query	target	ident	align	mismatch	qstart	qend	tstart	tend	eval	bits	qseq	target	length	representative	Member	organism	cluster	representative_name	domain-start1	domain-end1	domain-name1	domain-start2	domain-end2	domain-name2	domain-start3	domain-end3	domain-name3	domain-start4	domain-end4	domain-name4	domain-start5	domain-end5	domain-name5		
1	21NS	UniRef100_A049QWOC6	0.99	20	1	2	293	293	1.83E-100	296	598	296	296	Unclassified organism	UniRef100_A049QWOC6	Unclassified organism	Cluster: Putative mucin glycan binding protein (Fragment)																		
1	MN3	UniRef100_G6AYK8	0.671	204	65	31	234	101	1208	238	238	1243	1243	Prevotella stercorica DSM 18206	Prevotella stercorica DSM 18206	Prevotella stercorica DSM 18206	Cluster: Uncharacterized protein																		
2	MN3	UniRef100_A049G9JDF9	0.661	204	67	31	234	1121	1318	218	217	298	1353	Prevotella stercorica	Prevotella stercorica	Prevotella stercorica	Cluster: Lipocalin-like domain-containing protein																		
3	MN3	UniRef100_A049J3CQV6	0.632	209	75	27	235	464	668	1256	272	258	701	not retrieved	not retrieved	not retrieved	Cluster: Uncharacterized protein																		
4	MN3	UniRef100_R7GRV5	0.61	216	80	28	243	412	617	1.01E-100	252	298	849	Prevotella stercorica	Prevotella stercorica	Prevotella stercorica	Cluster: Lipocalin-like domain-containing protein																		
5	MU1	UniRef100_A046G9KE9	1	237	0	2	238	1	237	2.28E-156	496	238	237	Unclassified organism	Unclassified organism	Unclassified organism	Cluster: Putative mucin glycan binding protein (Fragment)																		
6	MU1	UniRef100_R6F8T1	0.89	174	19	65	238	1	171	1.28E-61	309	238	171	Prevotella sp. CAG-520	Prevotella sp. CAG-520	Prevotella sp. CAG-520	Cluster: Uncharacterized protein																		
7	MU1	UniRef100_G6AYK8	0.682	182	57	5	186	138	315	2.00E-70	248	238	1243	Prevotella stercorica DSM 18206	Prevotella stercorica DSM 18206	Prevotella stercorica DSM 18206	Cluster: Uncharacterized protein																		
8	MU1	UniRef100_A049RJDD9	0.672	182	58	5	186	138	315	3.75E-68	241	238	1353	Prevotella stercorica	Prevotella stercorica	Prevotella stercorica	Cluster: Lipocalin-like domain-containing protein																		
9	MU1	UniRef100_R6FV92	0.384	212	127	26	236	150	361	9.75E-43	168	238	362	Prevotella sp. CAG-520	Prevotella sp. CAG-520	Prevotella sp. CAG-520	Cluster: Uncharacterized protein																		
10	MU3	UniRef100_A046G9KCB4	1	193	0	2	194	1	193	1.83E-122	396	195	193	Unclassified organism	Unclassified organism	Unclassified organism	Cluster: Putative mucin glycan binding protein (Fragment)																		
11	MU3	UniRef100_A049RJDD9	0.938	194	12	1	194	161	758	1.29E-15	353	255	849	Prevotella stercorica	Prevotella stercorica	Prevotella stercorica	Cluster: Lipocalin-like domain-containing protein																		
12	MU3	UniRef100_G6AYK8	0.869	192	25	1	192	566	754	2.51E-102	338	195	1243	Prevotella stercorica DSM 18206	Prevotella stercorica DSM 18206	Prevotella stercorica DSM 18206	Cluster: Uncharacterized protein																		
13	MU3	UniRef100_A04264Y9S7	0.766	197	45	3	194	454	650	1.21E-61	307	195	1107	Prevotella sp. 885	Prevotella sp. 885	Prevotella sp. 885	Cluster: Uncharacterized protein																		
14	MU3	UniRef100_A046G9KE9	0.392	180	94	10	189	40	194	1.84E-20	101	195	237	Unclassified organism	Unclassified organism	Unclassified organism	Cluster: Putative mucin glycan binding protein (Fragment)																		
15	St-Glc5v2	UniRef100_A049R9K0L0	0.97	171	5	1	171	492	662	2.24E-109	357	172	733	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: Alpha-amylase	45		287	Alpha-amylase, cat	652		715	Starch-binding mod		45		287	Alpha-amylase, c	652		715	Starch-binding module 26	
16	St-Glc5v2	UniRef100_A047H1MV67	0.935	171	11	1	171	492	662	3.18E-106	347	172	733	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: Alpha-amylase	45		287	Alpha-amylase, cat	652		715	Starch-binding module 26										
17	St-Glc5v2	UniRef100_A043E4S4J2	0.929	171	12	1	171	492	662	4.36E-106	347	172	733	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: Alpha-amylase	45		287	Alpha-amylase, cat	652		715	Starch-binding module 26										
18	St-Glc5v2	UniRef100_A046A7UP88	0.935	171	11	1	171	492	662	5.98E-106	347	172	1081	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: Starch-binding protein	45		287	Alpha-amylase, cat	652		715	Starch-binding module 26										
19	St-Glc5v2	UniRef100_UP000010403D	0.929	171	12	1	171	492	662	1.55E-105	346	172	1083	Prevotella sp. Marseille-P4119	Prevotella sp. Marseille-P4119	Prevotella sp. Marseille-P4119	Cluster: Alpha-amylase family glycosyl hydrol	45		287	Alpha-amylase, cat	652		715	Starch-binding module 26										
20	St-Glc6	UniRef100_UP0019344099	0.931	205	14	1	205	192	396	1.56E-132	425	205	396	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: SusF/SusE family outer membrane p	177		303	Outer membrane protein SusF	177		303	Outer membrane protein SusF										
21	St-Glc6	UniRef100_A049R9K0L0	0.912	205	18	1	205	192	396	2.67E-131	422	205	396	Prevotella sp. AM34-19LB	Prevotella sp. AM34-19LB	Prevotella sp. AM34-19LB	Cluster: SusF/SusE family outer membrane p	177		303	Outer membrane protein SusF	177		303	Outer membrane protein SusF										
22	St-Glc6	UniRef100_A049R9K0L0	0.839	205	33	1	204	186	9.72E-118	383	205	397	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: SusF/SusE family outer membrane p	188		304	Outer membrane protein SusF	188		304	Outer membrane protein SusF											
23	St-Glc6	UniRef100_UP0015578378	0.669	205	68	1	205	192	396	2.05E-95	318	205	396	Prevotella sp. PCHR	Prevotella sp. PCHR	Prevotella sp. PCHR	Cluster: SusF/SusE family outer membrane p	177		303	Outer membrane protein SusF	177		303	Outer membrane protein SusF										
24	St-Glc6	UniRef100_A043D1HL84	0.631	205	75	1	205	192	396	1.31E-87	296	205	396	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: SusF domain-containing protein	186		302	Outer membrane protein SusF	186		302	Outer membrane protein SusF										
25	St-Si4	UniRef100_A046A7U73	0.995	224	1	1	224	174	397	4.25E-153	486	224	397	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: SusF/SusE family outer membrane p	182		304	Outer membrane protein SusF	182		304	Outer membrane protein SusF										
26	St-Si4	UniRef100_A046A7U73	0.929	224	1	1	224	174	397	1.36E-141	452	224	397	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: SusF/SusE family outer membrane p	182		304	Outer membrane protein SusF	182		304	Outer membrane protein SusF										
27	St-Si4	UniRef100_A047YV118	0.892	224	24	1	224	174	397	6.17E-137	439	224	397	Prevotella hominis	Prevotella hominis	Prevotella hominis	Cluster: SusF/SusE family outer membrane p	182		304	Outer membrane protein SusF	182		304	Outer membrane protein SusF										
28	St-Si4	UniRef100_A0437ABP42	0.892	224	24	1	224	174	397	1.16E-136	438	224	397	Prevotella sp. AM42-24	Prevotella sp. AM42-24	Prevotella sp. AM42-24	Cluster: SusF/SusE family outer membrane p	182		304	Outer membrane protein SusF	182		304	Outer membrane protein SusF										
29	St-Si4	UniRef100_A0437H026	0.879	224	27	1	224	174	397	5.81E-136	437	224	397	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: SusF domain-containing protein	182		304	Outer membrane protein SusF	182		304	Outer membrane protein SusF										
30	St-Si5	UniRef100_A049H147W8	0.675	108	34	1	108	161	266	1.63E-39	152	115	654	Prevotella sp. sp-65	Prevotella sp. sp-65	Prevotella sp. sp-65	Cluster: Starch-binding module 26	373		471	Starch-binding module 26	373		471	Starch-binding module 26										
31	St-Si5	UniRef100_UP0019610044	0.68	100	31	1	100	266	364	9.94E-38	147	115	369	Marella massiliensis	Marella massiliensis	Marella massiliensis	Cluster: Starch-binding protein	373		471	Starch-binding module 26	373		471	Starch-binding module 26										
32	St-Si5	UniRef100_UP000084E081	0.693	98	30	1	98	161	258	2.57E-37	146	115	369	Prevotella sp. P084	Prevotella sp. P084	Prevotella sp. P084	Cluster: Starch-binding protein	373		471	Starch-binding module 26	373		471	Starch-binding module 26										
33	St-Si5	UniRef100_UP000084E081	0.693	98	30	1	98	161	258	2.57E-37	146	115	369	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: Starch-binding module 26	373		471	Starch-binding module 26	373		471	Starch-binding module 26										
34	St-Si5	UniRef100_A041H4B20	0.632	98	36	1	98	171	268	8.31E-36	141	115	570	Prevotella sp. tC2-28	Prevotella sp. tC2-28	Prevotella sp. tC2-28	Cluster: Starch-binding module 26	399		465	Starch-binding module 26	399		465	Starch-binding module 26										
35	kin-Xyl8	UniRef100_R6XEY5	0.995	474	2	2	475	84	557	1.94E-316	972	476	800	Prevotella sp. CAG-732	Prevotella sp. CAG-732	Prevotella sp. CAG-732	Cluster: GH10 domain-containing protein	516		794	Glycosyl hydrolase	166		285	Carbohydrate binding domain										
36	kin-Xyl8	UniRef100_A049R9K0L0	0.985	474	149	2	474	88	560	8.52E-213	672	476	800	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		801	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
37	kin-Xyl8	UniRef100_A049R9K0L0	0.979	477	199	2	474	88	564	3.18E-188	543	476	816	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		816	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
38	kin-Xyl8	UniRef100_A049R9K0L0	0.973	477	202	2	474	88	564	3.18E-184	532	476	808	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		805	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
39	kin-Xyl8	UniRef100_A043S3E065	0.555	479	210	2	474	82	560	2.23E-163	528	476	812	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		810	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
40	kin-Xyl8	UniRef100_A043S3E065	0.555	479	210	2	474	82	560	2.23E-163	528	476	812	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		810	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
41	kin-Xyl8	UniRef100_A043S3E065	0.555	479	210	2	474	82	560	2.23E-163	528	476	812	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		810	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
42	kin-Xyl8	UniRef100_A043S3E065	0.555	479	210	2	474	82	560	2.23E-163	528	476	812	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		810	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
43	kin-Xyl8	UniRef100_A043S3E065	0.555	479	210	2	474	82	560	2.23E-163	528	476	812	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		810	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
44	kin-Xyl8	UniRef100_A043S3E065	0.555	479	210	2	474	82	560	2.23E-163	528	476	812	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516		810	Glycosyl hydrolase	170		289	Carbohydrate binding domain										
45	kin-Xyl8	UniRef100_A043S3E065	0.555	479	210	2	474	82	560	2.23E-163	528	476	812	Prevotella sp.	Prevotella sp.	Prevotella sp.	Cluster: GH10 domain-containing protein	516																	

110	Am-1	UniProt00_A0MAYB77	0.883	155	18	1	155	961	1114	1.0E+07	291	155	1114	Pivotella	cluster: Starch-binding protein	71	570	Alpha amylose, c	970	1045	Starch-binding module 26
111	Am-1	UniProt00_A0AD3IGW27	0.883	155	18	1	155	962	1115	4.10E+07	291	155	1115	Pivotella	cluster: Alpha-amylose	71	571	Alpha amylose, c	971	1046	Starch-binding module 26
112	Am-1	UniProt00_A0MAYB09	0.884	155	21	1	155	964	1117	7.72E+07	291	155	1117	Pivotella	cluster: Starch-binding protein	71	575	Alpha amylose, c	973	1048	Starch-binding module 26
113	Am-1	UniProt00_P0R177	0.881	155	29	1	155	789	922	9.1E+06	922	155	922	Pivotella	cluster: Alpha-amylose c	71	573	Alpha amylose, c	973	1049	Starch-binding module 26
114	Am-1	UniProt00_A0MAYB75	0.882	155	26	1	155	963	1116	2.83E+07	280	155	1116	Pivotella	cluster: Starch-binding protein	71	573	Alpha amylose, c	972	1047	Starch-binding module 26
115	Ap-2	UniProt00_A0A3E4SL8	0.999	300	3	2	301	793	1092	6.70E-195	611	302	1221	Pivotella	cluster: Alpha-amylose	71	573	Alpha amylose, c	975	1052	Starch-binding module 26
116	Ap-2	UniProt00_A0A1G5B82	0.983	300	5	2	301	795	384	6.34E-194	608	302	1223	Pivotella	cluster: Uncharacterized protein (Fragment)	277	354	Starch-binding module 26			
117	Ap-2	UniProt00_U0P001948A9	0.986	300	5	0.98	300	791	1090	1.4E+07	740	302	1118	Pivotella	cluster: Alpha-amylose family glycosyl hydrol	71	573	Alpha amylose, c	973	1050	Starch-binding module 26
118	Ap-2	UniProt00_A0A3RCN825	0.956	300	13	2	301	792	1089	7.98E-187	587	302	1118	Pivotella	cluster: Alpha-amylose	71	573	Alpha amylose, c	974	1049	Starch-binding module 26
119	Ap-2	UniProt00_A0A1X0B0M2	0.946	300	16	2	301	792	1089	3.18E-184	589	302	1118	Pivotella	cluster: Starch-binding protein	71	573	Alpha amylose, c	974	1049	Starch-binding module 26
120	Ap-2	UniProt00_U0P001933CF	0.987	293	4	0.98	293	1056	1234	6.24E-194	604	293	1118	Pivotella	cluster: Alpha-amylose family glycosyl hydrol	71	573	Alpha amylose, c	974	1049	Starch-binding module 26
121	Ap-2	UniProt00_A0A1H0M36	0.952	293	11	2	234	823	1055	5.20E-143	457	235	1117	Pivotella	cluster: Starch-binding protein	70	572	Alpha amylose, c	973	1048	Starch-binding module 26
122	Ap-2	UniProt00_A0A3RCN825	0.948	293	12	2	234	824	1056	3.45E-142	456	235	1118	Pivotella	cluster: Alpha-amylose	71	573	Alpha amylose, c	974	1049	Starch-binding module 26
123	Ap-2	UniProt00_A0A3RYG038	0.944	293	13	2	234	823	1055	4.70E-142	454	235	1117	Pivotella	cluster: Alpha-amylose	70	572	Alpha amylose, c	973	1048	Starch-binding module 26
124	Ap-2	UniProt00_A0A1X0B0M2	0.962	293	13	0.96	293	1099	234	824	1056	233	1118	Pivotella	cluster: Starch-binding protein	71	573	Alpha amylose, c	974	1049	Starch-binding module 26
125	LevLeu	UniProt00_A0A7AWA7G4	0.952	296	14	2	297	166	461	1.20E-196	616	297	461	Pivotella	cluster: DUF4950 domain-containing protein	204	461	Domain of unknown	41	192	Domain of unknown
126	LevLeu	UniProt00_R6PVV2	0.952	296	14	2	297	158	453	5.83E-196	614	297	453	Pivotella	cluster: DUF4950 domain-containing protein	196	453	Domain of unknown	33	184	Domain of unknown function (DUF508)
127	LevLeu	UniProt00_A0A03H11U2	0.956	296	16	0.956	296	1068	298	1.6E+07	608	296	1118	Pivotella	cluster: DUF4950 domain-containing protein	209	462	Domain of unknown	41	192	Domain of unknown function (DUF508)
128	LevLeu	UniProt00_A0A1X0K0H2	0.962	295	91	2	296	173	464	1.47E-173	434	297	465	Pivotella	cluster: Pivotella mirzabai	209	462	Domain of unknown	47	211	Domain of unknown
129	LevLeu	UniProt00_C8MN84	0.686	296	97	2	297	170	461	2.27E-131	427	297	461	Pivotella	cluster: DUF4950 domain-containing protein	207	461	Domain of unknown			

Table S6: Search_Result_dbCAN2_Sensitivity_8.5

query	target	fidet	alnlen	mismatch	gapopen	qstart	qend	tstart	tend	evalue	bits	query_length	target_length
St-Glc1	CBM26.aln	0.309	66	42	0	267	332	2	63	1.24E-10	58	370	77
St-Glc2	CBM26.aln	0.209	60	44	0	59	118	13	68	3.11E-10	55	232	77
St-St5	CBM26.aln	0.214	66	48	0	6	71	2	63	1.39E-04	35	115	77
Xln-Xyl8	CBM4.aln	0.167	129	105	0	84	212	5	131	8.24E-10	56	476	131
Xln-Xyl8	GH10.aln	0.333	57	37	0	4	59	32	88	1.39E-08	52	476	304
Xln-Xyl8	CBM16.aln	0.186	75	54	0	84	158	2	68	1.34E-04	39	476	131
Am-Am1	CBM26.aln	0.233	74	51	0	10	83	3	69	6.11E-12	58	155	77
Ap-Ap2	CBM26.aln	0.187	77	55	0	184	260	3	71	1.58E-10	57	302	77
Ap-Ap5	CBM26.aln	0.205	75	54	0	152	226	3	71	7.27E-11	57	235	77
BDG-Glc5	CBM27.aln	0.238	63	43	0	216	278	12	68	1.14E-09	54	279	166
BDG-Glc5	CBM23.aln	0.126	101	80	0	94	186	59	159	1.23E-04	38	279	160
PBGlcNAc-GlcNAc4F2	GT35.aln	0.018	273	235	0	1	273	154	393	2.10E-92	297	275	654
PBGlcNAc-GlcNAc9F2	GH29.aln	0.375	72	44	0	2	73	90	160	1.35E-35	122	74	335
PBGlcNAc-GlcNAc9F2	GH151.aln	0.154	69	54	0	4	72	1	65	2.78E-07	41	74	132
PBGlcNAc-GlcNAc17F2	GH106.aln	0.35	110	68	0	20	129	549	653	3.61E-14	64	142	794

