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Supplementary Materials for

The *Campylobacter jejuni* chemoreceptor Tlp10 has a bimodal ligand-binding domain and specificity for multiple classes of chemoeffectors

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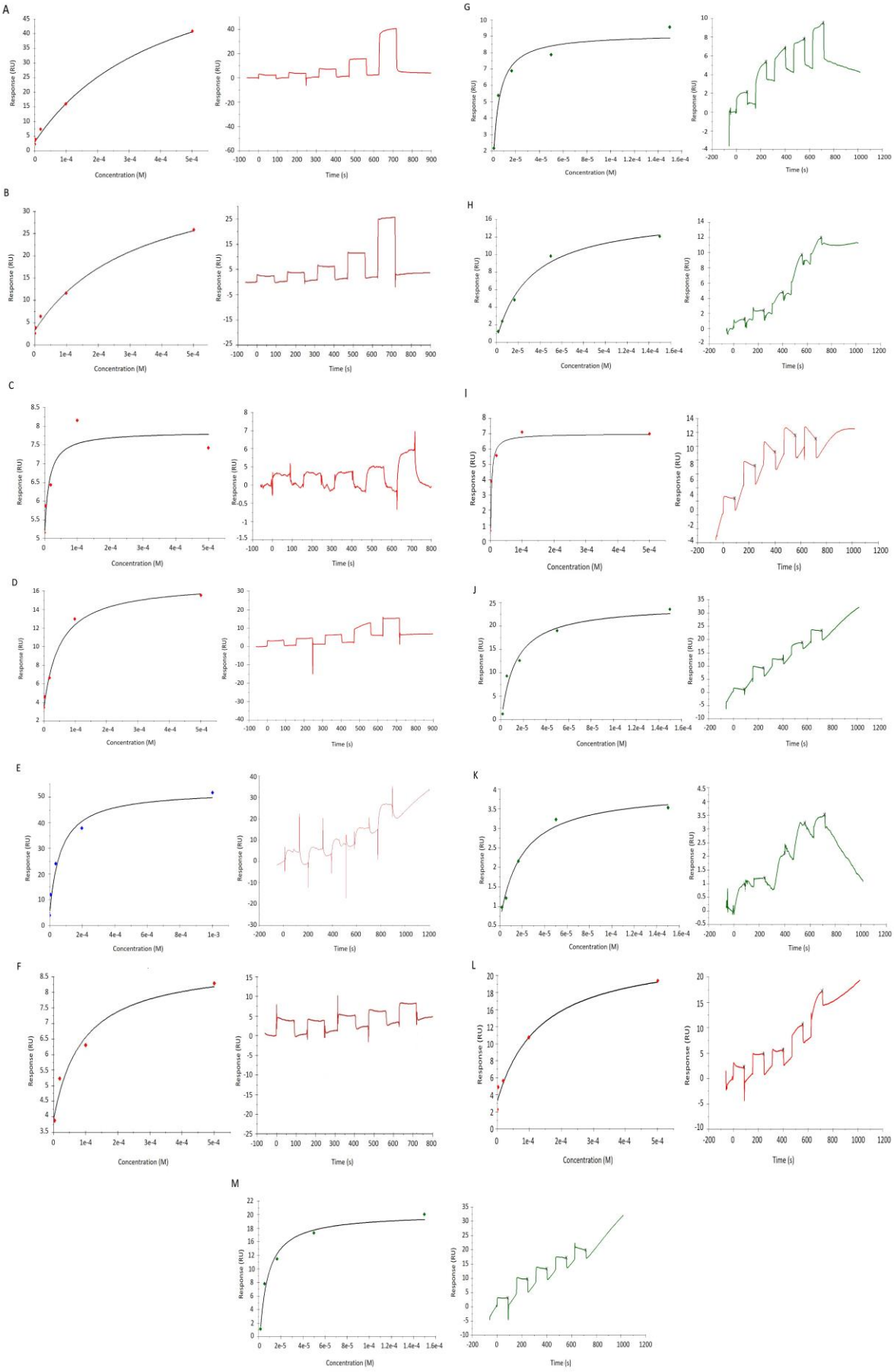
The PDF file includes:

Other Supplementary Material for this manuscript includes the following:

(available at stke.sciencemag.org/cgi/content/full/14/664/eabc8521/DC1)

Movie S1 (.avi format). *C. jejuni* migrate toward the attractant isoleucine.
Movie S2 (.avi format). Migration of *C. jejuni* cells toward the attractant isoleucine is reduced by addition of the repellent arginine.
Movie S3 (.avi format). PBS control for the effect of arginine on the migration of WT *C. jejuni* toward isoleucine.
Data file S1 (Microsoft Excel format). Proteins included in DAHL domain MSA.


A
Response (RU)
Concentration (M)
Response (RU)
Time (s)
B
Response (RU)
Concentration (M)
Response (RU)
Time (s)
C
Response (RU)
Concentration (M)
Response (RU)
Time (s)
D
Response (RU)
Concentration (M)
Response (RU)
Time (s)
E
Response (RU)
Concentration (M)
Response (RU)
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F
Response (RU)
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G
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H
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K
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Time (s)

Fig. S1. Representative sensorgrams from SPR analysis of the interaction of Tlp10^{LBD} with various ligands. Single-cycle SPR curves showing concentration-dependent interactions between Tlp10^{LBD} and **(A)** α-ketoglutarate; **(B)** malate; **(C)** aspartate; **(D)** thiamine; **(E)** fucose; **(F)** mannose; **(G)** sialic acid; **(H)** isoleucine; **(I)** galactose; **(J)** rhamnose; **(K)** purine; **(L)** fumarate; and **(M)** arginine. Data are representative of three independent experiments (n = 3).

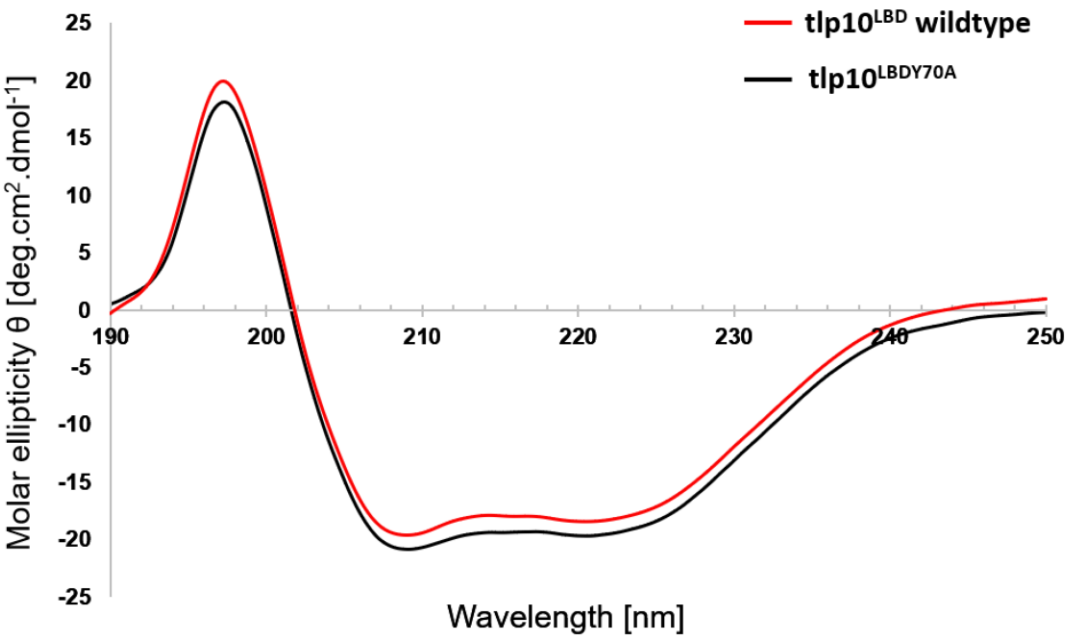

Fig. S2. Mutant Tlp10^{LBD} proteins are correctly folded. Far-UV CD (circular dichroism) spectrum for WT and Y70A Tlp10^{LBD}. This spectrum is representative of the similarity of all the mutant variants to that of the WT protein. Data are representative of three independent replicates (n = 3).

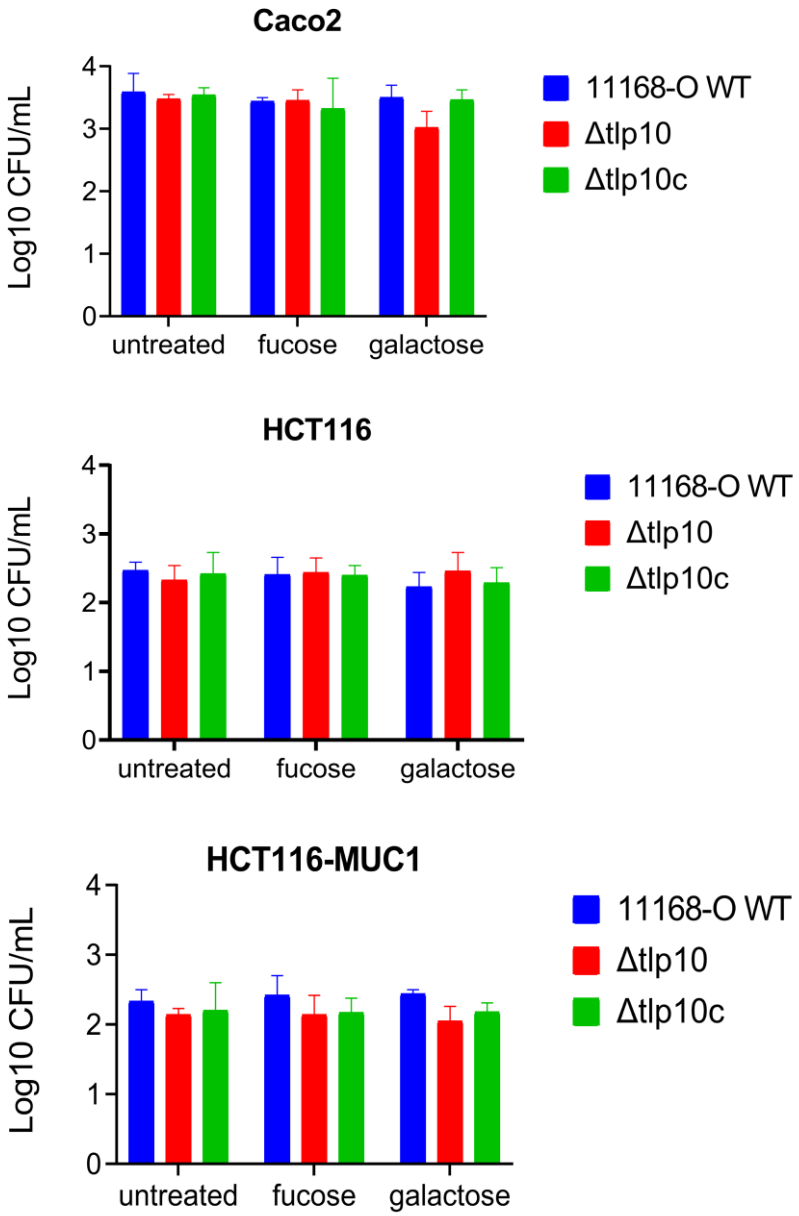

Fig. S3. Invasion of mammalian cells by WT and mutant *C. jejuni* in the presence and absence of fucose and galactose. Invasion analyses of Caco2, HCT166, and HCT166 overexpressing MUC1 (HCT116-MUC1) are presented as the mean of invasion from three technical replicates and are representative of three independent experiments (n = 3).

Table S1. HHpred search results for small subset of DAHL domains from various species. No known domain was detected in the periplasmic region of Tlp10 and homologous sequences. Low-confidence hits to partial human Nucleoporin_FG2 (Pfam accession number PF15967.5) domain and nuclear pore complex protein Nup155 are likely the result of α-helical nature of these proteins.

with TM regions excluded						
NCBI ID	Organism	Number of hits	Best hit	Probability	E-value	Score
WP_002865311.1	*C. jejuni subsp. jejuni NCTC 11168*	4	5IJO_T Nuclear pore complex Nup155	61	3.00E+02	28
WP_012478065.1	*Agrobacterium tumefaciens*	16	PF15967.5 ; Nucleoporin_FG2	83.4	54	29.7
WP_014473835.1	*Arcobacter sp. L*	9	5IJO_T Nuclear pore complex Nup155	85.6	43	30.3
WP_067981710.1	*Neptuniibacter pectenicola*	11	5IJO_T Nuclear pore complex Nup155	69.7	1.30E+02	27
WP_084274768.1	*Nitratiruptor tergarcus*	17	5IJO_T Nuclear pore complex Nup155	82.6	54	29.2
WP_069956973.1	*Magnetovibrio blakemorei*	10	PF15967.5 ; Nucleoporin_FG2	79.1	80	28.9
WP_010953844.1	*Pseudomonas putida KT2440*	19	5IJO_T Nuclear pore complex Nup155	88.4	31	31.6
WP_015153106.1	*Chroococcidiopsis thermalis*	16	PF15967.5 ; Nucleoporin_FG2	78.7	81	28.7

with TMs regions included						
NCBI ID	Organism	Number of hits	Best hit	Probability	E-value	Score
WP_002865311.1	*C. jejuni subsp. jejuni NCTC 11168*	73	PF15967.5 ; Nucleoporin_FG2	95.6	3.1	38.7
WP_012478065.1	*Agrobacterium tumefaciens*	44	5IJO_T Nuclear pore complex Nup155	92.8	11	34.2
WP_014473835.1	*Arcobacter sp. L*	84	5IJO_T Nuclear pore complex Nup155	94.9	4.8	37
WP_067981710.1	*Neptuniibacter pectenicola*	50	5IJO_T Nuclear pore complex Nup155	89	28	32
WP_084274768.1	*Nitratiruptor tergarcus*	41	5IJO_T Nuclear pore complex Nup155	89.5	27	32.2
WP_069956973.1	*Magnetovibrio blakemorei*	54	5IJO_T Nuclear pore complex Nup155	91.5	17	33.4
WP_010953844.1	*Pseudomonas putida KT2440*	78	5IJO_T Nuclear pore complex Nup155	91.4	19	33.7
WP_015153106.1	*Chroococcidiopsis thermalis*	29	5IJO_T Nuclear pore complex Nup155	89.8	25	32.3

Table S2. Molecules included in the glycan microarray.

Number	Spacer form of saccharide	Common name	Short name	Molecular weight
	MONOSACCHARIDES			
1	Fucα-sp3	L-α-Fuc	aF	221.3
2	Galα-sp3	α-Gal	aA	237.3
3	Galβ-sp3	β-Gal	bA	237.3
4	GalNAcα-sp0	TnSer	TnSer	308.3
5	GalNAcα-sp3	T_n	Tn	278.3
6	GalNAcβ-sp3	β-GalNAc	bAN	278.3
7	Glcα-sp3	α-Glc	aG	237.3
9	Glcβ-sp3	β-Glc	bG	237.3
10	GlcNAcβ-sp3	β-GlcNAc	GN	278.3
14	GlcN(Gc)β-sp4	β-GlcN(Gc)	bGN(Gc)	293.3
15	$HOCH_2(HOCH)_4CH_2NH_2$	aminoglucitol	glucitol	181.2
16	Manα-sp3	α-Man	aM	273.3
18	Manβ-sp4	β-Man	bM	236.2
19	ManNAcβ-sp4	β-ManAc	bMN	277.3
20	Rhaα-sp3	L-α-Rha	aR	221.3
22	GlcNAcβ-sp4	β-GlcNAc	GN-Gly	277.3
37	3-O-Su-Galβ-sp3	3-O-Su-β-Gal	bA3Su	317.3
38	3-O-Su-GalNAcα-sp3	3-O-Su-β-GalNac	bAN3Su	358.4
43	6-O-Su-GlcNAcβ-sp3	6-O-Su-β-GlcNAc	GN6su	358.4
44	GlcAα-sp3	α-glucoronic acid	aGU	251.2
45	GlcAβ-sp3	β-glucoronic acid	bGU	251.2
46	$6\text{-}H_2PO_3$Glcβ-sp4	β-Glc6P	G6P	316.2
47	$6\text{-}H_2PO_3$Manα-sp3	α-Man6P	M6P	339.2
48	Neu5Acα-sp3	α-Neu5Ac	Sia	366.4
49	Neu5Acα-sp9	α-Neu5AcBn	Sia-Bn	471.5
52	Neu5Gcα-sp3	α-Neu5Gc	aNeuGc	382.4
54	9-NAc-Neu5Acα-sp3	9-Nac-α-Neu5Ac	9NAcSia	407.4
55	3-O-Su-GlcNAcβ-sp3	3-O-Su-β-GlcNAc	GN3Su	358.4
	DISACCHARIDES			
71	Fucα1-2Galβ-sp3	H_{di}	Hdi	383.4
72	Fucα1-3GlcNAcβ-sp3		Fa3GN	424.5