Table S7a: Search_Result_pfamA_Full_Sensitivity_8.5

query	target	fidet	alnlen	mismatch	gapopen	qstart	qend	tstart	tend	evaluate	bits	query_length	target_length	pfam-family_description
Am-Am1	PF16738.8	0.16	74	56	0	10	83	19	86	1.34E-11	61	155	105	Starch-binding module 26
Ap-Ap2	PF16738.8	0.192	78	57	0	184	261	19	89	5.03E-12	66	302	105	Starch-binding module 26
Ap-Ap5	PF16738.8	0.168	76	58	0	152	227	19	89	4.03E-12	65	235	105	Starch-binding module 26
PBGal-Gal8	PF12836.10	0.269	63	45	0	215	277	22	84	9.05E-14	71	279	110	Helix-hairpin-helix motif
PBGlcNAc-GlcNAc4F2	PF00343.23	0.402	211	117	0	63	273	240	435	6.75E-78	259	275	722	Carbohydrate phosphorylase
PBGlcNAc-GlcNAc9F2	PF01120.20	0.352	71	45	0	3	73	136	205	7.77E-33	118	74	575	Alpha-L-fucosidase
PBGlcNAc-GlcNAc9F2	PF14871.9	0.191	72	56	0	3	74	54	123	1.01E-08	49	74	254	Hypothetical glycosyl hydrolase 6
StapPG-StapPG6	PF00271.34	0.381	55	33	0	2	56	260	314	8.51E-08	51	198	383	Helicase conserved C-terminal domain
Lev-Lev5	PF16324.8	0.328	258	171	0	40	297	21	275	8.72E-95	309	297	328	Domain of unknown function (DUF4960)
St-Glc1	PF16738.8	0.134	64	52	0	267	330	18	78	3.36E-10	61	370	105	Starch-binding module 26
St-Glc2	PF16738.8	0.272	65	44	0	59	123	29	90	3.22E-08	53	232	105	Starch-binding module 26
St-St4	PF16411.8	0.134	123	105	0	9	131	43	164	7.08E-13	67	224	400	Outer membrane protein SusF_SusE
St-St5	PF16738.8	0.22	75	55	0	3	77	15	85	5.86E-06	43	115	105	Starch-binding module 26
Xln-Xyl8	PF00331.23	0	58	56	0	4	60	151	208	3.88E-08	55	476	623	Glycosyl hydrolase family 10
Xln-Xyl8	PF02018.20	0.122	120	102	0	84	203	101	217	1.59E-07	53	476	293	Carbohydrate binding domain

Table S7b: Search_Result_pfamB_sensitivity_8.5

query	target	fidcnt	alnlen	mismatch	gapopen	qstart	qend	tstart	tend	evalue	bits	query_length	target_length
Am-Glc2	Pfam-B_132216	0.225	79	60	0	2	80	187	265	3.14E-05	46	197	342
AG-Gal2	Pfam-B_041373	0.252	335	248	0	2	333	33	367	1.23E-76	261	334	383
AG-Gal2	Pfam-B_129594	0.221	183	107	0	195	332	248	430	7.41E-13	72	334	447
AG-Gal2	Pfam-B_139034	0.316	138	87	0	196	333	295	422	1.09E-04	46	334	438
IlIn-Glc6	Pfam-B_098828	0.333	36	23	0	1	36	85	120	2.38E-05	47	232	177
PBGal-Gal8	Pfam-B_117300	0.37	62	38	0	44	105	85	146	9.82E-07	52	279	167
PBGlcNAc-GlcNAc4F2	Pfam-B_038544	0.118	173	133	0	64	236	258	409	7.44E-05	46	275	511
PBGlcNAc-GlcNAc17F2	Pfam-B_139651	0.024	119	114	0	13	130	138	256	1.82E-09	57	142	767
MethPG-MethPG8	Pfam-B_041373	0.346	165	107	0	118	282	219	383	2.80E-64	223	290	383
MethPG-MethPG8	Pfam-B_129594	0.224	195	113	0	131	277	248	442	2.43E-17	85	290	447
MethPG-MethPG8	Pfam-B_139034	0.32	151	97	0	132	282	295	438	2.23E-06	51	290	438
StapPG-GlcNAc6	Pfam-B_041373	0.236	263	199	0	1	261	100	362	4.12E-55	195	261	383
StapPG-GlcNAc6	Pfam-B_129594	0.212	179	106	0	127	261	248	426	2.38E-10	63	261	447
StapPG-StapPG6	Pfam-B_140635	0.389	95	37	0	50	144	1	61	2.02E-23	100	198	218
StapPG-StapPG6	Pfam-B_138624	0.428	70	39	0	2	71	49	118	1.30E-17	83	198	221
StapPG-StapPG6	Pfam-B_137648	0.103	74	65	0	2	75	32	105	1.30E-17	83	198	246
StapPG-StapPG6	Pfam-B_102152	0	46	45	0	2	47	15	60	7.36E-12	66	198	224
StapPG-StapPG6	Pfam-B_017071	0.05	59	54	0	15	73	1	58	3.49E-10	61	198	173
StapPG-StapPG6	Pfam-B_027443	0	41	40	0	2	42	41	81	3.42E-07	52	198	341
StapPG-StapPG6	Pfam-B_142319	0.02	48	45	0	5	52	89	135	3.19E-05	46	198	610
StapPG-StapPG6	Pfam-B_104506	0	43	40	0	19	59	73	115	1.43E-04	44	198	402
StapPG-StapPG6	Pfam-B_014096	0	22	21	0	26	47	88	109	6.38E-04	42	198	339
StapPG-StapPG6	Pfam-B_053823	0.047	42	38	0	16	56	108	149	6.38E-04	42	198	360
St-Glc1	Pfam-B_132216	0.241	141	104	0	6	143	125	265	1.17E-13	75	370	342
St-Glc1	Pfam-B_131236	0.216	125	97	0	18	142	168	292	1.30E-04	46	370	350
St-St4	Pfam-B_117833	0.152	114	85	0	10	123	204	304	1.03E-05	48	224	485

Table S8: Search_Result_All_Against_All_Input_Sensitivity_8.5

query	target	fident	alnlen	mismatch	qstart	qend	tstart	tend	evalue	bits	quer	target_length
PBGlcNAc-GlcNAc8	PBGlcNAc-GlcNAc8	1	88	0	1	88	1	88	6.43E-55	174	88	88
PBGlcNAc-GlcNAc9F2	PBGlcNAc-GlcNAc9F2	1	74	0	1	74	1	74	5.06E-53	168	74	74
StapPG-GlcNAc6	StapPG-GlcNAc6	1	261	0	1	261	1	261	3.99E-145	444	261	261
StapPG-GlcNAc6	AG-Gal2	0.84	265	42	1	261	64	328	4.26E-110	343	261	334
StapPG-GlcNAc6	MethPG-MethPG8	0.574	260	106	13	261	2	261	2.80E-54	182	261	290
StapPG-StapPG6	StapPG-StapPG6	1	198	0	1	198	1	198	7.13E-119	365	198	198
AG-Gal2	AG-Gal2	1	334	0	1	334	1	334	3.46E-187	570	334	334
AG-Gal2	StapPG-GlcNAc6	0.836	265	43	64	328	1	261	2.02E-106	336	334	261
AG-Gal2	MethPG-MethPG8	0.57	265	111	76	333	2	266	6.19E-55	187	334	290
IlIn-Glc6	IlIn-Glc6	1	232	0	1	232	1	232	6.62E-138	422	232	232
Am-Glc2	Am-Glc2	1	197	0	1	197	1	197	4.64E-135	411	197	197
Am-Glc2	St-Glc1	0.994	196	1	1	196	64	259	7.94E-134	408	197	370
Am-Glc2	St-Glc5V2	0.934	153	10	44	196	1	153	2.18E-97	303	197	172
Am-Glc2	St-Glc5V1	0.921	153	12	44	196	1	153	3.72E-96	299	197	172
Am-Glc2	Ap-Ap2	0.369	180	110	2	181	91	266	4.26E-26	97	197	302
Am-Glc2	Ap-Ap5	0.336	180	115	2	181	59	232	6.17E-24	91	197	235
Am-Glc2	St-Glc2	0.444	79	43	2	79	153	231	3.12E-15	65	197	232
Am-Glc2	Am-Am1	0.437	48	26	134	181	44	91	1.36E-09	48	197	155
MF12F2	MF12F2	1	59	0	1	59	1	59	6.51E-39	126	59	59
St-Glc1	St-Glc1	1	370	0	1	370	1	370	2.18E-256	771	370	370
St-Glc1	Am-Glc2	0.994	196	1	64	259	1	196	1.34E-130	408	370	197
St-Glc1	St-Glc5V2	0.935	171	11	107	277	1	171	3.79E-107	340	370	172
St-Glc1	St-Glc5V1	0.923	171	13	107	277	1	171	6.37E-106	337	370	172
St-Glc1	Ap-Ap2	0.334	240	149	5	244	43	266	1.12E-25	101	370	302
St-Glc1	Ap-Ap5	0.3	240	155	5	244	11	232	1.67E-23	94	370	235
St-Glc1	St-Glc2	0.351	138	82	5	142	105	231	4.36E-15	68	370	232
St-Glc1	Am-Am1	0.437	48	26	197	244	44	91	6.09E-09	48	370	155
St-Glc2	St-Glc2	1	232	0	1	232	1	232	6.29E-154	468	232	232
St-Glc2	Ap-Ap2	0.982	168	3	64	231	2	169	1.19E-107	334	232	302
St-Glc2	Ap-Ap5	0.963	136	5	96	231	2	137	3.74E-80	255	232	235
St-Glc2	St-Glc1	0.44	82	45	150	231	62	142	9.65E-14	61	232	370
St-Glc2	Am-Glc2	0.444	79	43	153	231	2	79	3.18E-13	60	232	197
St-Glc2	St-Glc5V2	0.289	105	63	8	97	2	106	1.30E-07	42	232	172
St-Glc2	St-Glc5V1	0.288	105	63	8	97	2	106	3.10E-07	41	232	172
Ap-Ap2	Ap-Ap2	1	302	0	1	302	1	302	3.60E-206	623	302	302
Ap-Ap2	Ap-Ap5	0.944	235	13	34	268	2	234	1.34E-147	454	302	235
Ap-Ap2	St-Glc2	0.982	168	3	2	169	64	231	6.56E-106	333	302	232
Ap-Ap2	Am-Am1	0.759	127	30	175	301	1	126	1.09E-60	202	302	155
Ap-Ap2	St-Glc1	0.368	183	112	88	266	62	244	1.00E-23	93	302	370

Ap-Ap2	Am-Glc2	0.369	180	110	91	266	2	181	3.33E-23	92	302	197
Ap-Ap2	St-Glc5V2	0.34	137	86	135	266	2	138	4.03E-16	70	302	172
Ap-Ap2	St-Glc5V1	0.34	137	86	135	266	2	138	9.70E-16	69	302	172
Ap-Ap2	St-St5	0.32	79	52	182	260	4	80	3.58E-05	35	302	115
St-Glc8	St-Glc8	1	205	0	1	205	1	205	3.49E-148	450	205	205
St-Glc8	St-St4	0.509	205	100	1	204	19	223	6.73E-69	221	205	224
St-St4	St-St4	1	224	0	1	224	1	224	4.46E-161	488	224	224
St-St4	St-Glc8	0.509	205	100	19	223	1	204	3.46E-70	226	224	205
StapPG-StapPG7	StapPG-StapPG7	1	256	0	1	256	1	256	8.50E-152	463	256	256
MG1	MG1	1	347	0	1	347	1	347	8.64E-239	719	347	347
MN3	MN3	1	298	0	1	298	1	298	2.86E-199	602	298	298
St-Glc5V2	St-Glc5V2	1	172	0	1	172	1	172	2.28E-120	368	172	172
St-Glc5V2	St-Glc5V1	0.988	172	2	1	172	1	172	3.91E-119	364	172	172
St-Glc5V2	St-Glc1	0.935	171	11	1	171	107	277	1.08E-112	346	172	370
St-Glc5V2	Am-Glc2	0.934	153	10	1	153	44	196	8.23E-100	308	172	197
St-Glc5V2	Ap-Ap2	0.34	137	86	2	138	135	266	4.31E-20	78	172	302
St-Glc5V2	Ap-Ap5	0.34	137	85	2	138	103	232	7.09E-19	75	172	235
St-Glc5V2	Am-Am1	0.437	48	26	91	138	44	91	7.59E-11	51	172	155
St-Glc5V2	St-Glc2	0.242	169	116	2	170	8	161	3.47E-10	49	172	232
Ap-Ap5	Ap-Ap5	1	235	0	1	235	1	235	1.76E-159	484	235	235
Ap-Ap5	Ap-Ap2	0.944	235	13	2	234	34	268	8.45E-149	453	235	302
Ap-Ap5	St-Glc2	0.963	136	5	2	137	96	231	7.98E-80	254	235	232
Ap-Ap5	Am-Am1	0.879	91	11	143	232	1	91	2.67E-54	181	235	155
Ap-Ap5	St-Glc1	0.336	183	117	56	232	62	244	3.93E-22	87	235	370
Ap-Ap5	Am-Glc2	0.336	180	115	59	232	2	181	1.34E-21	85	235	197
Ap-Ap5	St-Glc5V2	0.34	137	85	103	232	2	138	3.78E-15	66	235	172
Ap-Ap5	St-Glc5V1	0.34	137	85	103	232	2	138	9.29E-15	64	235	172
Ap-Ap5	St-St5	0.329	77	51	150	226	4	80	4.25E-06	38	235	115
BDG-Glc5	BDG-Glc5	1	279	0	1	279	1	279	1.14E-179	545	279	279
MU3	MU3	1	195	0	1	195	1	195	3.97E-131	400	195	195
MU3	MU1	0.392	160	94	10	169	41	195	1.30E-27	101	195	238
St-St5	St-St5	1	115	0	1	115	1	115	5.14E-80	248	115	115
St-St5	Ap-Ap5	0.329	77	51	4	80	150	226	8.70E-07	37	115	235
St-St5	Ap-Ap2	0.32	79	52	4	80	182	260	1.93E-05	33	115	302
St-St5	Am-Am1	0.294	77	53	14	89	17	93	3.57E-05	33	115	155
Xln-xyl8	Xln-xyl8	1	476	0	1	476	1	476	0.00E+00	979	476	476
Am-Am1	Am-Am1	1	155	0	1	155	1	155	1.60E-108	332	155	155
Am-Am1	Ap-Ap2	0.734	127	33	1	126	175	301	1.47E-63	203	155	302
Am-Am1	Ap-Ap5	0.879	91	11	1	91	143	232	3.69E-56	182	155	235
Am-Am1	St-Glc5V2	0.437	48	26	44	91	91	138	4.34E-10	48	155	172
Am-Am1	Am-Glc2	0.437	48	26	44	91	134	181	4.34E-10	48	155	197

Am-Am1	St-Glc1	0.437	48	26	44	91	197	244	4.34E-10	48	155	370
Am-Am1	St-Glc5V1	0.437	48	26	44	91	91	138	1.09E-09	47	155	172
Am-Am1	St-St5	0.294	77	53	17	93	14	89	4.27E-05	33	155	115
Lev-Lev5	Lev-Lev5	1	297	0	1	297	1	297	1.43E-212	641	297	297
Pec-Pec1	Pec-Pec1	1	239	0	1	239	1	239	3.73E-155	472	239	239
Pec-Pec1	Dex-Dex7	0.941	17	1	222	238	1	17	1.03E-05	36	239	213
St-Glc5V1	St-Glc5V1	1	172	0	1	172	1	172	3.44E-121	370	172	172
St-Glc5V1	St-Glc5V2	0.988	172	2	1	172	1	172	3.91E-119	364	172	172
St-Glc5V1	St-Glc1	0.923	171	13	1	171	107	277	1.85E-111	342	172	370
St-Glc5V1	Am-Glc2	0.921	153	12	1	153	44	196	1.41E-98	305	172	197
St-Glc5V1	Ap-Ap2	0.34	137	86	2	138	135	266	1.10E-19	77	172	302
St-Glc5V1	Ap-Ap5	0.34	137	85	2	138	103	232	1.80E-18	74	172	235
St-Glc5V1	Am-Am1	0.437	48	26	91	138	44	91	1.89E-10	50	172	155
St-Glc5V1	St-Glc2	0.242	169	116	2	170	8	161	8.61E-10	48	172	232
MU1	MU1	1	238	0	1	238	1	238	1.73E-164	499	238	238
MU1	MU3	0.392	160	94	41	195	10	169	8.85E-29	106	238	195
PBGlcNAc-GlcNAc17F2	PBGlcNAc-GlcNAc17F2	1	142	0	1	142	1	142	3.20E-95	293	142	142
MethPG-MethPG8	MethPG-MethPG8	1	290	0	1	290	1	290	5.98E-155	474	290	290
MethPG-MethPG8	AG-Gal2	0.567	265	111	2	266	76	333	1.28E-57	193	290	334
MethPG-MethPG8	StapPG-GlcNAc6	0.572	260	106	2	261	13	261	5.18E-53	179	290	261
BDG-BDG6	BDG-BDG6	1	170	0	1	170	1	170	5.04E-116	355	170	170
Dex-Dex7	Dex-Dex7	1	213	0	1	213	1	213	1.59E-139	425	213	213
Dex-Dex7	Pec-Pec1	0.941	17	1	1	17	222	238	1.11E-05	36	213	239
PBGal-Gal8	PBGal-Gal8	1	279	0	1	279	1	279	8.42E-190	574	279	279
PBGlcNAc-GlcNAc4F2	PBGlcNAc-GlcNAc4F2	1	275	0	1	275	1	275	1.80E-189	573	275	275
MF12F1	MF12F1	1	53	0	1	53	1	53	4.87E-32	106	53	53
PBGlcNAc-GlcNAc17F1	PBGlcNAc-GlcNAc17F1	1	96	0	1	96	1	96	1.50E-63	199	96	96
PBGlcNAc-GlcNAc9F1	PBGlcNAc-GlcNAc9F1	1	71	0	1	71	1	71	2.29E-46	149	71	71
PBGlcNAc-GlcNAc4F1	PBGlcNAc-GlcNAc4F1	1	251	0	1	251	1	251	5.13E-166	504	251	251