73	Fucα1-4GlcNAcβ-sp3	Le	LeC	424.5
75	Galα1-2Galβ-sp3		Aa2A	399.4
76	Galα1-3Galβ-sp3	B_{di}	Bdi	399.4
77	Galα1-3GalNAcβ-sp3	$T_{\alpha\beta}$	Tab	440.5
78	Galα1-3GalNAcα-sp3	$T_{\alpha\alpha}$	Taa	440.5
80	Galα1-3GlcNAcβ-sp3		Aa3GN	440.5
81	Galα1-4GlcNAcβ-sp3	α-LacNAc	aLN	440.5
83	Galα1-6Glcβ-sp4	Melibiose	Aa3G	398.4
84	Galβ1-2Galβ-sp3		Ab2A	399.4
85	Galβ1-3GlcNaAcβ-sp3	Le^c	LeC	440.5
87	Galβ1-3Galβ-sp3		Ab3A	399.4
88	Galβ1-3GalNAcβ-sp3	$T_{\beta\beta}$	Tbb	440.5
89	Galβ1-3GalNAcα-sp3	TF	TF	440.5
93	Galβ1-4Glcβ-sp4	Lac	Lac-Gly	398.4
94	Galβ1-4Galβ-sp4		Ab4A	398.4
97	Galβ1-4GlcNAcβ-sp3	LacNAc	LN	440.5
100	Galβ1-6Galβ-sp4		Ab6A	398.4
101	GalNAcα1-3GalNAcβ-sp3	Fs-2	Fs-2	481.5
102	GalNAcα1-3Galβ-sp3	A_{di}	Adi	440.5
103	GalNAcα1-3GalNAcα-sp3	core 5	core 5	481.5
104	GalNAcβ1-3Galβ-sp3		ANb3A	440.5
106	GalNAcβ1-4GlcNAcβ-sp3	LacdiNAc	LacdiNAc	481.5
110	Glcα1-4Glcβ-sp3	maltose	Malt2	399.4
111	Glcβ1-4Glcβ-sp4	cellobiose	cello	398.4
112	Glcβ1-6Glcβ-sp4	gentiobiose	gent	398.4
113	GlcNAcβ1-3GalNAcα-sp3	core 3	core 3	481.5
114	GlcNAcβ1-3Manβ-sp4		GN3M	439.4
115	GlcNAcβ1-4GlcNAcβ-Asn	chitobiose-Asn	Ch2-Asn	538.5
117	GlcNAcβ1-4GlcNAcβ-sp4	chitobiose	Ch2-Gly	480.5
118	GlcNAcβ1-6GalNAcα-sp3	core 6	core 6	481.5
119	Manα1-2Manβ-sp4		Ma2Mb	398.4
120	Manα1-3Manβ-sp4		Ma3M	398.4
121	Manα1-4Manβ-sp4		Ma4M	398.4
122	Manα1-6Manβ-sp4		Ma6M	398.4
123	Manβ1-4GlcNAcβ-sp4		Mb4GN	439.4

124	Manα1-2Manα-sp4		Ma2Ma	398.4
145	Galβ1-3(6-O-Su)GlcNAcβ-sp3	6-O-Su-Le^c	LeC6Su	520.5
146	Galβ1-4(6-O-Su)Glcβ-sp2	6-O-Su-Lac	Lac6Su	465.5
147	Galβ1-4(6-O-Su)GlcNAcβ-sp3	6-O-Su-LacNAc	LN6Su	520.5
149	GlcNAcβ1-4(6-O-Su)GlcNAcβ-sp2	6-O-Su-chitobiose	Ch2-6Su	547.5
150	3-O-Su-Galβ1-3GalNAcα-sp3	3`-O-Su-TF	TF3`Su	520.5
151	6-O-Su-Galβ1-3GalNAcα-sp3	6`-O-Su-TF	TF6`Su	520.5
152	3-O-Su-Galβ1-4Glcβ-sp2	SM3	Lac3`Su	465.3
153	6-O-Su-Galβ1-4Glcβ-sp2	6`-O-Su-Lac	Lac6`Su	465.3
155	3-O-Su-Galβ1-3GlcNAcβ-sp3	3`-O-Su-Le^c	LeC3`Su	520.5
157	3-O-Su-Galβ1-4GlcNAcβ-sp3	3`-O-Su-LacNAc	LN3`Su	520.5
159	4-O-Su-Galβ1-4GlcNAcβ-sp3	4`-O-Su-LacNAc	LN4`Su	520.5
161	6-O-Su-Galβ1-3GlcNAcβ-sp3	6`-O-Su-Le^c	LeC6`Su	520.5
163	6-O-Su-Galβ1-4GlcNAcβ-sp3	6`-O-Su-LacNAc	LN6`Su	520.5
164	GlcAβ1-3GlcNAcβ-sp3		GUb3GN	454.4
165	GlcAβ1-3Galβ-sp3		GUb3A	413.4
166	GlcAβ1-6Galβ-sp3		GUb6A	413.4
167	GlcNAcβ1-4-[HOOC(CH_3)CH]-3-O-GlcNAcβ-sp4	GlcNAc-Mur	GN-Mur	522.5
168	GlcNAcβ1--[HOOC(CH_3)CH]-3-O-GlcNAcβ-L-alanyl-D-i-glutaminyl-L-lysine	GMDP-Lys	GMDPLys	823.9
169	Neu5Acα2-3Galβ-sp3	GM4	GM4	528.5
170	Neu5Acα2-6Galβ-sp3		Sia6A	528.5
171	Neu5Acα2-3GalNAcα-sp3	3-SiaT_n	3-SiaTn	569.6
172	Neu5Acα2-6GalNAcα-sp3	SiaT_n	SiaTn	569.6
174	Neu5Gcα2-6GalNAcα-sp3	NeuGc-T_n	Neu5GCTn	585.6
176	3-O-Su-Galβ1-4(6-O-Su)Glcβ-sp2	3`,6-di-O-Su-Lac	Lac3`,6Su2	567.5 (Na+)
177	3-O-Su-Galβ1-4(6-O-Su)GlcNAcβ-sp2	3`,6-di-O-Su-LacNAc	LN3`6Su2	622.6 (Na+)
178	6-O-Su-Galβ1-4(6-O-Su)Glcβ-sp2	6,6`-di-O-Su-Lac	Lac6,6`Su2	567.5 (Na+)
179	6-O-Su-Galβ1-3(6-O-Su)GlcNAcβ-sp2	6,6`-di-O-Su-Le^c	LeC6,6`Su2	608.5 (Na+)
180	6-O-Su-Galβ1-4(6-O-Su)GlcNAcβ-sp2	6,6`-di-O-Su-LacNAc	LN66`Su2	608.5 (Na+)
181	3,4-O-Su_2-Galβ1-4GlcNAcβ-sp3	3`,4`-di-O-Su-LacNAc	LN3`4`Su2	622.6 (Na+)