Glycan ID	Glycan Name	MG1 (5 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124209 Slide# nCFG-172 Request# 3355 02/01/2017 7 RHB	StDev	%CV	MG1 (50 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124209 Slide# nCFG-172 Request# 3355 02/02/2017 7 RHB	StDev	%CV	MG1 (400 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124209 Slide# nCFG-172 Request# 3355 03/15/2017 7 RHB	StDev	%CV	MN3 (5 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124210 Slide# nCFG-173 Request# 3355 02/01/2017 7 RHB	StDev	%CV	MN3 (50 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124210 Slide# nCFG-173 Request# 3355 02/02/2017 7 RHB	StDev	%CV	MU1 (5 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124320 Slide# nCFG-174 Request# 3355 02/01/2017 7 RHB	StDev	%CV	MU1 (50 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124320 Slide# nCFG-174 Request# 3355 02/02/2017 7 RHB	StDev	%CV	MU3 (5 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124321 Slide# nCFG-175 Request# 3355 02/01/2017 7 RHB	StDev	%CV	MU3 (50 µg/ml) α- C-ter-His (1:2000) α- mIgG (5 µg/ml) 10124321 Slide# nCFG-175 Request# 3355 02/02/2017 7 RHB	StDev	%CV	
		StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV	StDev	%CV
1	Gala-Sp8	26	3	10	23	3	13	23	1	4	27	3	12	25	3	10	31	4	14	33	3	10	42	3	8	39	2	4	
2	Glcα-Sp8	22	2	11	23	4	15	13	9	71	29	2	6	28	8	30	27	4	14	30	2	7	36	4	11	31	4	14	
3	Mana-Sp8	21	3	14	21	6	26	12	7	59	20	2	9	22	2	10	22	2	7	23	5	20	31	2	7	31	3	10	
4	GalNAcα-Sp8	10	1	6	59	9	6	67	12	2	18	14	3	21	10	6	62	2	1	43	9	7	76	18	1	5	11	5	49
5	GalNAcα-Sp15	18	1	6	17	2	10	12	5	40	11	4	34	20	4	18	19	2	11	23	8	34	18	3	14	16	6	40	
6	Fuca-Sp8	13	6	49	12	5	41	17	7	42	13	3	25	16	4	24	10	7	75	13	10	79	20	2	10	21	10	47	
7	Fuca-Sp9	15	3	20	21	4	21	18	5	26	15	2	14	20	2	11	16	9	58	31	8	25	19	3	14	25	12	48	
8	Rhaa-Sp8	10	4	46	10	4	41	26	2	9	9	5	54	15	4	29	6	6	94	8	4	59	13	2	13	16	3	20	
9	Neu5Aca-Sp8	20	1	3	22	4	19	17	2	9	19	2	10	25	3	13	21	4	20	25	1	5	22	3	11	26	3	10	
10	Neu5Aca-Sp11	16	2	12	14	1	4	7	4	54	14	1	6	14	1	8	11	8	71	11	7	67	16	1	3	16	1	8	
11	Neu5Acaβ-Sp8	19	1	7	15	2	16	13	0	0	16	1	8	14	5	32	11	8	69	21	2	8	16	7	47	18	2	12	
12	Galβ-Sp8	17	10	58	19	4	21	11	4	40	21	7	32	19	6	30	25	2	9	23	12	50	22	11	51	32	2	6	
13	Glcβ-Sp8	24	3	12	15	4	24	18	5	29	22	3	15	20	5	25	18	9	49	27	5	18	28	3	10	24	6	24	
14	Manβ-Sp8	19	4	21	19	4	24	14	4	29	22	3	12	14	4	31	16	6	38	15	5	36	19	1	3	17	1	8	
15	GalNAcβ-Sp8	17	2	12	23	5	23	19	2	11	21	0	0	15	7	46	20	4	22	15	2	15	22	2	11	19	5	24	
16	GlcNAcβ-Sp0	15	2	14	14	7	50	11	5	49	13	7	56	10	6	67	7	6	88	14	6	46	15	4	27	13	7	52	
17	GlcNAcβ-Sp8	22	2	8	15	1	4	13	4	28	14	4	31	27	6	24	17	3	15	31	3	9	21	3	13	18	3	19	
18	GlcN(Glcβ-Sp8	21	2	9	32	5	15	36	4	10	20	6	29	25	2	8	20	3	15	20	5	23	24	3	12	27	4	15	
19	Galβ1-4GlcNAcβ1-6Galβ1-4GlcNAcβ1-3GalNAcα-Sp8	12	7	57	16	1	8	107	5	5	17	1	7	304	23	8	31	6	19	1118	68	6	16	1	6	15	2	11	
20	Galβ1-4GlcNAcβ1-6Galβ1-4GlcNAcβ1-3GalNAcα-Sp14	12	6	53	34	17	50	39	2	6	14	4	25	128	19	15	17	2	14	31	8	25	16	3	22	29	5	16	
21	GlcNAcβ1-6GlcNAcβ1-4GlcNAcβ1-3GlcNAcα-Sp8	11	6	59	10	5	48	6	6	99	13	3	20	15	2	13	8	7	87	10	6	61	17	1	7	15	2	14	
22	6S(3S)Galβ1-4(6S)GlcNAcβ-Sp0	11	6	58	13	7	49	10	5	56	15	1	3	15	1	3	21	6	28	22	2	8	19	1	7	16	4	25	
23	6S(3S)Galβ1-4GlcNAcβ-Sp0	27	1	5	24	5	20	17	5	27	24	1	5	23	1	4	23	5	20	22	3	12	24	4	19	22	1	4	
24	(3S)Galβ1-4Fuca1-3(6S)Glc-Sp0	33	1	2	44	3	8	38	3	8	35	6	17	35	3	10	31	5	16	46	5	10	36	2	7	38	5	12	
25	(3S)Galβ1-4Glcβ-Sp8	22	1	6	22	2	10	17	2	9	24	2	8	22	2	11	27	9	32	22	10	48	31	3	10	31	2	5	
26	(3S)Galβ1-4(6S)Glcβ-Sp0	23	3	15	22	3	13	9	6	67	25	3	10	22	1	5	27	2	6	24	3	11	31	2	6	28	3	9	
27	(3S)Galβ1-4(6S)Glcβ-Sp8	17	1	5	20	2	10	15	3	21	21	2	12	22	2	10	24	4	16	39	2	6	26	3	13	25	2	9	
28	(3S)Galβ1-3Fuca1-4GlcNAcβ-Sp8	15	3	17	11	6	53	11	6	57	11	6	57	17	3	15	13	6	48	21	7	32	20	1	6	16	8	50	
29	(3S)Galβ1-3GalNAcα-Sp8	15	1	6	14	6	43	8	5	68	17	5	28	20	2	9	23	5	23	21	2	9	18	1	5	12	8	64	
30	(3S)Galβ1-3GlcNAcβ-Sp0	11	5	49	9	5	55	9	7	77	10	7	70	9	6	67	3	1	23	18	4	20	12	5	41	10	7	69	
31	(3S)Galβ1-3GlcNAcβ-Sp8	15	2	15	14	3	25	3	1	27	8	4	44	13	6	47	7	6	86	20	9	45	18	1	3	18	2	12	
32	(3S)Galβ1-4Fuca1-3GlcNAcα-Sp0	9	7	76	12	8	63	14	5	35	6	5	89	12	9	74	9	8	90	21	10	49	13	6	52	16	5	31	
33	(3S)Galβ1-4Fuca1-3GlcNAcα-Sp8	21	2	7	22	1	3	12	5	44	15	4	30	20	3	16	15	8	54	23	3	13	17	4	21	22	6	30	
34	(3S)Galβ1-4(6S)GlcNAcβ-Sp0	9	6	72	15	4	28	11	5	43	15	2	12	16	4	24	8	6	85	18	9	53	13	6	46	16	1	3	
35	(3S)Galβ1-4(6S)GlcNAcβ-Sp8	19	3	17	21	1	6	16	5	29	16	1	8	15	5	30	23	3	11	27	5	20	17	7	40	18	5	30	
36	(3S)Galβ1-4GlcNAcβ-Sp0	6	4	63	15	1	6	9	5	58	10	5	48	13	5	42	13	6	46	17	8	48	15	3	20	16	1	8	
37	(3S)Galβ1-4GlcNAcβ-Sp8	18	4	20	21	2	11	18	6	33	16	5	28	12	6	48	20	1	4	19	3	18	24	3	14	16	8	51	
38	(3S)Galβ-Sp8	16	7	44	17	3	16	17	1	8	18	5	28	18	5	26	17	7	44	17	9	55	20	5	25	19	1	5	
39	(6S)Galβ1-4GlcNAcβ-Sp0	18	1	3	16	2	11	12	5	41	13	5	36	13	5	40	14	6	45	17	2	13	14	6	48	13	6	42	
40	(4S)Galβ1-4GlcNAcβ-Sp8	11	5	49	18	1	6	64	17	2	11	14	8	54	7	7	108	17	5	31	14	7	47	9	6	72			
41	(6P)Mana-Sp8	20	2	7	21	1	7	18	5	28	18	2	10	18	8	43	11	8	77	15	7	46	25	2	8	22	2	8	
42	(6S)Galβ1-4Glcβ-Sp0	22	1	5	22	7	32	18	4	25	20	2	10	19	1	7	12	6	52	22	2	10	23	3	11	17	7	44	
43	(6S)Galβ1-4Glcβ-Sp8	6																											

66	Fuca1-2Galb1-3GlcNAcb1-3Galb1-4Glc-Sp10	10	5	55	13	4	26	56	3	6	11	5	48	8	6	71	2	1	22	4	1	13	12	2	17	9	7	77	
67	Fuca1-2Galb1-3GlcNAcb-Sp0	20	2	10	25	4	16	22	5	24	13	7	50	27	3	12	4	1	26	13	8	64	20	2	10	18	8	45	
68	Fuca1-2Galb1-3GlcNAcb-Sp8	15	2	15	23	6	25	14	6	42	15	5	30	28	14	49	10	7	76	17	4	22	18	2	11	20	4	20	
69	Fuca1-2Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	16	2	14	26	3	11	28	7	24	15	2	13	67	11	16	90	5	6	3878	124	3	17	2	13	21	3	15	
70	Fuca1-2Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	13	9	68	27	6	24	49	3	7	18	3	18	83	10	12	148	15	10	4336	921	21	19	4	24	21	2	11	
71	Fuca1-2Galb1-4(Fuca1-3)GlcNAcb-Sp0	21	4	21	32	11	33	29	5	19	19	3	15	93	25	27	13	6	46	23	3	11	23	2	8	34	3	9	
72	Fuca1-2Galb1-4(Fuca1-3)GlcNAcb-Sp8	21	2	10	20	2	11	17	2	13	19	1	4	84	14	16	22	2	10	29	3	9	27	3	12	27	3	12	
73	Fuca1-2Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	16	1	4	30	9	29	238	14	6	22	1	4	402	54	13	240	11	5	5740	419	7	15	4	25	25	7	27	
74	Fuca1-2Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	16	1	5	52	11	22	315	17	5	21	2	12	657	64	10	273	25	9	6247	464	7	19	2	13	23	6	24	
75	Fuca1-2Galb1-4GlcNAcb-Sp0	19	4	22	17	3	15	16	1	4	22	2	9	52	2	3	15	3	17	21	3	13	19	4	22	21	2	12	
76	Fuca1-2Galb1-4GlcNAcb-Sp8	10	6	65	27	4	15	92	30	33	18	1	7	506	32	6	3	1	40	33	5	17	17	2	14	21	3	16	
77	Fuca1-2Galb1-4Glc-Sp0	13	6	47	33	6	19	24	6	26	19	4	23	100	18	18	13	6	47	41	8	19	21	2	8	25	4	14	
78	Fuca1-2Galb-Sp8	17	3	17	28	4	13	36	8	21	20	2	10	30	9	29	20	3	16	33	3	9	24	1	3	22	4	20	
79	Fuca1-3GlcNAcb-Sp8	3	1	38	16	6	39	14	7	49	6	3	57	10	4	46	3	2	77	13	6	49	5	3	69	22	5	23	
80	Fuca1-4GlcNAcb-Sp8	8	6	74	16	4	29	23	6	24	13	1	7	19	3	16	3	1	35	13	6	48	10	5	48	12	4	35	
81	Fucb1-3GlcNAcb-Sp8	4	3	68	18	3	18	7	3	43	11	3	30	15	4	30	3	1	23	28	13	46	10	5	49	18	5	28	
82	GalNAca1-3(Fuca1-2)Galb1-3GlcNAcb-Sp0	13	2	18	17	1	3	6	5	86	13	3	21	19	5	25	7	6	98	6	1	17	17	2	12	20	6	28	
83	GalNAca1-3(Fuca1-2)Galb1-4(Fuca1-3)GlcNAcb-Sp0	20	3	15	37	5	13	32	13	40	17	4	25	38	17	44	16	3	20	34	15	44	14	6	45	40	9	24	
84	(3S)Galb1-4(Fuca1-3)Glc-Sp0	22	3	15	41	10	26	32	10	32	25	2	8	45	15	34	21	4	21	41	10	26	27	1	4	30	5	16	
85	GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb-Sp0	21	3	14	18	3	15	21	3	16	17	3	16	16	1	5	14	10	70	19	1	5	21	1	6	18	1	5	
86	GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb-Sp8	10	4	41	11	5	49	9	4	45	6	6	100	4	1	20	3	1	23	5	1	13	7	5	64	7	3	46	
87	GalNAca1-3(Fuca1-2)Galb1-4Glc-Sp0	8	5	62	14	1	10	15	3	20	12	2	14	12	4	39	12	6	51	13	6	42	16	1	6	17	2	12	
88	GlcNAcb1-3Galb1-3GalNAca-Sp8	22	1	4	20	1	5	16	1	8	23	2	11	20	2	9	20	2	8	20	1	3	26	3	11	21	1	6	
89	GalNAca1-3(Fuca1-2)Galb-Sp8	18	2	10	17	1	6	15	2	15	15	5	34	18	3	19	13	6	52	19	3	17	17	3	14	18	3	17	
90	GalNAca1-3(Fuca1-2)Galb-Sp18	13	1	7	13	3	24	6	2	35	5	4	88	11	5	46	2	1	22	7	3	46	6	6	115	13	2	17	
91	GalNAca1-3GalNAcb-Sp8	10	5	50	18	2	11	8	5	67	9	7	76	11	5	46	3	1	40	14	7	48	17	2	12	16	2	11	
92	GalNAca1-3Galb-Sp8	11	7	67	11	7	64	12	7	56	12	6	52	12	2	15	7	5	69	19	10	56	19	1	7	18	2	8	
93	GalNAca1-4(Fuca1-2)Galb1-4GlcNAcb-Sp8	18	2	12	20	5	25	19	2	12	15	2	15	25	8	34	3	1	23	16	3	20	18	2	11	22	5	21	
94	GalNAcb1-3GalNAca-Sp8	14	2	13	15	3	17	6	3	52	15	1	9	11	5	50	2	1	55	4	1	37	11	7	63	16	2	10	
95	GalNAcb1-3(Fuca1-2)Galb-Sp8	21	5	25	21	3	13	17	2	9	18	2	10	24	6	25	14	9	64	13	8	64	21	3	13	14	8	55	
96	GalNAcb1-3Galb1-4Galb1-4GlcNAcb-Sp0	19	1	7	23	2	7	18	5	26	15	1	4	23	2	9	14	6	43	24	4	17	20	1	5	26	1	5	
97	GalNAcb1-4(Fuca1-3)GlcNAcb-Sp0	22	4	19	34	5	14	31	12	40	20	3	15	44	5	11	21	1	5	24	2	7	23	2	7	27	1	5	
98	GalNAcb1-4GlcNAcb-Sp0	17	2	11	19	4	22	13	3	26	18	1	7	17	3	20	6	4	67	22	1	6	17	1	7	18	2	10	
99	GalNAcb1-4GlcNAcb-Sp8	9	6	21	3	13	2	16	24	2	8	19	2	11	8	9	104	19	9	49	22	3	13	19	23	1	6		
100	Galb1-2Galb-Sp8	23	3	15	23	15	17	19	30	3	10	22	4	17	23	8	35	30	3	43	3	6	38	3	7	3	38	3	7
101	Galb1-3(Fuca1-2)Galb1-3GlcNAcb-Sp0	22	1	6	14	3	20	15	2	16	20	2	9	19	1	4	16	7	43	15	8	52	21	3	14	19	5	28	
102	Galb1-3(Fuca1-2)Galb1-3GlcNAcb-Sp8	18	1	7	19	2	9	11	5	41	21	2	11	22	3	14	19	1	7	17	9	52	29	3	9	24	6	27	
103	Galb1-3(Fuca1-2)Galb1-4(Fuca1-3)GlcNAcb-Sp0	17	2	9	15	1	9	14	3	18	10	5	51	22	6	26	13	3	23	27	7	27	16	1	5	17	4	23	
104	Galb1-3(Fuca1-2)Galb1-4(Fuca1-3)GlcNAcb-Sp8	18	1	6	25	5	18	18	7	38	18	4	21	30	4	13	15	6	42	27	5	18	18	1	7	41	13	31	
105	Galb1-3(Fuca1-2)Galb1-4GlcNAcb-Sp0	15	4	27	17	4	22	10	2	18	16	2	10	15	1	6	11	5	41	21	4	18	16	2	14	16	4	26	
106	Galb1-3(Fuca1-2)Galb1-4Glc-Sp0	18	3	20	29	7	26	26	10	39	18	2	10	37	12	33	21	3	16	36	2	6	26	4	17	28	6	22	
107	Galb1-3(Fuca1-2)Galb-Sp8	19	1	6	24	6	25	15	8	50	18	3	16	29	14	51	9	7	83	19	10	54	22	3	11	27	7	25	
108	Galb1-3(Fuca1-2)Galb-Sp18	16	1	6	19	2	9	8	3	38	13	6	47	17	3	20	4	1	12	8	7	84	17	2	10	17	4	23	
109	Galb1-4(Galb1-3)Galb1-4GlcNAcb-Sp8	22	3	12	18	2	8	13	1	7	21	4	19	19	3	15	7	6	81	16	7	42	26	1	4	17	2	12	
110	Galb1-3GalNAca-Sp8	22	2	9	18	1	5	13	5	35	24	1	4	17	3	16	17	11	66	18	5	184	2	5	184	2	10	2	
111	Galb1-3GalNAca-Sp18	13	5	38	17	3	17	16	4	23	16	1	5	27	5	20	16	1	4	24	2	9	20	2	8	19	4	18	
112	Galb1-3GalNAcb-Sp8	24	4	17	20	4	22	15	6	40	22	1	4	17	4	22	18	2	12	21	7	32	28	3	9	24	1	4	
113	Galb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp8	17	1	6	18	2	10	12	5	40	8	4	50	13	4	29	14	5	39	10	7	64	16	2	10	19	4	21	
114	Galb1-3Galb1-3GlcNAcb-Sp0	12	5	41	13	7	55	16	2	15	15	3	22	16	4	22	11	6	52	6	3	50	10	6	63	19	2	11	
115	Galb1-3Galb1-4GlcNAcb-Sp8	18	2	12	17	1	5	13	2	19	18	2	12	20	2	10	17	0	0	11	7	65	20	1	5	17	2	12	
116	Galb1-3Galb1-4Glc-Sp0	23	4	16	19	4	22	21	6	31	21	5	23	23	3	12	27	3	11	27	4	14	34	2	6	30	2	7	
117	Galb1-3Galb1-4Glc-Sp10	12	6	54	16	7	46	46	3	7	15	1	6	11	5	41	6	7	113	15	7	45	12	3	24	16	1	3	
118	Galb1-3Galb-Sp8	25	5	20	25	5	20	19	4	19	25	2	7	26	8	29	23	2	9	29	3	11	31	2	8	26	2	6	
119	Galb1-4(Fuca1-2)Galb1-4GlcNAcb-Sp8	19	1	4	24	5	22	18	5	29	17	1	3	27	6	21	15	4	28	35	2	6	21	2	12	25	2	8	
120	Galb1-4Galb1-4GlcNAcb-Sp0	17	1	6	19	3	15	13	4	27	14	2	17	18	4	21	6	4	73	25	4	17	19	4	19	21	6	29	
121	Galb1-4Galb1-4GlcNAcb-Sp8	20	1	7	24	2	7	19	2	9	21	3	16	21	1	5	14	7	48	38	5	12	28	2	5	24	2	10	
122	Galb1-4Galb1-4Glc-Sp0	19	3	14	23	6	27	10	7	67	17	4	23	20	3	12	7	3	46	21	5	24	24	2	8	30	4	14	
123	Galb1-4GlcNAcb-Sp8	14	7	48	11	5	48	10	6	58	14																		