182	3,6-O-Su_2-Galβ1-4GlcNAcβ-sp2	3`,6`-di-O-Su-LacNAc	LN3`6`Su2	608.5 (Na+)
183	4,6-O-Su_2-Galβ1-4GlcNAcβ-sp2	4`,6`-di-O-Su-LacNAc	LN4`6`Su2	608.5 (Na+)
184	4,6-O-Su_2-Galβ1-4GlcNAcβ-sp3	4`,6`-di-O-Su-LacNAc	LN4`6`Su2-C3	622.6 (Na+)
186	Neu5Acα2-8Neu5Acα2-sp3	$(Sia)_2$	(Sia)2	679.6 (Na+)
189	3,6-O-Su_2-Galβ1-4(6-O-Su)GlcNAcβ-sp2	3`,6,6`-tri-O-Su-LacNAc	LN3`66`Su3	710.6 (Na+)
192	GalNAcβ1-4(6-O-Su)GlcNAcβ-sp3	6-O-Su-LacdiNAc	LacdiNAc6Su	561.5
193	3-O-Su-GalNAcβ1-4GlcNAcβ-sp3	3`-O-Su-LacdiNAc	LacdiNAc3`Su	561.5
194	6-O-Su-GalNAcβ1-4GlcNAcβ-sp3	6`-O-Su-LacdiNAc	LacdiNAc6`Su	561.5
195	6-O-Su-GalNAcβ1-4-(3-O-Su)GlcNAcβ-sp3	6`-Su-3-O-Ac-LacdiNAc	3Ac-LacdiNAc6`Su	603.5
196	3-O-Su-GalNAcβ1-4(3-O-Su)-GlcNAcβ-sp3	3,3`-O-Su_2-LacdiNAc	LacdiNAc3,3`Su2	663.5(Na+)
197	3,6-O-Su_2-GalNAcβ1-4GlcNAcβ-sp3	3`,6`-Su_2-LacdiNAc	LacdiNAc3`,6`Su2	663.5(Na+)
198	4,6-O-Su_2-GalNAcβ1-4GlcNAcβ-sp3	4`,6`-Su_2-LacdiNAc	LacdiNAc4`,6`Su2	663.5(Na+)
199	4,6-O-Su_2-GalNAcβ1-4-(3-O-Ac)GlcNAcβ-sp3	4`,6`-Su_2-3-O-Ac-LacdiNAc	3Ac-LacdiNAc4`,6`Su2	705.5(Na+)
200	4-O-Su-GalNAcβ1-4GlcNAcβ-sp3	4`-O-Su-LacdiNAc	LacdiNAc4`Su	561.5
201	3,4-O-Su_2-Galβ1-4GlcNAcβ-sp3	3`,4`-Su_2-LacdiNAc	LacdiNAc3`,4`Su2	663.5(Na+)
202	6-O-Su-GalNAcβ1-4(6-O-Su)GlcNAcβ-sp3	6,6`-O-Su-LacdiNAc	LacdiNAc6,6`Su2	663.5(Na+)
203	Galβ1-4(6-O-Su)GlcNAcβ-sp2	6-O-Su-LacNAc	LN6Su	506.5
204	4-O-Su-GalNAcβ1-4GlcNAcβ-sp2	4`-O-Su-LacdiNAc	LacdiNAc4`Su-C2	547.5
205	Neu5Acα2-6GalNAcβ-sp3		6SiaANb	569.6
206	Neu5Gcα2-3Gal-sp3	NeuGcα3Gal	Neu5Gc3A	544.5
TRISACCHARIDES				
215	Fucα1-2Galβ1-3GlcNAcβ-sp3	$Le^{d,}$ H (type 1)	LeD	586.6
216	Fucα1-2Galβ1-4GlcNAcβ-sp3	H (type 2)	Htype2	586.6
217	Fucα1-2Galβ1-3GalNAcα-sp3	H (type 3)	Htype3	586.6
219	Fucα1-2Galβ1-4Glcβ-sp4	H (type 6	Htype6	544.5
220	Galα1-3Galβ1-4Glcβ-sp2		Aa3`Lac-C2	547.5

222	Galα1-3Galβ1-4GlcNAcβ-sp3	Galili (tri)	Galili3	602.6
224	Galα1-4Galβ1-4Glcβ-sp3	P^k, Gb3, $GbOse_3$	Pk	561.5
225	Galα1-4Galβ1-4GlcNAc-sp2	P_1	P1	588.6
226	Fucα1-2(Galα1-3)Galβ-sp3	B_{tri}	Btri	545.5
228	Galβ1-2Galα1-4GlcNAcβ-sp4		Ab2aLN	601.6
229	Galβ1-3Galβ1-4GlcNAcβ-sp4		Ab3`LN	601.6
231	Galβ1-4GlcNAcβ1-3GalNAcα-sp3		LN3Tn	643.6
232	Galβ1-4GlcNAcβ1-6GalNAcα-sp3		LN6Tn	643.6
233	Galβ1-3(Fucα1-4)GlcNAcβ-sp3	Le^a	LeA	586.6
234	Fucα1-3(Galβ1-4)GlcNAcβ-sp3	Le^x	LeX	586.6
235	Fucα1-2(GalNAcα1-3)Galβ-sp3	A_{tri}	Atri	586.6
238	GalNAcβ1-4Galβ1-4Glcβ-sp3	GA_2, $GgOse_3$	GA2	602.6
240	$(Glcα1-4)_3β$-sp4	maltotriose	(Ga4)3b	560.5
241	$(Glcα1-6)_3β$-sp4	isomaltotriose	(Ga6)3b	560.5
246	GlcNAcβ1-2Galβ1-3GalNAcα-sp3		GN2`TF	643.6
247	GlcNAcβ1-3Galβ1-3GalNAcα-sp3		GN3`TF	643.6
248	GlcNAcβ1-3Galβ1-4Glcβ-sp2		GN3`Lac	588.6
250	GlcNAcβ1-3Galβ1-4GlcNAcβ-sp3		GN3`LN	643.6
251	GlcNAcβ1-4Galβ1-4GlcNAcβ-sp2		GN4`LN	629.6
252	GlcNAcβ1-4GlcNAcβ1-4GlcNAcβ-sp4	chitotriose	Ch3	683.6
253	GlcNAcβ1-6Galβ1-4GlcNAcβ-sp2		GN6`LN	629.6
254	Galβ1-3(GlcNAcβ1-6)GalNAcα-sp3	core 2	core 2	643.6
255	GlcNAcβ1-3(GlcNAcβ1-6)GalNAcα-sp3	core 4	core 4	684.7
258	Manα1-3(Manα1-6)Manβ-sp4	Man_3	(Ma)3b	560.5
262	Galβ1-3GalNAcβ1-3Gal-sp4	$T_{ββ}$-Gal	Tbb-A	601.6
264	Galβ1-4Galβ1-4GlcNAc-sp3		Ab4`LN	602.6
287	3-O-Su-Galβ1-3(Fucα1-4)GlcNAcβ-sp3	Su-Le^a	3`SuLeA	666.7
288	Fucα1-3(3-O-Su-Galβ1-4)GlcNAcβ-sp3	Su-Le^x	3`SuLeX	666.7
289	Galα1-3(Neu5Acα2-	6-SiaTF	6SiaTF	731.7

	6)GalNAcα-sp3			
290	Galβ1-3(Neu5Acα2-6) GalNAcα-sp3		A3a(Sia) Tn	731.7
292	Neu5Acα2-3Galβ1-3GalNAcα-sp3	3`-Sia-TF	Sia3`TF	731.7
293	Neu5Acα2-3Galβ1-4Glcβ-sp3	3`SL	3`SL	690.7
294	Neu5Acα2-3Galβ1-4Glcβ-sp4	3`SL	3`SL-Gly	689.6
295	Neu5Acα2-6Galβ1-4Glcβ-sp2	6`SL	6`SL-C2	676.6
298	Neu5Acα2-3Galβ1-4GlcNAcβ-sp3	3`SLN	3`SLN	731.7
299	Neu5Acα2-3Galβ1-3GlcNAcβ-sp3	3`-SiaLe^{c}	3`SiaLeC	731.7
300	Neu5Acα2-6Galβ1-4GlcNAcβ-sp3	6`SLN	6`SLN	731.7
303	Neu5Gcα2-3Galβ1-4GlcNAcβ-sp3	3`SLN (Gc)	3`SLN(Gc)	747.7
304	Neu5Gcα2-6Galβ1-4GlcNAcβ-sp3	6`SLN (Gc)	6`SLN(Gc)	747.7
306	9-NAc-Neu5Acα2-6Galβ1-4GlcNAcβ-sp3		9NAc-6`SLN	788.8
315	Neu5Acα2-3Galβ1-4-(6-O-Su)GlcNAcβ-sp3	6-Su-3`SLN	3`SLN6Su	833.8 (Na+)
317	Neu5Acα2-3Galβ1-3-(6-O-Su)GalNAcβ-sp3	6-Su-3`SiaTF	3`SiaTF6Su	833.8 (Na+)
318	Neu5Acα2-6Galβ1-4-(6-O-Su)GlcNAcβ-sp3	6-Su-6`SLN	6`SLN6Su	833.8 (Na+)
319	Neu5Acα2-3-(6-O-Su)Galβ1-4GlcNAcβ-sp3	6`-Su-3`SLN	3`SLN6`Su	833.8 (Na+)
321	$(Neu5Ac\alpha2\text{-}8)_3$-sp3	$(Sia)_3$	(Sia)3	992.9 (Na+)
323	Neu5Acα2-6Galβ1-3GlcNAc-sp3	6`-SiaLe^{c}	6`SiaLeC	731.7
324	Neu5Acα2-6Galβ1-3(6-O-Su)GlcNAc-sp3	6Su-6`-SiaLe^{c}	6`SiaLeC 6Su	883.8 (Na+)
331	Neu5Gcα2-3Galβ1-3GlcNAcβ-sp3	3`SiaLe^{c} (Gc)	3`SiaLeC (GC)	747.7
TETRASACCHARIDES				
359	Fucα1-2(Galα1-3)Galβ1-3GlcNAcβ-sp3	B (type 1)	Btype1	748.7
360	Fucα1-2(Galα1-3)Galβ1-4GlcNAcβ-sp3	B (type 2)	Btype2	748.7
362	Fucα1-2(Galα1-3)Galβ1-3GalNAcα-sp3	B (type 3)	Btype3	748.7
363	Fucα1-2(Galα1-3)Galβ1-3GalNAcβ-sp3	B (type 4)	Btype4	748.7
364	Fucα1-3(Galα1-3Galβ1-4)GlcNAcβ-sp3	αGalLe^{x}	aGalLeX	748.7

366	Fucα1-2(GalNAcα1-3)Galβ1-3GlcNAcβ-sp3	A (type 1)	Atype1	789.8
368	Fucα1-2(GalNAcα1-3)Galβ1-4GlcNAcβ-sp3	A (type 2)	Atype2	789.8
371	Fucα1-2Galβ1-3(Fucα1-4)GlcNAcβ-sp3	Le^b	LeB	732.7
372	Fucα1-3(Fucα1-2Galβ1-4)GlcNAcβ-sp3	Le^y	LeY	732.7
373	Galα1-3Galβ1-4GlcNAcβ1-3Galβ-sp3	Galili (tetra)	Galili4	764.7
375	Galα1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-sp3		aLN3`LN	805.8
376	Galβ1-3GlcNAcβ1-3Galβ1-4Glcβ-sp4	LNT	LNT	763.7
377	Galβ1-3GlcNAcβ1-3Galβ1-3GlcNAcβ-sp2		LeCb3`LeC	791.8
378	Galβ1-3GlcNAcα1-3Galβ1-4GlcNAcβ-sp3		LeCa3`LN	805.8
379	Galβ1-3GlcNAcβ1-3Galβ1-4GlcNAcβ-sp3		LeCb3`LN	805.8
380	Galβ1-3GlcNAcα1-6Galβ1-4GlcNAcβ-sp2		LeCa6`LN	791.8
381	Galβ1-3GlcNAcβ1-6Galβ1-4GlcNAcβ-sp2		LeCb6`LN	791.8
382	Galβ1-3GalNAcβ1-4Galβ1-4Glcβ-sp3	Asialo-GM1	aGM1	764.7
383	Galβ1-4GlcNAcβ1-3Galβ1-4Glcβ-sp2	LNnT	LNnT	763.7
385	Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-sp3	i	LNb3`LN	805.8
387	Galβ1-4GlcNAcβ1-6Galβ1-4GlcNAcβ-sp2		LNb6`LN	791.7
388	Galβ1-3(Galβ1-4GlcNAcβ1-6)GalNAcα-sp3		LNb6TF	805.8
389	GalNAcβ1-3Galα1-4Galβ1-4Glcβ-sp3	Gb4, P	Gb4	764.7
390	$(Glcα1\text{-}4)_4β$-sp4	maltotetraose	(Ga4)4b	722.7
391	$(Glcα1\text{-}6)_4β$-sp4	isomaltotetraose	(Ga6)4b	722.7
392	Fucα1-2(GalNAcα1-3)Galβ1-3GalNAcα-sp3	A (type 3)	A(type3)	789.8
395	GlcNAcβ1-3(GlcNAcβ1-6)Galβ1-4GlcNAcβ-sp3	Tk	Tk	832.8
401	Galβ1-3GlcNAcβ1-3Galβ1-3GlcNAcβ-sp3	Le^c3Le^c	Le^c3Le^c	805.8
419	3-O-SuGalβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-sp3		(3`SuLN)3`LN	907.8
420	4-O-SuGalβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-sp3		(4`SuLN)3`LN	907.8

421	Neu5Acα2-3(GalNAcβ1-4)Galβ1-4Glcβ-sp2	GM2	GM2	879.8
422	Neu5Acα2-3Galβ1-4GlcNAcβ1-3Galβ-sp3		3`SLNb3A	893.9
423	Fucα1-3(Neu5Acα2-3Galβ1-4)GlcNAcβ-sp3	$SiaLe^x$	SiaLeX	877.9
426	Neu5Acα2-3Galβ1-3(Fucα1-4)GlcNAcβ-sp3	$SiaLe^a$	SiaLeA	877.9
428	Fucα1-3(Neu5Acα2-3Galβ1-4)6-O-Su-GlcNAcβ-sp3		SiaLeX6Su	979.9
429	Fucα1-3(Neu5Acα2-3(6-O-Su)Galβ1-4)GlcNAcβ-sp3		SiaLeX6`Su	979.9
433	Neu5Acα2-3Galβ1-3(Neu5Acα2-6)GalNAcα-sp3	Sia_2-TF	Sia2-3`,6TF	1044.9
434	Neu5Acα2-8Neu5Acα2-3Galβ1-4Glcβ-sp4	GD3	GC3	1002.9 (Na+)
PENTA-NONA SACCHARIDES				
479	Fucα1-2Galβ1-3GlcNAcβ1-3Galβ1-4Glcβ-sp4	LNFP-I	Htype1Lac	909.9
480	Fucα1-2Galβ1-3GlcNAcβ1-3Galβ1-4GlcNAcβ-sp2	H (type1) penta	HtypeILN	937.91
481	Galα1-3Galβ1-4GlcNAcβ1-3Galβ1-4Glcβ-sp4	Galili (penta)	Galili5	925.8
483	Fucα1-3(Fucα1-2 (Galα1-3)Galβ1-4)GlcNAcβ-sp3	Ble^y	BLeY	894.9
488	Galβ1-4GlcNAcβ1-3(Galβ1-4GlcNAcβ1-6)GalNAcα-sp3		LN2-3,6Tn	1008.9
489	Galβ1-4GlcNAcβ1-3(GlcNAcβ1-6)Galβ1-4GlcNAc-sp2		LN3`(GN6`)LN	994.9
490	GlcNAcβ1-3(Galβ1-4GlcNAcβ1-6)Galβ1-4GlcNAcβ-sp2		LN6`(GN3`)LN	994.9
492	$(Glcα1\text{-}6)_5β$-sp4	isomaltopentaose	(Ga6)5b	884.8
493	$(GlcNAcβ1\text{-}4)_5β$-sp4	chitopentaose	Ch5	1090
495	Manα1-3(Manα1-3(Manα1-6)Manα1-6)Manβ-sp4	Man5	(Ma)5b	966.9
496	Fucα1-2Galβ1-3(Fucα1-4)GlcNAcβ1-3Galβ1-4Glcβ-sp4	Le^b-Lac	LeBLac	1056
497	Fucα1-3(Fucα1-2Galβ1-4)GlcNAcβ1-3Galβ1-4Glcβ-sp4	Le^y-Lac	LeYLac	1056
498	$(Galβ1\text{-}4GlcNAcβ1\text{-}3)_3$-sp3	$(LN)_3$	(LNb3`)3	1171.1
499	Galβ1-4GlcNAcβ1-3(Galβ1-4GlcNAcβ1-6)Galβ1-4GlcNAc-sp2	I	LN2-3`,6`LN	1157.1