152	Galb1-4(Fuca1-3)GlcNAcb-Sp8	18	2	10	19	4	21	16	1	6	16	5	32	124	57	46	12	9	76	11	6	58	22	2	8	25	3	13	
153	Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	23	1	6	39	10	25	36	4	11	20	5	24	101	42	42	148	14	9	3752	390	10	22	3	13	37	7	18	
154	Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	11	2	15	14	1	4	23	3	15	15	1	9	98	12	13	128	9	7	6758	1055	16	12	1	4	17	4	21	
155	Galb1-4(6S)GlcNb-Sp0	23	4	15	19	1	5	17	2	12	24	2	6	23	4	19	23	9	41	34	4	12	30	1	4	28	1	5	
156	Galb1-4(6S)GlcNb-Sp8	20	3	13	21	4	17	13	2	11	15	8	57	21	3	16	17	13	81	21	2	7	26	1	4	20	8	39	
157	Galb1-4GalNAcb1-3(Fuca1-2)Galb1-4GlcNAcb-Sp8	18	2	9	16	4	25	11	8	67	17	1	7	15	3	22	20	1	4	22	2	9	16	3	18	13	4	31	
158	Galb1-4GalNAcb1-3(Fuca1-2)Galb1-4GlcNAcb-Sp8	19	1	3	16	4	26	24	4	16	21	2	10	13	2	17	19	3	14	36	2	6	20	1	5	19	3	16	
159	Galb1-4GlcNAcb1-3GalNAcb-Sp8	14	2	14	11	5	45	14	4	27	13	6	46	113	17	15	18	2	9	289	32	11	13	6	47	12	5	44	
160	Galb1-4GlcNAcb1-3GalNAcb-Sp14	5	5	99	8	5	65	15	2	16	14	1	7	100	39	39	18	2	11	47	4	8	13	6	50	8	9	117	
161	Galb1-4GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	14	1	7	21	5	22	115	8	7	7	6	87	106	22	21	165	10	6	5112	883	17	15	2	12	17	1	8	
162	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	11	5	43	21	8	36	157	21	14	14	2	14	117	18	16	315	47	15	7219	350	5	12	2	13	12	2	17	
163	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	16	1	6	14	5	32	149	18	12	17	3	20	93	8	8	356	31	9	5963	236	4	8	5	62	11	4	42	
164	Galb1-4GlcNAcb1-3Galb1-4GlcNb-Sp0	13	2	17	14	3	20	43	2	5	18	2	14	104	54	52	239	9	4	5538	311	6	17	2	10	15	4	29	
165	Galb1-4GlcNAcb1-3Galb1-4GlcNb-Sp8	14	2	13	19	1	3	83	17	20	15	1	8	144	10	7	194	14	7	6730	548	8	16	2	11	17	7	39	
166	Galb1-4GlcNAcb1-6(Galb1-3)GalNAcb-Sp8	9	4	49	17	2	12	33	7	20	16	1	5	58	4	7	3	1	35	5	1	16	17	2	14	17	2	10	
167	Galb1-4GlcNAcb1-6(Galb1-3)GalNAcb-Sp14	17	3	16	26	6	24	33	5	16	19	3	15	153	14	9	9	3	30	28	4	14	22	4	16	31	4	14	
168	Galb1-4GlcNAcb-Sp0	17	5	31	18	5	26	13	9	70	17	4	23	144	63	44	3	1	39	12	7	59	25	4	16	17	4	25	
169	Galb1-4GlcNAcb-Sp8	18	4	21	9	6	59	6	5	84	14	7	52	53	4	7	12	8	61	24	5	21	27	3	10	19	5	26	
170	Galb1-4GlcNAcb-Sp23	7	4	56	6	3	57	15	5	35	15	2	14	45	6	14	5	7	134	13	6	49	13	7	54	14	7	49	
171	Galb1-4GlcNb-Sp0	17	1	8	5	5	86	8	6	83	11	5	43	8	9	115	7	8	111	22	4	18	26	1	2	23	3	11	
172	Galb1-4GlcNb-Sp8	16	1	9	16	4	25	15	1	5	19	3	14	11	8	75	7	6	81	19	10	55	2	6	23	2	7		
173	GlcNAcb1-3Galb1-4GlcNAcb-Sp8	5	4	82	11	6	53	8	3	37	6	4	67	16	9	98	12	8	66	7	7	96	13	6	51	14	1	7	
174	GlcNAcb1-6Galb1-4GlcNAcb-Sp8	8	6	67	10	4	36	7	3	42	12	3	25	14	2	14	3	1	29	8	5	62	15	2	12	15	1	8	
175	GlcNAcb1-2Galb1-3GalNAcb-Sp8	8	6	67	16	1	8	6	3	49	13	4	31	13	5	35	4	3	62	18	8	47	18	1	6	18	2	12	
176	GlcNAcb1-6(GlcNAcb1-3)GalNAcb-Sp8	11	5	48	14	6	44	7	3	43	12	5	46	14	3	22	3	1	47	5	1	28	15	1	6	14	4	30	
177	GlcNAcb1-6(GlcNAcb1-3)GalNAcb-Sp14	15	1	8	13	1	7	8	4	46	14	3	19	7	4	67	3	1	15	7	7	92	15	2	15	11	7	61	
178	GlcNAcb1-6(GlcNAcb1-3)Galb1-4GlcNAcb-Sp8	12	6	46	16	2	11	14	1	9	16	1	9	17	5	27	2	1	22	4	1	26	20	1	7	14	6	40	
179	GlcNAcb1-3GalNAcb-Sp8	14	7	52	17	1	6	10	3	35	17	3	16	17	2	10	1	1	128	2	1	22	21	4	19	19	1	7	
180	GlcNAcb1-3GalNAcb-Sp14	15	7	45	13	4	32	8	4	49	14	3	20	6	5	79	7	5	76	13	2	17	14	3	22	12	4	30	
181	GlcNAcb1-3Galb-Sp8	20	2	9	19	2	11	18	4	24	19	5	23	17	5	31	23	2	8	24	4	15	28	2	7	25	4	15	
182	GlcNAcb1-3Galb1-4GlcNAcb-Sp0	12	3	26	11	4	31	8	4	46	14	2	18	6	4	67	11	5	46	10	7	75	11	6	53	8	4	55	
183	GlcNAcb1-3Galb1-4GlcNAcb-Sp8	12	6	50	12	1	4	9	3	37	11	3	4	11	8	75	12	5	46	15	2	11	15	2	12	14	1	10	
184	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	7	3	44	6	3	4	42	47	6	12	10	4	41	3	5	14	11	4	37	126	6	5	11	3	27	5	7	
185	GlcNAcb1-3Galb1-4GlcNb-Sp0	18	3	16	15	1	3	14	1	7	20	2	12	13	3	27	17	1	6	14	6	44	18	2	10	15	2	10	
186	GlcNAcb1-4-MDPLys	9	6	75	13	3	20	21	5	25	9	4	51	24	6	23	5	4	74	24	20	84	11	5	48	19	3	17	
187	GlcNAcb1-6(GlcNAcb1-4)GalNAcb-Sp8	14	3	23	14	6	43	11	4	37	13	1	10	12	5	45	5	5	107	11	8	75	17	1	3	15	1	8	
188	GlcNAcb1-4Galb1-4GlcNAcb-Sp8	15	1	6	11	6	57	8	4	56	14	3	20	9	6	48	2	1	22	13	7	52	17	2	10	16	2	13	
189	GlcNAcb1-4GlcNAcb1-4GlcNAcb1-4GlcNAcb1-4GlcNAcb1-4GlcNAcb1-Sp8	9	5	54	12	5	40	13	4	29	6	4	66	10	8	80	2	1	58	6	3	57	8	4	55	13	6	47	
190	GlcNAcb1-4GlcNAcb1-4GlcNAcb1-4GlcNAcb1-4GlcNAcb1-Sp8	11	3	30	11	2	23	4	1	26	8	5	64	14	1	9	6	5	91	10	6	56	13	3	21	7	6	86	
191	GlcNAcb1-4GlcNAcb1-4GlcNAcb-Sp8	14	1	9	13	6	45	11	5	49	10	5	49	14	3	24	10	8	82	13	6	46	8	7	81	10	6	59	
192	GlcNAcb1-6GalNAcb-Sp8	16	2	13	15	3	18	8	3	40	16	1	9	18	1	7	6	9	164	11	8	75	17	2	13	13	4	33	
193	GlcNAcb1-6GalNAcb-Sp14	13	2	13	11	5	43	6	2	36	15	3	22	11	8	74	12	5	42	10	6	63	14	1	10	15	6	38	
194	GlcNAcb1-6Galb1-4GlcNAcb-Sp8	16	2	12	19	3	18	13	1	10	20	3	17	23	2	10	6	1	23	20	7	37	31	1	5	30	2	7	
195	Glc1-4GlcNb-Sp8	21	2	8	20	2	10	15	3	16	24	2	7	22	5	21	12	8	68	22	4	17	30	2	8	26	1	5	
196	Glc1-4GlcNb-Sp8	20	8	41	18	4	24	19	4	23	24	2	7	28	4	14	26	1	5	30	4	14	29	2	6	25	3	13	
197	Glc1-6Glc1-6GlcNb-Sp8	8	7	81	10	5	51	7	1	15	14	2	12	9	6	60	3	2	53	17	8	45	11	5	48	10	6	62	
198	Glc1-4GlcNb-Sp8	11	5	50	10	4	41	34	2	5	10	5	45	8	5	67	9	7	72	10	8	82	18	3	14	13	2	11	
199	Glc1-6GlcNb-Sp8	11	5	48	7	5	26	19	4	20	13	6	46	20	4	21	14	6	43	23	5	22	19	4	24	16	5	29	
200	G-cs-Sp8	11	6	53	7	6	88	7	3	48	11	5	49	7	14	3	18	3	1	29	19	10	54	17	1	8	17	1	6
201	Glc1-6-Sp8	15	2	15	19	6	34	18	4	20	13	7	54	18	2	14	5	2	38	10	9	83	18	2	9	17	5	28	
202	GlcAb-Sp8	14	2	17	9	5	54	17	10	58	14	2	12	13	1	9	7	6	92	15	7	48	14	6	40	2	12		
203	GlcAb1-3Galb-Sp8	21	3	15	15	8	54	19	2	8	17	6	36	18	3	15	17	8	47	22	2	10	23	5	22	21	12	56	
204	GlcAb1-6Galb-Sp8	15	3	17	16	2	15	4	1	26	13	2	17	21	5	26	14	6	40	22	1	4	20	2	11	15	8	54	
205	KDNa2-3Galb1-3GlcNAcb-Sp0	19	3	17	25	6	22	29	2	8	21	5	26	38	7	17	30	3	9	33	4	13	30	6	19	34	4	13	
206	KDNa2-3Galb1-4GlcNAcb-Sp0	20	2	7	15	2	12	12	2	15	17	3	17	19	5	25	19	5	25	14	7	51	24	3	11	20	2	12	
207	Mana1-2Mana1-2Mana1-3Mana-Sp9	21	3	14	29	6	22	22	4	16	20	2	8	28	10	37	20	3	14	25	2	6	29	2	6	21	4	18	
208	Mana1-2Mana1-6(Mana1-2Mana1-3)Mana-Sp9	16	2	14	15	3	16	15	6	38	18	3	14	14	2	15	17	2	10	17	3	19	22	1	6	19	2	9	
209	Mana1-2Mana1-3Mana-Sp9	18	1	7	22	6	28	14	5	36	16																		