501	Galβ1-3GalNAcβ1-3Galα1-4Galβ1-4Glcβ-sp4	Gb5	Gb5	925.8
502	$(Glc\alpha1\text{-}6)_6\beta$-sp4	maltohexaose	(Ga6)6b	1046.9
503	$(GlcNAc\beta1\text{-}4)_6\beta$-sp4	chitohexaose	Ch6	1293.3
504	$(A\text{-}GN\text{-}M)_2$-3,6-M-GN-GNβ-sp4	9-OS	9-OS	1697.6
505	$(GN\text{-}M)_2$-3,6-M-GN-GNβ-sp4	7-OS	7-OS	1373.3
527	Neu5Acα2-3Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-sp2	3`SLN-LacNAc	3`SLN-LN	1083
528	Fucα1-3(Neu5Acα2-3 Galβ1-4)GlcNAcβ1-3Galβ-sp3	$SiaLe^x$-3Gal	SiaLeX3 A	1040
529	Neu5Acα2-6(Galβ1-3)GlcNAcβ1-3Galβ1-4Glcβ-sp4	LSTb	LSTb	1055
531	GalNAcβ1-4(Neu5Acα2-8Neu5Acα2-3)Galβ1-4Glc-sp2	GD2	GD2-C2	1193.1 (Na+)
532	Neu5Acα2-8Neu5Acα2-8Neu5Acα2-3Galβ1-4Glc-sp2	GT3	GT3	1303.1 (2Na+)
533	(Neu5Acα2-8)2Neu5Acα2-3(GalNAcβ1-4)Galβ1-4Glc-sp2	GT2	GT2	1506.3 (2Na+)
534	Neu5Acα2-3Galβ1-4GlcNAcβ1-3Galβ1-4GlcNAcβ-sp3	6`SLN-LacNAc	6`SLN-LN	1097.1
536	Neu5Acα2-3Galβ1-3GlcNAcβ1-3Galβ1-4Glcβ-sp4	LSTa	LSTa	1055
537	Neu5Acα2-3Galβ1-4GlcNAcβ1-3Galβ1-4Glcβ-sp4	LSTd	LSTd	1055
538	Le^x1-6'(Le^c1-3')Lac-sp4	MFLNH III	MFLNH III	1389.2
539	LacNAc1-6'(Le^d1-3')Lac-sp4	MFLNH I	MFLNH I	1389.2
540	Le^x1-6'(6'SLN1-3')Lac-sp4	MSMFLNnH	MSMFLNnH	1566.5
541	Le^x1-6'(Le^d1-3')Lac-sp4	DFLNH (a)	DFLNH (a)	1535.4
542	Le^cLe^x1-6'(Le^c1-3')Lac-sp4	MF(1-3)iLNO	MF(1-3)iLNO	1754.6
543	Le^x1-6'(Le^b1-3')Lac-sp4	TFLNH	TFLNH	1681.5
HIGER OLIGOSACCHARIDES				
625	$(GlcA\beta1\text{-}4GlcNAc\beta1\text{-}3)_8\text{-}NH_2$-ol	hyaluroninc acid	HyalU-ol	3207.5
627	$(Sia2\text{-}6A\text{-}GN\text{-}M)_2$-3,6-M-GN-GNβ-sp4	11-OS, YDS	11-OS	2302.1 (Na+)

TERMINAL GALACTOSE				
1A	Galβ1-3GlcNAc	Lacto-N-Biose I		383.35
1B	Galβ1-4GlcNAc	N-Acetyllactosamine		383.35
1C	Galβ1-4Gal	β-1-4-galactosyl-galactose		342.3
1D	Galβ1-6GlcNAc	β-1-6 Galactosyl-N-acetyl glucosamine		383.35
1E	Galβ1-3GalNAc	β-1-3 Galactosyl-N-acetyl galactosamine		383.35
1F	Galβ1-3GalNAcβ1-4Galβ1-4Glc	asialo GM1		707.63
1G	Galβ1-3GlcNAcβ1-3Galβ1-4Glc	Lacto-N-tetraose		707.63
1H	Galβ1-4GlcNAcβ1-3Galβ1-4Glc	Lacto-N-neotetraose		707.63
1I	Galβ1-4GlcNAcβ1-6(Galβ1-4GlcNAcβ1-3)Galβ1-4Glc	Lacto-N-neohexaose		1072.96
1J	Galβ1-4GlcNAcβ1-6(Galβ1-3GlcNAcβ1-3)Galβ1-4Glc	Lacto-N-hexaose		1072.96
1K	Galα1-4Galβ1-4Glc	Globotriose		504.44
1L	GalNAcα1-O-Ser	Tn Antigen GalNAcα1-O-Ser		308.29
1M	Galβ1-3GalNAcα1-O-Ser	Galactosyl-Tn Antigen		470.43
1N	Galα1-3Gal	α1-3 Galactobiose		342.24
1O	Galα1-3Galβ1-4GlcNAc	Linear B-2 Trisaccharide		545.49
1P	Galα1-3Galβ1-4Glc	Linear B-6 Trisaccharide		504.44
2A	Galα1-3Galβ1-4Galα1-3Gal	α1-3, β1-4,α1-3 Galactotetraose		666.58
2B	Galβ1-6Gal	beta1-6galactobiose		342.3
2C	GalNAcβ1-3Gal	terminal disaccharide of Globotriose		383.35
2D	GalNAcβ1-4Gal	receptor for P.aureginosa		383.35
2E	Galα1-4Galβ1-4GlcNAc	P1 antigen		545.49
2F	GalNAcα1-3Galβ1-4Glc	a-D-N-acetylgalactosamine 1-3Galβ1-4Glc		545.49
2G	Galβ1-3GlcNAcβ1-3Galβ1-4GlcNAcβ1-6(Galβ1-3GlcNAcβ1-3)Galβ1-4Glc	iso-Lacto-N-octaose (iLNO)		1438.3
2H	Galβ1-3GlcNAcβ1-3Galβ1-4GlcNAcβ1-3Galβ1-4Glc	para-Lacto-N-hexaose (pLNH)		1072.96
18B	Galβ1-3GalNAcβ1-3Galα1-4Galβ1-4Glc	Globopentaose		869.76

18C	Galβ1-3GalNAcβ1-3Gal	Core type 4/Gb5 triose structure		545.48
18L	Galβ1-4Glc	4-O-(B-D-galactopyranosyl)-B-D-glucose		342.3
18M	Galβ1-4Gal	4-O-(B-D-galactopyranosyl)-B-D-galactose		360.3
18N	Galβ1-6Gal	6-O-(B-D-galactopyranosyl)-B-D-galactose		342.3
TERMINAL GlcNAc				
4A	GlcNAcβ1-4GlcNAc	N,N'-Diacetyl chitobiose		424.4
4B	GlcNAcβ1-4GlcNAcβ1-4GlcNAc	N,N',N''-Triacetyl chitotriose		627.59
4C	GlcNAcβ1-4GlcNAcβ1-4GlcNAcβ1-4GlcNAc	N,N',N'',N'''-Tetraacetyl chitotetraose		830.79
4D	GlcNAcβ1-4GlcNAcβ1-4GlcNAcβ1-4GlcNAcβ1-4GlcNAc	N,N',N'',N''',N'''',N'''''-Hexaacetyl chitohexaose		1237.17
4E	Bacterial cell wall muramyl discaccharide	GlcNAcβ1-4MurNAc		496.46
4F	GlcNAcβ1-4GlcNAcβ1-4GlcNAcβ1-4GlcNAcβ1-4GlcNAc	Pentacetyl chitopentaose		1033.98
18G	6-O-Su-GlcNAc	N-Acetyl-D-Glucosamine 6-O-sulfate		323.25
18H	GlcNAc	N-Acetyl-D-Glucosamine		221.21
MANNOSYL CONTAINING GLYCANS				
5A	GlcNAcβ1-2Man	β1-2 N-Acetylglucosamine-mannose		383.35
5B	GlcNAcβ1-2Manα1-6(GlcNAcβ1-2Manα1-3)Man	Bianntennary N-linked core pentasaccharide		910.8
5C	Manα1-2Man	α1-2-Mannobiose		342.3
5D	Manα1-3Man	α1-3-Mannobiose		342.3
5E	Manα1-4Man	α1-4-Mannobiose		342.3
5F	Manα1-6Man	α1-6-Mannobiose		342.3
5G	Manα1-6(Manα1-3)Man	α1-3,α1-6-Mannobiose		504.44
5H	Manα1-6(Manα1-3)Manα1-6(Manα1-3)Man	α1-3,α1-3,α1-6-Mannopentaose		828.72
FUCOSYLATED GLYCANS				
7A	Fucα1-2Galβ1-3GlcNAcβ1-3Galβ1-4Glc	Lacto-N-fucopentaose I		853.77
7B	Galβ1-3(Fucα1-4)GlcNAcβ1-3Galβ1-4Glc	Lacto-N-fucopentaose II		853.77

7C	Galβ1-4(Fucα1-3)GlcNAcβ1-3Galβ1-4Glc	Lacto-N-fucopentaose III		853.77
7D	Fucα1-2Galβ1-3(Fucα1-4)GlcNAcβ1-3Galβ1-4Glc	Lacto-N-difucohexaose I		999.91
7E	Galβ1-3(Fucα1-4)GlcNAcβ1-3Galβ1-4(Fucα1-3)Glc	Lacto-N-difucohexaose II		999.91
7F	Fucα1-2Gal	H-disaccaride		326.3
7G	Fucα1-2Galβ1-4Glc	2'-Fucosyllactose		488.44
7H	Galβ1-4(Fucα1-3)Glc	3'-Fucosyllactose		488.44
7I	Galβ1-4(Fucα1-3)GlcNAc	Lewis^{x}		529.49
7J	Galβ1-3(Fucα1-4)GlcNAc	Lewis^{a}		529.49
7K	GalNAcα1-3(Fucα1-2)Gal	Blood Group A trisaccharide		529.49
7L	Fucα1-2Galβ1-4(Fucα1-3)Glc	Lactodifucotetraose (LDFT)		
7M	Galβ1-3(Fucα1-2)Gal	Blood Group B Trisaccharide		488.44
7N	Fucα1-2Galβ1-4(Fucα1-3)GlcNAc	Lewis^{y}		675.63
7O	Fucα1-2Galβ1-3GlcNAc	Blood Group H Type II Trisaccharide		529.49
7P	Fucα1-2Galβ1-3(Fucα1-4)GlcNAc	Lewis^{b} tetrasaccharide		675.63
8A	SO_3-3Galβ1-3(Fucα1-4)GlcNAc	Sulpho Lewis^{a}		631.53
8B	SO_3-3Galβ1-4(Fucα1-3)GlcNAc	Sulpho Lewis^{x}		631.53
8C	Galβ1-3GlcNAcβ1-3Galβ1-4(Fucα1-3)GlcNAcβ1-3Galβ1-4Glc	Monofucosyl-para-Lacto-N-hexaose IV		1219.1
8D	Galβ1-4(Fucα1-3)GlcNAcβ1-6(Galβ1-3GlcNAcβ1-3)Galβ1-4Glc	Monofucosyllacto-N-hexaose III		1219.1
8E	Galβ1-4(Fucα1-3)GlcNAcβ1-6(Fucα1-2Galβ1-3GlcNAcβ1-3)Galβ1-4Glc	Difucosyllacto-N-hexaose		1365.25
8F	Galβ1-4(Fucα1-3)GlcNAcβ1-6(Fucα1-2Galβ1-3(Fucα1-4)GlcNAcβ1-3)Galβ1-4Glc	Trifucosyllacto-N-hexaose		1511.39
8G	Galβ1-4GlcNAcβ1-3Galβ1-4(Fucα1-3)Glc	Lacto-N-fucopentaose VI (LNFP VI)		853.77
8H	Fucα1-2Galβ1-4(Fucα1-3)GlcNAcβ1-3Galβ1-4Glc	Lacto-N-neodifucohexaose I (LNnDFH I)		999.91
8I	Fucα1-3Galβ1-4GlcNAcβ1-3Galβ1-4(Fucα1-3)Glc	Lacto-N-neodifucohexaose II (LNnDFH II)		999.91
8J	Fucα1-2Galb1-4(Fucα1-3)GlcNAcb1-3(Fucα1-2)Galb1-4Glc	Trifucosyllacto-N-neoteraose I (TFLNnTI)		1146.05

8K	Galβ1-4(Fucα1-3)GlcNAcβ1-6(Galβ1-4GlcNAcβ1-3)Galβ1-4Glc	Monofucosyllacto- N-neohexaose I (MFLNnH I)	1219.1
8L	Galβ1-4(Fucα1-3)GlcNAcβ1-6(Galβ1-4(Fucα1-3)GlcNAcβ1-3)Galβ1-4Glc	Difucosyllacto-N-neohexaose I (DFLNnH I)	1365.25
8M	Fucα1-2Galβ1-4(Fucα1-3)GlcNAcβ1-6(Galβ1-4GlcNAcβb1-3)Galβ1-4Glc	Difucosyllacto-N-neohexaose II (DFLNnH II)	1365.25
8N	Galβ1-3GlcNAcβ1-3Galβ1-4(Fucα1-3)GlcNAcβ1-6(Galβ1-3GlcNAcβ1-3)Galβ1-4Glc	Monofucosyl(1-3)-iso-lacto-N-octaose (MFiLNO)	1584.44
8O	Fucα1-2Galβ1-3GlcNAcβ1-3Galβb1-4(Fucα1-3)GlcNAcβ1-6(Galβ1-3GlcNAcβ1-3)Galβ1-4Glc	Trifucosyl(1-2,1-2,1-3)-iso-lacto-N-octaose (TFiLNO (1-2,1-2,1-3))	1876.72
8P	GalNAcα1-3(Fucα1-2)Galβ1-4GalNAc	Blood Group A tetrasaccharide	732.68
9A	Galα1-3(Fucα1-2)Galβ1-4(Fucα1-3)Glc	Blood Group B pentasaccharide	796.72
9B	Galβ1-4GlcNAcβ1-6(Fucα1-2Galβ1-3GlcNAcβ1-3)Galβ1-4Glc	Monofucosyllacto-N-hexaose I	1219.1
18D	Galα1-3(Fucα1-2)Galβ1-4Glc	Blood group B antigen tetraose type 5	650.57
18E	GalNAcα1-3(Fucα1-2)Galβ1-4(Fucα1-3)Glc	Blood group A pentasaccharide	837.77
19J	Galβ1-4(Fucα1-3)GlcNAcβ1-3Gal	Lewis^{x} tetraose	691.62
19L	Fucα1-2Galβ1-4(Fucα1-3)GlcNAcβ1-3Gal	Lewis^{y} pentaose	837.77
19M	Galβ1-3(Fucα1-4)GlcNAcβ1-3Gal	Lewis^{a} tetraose	691.62
19N	Fucα1-2Galβ1-3(Fucα1-4)GlcNAcβ1-3Gal	Lewis^{b} pentaose	837.77
20A	Fucα1-2Galβ1-3GalNAcβ1-3Gal	Blood group H antigen tetraose type 4	691.27
20B	GalNAcα1-3(Fucα1-2)Galβ1-3GalNAcβ1-3Gal	Blood group A antigen pentaose type 4	894.82
20C	Galα1-3(Fucα1-2)Galβ1-3GalNAcβ1-3Gal	Blood group B antigen pentasaccaride type 4	853.76
SIALYLATED GLYCANS			
10A	Neu5Acα2-3Galβ1-3(Fucα1-4)Glc*N*Ac	Sialyl Lewis^{a} (S Lea)	820.74
10B	Neu5Acα2-3Galβ1-4(Fucα1-3)Glc*N*Ac	Sialyl Lewis^{x} (S Lex)	820.74
10C	Neu5Acα2-3Galβ1-3Glc*N*Acβ1-3Galβ1-4Glc	Sialyllacto-N-tetraose a	