229	Neu5Aca2-8Neu5Aca2-8Neu5Aca-Sp8	14	5	33	6	3	56	6	4	67	17	1	3	14	1	7	7	6	87	9	5	53	20	2	8	17	2	11	
230	GalNAcb1-4(Neu5Aca2-3)Galb1-4GlcNAcb-Sp0	19	3	14	19	3	15	19	1	4	18	0	0	19	2	11	21	2	9	21	2	10	22	1	3	22	3	14	
231	GalNAcb1-4(Neu5Aca2-3)Galb1-4GlcNAcb-Sp8	10	4	42	16	5	30	14	4	27	6	2	43	8	3	36	5	3	60	8	2	25	9	6	70	14	3	19	
232	GalNAcb1-4(Neu5Aca2-3)Galb1-4Glc-Sp0	16	2	11	13	10	79	10	4	44	13	1	10	12	2	12	6	5	84	6	4	67	15	2	16	16	1	8	
233	Neu5Aca2-3Galb1-3GalNAcb1-4(Neu5Aca2-3)Galb1-4Glc-Sp0	9	4	47	25	6	24	16	7	44	10	4	35	16	2	15	4	1	16	23	6	28	16	2	14	23	10	45	
234	Neu5Aca2-6(Neu5Aca2-3)GalNAca-Sp8	11	1	9	11	3	20	4	1	30	5	3	81	12	2	17	3	1	29	3	1	27	8	6	73	5	3	6	
235	Neu5Aca2-3GalNAca-Sp8	5	3	60	13	5	41	6	3	57	10	5	50	12	3	25	5	3	63	9	7	76	11	3	31	14	2	15	
236	Neu5Aca2-3GalNAcb1-4GlcNAcb-Sp0	7	5	68	6	5	83	7	3	41	7	4	59	8	5	64	3	1	23	5	2	53	4	1	13	11	6	54	
237	Neu5Aca2-3Galb1-3(6S)GlcNAcb-Sp8	15	1	4	13	6	44	9	4	40	8	6	76	10	6	56	13	7	53	20	9	47	18	1	7	15	2	16	
238	Neu5Aca2-3Galb1-3(Fuca1-4)GlcNAcb-Sp8	14	1	6	13	1	11	4	1	34	12	4	29	16	6	35	3	1	27	7	5	78	15	3	20	17	4	25	
239	Neu5Aca2-3Galb1-3(Fuca1-4)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	19	1	7	40	2	4	39	7	18	20	3	16	52	5	9	20	3	15	42	6	13	18	4	22	46	6	13	
240	Neu5Aca2-3Galb1-4(Neu5Aca2-3Galb1-3)GlcNAcb-Sp8	14	1	9	12	2	17	7	4	60	12	6	45	14	2	11	3	2	53	5	1	18	14	2	14	12	6	48	
241	Neu5Aca2-3Galb1-3(6S)GalNAca-Sp8	14	3	21	8	5	57	11	2	19	16	2	9	14	1	10	17	3	17	19	2	8	21	4	20	19	3	16	
242	Neu5Aca2-6(Neu5Aca2-3Galb1-3)GalNAca-Sp8	7	6	91	3	2	69	3	2	62	8	5	59	4	4	106	3	2	53	4	2	55	6	5	92	6	5	89	
243	Neu5Aca2-6(Neu5Aca2-3Galb1-3)GalNAca-Sp14	15	3	21	24	3	13	26	3	10	16	2	11	32	10	32	20	5	24	28	8	29	28	2	6	32	3	9	
244	Neu5Aca2-3Galb-Sp8	15	2	11	13	5	41	10	6	62	15	3	20	10	7	69	10	7	64	21	6	28	19	1	7	15	3	21	
245	Neu5Aca2-3Galb1-3GalNAcb1-3Gala1-4Galb1-4Glc-Sp0	13	2	17	29	6	19	29	8	26	11	2	22	26	5	19	5	1	28	15	6	38	17	3	20	20	3	16	
246	Neu5Aca2-3Galb1-3GlcNAcb1-3Galb1-4GlcNAcb-Sp0	13	1	4	6	1	24	10	5	53	11	2	21	13	1	10	9	6	62	13	6	42	15	2	13	9	6	70	
247	Fuca1-2(6S)Galb1-4Glc-Sp0	16	3	21	47	11	24	35	7	19	19	1	7	51	7	15	16	7	43	22	1	6	23	2	10	29	3	9	
248	Neu5Aca2-3Galb1-3GlcNAcb-Sp0	18	1	8	17	4	25	17	3	14	20	4	18	17	1	7	18	9	50	20	3	16	22	1	6	22	2	11	
249	Neu5Aca2-3Galb1-4(6S)GlcNAcb-Sp8	15	2	11	14	2	16	14	2	15	18	1	7	18	2	12	23	4	18	20	3	17	21	3	12	16	2	11	
250	Neu5Aca2-3Galb1-4(Fuca1-3)(6S)GlcNAcb-Sp8	20	3	16	16	3	16	10	5	54	17	2	13	19	6	32	12	6	50	13	7	54	20	2	9	18	5	30	
251	Neu5Aca2-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	19	1	7	24	1	2	23	2	11	20	2	8	27	4	15	20	2	9	28	8	29	19	1	4	23	4	18	
252	Neu5Aca2-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	16	3	15	19	4	23	17	4	26	16	5	29	21	6	30	11	4	39	24	7	29	17	2	9	17	3	19	
253	Neu5Aca2-3Galb1-4(Fuca1-3)GlcNAcb-Sp8	11	5	45	13	5	35	9	5	59	12	2	13	13	2	12	10	5	51	3	1	15	13	2	17	10	3	29	
254	Neu5Aca2-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb-Sp8	17	3	17	13	1	9	14	7	50	11	6	51	15	2	12	12	6	45	16	3	18	15	3	17	14	2	12	
255	Neu5Aca2-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4GlcNAcb-Sp8	30	2	7	39	6	17	35	6	18	27	4	14	36	5	15	29	4	12	42	2	5	27	4	14	41	8	20	
256	Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	12	2	14	12	5	41	77	13	17	11	5	43	13	5	37	7	4	55	13	7	51	12	2	18	11	1	12	
257	Neu5Aca2-3Galb1-4GlcNAcb-Sp0	17	3	17	15	2	12	14	5	39	14	3	23	15	2	15	8	6	85	20	2	10	14	2	18	17	2	14	
258	Neu5Aca2-3Galb1-4GlcNAcb-Sp8	8	6	67	4	1	16	3	5	36	8	4	50	9	4	43	3	1	23	3	2	55	11	5	48	8	6	73	
259	Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	3	4	3	77	9	6	68	6	5	87	2	1	41	10	5	53	3	1	18	4	1	26	11	5	49	10	6	
260	Fuca1-2Gal1-4(6S)Glc-Sp0	18	3	16	37	8	22	30	4	15	20	2	11	46	10	23	14	9	64	29	12	42	26	1	1	5	39	6	15
261	Neu5Aca2-3Galb1-4Glc-Sp0	21	4	18	20	1	4	20	14	70	19	1	5	22	2	9	18	4	20	13	8	62	25	2	8	25	3	11	
262	Neu5Aca2-3Galb1-4Glc-Sp8	16	1	8	19	7	36	30	3	9	9	5	52	16	2	14	9	6	65	18	8	46	15	2	12	18	1	8	
263	Neu5Aca2-6GalNAca-Sp8	15	3	19	11	6	51	9	4	46	11	5	44	12	1	8	9	6	65	5	1	11	25	3	13	17	3	19	
264	Neu5Aca2-6GalNAcb1-4GlcNAcb-Sp0	2	2	86	7	5	84	12	10	84	6	6	100	4	5	137	2	1	67	1	1	82	0	1	200	2	2	98	
265	Neu5Aca2-6Galb1-4(6S)GlcNAcb-Sp8	9	6	71	13	2	13	8	4	44	15	2	14	11	5	44	7	5	72	15	2	16	19	3	17	18	3	16	
266	Neu5Aca2-6Galb1-4GlcNAcb-Sp0	9	4	49	14	3	24	12	2	20	14	2	12	13	1	11	8	4	49	15	2	14	16	1	8	11	5	43	
267	Neu5Aca2-6Galb1-4GlcNAcb-Sp8	6	6	94	9	6	67	8	6	79	13	5	42	9	5	55	5	4	68	10	8	78	19	1	5	22	12	55	
268	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	14	5	32	26	2	7	24	4	18	14	2	13	24	3	13	15	6	41	26	6	22	19	2	9	26	5	20	
269	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	10	5	52	7	3	37	7	4	56	10	5	51	9	6	65	4	0	0	9	3	38	16	7	42	15	3	16	
270	Neu5Aca2-6Galb1-4Glc-Sp0	16	6	38	19	4	20	18	4	21	21	1	3	23	6	27	9	5	50	18	3	16	22	1	2	16	6	39	
271	Neu5Aca2-6Galb1-4Glc-Sp8	9	7	72	11	6	57	8	6	73	11	5	44	14	3	22	5	1	13	12	7	60	15	3	23	12	5	45	
272	Neu5Aca2-6Galb-Sp8	20	1	7	18	3	16	15	2	14	24	1	2	20	4	19	15	7	47	20	9	44	30	4	14	28	3	11	
273	Neu5Aca2-8Neu5Aca-Sp8	20	2	8	15	2	11	9	4	44	21	2	9	19	2	11	14	8	56	17	6	35	23	4	17	20	2	11	
274	Neu5Aca2-8Neu5Aca2-3Galb1-4Glc-Sp0	19	3	17	20	3	16	17	2	12	16	4	22	18	2	12	18	2	8	20	1	4	20	2	9	18	0	0	
275	Galb1-3(Fuca1-4)GlcNAcb1-3Galb1-3(Fuca1-4)GlcNAcb-Sp0	20	3	13	30	4	15	30	9	31	19	2	9	32	3	9	16	2	14	42	5	11	24	2	9	35	7	19	
276	Neu5Acb2-6GalNAca-Sp8	13	6	46	14	2	14	11	2	20	15	2	15	12	1	8	16	2	11	12	8	64	16	1	6	12	2	15	
277	Neu5Acb2-6Galb1-4GlcNAcb-Sp8	14	3	18	18	4	21	17	8	45	17	1	8	16	1	3	17	8	40	17	3	18	19	3	14	19	2	11	
278	Neu5Gca2-3Galb1-3(Fuca1-4)GlcNAcb-Sp0	13	3	22	18	2	11	12	5	43	17	2	11	17	2	10	14	2	14	26	4	14	18	2	8	23	3	13	
279	Neu5Gca2-3Galb1-3GlcNAcb-Sp0	18	2	14	18	2	9	17	6	33	19	1	4	23	3	11	18	3	14	26	2	8	22	2	10	19	1	4	
280	Neu5Gca2-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	19	2	12	26	3	13	16	2	12	15	1	8	38	4	12	19	3	16	27	4	13	20	3	14	32	2	5	
281	Neu5Gca2-3Galb1-4GlcNAcb-Sp0	17	1	6	16	4	24	11	5	43	18	2	10	17	4	25	10	6	64	16	7	40	20	3	15	18	2	12	
282	Neu5Gca2-3Galb1-4Glc-Sp0	28	3	9	51	9	18	36	11	32	31	2	7	53	17	32	29	3	11	49	4	9	33	6	17	50	5	10	
283	Neu5Gca2-6GalNAca-Sp0	21	2	7	19	2	12	16	1	6	18	2	11	17	2	13	16	3	17	23	3	11	21	4	19	16	3	17	
284	Neu5Gca2-6Galb1-4GlcNAcb-Sp0	17	3	17	17	3	15	10	4	37	19	1	6	26	3	12	20	2	12	21	2	11	23	2	7	51	38	75	
285	Neu5																												

308	GlcNAcb1-4GlcNAcb-Sp10	7	5	67	13	1	4	11	9	85	9	4	44	10	4	45	5	4	78	11	7	68	9	6	71	8	6	70
309	GlcNAcb1-4GlcNAcb-Sp12	11	4	39	15	2	12	4	1	26	11	6	53	14	1	8	9	5	59	15	8	49	14	1	7	15	4	31
310	MurNAcb1-4GlcNAcb-Sp10	12	2	18	15	3	18	9	2	28	10	4	46	12	4	30	15	1	6	12	5	39	11	1	9	14	2	15
311	Mana1-6Manb-Sp10	18	1	3	20	2	11	15	8	57	17	2	9	15	2	12	4	2	35	14	9	63	24	4	16	29	5	16
312	Mana1-6(Mana1-3)Mana1-6(Mana1-3)Manb-Sp10	12	1	8	17	3	20	13	5	38	14	1	4	20	4	21	7	2	29	10	4	39	13	3	25	17	2	12
313	Mana1-2Mana1-6(Mana1-3)Mana1-6(Mana1-2)Mana1-3)Mana-Sp9	12	1	4	15	2	11	14	3	20	13	2	15	16	4	24	14	1	10	15	1	8	14	2	14	13	1	9
314	Mana1-2Mana1-6(Mana1-2)Mana1-3)Mana1-6(Mana1-2)Mana1-2)Mana1-3)Mana-Sp9	13	1	5	12	2	15	11	2	18	13	3	25	11	2	22	9	5	58	13	2	19	14	0	0	11	2	13
315	Neu5Aca2-3Galb1-4GlcNAcb1-6(Neu5Aca2-3Galb1-3)GalNAca-Sp14	17	1	8	19	8	42	16	3	17	15	2	14	14	2	16	17	2	13	19	6	33	17	1	8	17	1	8
316	Neu5Aca2-6Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	10	2	22	5	3	74	11	2	20	8	3	35	17	2	14	53	1	3	514	53	10	11	5	49	10	6	63
317	Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	6	3	57	7	4	60	19	2	11	18	4	22	328	40	12	81	6	7	6821	1519	22	62	8	12	112	50	45
318	Neu5Aca2-8Neu5Acb-Sp17	22	1	6	19	5	27	17	1	8	20	1	4	22	3	12	19	1	5	21	1	5	22	3	11	25	3	13
319	Neu5Aca2-8Neu5Aca2-8Neu5Acb-Sp8	14	2	11	11	5	51	10	4	43	10	3	24	11	5	44	13	5	44	5	2	53	14	2	13	11	5	45
320	Neu5Gcb2-6Galb1-4GlcNAcb-Sp8	28	2	5	26	2	7	18	3	15	30	4	13	26	4	16	25	1	2	24	3	11	31	2	5	29	2	7
321	Galb1-3GlcNAcb1-2Mana1-6(Galb1-3GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp19	43	3	8	34	8	23	33	2	7	37	5	13	43	9	22	51	5	9	52	7	14	44	1	3	43	1	3
322	Neu5Aca2-3Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	12	1	7	13	1	6	10	2	22	14	2	15	13	4	33	15	7	47	18	3	18	13	1	7	9	3	30
323	Neu5Aca2-3Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	7	4	61	9	4	43	10	2	18	7	4	54	5	2	36	13	5	37	140	19	13	29	12	40	37	10	27
324	Galb1-4(Fuca1-3)GlcNAcb1-2Mana1-6(Galb1-4(Fuca1-3)GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp20	8	6	73	20	6	31	27	7	25	63	5	8	937	118	13	103	11	11	4196	651	16	12	6	52	24	2	10
325	Neu5Aca2-3Galb1-4GlcNAcb-Sp0	8	3	42	4	4	91	3	1	15	12	2	15	7	4	51	8	6	74	16	3	17	10	5	44	6	4	79
326	Neu5Aca2-3Galb1-3GlcNAcb-Sp0	10	4	44	4	1	26	4	3	68	11	3	25	8	4	49	2	1	22	4	2	55	10	5	48	16	3	15
327	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-3GlcNAcb-Sp0	9	3	37	14	5	40	20	12	61	10	3	34	15	5	36	13	4	26	25	6	23	23	7	30	39	9	22
328	Neu5Aca2-3Galb1-3(Fuca1-4)GlcNAcb1-3Galb1-3(Fuca1-4)GlcNAcb-Sp0	15	2	12	26	9	35	19	4	23	15	1	5	34	12	34	16	3	17	30	6	21	15	1	3	28	4	13
329	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	10	2	20	10	2	15	18	3	17	11	2	17	8	2	19	7	4	52	13	6	42	31	16	53	37	7	18
330	Gala1-4Galb1-4GlcNAcb1-3Galb1-4Glc-Sp0	14	2	12	20	5	23	10	3	36	13	6	46	19	5	27	3	1	39	6	4	58	17	3	19	25	3	13
331	GalNAcb1-3Gala1-4Galb1-4GlcNAcb1-3Galb1-4Glc-Sp0	11	1	5	10	3	29	27	2	9	9	2	18	20	4	21	8	4	49	17	2	10	9	4	41	18	2	12
332	GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	9	2	27	12	1	8	40	6	14	8	4	51	11	2	13	4	1	20	8	3	44	12	2	16	9	2	18
333	GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	17	3	14	30	1	4	128	16	13	17	2	9	72	23	32	35	4	12	538	65	12	26	3	10	40	5	13
334	Neu5Aca2-3Galb1-4(Fuca1-3)GlcNAcb1-6(Neu5Aca2-3Galb1-3)GalNAc-Sp14	26	4	17	37	2	5	36	8	22	26	1	5	39	4	10	25	2	9	47	2	4	26	2	6	38	3	8
335	GlcNAca1-4Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	12	1	7	14	2	14	41	4	9	12	1	4	15	2	11	11	6	53	13	5	35	11	1	9	17	1	8
336	GlcNAca1-4Galb1-4GlcNAcb-Sp0	17	2	13	20	2	9	16	2	13	15	5	33	19	3	15	18	3	15	29	4	15	20	4	18	21	3	16
337	GlcNAca1-4Galb1-3GlcNAcb-Sp0	18	1	5	27	3	10	14	5	34	16	2	9	19	4	23	14	6	43	25	7	28	18	1	3	28	7	24
338	GlcNAca1-4Galb1-4GlcNAcb1-3Galb1-4Glc-Sp0	13	2	12	16	3	16	19	2	9	13	2	17	16	5	29	3	1	15	18	9	52	11	7	62	18	4	20
339	GlcNAca1-4Galb1-4GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb-Sp0	37	3	9	39	5	14	29	3	11	31	4	14	34	1	2	30	5	18	94	5	5	38	5	12	30	7	25
340	GlcNAca1-4Galb1-4GlcNAcb1-3Galb1-4GlcNAcb-Sp0	14	6	43	20	4	18	20	2	8	15	1	5	23	4	19	15	2	16	68	2	2	18	2	10	21	8	38
341	GlcNAca1-4Galb1-3GalNAc-Sp14	16	3	18	21	9	41	20	3	17	15	1	9	17	2	12	10	4	42	22	3	12	13	1	9	22	3	15
342	Neu5Aca2-6Galb1-4GlcNAcb1-2Mana1-6(Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp12	10	4	42	10	3	29	10	4	35	10	4	43	13	1	10	8	6	72	26	3	12	20	5	23	17	4	22
343	Mana1-6(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp12	11	1	7	19	3	17	25	6	22	13	2	17	26	6	22	15	4	27	51	6	11	32	15	47	39	21	53
344	Neu5Aca2-6Galb1-4GlcNAcb1-2Mana1-6Manb1-4GlcNAcb1-4GlcNAc-Sp12	15	2	12	12	1	8	12	1	8	14	1	10	12	5	40	21	1	5	70	6	9	19	2	10	17	3	15
345	Neu5Aca2-6Galb1-4GlcNAcb1-2Mana1-3Manb1-4GlcNAcb1-4GlcNAc-Sp12	11	4	37	12	1	7	13	1	9	11	2	21	12	3	24	17	2	13	49	4	8	24	4	16	26	8	31
346	Galb1-4GlcNAcb1-2Mana1-3Manb1-4GlcNAcb1-4GlcNAc-Sp12	8	6	77	11	2	20	14	1	6	17	2	14	896	65	7	119	11	10	5508	691	13	14	1	6	18	6	34
347	Galb1-4GlcNAcb1-2Mana1-6Manb1-4GlcNAcb1-4GlcNAc-Sp12	9	4	46	10	4	39	13	4	33	24	1	2	620	73	12	143	12	9	5040	564	11	12	5	45	11	4	42
348	Mana1-6(Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp12	10	2	15	21	3	17	23	3	13	15	2	15	941	57	6	95	6	6	5299	641	12	12	2	21	16	3	16
349	GlcNAcb1-2Mana1-6(GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	13	2	15	23	6	27	24	4	17	12	1	10	30	8	27	15	1	6	20	2	7	15	2	12	33	5	14
350	Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	19	2	9	40	9	23	92	14	15	27	4	15	1123	149	13	58	9	15	6166	724	12	23	7	32	42	8	19
351	Galb1-3GlcNAcb1-2)Mana1-6(Galb1-3GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	11	3	28	38	2	5	34	10	30	13	1	4	34	9	27	11	5	45	24	8	33	13	2	17	45	12	28
352	(6S)GlcNAcb1-3Galb1-4GlcNAcb-Sp0	14	2	13	28	7	26	22	3	12	15	3	21	99	13	13	21	2	10	27	5	18	16	3	21	24	2	10
353	KDNa2-3Galb1-4(Fuca1-3)GlcNAc-Sp0	16	2	11	42	14	33	30	4	13	17	3	17	32	8	25	20	3	13	129	11	9	19	2	13	34	4	10
354	KDNa2-6Galb1-4GlcNAc-Sp0	17	2	10	23	1	4	19	2	12	17	1	6	27	7	27	17	4	21	30	5	17	47	13	29	79	21	26
355	KDNa2-3Galb1-4Glc-Sp0	13	2	11	18	2	11	14	2	11	10	4	43	21	2	8	13	6	46	24	2	10	14	1	9	18	2	11
356	KDNa2-3Galb1-3GalNAc-Sp14	19	1	7	51	4	8	50	15	31	16	2	11	46	4	8	34	6	18	254	32	12	25	1	5	43	6	14
357	Fuca1-2Galb1-3GlcNAcb1-2)Mana1-6(Fuca1-2Galb1-3GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp20	29	3	12	34	2	6	38	3	8	30	1	3	36	7	20	31	4	13	39	7	18	31	5	17	37	7	18
358	Fuca1-2Galb1-4GlcNAcb1-2)Mana1-6(Fuca1-2Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp20	25	1	5	36	5	13	158	27	17	119	13	11	679	35	5	87	2	3	4664	383	8	30	3	9	39	4	10
359	Fuca1-2Galb1-4(Fuca1-3)GlcNAcb1-2)Mana1-6(Fuca1-2Galb1-4(Fuca1-3)GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp20	35	1	1	42	5	11	37	2	6	39	9	22	109	11	10	105	5	5	2294	80	3	37	2	6	38	1	1
360	Gala1-3Galb1-4GlcNAcb1-2)Mana1-6(Gala1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp20	16	2	11	20	5	25	18	2	13	14	2	11	21	3	16	18	1	3	26								

363	Neu5Aca2-6GlcNAcb1-4GlcNAc-Sp21	13	2	15	9	3	34	11	2	17	12	2	17	12	2	15	12	8	63	13	7	55	15	3	19	15	3	18
364	Neu5Aca2-6GlcNAcb1-4GlcNAcb1-4GlcNAc-Sp21	11	4	42	10	4	43	8	2	27	12	0	0	14	3	21	6	4	73	11	7	64	13	2	16	13	5	40
365	Galb1-4(Fuca1-3)GlcNAcb1-6(Fuca1-2Galb1-4GlcNAcb1-3)Galb1-4Glc-Sp21	14	2	13	18	3	17	18	3	16	15	2	10	50	12	25	14	6	41	36	1	2	16	1	5	19	4	20
366	Galb1-4GlcNAcb1-2MAna1-6(Galb1-4GlcNAcb1-4)(Galb1-4GlcNAcb1-2)MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	14	1	10	18	2	9	59	6	10	34	2	6	399	38	9	38	2	6	6783	797	12	15	1	9	25	11	43
367	GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp20	18	1	3	23	1	6	22	2	8	18	2	9	31	2	5	54	3	6	416	43	10	21	1	5	26	3	11
368	Gala1-3(Fuca1-2)Galb1-4GlcNAcb1-2MAna1-6(Gala1-3(Fuca1-2)Galb1-4GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp20	22	3	12	22	5	23	26	3	13	21	3	12	94	22	23	91	5	6	2022	217	11	23	2	10	32	5	16
369	Gala1-3Galb1-4(Fuca1-3)GlcNAcb1-2MAna1-6(Gala1-3Galb1-4(Fuca1-3)GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp20	26	3	12	37	3	8	31	2	6	25	2	7	44	8	18	29	1	4	46	11	24	28	2	7	39	6	16
370	GalNAca1-3(Fuca1-2)Galb1-3GlcNAcb1-2MAna1-6(GalNAca1-3(Fuca1-2)Galb1-3GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp20	19	1	7	27	5	20	20	1	4	19	1	7	25	3	13	17	2	10	22	2	10	19	1	7	22	3	12
371	Fuca1-4(Fuca1-2Galb1-3)GlcNAcb1-2MAna1-3(Fuca1-4(Fuca1-2Galb1-3)GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp19	20	4	19	33	2	7	31	8	25	23	3	11	29	1	4	20	4	20	41	2	5	26	6	22	30	3	9
372	Neu5Aca2-3Galb1-4GlcNAcb1-3GalNAc-Sp14	4	1	35	9	2	76	10	2	18	8	6	67	7	5	70	6	4	67	15	8	54	12	1	5	14	3	24
373	Neu5Aca2-6Galb1-4GlcNAcb1-3GalNAc-Sp14	13	3	25	25	9	38	27	6	22	7	2	35	29	7	23	14	2	15	28	6	21	12	4	32	32	5	17
374	Neu5Aca2-3Galb1-4(Fuca1-3)GlcNAcb1-3GalNAca-Sp14	29	4	15	37	2	5	32	1	4	22	7	33	41	9	22	33	8	26	41	11	28	35	12	34	44	7	16
375	GalNAcb1-4GlcNAcb1-2MAna1-6(GalNAcb1-4GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp12	23	1	6	39	11	27	50	10	21	28	2	9	53	10	19	142	32	22	4520	474	10	31	3	9	35	4	12
376	Galb1-3GalNAca1-3(Fuca1-2)Galb1-4Glc-Sp0	13	3	25	14	6	42	11	5	40	9	4	39	17	11	68	7	7	96	16	11	70	14	1	7	20	3	13
377	Galb1-3GalNAca1-3(Fuca1-2)Galb1-4GlcNAc-Sp0	9	4	43	16	7	46	43	4	10	3	1	35	12	1	11	4	1	37	20	1	7	8	4	54	10	4	43
378	Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-3GlcNAcb1-3)Galb1-4Glc-Sp0	11	1	4	32	6	17	212	98	46	13	2	14	38	13	34	10	5	49	17	3	16	12	3	24	13	2	15
379	Galb1-4(Fuca1-3)GlcNAcb1-6(Galb1-3GlcNAcb1-3)Galb1-4Glc-Sp21	7	4	60	6	4	64	7	4	56	10	2	22	79	7	8	9	6	72	20	4	17	9	4	47	8	6	71
380	Galb1-4GlcNAcb1-6(Fuca1-4(Fuca1-2Galb1-3)GlcNAcb1-3)Galb1-4Glc-Sp21	18	2	8	26	6	24	44	11	24	20	2	12	162	4	2	156	9	6	1401	69	5	15	2	10	26	7	25
381	Galb1-4(Fuca1-3)GlcNAcb1-6(Fuca1-4(Fuca1-2Galb1-3)GlcNAcb1-3)Galb1-4Glc-Sp21	13	2	16	16	2	14	17	2	10	14	1	8	70	9	12	93	9	9	633	53	8	15	1	5	14	2	12
382	Galb1-3GlcNAcb1-3Galb1-4(Fuca1-3)GlcNAcb1-6(Galb1-3GlcNAcb1-3)Galb1-4Glc-Sp21	9	4	49	11	1	9	15	4	29	9	4	41	113	3	3	97	12	13	564	43	8	17	1	7	11	5	43
383	Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-2)MAna1-6(Galb1-4GlcNAcb1-4)(Galb1-4GlcNAcb1-2)MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	12	2	17	17	4	22	94	5	6	159	12	8	734	93	13	79	15	19	7312	620	8	13	1	10	12	6	51
384	GlcNAcb1-2MAna1-6(GlcNAcb1-4)(GlcNAcb1-2)MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	12	2	13	11	2	13	11	3	24	4	5	133	52	3	6	39	2	4	314	20	6	12	1	7	13	1	4
385	Fuca1-2Galb1-3GalNAca1-3(Fuca1-2)Galb1-4Glc-Sp0	17	2	11	39	4	11	51	9	18	21	4	17	36	3	10	20	2	9	42	13	31	19	3	15	31	7	22
386	Fuca1-2Galb1-3GalNAca1-3(Fuca1-2)Galb1-4GlcNAc-Sp0	7	4	65	4	2	35	56	13	22	5	2	36	7	4	52	5	2	36	9	5	49	11	4	36	7	3	53
387	Galb1-3GlcNAcb1-3GalNAca-Sp14	15	1	6	18	10	57	24	4	16	16	1	8	17	6	34	7	6	87	26	11	41	13	5	37	10	5	45
388	GalNAcb1-4(Neu5Aca2-3)Galb1-4GlcNAcb1-3GalNAca-Sp14	11	4	35	31	1	2	43	4	10	10	2	22	36	4	11	15	1	6	48	5	11	15	5	36	24	3	13
389	GalNAca1-3(Fuca1-2)Galb1-3GalNAca1-3(Fuca1-2)Galb1-4GlcNAc-Sp0	8	4	53	7	5	78	7	3	48	7	5	64	11	4	39	3	1	47	5	3	48	6	5	79	11	11	103
390	Gala1-3Galb1-3GlcNAcb1-2MAna1-6(Gala1-3Galb1-3GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp19	29	7	24	37	4	10	42	9	21	24	4	16	30	8	26	22	3	16	27	1	2	25	4	17	37	7	19
391	Gala1-3Galb1-3(Fuca1-4)GlcNAcb1-2MAna1-6(Gala1-3Galb1-3(Fuca1-4)GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp19	35	4	11	30	3	10	29	6	20	36	5	14	34	12	35	38	4	10	35	3	8	49	3	7	35	9	27
392	Neu5Aca2-3Galb1-3GlcNAcb1-2MAna1-6(Neu5Aca2-3Galb1-3GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp19	8	6	70	26	6	23	22	1	6	14	3	19	27	4	16	7	4	58	35	2	5	17	1	6	28	6	21
393	GlcNAcb1-2MAna1-6(Galb1-4GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp12	13	3	20	15	2	15	16	2	11	22	3	15	547	43	8	100	10	10	6805	518	8	12	2	13	15	2	12
394	Galb1-4GlcNAcb1-2MAna1-6(GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp12	10	2	23	8	4	44	14	3	21	11	4	37	598	25	4	77	5	6	5162	941	18	6	5	89	16	5	29
395	Neu5Aca2-3Galb1-3GlcNAcb1-3GalNAca-Sp14	8	5	65	17	10	57	8	4	52	6	5	83	20	9	46	7	4	64	18	5	26	13	1	9	16	4	27
396	Fuca1-2Galb1-4GlcNAcb1-3GalNAca-Sp14	15	3	22	34	10	28	32	4	11	13	7	54	225	56	25	22	5	23	100	8	8	20	1	7	39	15	38
397	Galb1-4(Fuca1-3)GlcNAcb1-3GalNAca-Sp14	19	3	16	29	6	21	30	6	21	15	2	12	77	25	32	18	1	5	50	16	31	20	1	6	28	8	29
398	GalNAca1-3GalNAcb1-3Gala1-4Galb1-4GlcNAc-Sp0	4	2	59	11	7	65	4	3	75	8	4	55	5	3	52	3	1	18	4	1	37	6	4	76	7	5	73
399	Gala1-4Galb1-3GlcNAcb1-2MAna1-6(Gala1-4Galb1-3GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp19	20	3	15	35	5	15	21	9	42	20	2	9	31	4	13	19	2	13	38	9	24	17	2	9	27	5	18
400	Gala1-4Galb1-4GlcNAcb1-2MAna1-6(Gala1-4Galb1-4GlcNAcb1-2MAna1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp24	38	1	2	47	15	32	40	9	22	35	2	6	91	16	17	109	1	1	2685	32	1	38	2	6	58	15	25
401	Gala1-3Galb1-4GlcNAcb1-3GalNAca-Sp14	5	2	43	9	4	52	6	5	91	3	1	18	10	2	23	8	6	75	10	5	50	7	4	63	9	4	41
402	Galb1-3GlcNAcb1-6Galb1-4GlcNAc-Sp0	11	5	48	18	2	12	10	4	37	7	5	68	9	5	52	2	1	22	3	1	23	15	1	3	16	2	15
403	Galb1-3GlcNAca1-6Galb1-4GlcNAc-Sp0	5	3	60	6	4	71	4	1	16	4	3	75	4	3	75	4	3	74	18	4	23	3	1	23	9	6	68
404	GalNAcb1-3Gala1-6Galb1-4Glc-Sp8	21	6	27	22	5	21	14	3	22	18	1	5	19	4	23	18	2	14	18	3	19	20	2	8	16	5	30
405	Gala1-3(Fuca1-2)Galb1-4(Fuca1-3)Glc-Sp21	17	4	25	15	2	14	16	2	10	15	1	6	18	4	21	17	2	13	38	3	7	18	3	14	14	2	15
406	Galb1-4GlcNAcb1-6(Neu5Aca2-6Galb1-3GlcNAcb1-3)Galb1-4Glc-Sp21	12	4	38	12	4	32	7	4	56	9	4	42	8	4	52	6	4	63	31	5	17	12	6	49	8	3	40
407	Galb1-3GalNAcb1-4(Neu5Aca2-8Neu5Aca2-3)Galb1-4Glc-Sp0	26	2	7	29	3	12	23	2	10	26	4	14	30	1	2	23	1	5	28	4	15	25	3	13	27	1	5
408	Neu5Aca2-3Galb1-3GalNAcb1-4(Neu5Aca2-8Neu5Aca2-3)Galb1-4Glc-Sp0	26	2	9	31	1	2	25	4	18	22	1	6	26	5	19	18	2	12	32	3	8	21	1	6	33	6	18
409	Gala1-3(Fuca1-2)Galb1-4GlcNAcb1-3GalNAca-Sp14	9	6	70	17	5	27	15	5	30	7	4	61	21	3	14	2	1	22	14	11	77	4	1	37	21	8	37
410	GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb1-3GalNAca-Sp14	3	1	23	16	16	104	12	8	69	5	3	65	10	6	61	2	1	22	27	13	49	5	4	74	11	9	86
411	GalNAca1-3GalNAcb1-3Gala1-4Galb1-4Glc-Sp0	12	1	11	14	2	17	9	6	70	10	3	27	11	3	32	4	1	26	13	5	40	14	1	6	11	5	46
412	Fuca1-2Galb1-4(Fuca1-3)GlcNAcb1-3GalNAca-Sp14	18	1	5	42	3	6	55	4	8	19	2	13	50	5	10	37	3	7	177	10	6	19	2	13	32	4	14
413	Gala1-3(Fuca1-2)Galb1-4(Fuca1-3)GlcNAcb1-3GalNAc-Sp14	14	3	19	37	16	44	25	6	24	17	1	6	31	3	11	4	1	29	27	2	6	16	4	25	19	6	31
414	GalNAca1-3(Fuca1-2)Galb1-4(Fuca1-3)GlcNAcb1-3GalNAc-Sp14	22	5	21	23	4	17	30	4	12	17	4	25	30	5	16	17	3	20	29	4	14	25	4				

416	Fuca1-2Galb1-4GlcNAcb1-2Mana1-6(Fuca1-2Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	24	2	10	36	10	28	66	4	6	26	1	4	258	18	7	93	6	7	2881	130	5	26	2	9	33	6	17
417	GlcNAcb1-2(GlcNAcb1-6)Mana1-6(GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp19	25	1	5	23	2	9	17	3	16	25	1	5	21	4	18	22	2	8	29	5	17	21	1	7	22	1	4
418	Fuca1-2Galb1-3GlcNAcb1-3GalNAc-Sp14	20	1	4	15	1	5	11	2	15	19	2	5	17	2	13	14	6	44	24	2	10	20	1	2	19	1	7
419	Gala1-3(Fuca1-2)Galb1-3GlcNAcb1-3GalNAc-Sp14	3	1	38	9	8	87	4	1	26	4	1	12	10	10	98	2	1	43	11	3	27	9	6	69	9	3	36
420	GalNAca1-3(Fuca1-2)Galb1-3GlcNAcb1-3GalNAc-Sp14	14	1	10	18	5	25	14	3	19	17	4	22	27	3	12	16	3	18	25	2	6	17	2	9	23	4	17
421	Gala1-3Galb1-3GlcNAcb1-3GalNAc-Sp14	4	1	20	14	7	49	8	2	23	11	1	9	29	9	31	4	1	26	26	5	19	10	5	48	25	7	29
422	Fuca1-2Galb1-3GlcNAcb1-2Mana1-6(Fuca1-2Galb1-3GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	22	2	10	32	4	12	26	8	32	21	4	17	45	12	27	24	3	12	47	9	20	22	4	19	43	7	17
423	Gala1-3(Fuca1-2)Galb1-4GlcNAcb1-2Mana1-6(Gala1-3(Fuca1-2)Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	18	2	12	43	8	19	41	19	47	16	4	22	46	19	42	19	2	9	84	27	32	21	1	4	32	4	13
424	Galb1-3GlcNAcb1-6(Galb1-3GlcNAcb1-2)Mana1-6(Galb1-3GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp19	21	3	14	34	3	10	84	12	15	20	3	17	62	23	37	23	3	11	39	8	21	24	1	4	43	12	29
425	Galb1-4GlcNAcb1-6(Fuca1-2Galb1-3GlcNAcb1-3)Galb1-4Glc-Sp21	7	2	27	13	1	6	40	1	4	12	1	11	101	21	21	12	5	40	21	5	27	8	4	45	7	3	47
426	Fuca1-3GlcNAcb1-6(Galb1-4GlcNAcb1-3)Galb1-4Glc-Sp21	3	1	15	11	3	23	46	6	12	9	4	44	205	30	15	116	20	17	5545	105	2	10	2	15	16	12	73
427	GlcNAcb1-2Mana1-6(GlcNAcb1-4)GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	4	4	91	3	1	38	3	1	15	3	0	0	5	2	53	2	1	29	5	3	53	3	1	27	5	3	52
428	GlcNAcb1-2Mana1-6(GlcNAcb1-4)GlcNAcb1-4(GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	8	4	49	12	3	27	10	3	35	12	3	25	12	2	13	7	4	51	15	2	12	7	3	42	15	3	23
429	GlcNAcb1-6(GlcNAcb1-2)Mana1-6(GlcNAcb1-4)GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	11	1	9	8	4	44	5	2	32	9	3	40	8	2	27	6	4	63	5	1	29	11	2	13	9	1	16
430	GlcNAcb1-6(GlcNAcb1-2)Mana1-6(GlcNAcb1-4)GlcNAcb1-4(GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	6	4	74	7	4	52	5	3	60	3	1	39	4	1	29	3	1	18	4	1	35	7	4	54	6	3	49
431	Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-4)Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	7	6	81	8	5	60	11	7	61	13	2	11	240	71	30	106	11	11	4471	1019	23	12	2	15	11	4	33
432	Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-4)Galb1-4GlcNAcb1-4(Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	6	3	53	7	3	46	39	2	5	79	6	8	718	82	11	194	7	4	6089	266	4	14	2	11	20	2	9
433	Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-4)Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	9	3	37	11	3	32	43	3	6	23	4	17	623	11	2	93	6	7	5175	153	3	14	4	25	15	2	12
434	Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-4)Galb1-4GlcNAcb1-4(Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp21	8	3	46	7	3	39	68	11	17	53	4	7	677	61	9	134	8	6	5580	305	5	18	5	30	21	8	40
435	Galb1-4Galb-Sp10	14	3	20	11	8	78	6	5	75	9	6	72	6	6	94	4	1	29	10	6	67	14	2	17	13	7	57
436	Galb1-6Galb-Sp10	7	5	74	10	6	57	8	4	44	13	1	8	9	5	61	4	1	26	14	6	40	14	2	12	10	7	65
437	Neu5Aca2-3Galb1-4GlcNAcb1-3Galb-Sp8	14	4	27	14	7	48	18	9	52	5	3	67	12	5	46	2	0	0	9	8	85	12	6	49	22	5	22
438	GalNAca1-6GalNAcb-Sp8	5	2	53	12	5	44	4	1	16	15	1	8	9	5	61	2	1	29	2	1	71	10	7	63	9	6	67
439	(6S)Galb1-3GlcNAcb-Sp0	10	7	71	10	7	74	9	6	72	17	3	16	16	3	16	14	11	75	22	6	25	19	5	28	16	1	5
440	(6S)Galb1-3GlcNAcb-Sp0	21	2	7	26	4	17	20	1	7	20	4	18	25	3	11	23	6	26	27	3	12	23	6	27	25	3	14
441	Fuca1-2Galb1-4GlcNAcb1-2Mana1-6(Fuca1-2Galb1-4GlcNAcb1-2)Fuca1-2Galb1-4GlcNAcb1-4)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	27	2	7	32	2	7	80	6	7	39	2	6	299	25	8	184	17	9	2891	171	6	25	1	4	27	3	11
442	Fuca1-2Galb1-4(Fuca1-3)GlcNAcb1-2Mana1-6(Fuca1-2Galb1-4)Fuca1-3)GlcNAcb1-4(Fuca1-2Galb1-4)Fuca1-3)GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	18	1	5	34	3	10	60	18	29	30	1	3	436	16	4	223	39	18	2476	75	3	24	1	3	28	5	19
443	Galb1-4(Fuca1-3)GlcNAcb1-6GalNAc-Sp14	19	3	15	24	4	15	32	5	15	16	2	9	38	6	16	18	3	19	40	6	14	22	5	22	24	2	10
444	Galb1-4GlcNAcb1-2Mana-Sp0	21	2	9	26	2	8	20	4	20	20	3	15	28	2	8	21	2	10	24	2	8	24	1	3	22	2	7
445	Fuca1-2Galb1-4GlcNAcb1-6(Fuca1-2Galb1-4GlcNAcb1-3)GalNAc-Sp14	13	4	33	32	5	16	224	16	7	17	3	17	637	17	3	10	5	49	49	8	15	12	7	61	28	3	11
446	Gala1-3(Fuca1-2)Galb1-4GlcNAcb1-6(Gala1-3(Fuca1-2)Galb1-4GlcNAcb1-3)GalNAc-Sp14	6	5	78	20	6	29	12	10	84	5	3	69	44	13	30	4	1	13	25	6	24	6	5	79	16	8	49
447	GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb1-6(GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb1-3)GalNAc-Sp14	3	1	52	12	8	65	24	10	44	6	4	79	99	45	45	4	1	37	18	11	63	3	1	23	9	10	106
448	Neu5Aca2-8Neu5Aca2-3Galb1-3GalNAcb1-4(Neu5Aca2-8Neu5Aca2-3)Galb1-4Glc-Sp0	69	4	6	72	4	6	46	1	3	65	4	6	343	18	5	93	6	6	4276	219	5	66	7	10	66	2	4
449	GalNAca1-4Galb1-4Glc-Sp0	18	2	11	21	3	12	19	5	26	20	3	14	26	6	23	15	8	52	23	4	19	19	2	11	21	4	20
450	GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb1-2Mana1-6(GalNAca1-3(Fuca1-2)Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	17	5	26	57	12	21	39	9	22	17	1	6	64	15	24	19	3	14	58	11	20	19	1	5	55	4	7
451	Gala1-3(Fuca1-2)Galb1-3GlcNAcb1-2Mana1-6(Gala1-3(Fuca1-2)Galb1-3GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	15	2	14	56	32	57	41	26	63	16	4	26	31	17	57	5	4	75	61	8	13	18	3	18	58	19	32
452	Neu5Aca2-6Galb1-4GlcNAcb1-6(Fuca1-2Galb1-3GlcNAcb1-3)Galb1-4Glc-Sp21	16	1	9	23	7	31	20	3	14	44	31	69	65	27	42	13	1	6	27	2	6	21	3	12	22	3	12
453	GalNAca1-3(Fuca1-2)Galb1-3GlcNAcb1-2Mana1-6(GalNAca1-3(Fuca1-2)Galb1-3GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp22	20	2	8	39	7	18	33	5	15	18	2	10	32	9	30	17	1	6	36	5	14	23	3	15	28	1	5
454	Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp19	12	6	45	34	6	18	35	6	16	17	3	16	27	10	38	10	8	78	19	7	35	19	4	24	39	15	38
455	Neu5Aca2-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-4)Neu5Aca2-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	8	4	55	12	7	59	12	4	33	8	1	15	11	5	50	10	7	71	20	2	12	10	5	47	10	4	37
456	Neu5Aca2-3Galb1-4GlcNAcb1-4Mana1-6(GlcNAcb1-4)Neu5Aca2-3Galb1-4GlcNAcb1-4(GlcNAcb1-4)Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	7	4	61	7	2	24	9	3	28	7	3	46	11	5	43	4	1	26	14	2	13	10	4	41	9	3	31
457	Neu5Aca2-3Galb1-4GlcNAcb1-6(Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-4)Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	8	5	56	10	3	35	11	2	20	10	2	23	11	2	23	10	5	56	24	1	2	11	1	12	11	2	16
458	Neu5Aca2-3Galb1-4GlcNAcb1-6(Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-4)Neu5Aca2-3Galb1-4GlcNAcb1-4(Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	5	3	59	9	4	44	7	3	49	7	4	51	17	7	41	9	3	36	20	2	12	10	2	18	7	7	99

459	Neu5Aca2-6Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-4)(Neu5Aca2-6Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	12	1	8	14	5	34	42	2	6	9	4	47	17	5	27	15	1	6	324	14	4	65	41	64	287	168	58
460	Neu5Aca2-6Galb1-4GlcNAcb1-4Mana1-6(GlcNAcb1-4)(Neu5Aca2-6Galb1-4GlcNAcb1-4)(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	9	3	29	14	1	10	41	3	7	8	4	54	15	4	27	10	6	56	296	5	2	95	24	26	719	361	50
461	Neu5Aca2-6Galb1-4GlcNAcb1-6(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-4)(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	7	3	49	7	4	68	37	4	10	6	3	53	9	7	75	10	7	76	363	16	4	71	34	48	541	211	39
462	Neu5Aca2-6Galb1-4GlcNAcb1-6(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-4)(Neu5Aca2-6Galb1-4GlcNAcb1-4)(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	10	4	44	11	2	20	35	4	12	11	7	59	20	5	25	15	8	50	385	37	10	112	20	18	464	50	11
463	Gala1-3(Fuca1-2)Galb1-3GalNAcb-Sp8	17	3	14	13	1	11	12	7	55	16	1	5	15	3	18	8	4	44	19	3	15	20	2	8	17	2	14
464	Gala1-3(Fuca1-2)Galb1-3GalNAcb-Sp8	25	3	11	27	2	9	15	3	19	28	3	10	28	1	3	18	4	24	31	4	14	30	5	16	33	2	7
465	GlcA1-6GlcA1-6GlcA1-6GlcA-Sp10	4	1	13	24	7	29	11	5	46	10	3	27	21	5	23	5	1	13	23	11	51	9	6	75	22	11	52
466	GlcA1-4GlcA1-4GlcA1-4GlcA-Sp10	7	5	76	17	3	17	11	12	105	10	4	42	12	3	22	4	1	12	22	3	14	14	5	39	29	7	24
467	Neu5Aca2-3Galb1-4GlcNAcb1-6(Neu5Aca2-3Galb1-4GlcNAcb1-3)GalNAcb-Sp14	6	4	67	12	1	5	6	3	48	6	5	82	8	5	64	6	7	104	9	7	78	10	6	68	6	4	62
468	Fuca1-2Galb1-4(Fuca1-3)GlcNAcb1-2Mana1-6(Fuca1-2Galb1-4(Fuca1-3)GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	45	3	6	44	2	4	53	6	11	57	10	18	475	47	10	58	3	6	3516	243	7	74	12	16	67	5	7
469	Fuca1-2Galb1-3(Fuca1-4)GlcNAcb1-2Mana1-6(Fuca1-2Galb1-3(Fuca1-4)GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb1-4(Fuca1-3)GlcNAcb-Sp19	40	4	11	36	7	19	33	5	15	39	3	9	42	12	30	45	6	14	54	4	7	48	7	14	64	8	13
470	GlcNAcb1-6(GlcNAcb1-2)Mana1-6(GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	32	4	13	40	3	7	43	6	14	28	1	5	47	3	6	31	4	12	62	18	28	35	5	14	47	8	16
471	Galb1-3GlcNAcb1-2)Mana1-6(GlcNAcb1-4)(Galb1-3GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	38	5	13	52	3	6	49	9	19	33	8	23	49	9	18	28	1	5	52	10	20	38	5	13	42	7	17
472	Neu5Aca2-6Galb1-4GlcNAcb1-6(Galb1-3GlcNAcb1-3)Galb1-4GlcA-Sp21	12	4	32	13	3	27	6	1	20	6	5	79	40	6	15	9	7	74	27	3	11	12	3	22	7	4	52
473	Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana-Sp0	19	2	12	32	3	8	30	10	33	18	1	5	29	12	41	22	4	17	58	4	7	22	5	23	27	4	14
474	Neu5Aca2-3Galb1-4GlcNAcb1-6GalNAcb-Sp14	8	6	71	6	3	45	8	2	27	9	4	45	15	4	25	2	1	29	8	6	74	12	5	44	12	5	43
475	Neu5Aca2-6Galb1-4GlcNAcb1-6GalNAcb-Sp14	13	7	53	30	13	42	38	8	22	16	2	14	29	8	26	16	7	43	31	3	11	20	0	0	32	5	16
476	Neu5Aca2-6Galb1-4GlcNAcb1-6(Neu5Aca2-6Galb1-4GlcNAcb1-3)GalNAcb-Sp14	40	2	4	50	2	3	54	4	8	39	5	13	53	4	7	57	3	5	296	21	7	114	14	12	203	78	39
477	Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-6(Neu5Aca2-6Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	32	2	8	52	8	16	67	11	16	41	5	11	71	7	9	45	5	12	224	10	4	105	23	22	349	94	27
478	Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-6(Neu5Aca2-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	26	4	16	37	4	11	38	2	5	30	2	6	31	5	15	28	6	21	48	13	27	32	1	3	43	16	39
479	Mana1-6(Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp19	24	3	14	43	6	14	35	4	13	28	3	12	39	7	18	26	4	14	36	5	14	28	3	11	38	11	28
480	Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	35	6	16	58	5	9	179	10	5	117	17	15	629	74	12	75	4	6	4063	165	4	44	1	3	70	9	12
481	Neu5Aca2-3Galb1-3GlcNAcb1-2)Mana1-6(GlcNAcb1-4)(Neu5Aca2-3Galb1-3GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp21	12	6	51	30	14	48	21	13	63	13	3	21	29	6	22	10	8	81	28	7	26	13	6	52	13	9	67
482	Neu5Aca2-6Galb1-4GlcNAcb1-6(Fuca1-2Galb1-4)(Fuca1-3)GlcNAcb1-3)Galb1-4Glc-Sp21	11	3	27	18	5	30	15	6	42	11	2	23	30	2	7	6	4	67	21	2	9	9	4	49	16	6	41
483	Galb1-3GlcNAcb1-6GalNAcb-Sp14	11	4	38	19	16	81	15	1	6	9	5	54	36	4	11	12	6	50	10	9	90	13	6	48	17	2	11
484	Gala1-3Galb1-3GlcNAcb1-6GalNAcb-Sp14	8	3	41	16	3	18	16	3	20	6	5	91	10	6	65	5	5	104	14	7	47	12	8	64	11	7	69
485	Galb1-3(Fuca1-4)GlcNAcb1-6GalNAcb-Sp14	23	4	17	40	6	14	37	2	5	23	2	9	31	5	17	15	5	30	36	3	7	24	2	7	38	11	29
486	Neu5Aca2-3Galb1-3GlcNAcb1-6GalNAcb-Sp14	6	5	84	31	6	19	27	2	7	10	5	49	33	4	13	8	6	76	28	5	19	15	2	12	37	13	36
487	(3S)Galb1-3(Fuca1-4)GlcNAcb-Sp0	20	1	7	34	1	3	60	6	9	15	2	16	97	13	13	37	3	7	336	33	10	21	2	11	49	13	27
488	Galb1-4(Fuca1-3)GlcNAcb1-6(Neu5Aca2-6Galb1-3)GlcNAcb1-3)Galb1-4Glc-Sp21	18	3	14	41	6	15	45	13	30	16	3	18	88	12	14	24	3	12	123	7	5	22	7	33	42	8	18
489	Fuca1-2Galb1-4GlcNAcb1-6GalNAcb-Sp14	17	1	6	40	8	21	35	3	9	18	1	7	198	51	26	18	8	48	77	13	17	18	2	12	56	10	17
490	Gala1-3Galb1-4GlcNAcb1-6GalNAcb-Sp14	8	4	56	5	2	39	7	4	58	5	4	74	9	6	63	6	6	96	26	11	42	19	2	11	21	3	13
491	Galb1-4(Fuca1-3)GlcNAcb1-2)Mana-Sp0	21	4	20	28	12	42	20	9	47	22	2	10	88	8	9	145	60	42	1641	392	24	22	4	20	34	6	17
492	Fuca1-2(6S)Galb1-3GlcNAcb-Sp0	4	5	122	6	3	46	3	1	39	6	4	67	3	1	18	3	1	23	14	7	49	16	2	15	14	5	39
493	Gala1-3(Fuca1-2)Galb1-4GlcNAcb1-6GalNAcb-Sp14	8	5	70	4	2	49	3	1	46	5	4	74	3	1	15	2	1	22	6	5	76	4	1	16	3	2	63
494	Fuca1-2Galb1-4GlcNAcb1-2)Mana-Sp0	10	5	54	16	5	33	7	2	28	12	5	45	30	12	40	61	5	9	499	43	9	19	2	10	17	6	37
495	Fuca1-2Galb1-3(6S)GlcNAcb-Sp0	21	5	26	28	1	4	27	2	8	19	4	19	62	8	12	20	3	17	33	8	25	23	2	11	30	8	28
496	Fuca1-2(6S)Galb1-3(6S)GlcNAcb-Sp0	27	5	18	24	3	12	38	5	14	15	3	19	25	4	18	30	3	11	42	12	29	27	6	23	27	4	14
497	Neu5Aca2-6Galb1-4GlcNAcb1-6(GlcNAcb-Sp8	11	4	41	16	5	29	16	8	50	9	3	37	20	5	24	8	7	94	12	2	15	9	6	65	21	7	33
498	GalNAcb1-4(Fuca1-3)(6S)GlcNAcb-Sp8	14	2	15	27	6	23	35	6	18	12	5	41	28	8	28	17	3	20	32	5	15	17	1	6	26	7	26
499	(3S)Galb1-4(Fuca1-3)GlcNAcb-Sp8	23	4	15	34	7	21	26	4	16	21	1	6	39	4	10	22	9	40	40	8	21	28	3	10	26	2	7
500	Fuca1-2Galb1-3GlcNAcb1-6(Fuca1-2Galb1-3GlcNAcb1-3)GalNAcb-Sp14	21	4	21	47	11	24	65	23	35	24	3	11	55	4	8	15	10	72	30	6	21	27	5	17	40	5	12
501	GalNAcb1-3(Fuca1-2)Galb1-3GlcNAcb1-6GalNAcb-Sp14	6	4	71	12	6	48	13	1	9	5	2	43	12	5	44	4	1	13	25	8	34	10	2	20	25	11	43
502	GlcNAcb1-6(GlcNAcb1-2)Mana1-6(GlcNAcb1-4)(GlcNAcb1-4)(GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp21	11	1	11	16	4	23	17	1	3	11	2	17	11	3	31	8	2	31	19	9	49	14	1	4	13	2	15
503	Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-4)Galb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp21	7	3	38	30	9	31	90	4	4	136	9	6	711	67	9	140	17	12	5377	157	3	23	9	38	32	8	24
504	Galb1-3GlcNAcb1-3Galb1-4GlcNAcb-Sp8	8	6	69	8	7	81	11	6	54	10	4	40	8	4	51	7	6	92	9	3	37	7	5	80	7	5	77
505	Galb1-3(6S)GlcNAcb-Sp8	6	4	73	8	3	44	7	6	85	14	3	19	48	8	16	4	1	16	14	7	52	13	2	14	13	3	20
506	(6S)(4S)GalNAcb1-4GlcNAcb-Sp8	15	1	6	8	5	65	12	1	11	14	2	15	10	5	52	20	4	22	21	4	17	16	2	15	17	3	20
507	(6S)GalNAcb1-4GlcNAcb-Sp8	12	2	14	6	4	67	8	4	49	11	3	30	7	3	50	2	1	22	6	4	70	14	2	14	5	3	61
508	(3S)GalNAcb1-4(3S)GlcNAcb-Sp8	9	5	53	10	3	26	9	4	47	15	1	9	16	2	9	24	1	5	22	2	9	13	6	42	15	4	24
509	GalNAcb1-4(6S)GlcNAcb-Sp8	9	4	45	7	6	87	23	5	22	3	1	27	6	4	79	10	6	62	13	9	67	13	2	17	16	3	16
510	(3S)GalNAcb1-4GlcNAcb-Sp8	10	2	22	13	2	16	9	2	24	9	4	45	19	7	36	9	6	62	18	2	9	13	3	22	13	5	40
511	(4S)GalNAcb-Sp10	13																										

515	Neu5Aca2-6Galb1-4GlcNAcb1-2Man-Sp0	2	1	22	4	1	34	4	3	77	6	4	71	11	5	49	3	1	15	19	5	25	6	5	89	10	6	57
516	Gala1-3Galb1-4GlcNAcb1-2Mana-Sp0	4	3	62	9	4	48	6	3	42	11	2	13	9	5	49	3	1	35	11	5	51	14	2	15	11	5	43
517	Gala1-3Fuca1-2Galb1-4GlcNAcb1-2Mana-Sp0	11	4	35	14	3	20	14	1	4	15	6	38	116	27	24	143	31	22	2476	259	10	21	2	9	25	2	9
518	GalNAca1-3Fuca1-2Galb1-4GlcNAcb1-2Mana-Sp0	9	5	55	13	6	45	5	1	11	13	1	4	9	6	60	4	3	75	8	7	87	15	0	0	7	5	72
519	Galb1-3GlcNAcb1-2Mana-Sp0	27	3	10	53	13	25	48	20	41	25	5	19	50	16	33	32	5	15	50	20	40	27	2	9	59	13	22
520	Gala1-3Fuca1-2Galb1-3GlcNAcb1-6GalNAc-Sp14	15	1	5	9	4	22	14	5	40	4	2	59	18	2	12	4	1	16	14	6	44	7	5	74	20	13	67
521	Neu5Aca2-3Galb1-3GlcNAcb1-2Mana-Sp0	19	4	18	18	3	14	4	4	77	10	2	17	5	2	43	3	1	5	5	1	11	18	4	24	18	3	18
522	Gala1-3Galb1-3GlcNAcb1-2Mana-Sp0	9	4	18	18	3	14	4	4	31	20	2	8	37	7	19	26	1	5	2194	52	2	26	5	18	23	2	8
523	GalNAca1-4GlcNAcb1-2Mana-Sp0	19	2	10	15	3	18	9	5	55	21	2	9	56	17	31	40	3	7	2561	116	5	25	3	12	21	1	2
524	Neu5Aca2-3Galb1-3GalNAcb1-4Galb1-4Glc-Sp0	11	5	48	11	4	37	9	8	85	10	5	47	12	9	80	5	3	67	18	15	84	9	5	57	16	3	20
525	GlcNAcb1-2 Mana1-6(GlcNAcb1-4)GlcNAcb1-2Mana1-3Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAc-Sp21	10	2	15	18	4	21	9	4	42	6	4	71	14	8	62	7	7	98	15	7	45	9	3	32	13	2	12
526	Galb1-4GlcNAcb1-2 Mana1-6(GlcNAcb1-4)GlcNAcb1-4GlcNAcb1-2Mana1-3Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAc-Sp21	8	4	53	12	3	21	44	2	4	42	4	10	777	100	13	71	10	15	5082	410	8	20	3	14	21	4	17
527	Galb1-4GlcNAcb1-2 Mana1-6(GlcNAcb1-4)GlcNAcb1-4GlcNAcb1-2Mana1-3Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAc-Sp21	11	1	12	18	4	21	88	6	7	35	24	68	869	22	2	98	9	9	8208	1170	14	12	2	18	18	5	29
528	Fuca1-4(Galb1-3)GlcNAcb1-2 Mana-Sp0	87	36	41	76	19	25	65	12	19	71	13	18	87	15	17	46	8	17	70	16	24	71	14	21	86	26	30
529	Neu5Aca2-3Galb1-4(Fuca1-3)GlcNAcb1-2Mana-Sp0	9	6	63	19	7	38	7	3	48	8	2	32	18	3	19	3	1	18	16	8	51	14	1	10	16	5	29
530	GlcNAcb1-3Galb1-4GlcNAcb1-6(GlcNAcb1-3)Galb1-4GlcNAc-Sp0	6	5	84	11	5	47	12	3	22	7	4	58	10	4	40	7	6	81	15	2	10	12	3	28	9	4	39
531	GalNAca1-3(Fuca1-2)Galb1-3GalNAcb1-3Gala1-4Galb1-4Glc-Sp21	4	3	84	9	6	63	5	1	20	3	2	46	12	2	20	4	2	46	5	1	22	13	3	23	15	3	18
532	Gala1-3(Fuca1-2)Galb1-3GalNAcb1-3Gala1-4Galb1-4Glc-Sp21	7	5	73	12	7	57	5	2	33	7	3	41	9	3	31	3	1	15	8	3	39	15	2	10	10	6	63
533	Galb1-3GalNAcb1-3Gal-Sp21	11	1	5	6	4	79	2	1	55	10	3	31	15	5	30	11	9	80	13	7	51	17	3	17	11	9	81
534	GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	10	3	33	8	4	52	10	2	22	7	5	67	7	4	63	16	9	56	39	3	7	13	2	16	15	1	8
535	GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp25	26	4	14	29	7	25	32	4	13	25	3	13	31	6	20	49	8	17	254	20	8	38	9	23	29	6	22
536	Fuca1-2Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Fuca1-2Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp24	38	8	22	122	60	49	356	56	16	39	2	4	995	26	3	129	13	10	7556	154	2	37	2	5	42	6	15
537	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	27	3	11	48	7	14	80	17	22	24	2	7	48	2	5	35	3	8	114	10	9	32	3	8	66	22	33
538	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp25	28	2	8	40	2	4	206	16	8	27	2	8	40	8	20	33	4	13	44	2	5	34	4	12	40	6	15
539	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	32	5	14	44	5	11	126	11	9	33	4	13	119	7	6	131	12	9	7740	768	10	36	4	10	44	3	7
540	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp24	29	5	16	64	5	8	309	19	6	24	3	12	427	46	11	188	13	7	9927	545	5	31	3	10	33	4	11
541	Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp25	21	4	20	39	8	20	119	11	9	18	4	24	38	2	5	22	7	30	56	6	10	21	4	21	26	6	21
542	Neu5Gca2-8Neu5Gca2-3Galb1-4GlcNAc-Sp0	15	1	9	13	2	13	12	2	19	10	3	32	12	2	18	13	3	22	13	2	17	16	2	14	14	3	24
543	Neu5Aca2-8Neu5Gca2-3Galb1-4GlcNAc-Sp0	5	3	72	4	3	59	7	4	56	3	1	38	7	2	32	2	1	22	9	5	56	12	3	29	3	1	35
544	Neu5Gca2-8Neu5Gca2-3Galb1-4GlcNAc-Sp0	8	6	77	9	3	30	4	1	29	5	5	87	5	4	82	5	1	22	4	1	23	11	6	55	7	3	49
545	Neu5Gca2-8Neu5Gca2-3Galb1-4GlcNAc-Sp0	7	2	29	8	3	37	5	1	16	5	3	61	8	5	60	7	5	72	8	2	27	9	3	39	4	2	35
546	Neu5Gca2-8Neu5Gca2-6Galb1-4GlcNAc-Sp0	16	2	13	13	2	14	13	2	14	13	2	14	12	3	24	15	3	22	17	3	15	20	2	11	15	3	20
547	Neu5Aca2-8Neu5Aca2-3Galb1-4GlcNAc-Sp0	2	1	43	4	2	49	6	6	97	4	3	89	3	1	15	2	1	29	3	1	29	7	2	25	3	1	29
548	GlcNAcb1-3Galb1-4GlcNAcb1-6(GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-2Man a1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp24	29	4	13	39	5	13	64	6	9	30	3	9	46	4	9	56	3	6	305	22	7	28	2	6	38	3	7
549	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp24	21	4	20	44	5	10	99	17	17	20	1	6	94	8	8	118	18	16	4325	529	12	20	3	12	37	4	11
550	Gala1-3Galb1-4GlcNAcb1-2Mana1-6(Gala1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAc-Sp24	33	1	4	32	8	26	50	4	9	25	2	8	33	2	6	27	5	17	45	4	9	35	1	4	39	8	20
551	GlcNAcb1-3Galb1-4GlcNAcb1-6(GlcNAcb1-3Galb1-3)GalNAca-Sp14	9	1	7	6	3	45	4	1	26	7	5	68	14	4	30	13	5	42	17	7	42	12	6	53	13	2	17
552	GalNAcb1-3GlcNAcb-Sp0	10	5	48	7	4	57	4	3	68	10	5	52	18	16	90	2	1	38	4	1	20	13	3	27	12	5	44
553	GalNAcb1-4GlcNAcb1-3GalNAcb1-4GlcNAcb-Sp0	7	4	63	18	2	12	102	6	6	12	2	17	12	1	7	67	12	17	4173	145	3	15	3	17	15	3	17
554	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp25	17	1	7	27	1	5	405	42	10	17	2	12	25	3	14	19	5	28	24	4	15	14	2	13	19	1	5
555	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp25	19	2	11	109	11	10	482	68	14	20	1	4	246	13	5	61	4	6	8848	426	5	27	2	7	34	5	15
556	GlcNAcb1-3Galb1-3GalNAc-Sp14	11	5	43	5	2	32	4	1	16	8	5	62	18	10	59	8	7	94	9	4	45	9	6	67	12	3	21
557	Galb1-3GlcNAcb1-6(Galb1-3)GalNAc-Sp14	13	2	15	23	5	20	18	3	17	16	1	6	45	11	25	6	1	9	22	6	26	13	3	25	22	8	34
558	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp25	22	2	8	41	3	7	241	45	19	21	3	15	173	25	14	103	6	5	7876	1097	14	20	1	4	29	6	22
559	(3S)GlcAb1-3Galb1-4GlcNAcb1-3Galb1-4Glc-Sp0	5	3	55	14	4	31	5	3	57	8	6	71	4	3	68	5	4	80	5	1	13	12	3	22	14	2	15
560	(3S)GlcAb1-3Galb1-4GlcNAcb1-2Mana-Sp0	16	3	16	17	3	19	14	2	13	16	2	14	14	2	13	22	2	10	17	7	44	22	3	14	15	6	42

561	Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	22	2	9	40	6	15	107	19	18	25	4	14	73	9	12	25	5	18	49	2	4	31	4	12	32	2	6
562	Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(Galb1-3GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	32	3	8	34	2	7	73	4	6	29	3	10	63	11	18	40	3	8	129	22	17	43	7	16	44	4	9
563	Neu5Aca2-8Neu5Aca2-3Galb1-3GalNAcb1-4(Neu5Aca2-3)Galb1-4GlcNAcb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	9	4	45	14	2	12	10	5	49	7	4	56	12	5	41	21	2	11	25	5	21	14	4	25	15	3	20
564	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	27	2	7	27	3	13	25	1	4	24	4	15	37	3	7	56	7	12	227	13	6	29	1	3	32	6	19
565	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	22	2	10	41	4	10	242	15	6	24	2	10	184	16	9	158	2	1	7905	599	8	26	1	2	34	5	14
566	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	7	6	95	40	29	72	279	19	7	7	6	84	35	19	54	11	9	88	32	19	60	4	1	23	51	20	40
567	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	18	3	16	76	16	21	379	64	17	20	4	20	324	31	10	168	8	5	8031	443	6	19	4	21	54	7	13
568	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	19	2	12	50	7	13	384	14	4	18	2	9	61	9	14	26	2	7	54	3	6	20	3	14	75	4	6
569	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	24	3	12	69	4	6	441	48	11	25	5	20	245	22	9	157	5	3	8039	542	7	23	3	11	38	5	14
570	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp19	14	8	54	52	24	47	316	88	28	17	6	35	42	8	18	22	13	61	64	24	38	18	8	43	36	11	31
571	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp19	27	1	4	70	3	4	471	25	5	26	1	4	354	43	12	138	9	6	10843	933	9	26	1	5	42	7	17
572	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	24	3	12	51	7	14	280	31	11	29	2	7	309	35	11	178	15	8	8010	341	4	24	4	16	43	3	8
573	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	34	2	6	50	8	16	117	14	12	29	2	8	41	3	7	37	1	3	51	6	11	35	3	8	40	2	4
574	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	24	5	23	58	5	8	294	17	6	23	2	9	298	34	11	114	12	11	8051	247	3	23	1	5	41	6	15
575	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	32	1	2	42	5	12	134	19	14	29	1	3	54	1	3	38	1	3	51	5	9	33	2	7	50	5	9
576	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	25	1	2	75	4	5	358	33	9	35	16	45	344	27	8	87	2	3	10512	96	1	27	2	6	40	2	6
577	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	38	0	0	47	7	14	201	15	7	37	2	5	76	5	7	65	4	7	1203	143	12	38	1	3	45	6	13
578	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp24	34	3	9	110	25	23	406	12	3	32	1	4	356	27	8	101	2	2	11904	1243	10	31	4	13	46	7	16
579	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3GalNAcA-Sp14	18	1	5	37	3	8	70	6	9	17	6	33	67	13	20	107	11	10	3601	349	10	20	3	12	37	6	17
580	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-3)GalNAcA-Sp14	19	1	3	61	37	60	142	30	21	22	4	19	84	16	19	212	13	6	4283	465	11	20	1	7	38	6	16
581	Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-6(Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2)Mana1-3)Manb1-4GlcNAcb1-4(Fuca1-6)GlcNAcb-Sp14	18	1	5	43	2	5	104	5	5	17	2	11	103	9	9	113	7	6	5326	681	13	19	2	9	43	3	6
582	Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3GalNAcA-Sp14	6	5	76	4	3	75	6	4	63	2	1	22	9	5	56	2	0	0	9	4	44	10	5	47	9	5	58
583	GlcNAcb1-3Galb1-4GlcNAcb1-3GalNAcA-Sp14	5	1	28	16	3	17	5	2	43	7	4	57	10	6	60	4	2	55	23	4	15	14	3	19	11	5	50
584	GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-3)GalNAcA-Sp14	5	4	82	7	4	58	7	3	37	10	1	6	13	6	49	9	5	62	10	5	49	13	2	19	11	8	75
585	GlcNAcb1-3Galb1-4GlcNAcb1-6(GlcNAcb1-3Galb1-4GlcNAcb1-3)GalNAcA-Sp14	13	1	11	27	11	39	22	1	6	13	2	13	31	3	9	11	9	81	34	5	16	20	2	11	41	7	17

586	Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3)GalNAca-Sp14	14	3	19	35	4	11	89	15	17	11	5	43	124	31	25	51	6	11	1797	92	5	15	4	24	43	2	6
587	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3GalNAca-Sp14	3	1	23	6	3	57	9	4	46	9	5	51	7	5	72	5	5	102	10	6	60	6	5	92	5	1	16
588	GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3GalNAca-Sp14	7	4	61	23	2	10	22	2	10	9	5	53	20	3	15	8	4	50	25	3	11	10	4	45	17	3	15
589	Galb1-4GlcNAcb1-3Galb1-3GalNAca-Sp14	7	5	67	8	7	84	7	7	99	9	4	47	81	26	32	140	18	13	3397	255	8	9	5	56	13	5	39
590	Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-3)GalNAca-Sp14	4	3	68	13	5	36	54	15	27	5	4	99	26	10	37	3	1	23	24	16	67	11	6	56	23	4	19
591	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Galb1-3)GalNAca-Sp14	24	4	15	38	5	13	46	9	19	27	6	22	43	12	28	11	12	109	27	4	13	19	7	39	45	13	28
592	Neu5Aca2-6Galb1-4GlcNAcb1-6(Galb1-3)GalNAca-Sp14	12	5	47	19	2	11	23	2	10	11	6	53	39	15	38	5	1	16	25	1	4	20	1	6	30	7	23
593	Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	10	6	61	39	11	27	80	22	28	12	2	15	64	47	74	90	41	45	1579	454	29	17	2	12	38	7	19
594	GlcNAcb1-6(Neu5Aca2-3Galb1-3)GalNAca-Sp14	6	4	70	5	6	114	4	1	29	3	1	35	8	3	34	4	1	16	5	1	29	9	5	56	9	4	46
595	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-6(Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3)GalNAca-Sp14	14	2	11	42	21	49	36	12	34	17	3	15	30	8	27	21	3	15	45	4	8	27	11	40	53	6	12
596	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	7	4	54	29	5	19	68	24	36	10	3	34	38	12	31	9	8	84	67	3	4	50	17	35	68	30	44
597	Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	38	10	28	49	5	11	66	12	19	30	3	10	64	19	30	52	8	15	327	30	9	32	4	12	61	7	12
598	Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-6(Neu5Aca2-6Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-3Galb1-4GlcNAcb1-2Mana1-3)Manb1-4GlcNAcb1-4GlcNAcb-Sp12	16	4	25	26	5	18	66	11	16	11	7	59	83	18	22	144	17	12	3224	1107	34	20	4	17	19	8	44
599	GlcNAcb1-3Fuca-Sp21	2	1	22	27	7	27	18	3	20	5	5	91	29	11	37	7	6	82	36	6	16	16	1	8	48	10	20
600	Galb1-3GalNAcb1-4(Neu5Aca2-8Neu5Aca2-8Neu5Aca2-3)Galb1-4Glc-Sp21	11	1	7	11	5	46	6	2	30	8	5	60	15	2	10	20	9	48	27	1	5	11	5	45	12	3	26