10D	Galβ1-4(Fucα1-3)Glc*N*Acβ1-6(Neu5Acα2-6Galβ1-4Glc*N*Acβ1-3)Galβ1-4Glc	Monosialyl, monofucosyllacto-N-neohexose		1510.36
10E	Neu5Acα2-3Galβ1-3(Neu5Acα2-6)GalNAc	Disialyl-TF		965.86
10H	Neu5Acα2-6Galβ1-3GlcNAcβ1-3Galβ1-4(Fucα1-3)Glc	Sialyllacto-N-fucopentaose VI		1145.03
10I	Galβ1-3GlcNAcβ1-3(Neu5Acα2-6Galβ1-4GlcNAcβ1-6)Galβ1-4Glc	Monosialyllacto-N-hexaose		1364.22
10J	Neu5Acα2-6Galβ1-3GlcNAcβ1-3(Galβ1-4GlcNAcβ1-6)Galβ1-4Glc	Monosialyllacto-N-neohexaose		1364.22
10K	Neu5Acα2-3Galβ1-4Glc*N*Ac	3'-Sialyllactosamine		674.6
10L	Neu5Acα2-6Galβ1-4Glc*N*Ac	6'-Sialyllactosamine		674.6
10M	Neu5Acα2-3Galβ1-3GlcNAcβ1-3Galβ1-4Glc	LS-Tetrasaccharide a (LSTa)		998.88
10N	Galβ1-3(Neu5Acα2-6)Glc*N*Acβ1-3Galβ1-4Glc	LS-Tetrasaccharide b (LSTb)		998.88
10O	Neu5Acα2-6Galβ1-4Glc*N*Acβ1-3Galβ1-4Glc	LS-Tetrasaccharide c (LSTc)		998.88
10P	Neu5Acα2-3Galβ1-3(Neu5Acα2-6)Glc*N*Acβ1-3Galβ1-4Glc	Disialyllacto-N-tetraose		1290.14
11A	Neu5Acα2-3Galβ1-4Glc	3'-Sialyllactose		633.55
11B	Neu5Acα2-6Galβ1-4Glc	6'-Sialyllactose		633.55
11C	(Neu5Acα2-8Neu5Ac)n (n<50)	Colominic acid		
18A	Neu5Acα2-3Galβ1-4GlcNAcβ1-3Galβ1-4Glc	LS-Tetrasaccharide d		1020.86
18K	9-NAc-Neu5Ac	9-acetamido-9-deoxy-N-acetyl-a-D-neurminic acid		351.31
18O	Neu5Gc	N-glycolylneuraminic acid		325.27
19K	Neu5Acα2-3Galβ1-4(Fucα1-3)GlcNAcβ1-3Gal	Sialyl lewis X pentaose		1004.86
GLYCOSAMINOGLYCANS - high and low molecular weight				
12A	Neocarratetraose-41, 3-di-O-sulphate (Na+)	$C_{24}H_{36}O_{25}S_2Na_2$ (Mixed anomers. Tetrasaccharide of regular κ - carrageenan)		834.64
12B	Neocarratetraose-41-O-sulphate (Na+)	$C_{24}H_{37}O_{22}SNa$ (Mixed anomers. Derived from C1003 by removal of the non-reducing terminal 4-sulphate)		732.59

12C	Neocarrahexaose-24,41, 3, 5-tetra-O-sulphate (Na+)	$C_{36}H_{52}O_{40}S_4Na_4$ (Mixed anomers. A hybrid sequence comprising carrageenan disaccharides in the order k-i-k, derived from the carrageenan from *Chondrus crispus*)	1344.99
12D	Neocarrahexaose-41, 3, 5-tri-O-sulphate (Na+)	$C_{36}H_{53}O_{37}S_3Na_3$ (Mixed anomers. Hexasaccharide of regular κ-carrageenan)	1242.95
12E	Neocarraoctaose-41, 3, 5, 7-tetra-O-sulphate (Na+)	$C_{48}H_{70}O_{49}S_4Na_4$ (Mixed anomers. Octasaccharide of regular κ-carrageenan)	1651.26
12F	Neocarradecaose-41, 3, 5, 7, 9-penta-O-sulphate (Na+)	$C_{60}H_{87}O_{61}S_5Na_5$ (Mixed anomers. Decasaccharide of regular κ- carrageenan)	2059.57
12G	ΔUA-2S-GlcNS-6S	$C_{12}H_{15}NO_{19}S_3Na_4$ (Predominant disaccharide produced from heparin by heparinase I and II)	665.4
12H	ΔUA-GlucNS-6S	$C_{12}H_{16}NO_{16}S_2Na_3$ (Produced from heparinase II digestion of heparin and heparin sulphate)	563.35
12I	ΔUA-2S-GlucNS	$C_{12}H_{16}NO_{16}S_2Na_3$ (Produced from heparin by digestion with heparinase I and II)	563.35
12J	ΔUA-2S-GlcNAc-6S	$C_{14}H_{18}NO_{17}S_2Na_3$ (Minor component produced from heparin by heparinase II)	605.39
12K	ΔUA-GlcNAc-6S	$C_{14}H_{19}NO_{14}SNa_2$ (Product of the action of heparinases II and III on heparin and heparan sulphate)	503.34
12L	ΔUA-2S-GlcNAc	$C_{14}H_{19}NO_{14}SNa_2$ (Minor product of the action of heparinase II on heparin)	503.34
12M	ΔUA-GlcNAc	$C_{14}H_{20}NO_{11}Na$ (Produced from heparin sulphate by digestion With heparinase III)	401.3
12N	ΔUA-GalNAc-4S (Delta Di-4S)	$C_{14}H_{19}NO_{14}SNa_2$ (Produced from various chondroitin sulphates By the action of chondroitinases ABC, B and AC-1)	503.34
12O	ΔUA-GalNAc-6S (Delta Di-6S)	$C_{14}H_{19}NO_{14}SNa_2$ (Produced from various chondroitin sulphates By the action of chondroitinases ABC, AC-1 and C)	503.34

12P	ΔUA-GalNAc-4S,6S (Delta Di-disE)	$C_{14}H_{18}NO_{17}S_2Na_3$ (Produced from various chondroitin sulphates By the action of chondroitinases ABC, B and AC-1)	605.39
13A	ΔUA-2S-GalNAc-4S (Delta Di-disB)	$C_{14}H_{18}NO_{17}S_2Na_3$ (Produced from various chondroitin sulphates by action of chondroitinase ABC and/or B. Most typically from chondroitin sulphate B (dermatan sulphate))	605.39
13B	ΔUA-2S-GalNAc-6S (Delta Di-disD)	$C_{14}H_{18}NO_{17}S_2Na_3$ (Produced from various chondroitin sulphates by the action of chondroitinase ABC)	605.39
13C	ΔUA-2S-GalNAc-4S-6S (Delta Di-tisS)	$C_{14}H_{17}NO_{20}S_3Na_4$ (Produced as a minor component by the action of chondroitinase ABC on various chondroitin sulphates, particularly B)	707.43
13D	ΔUA-2S-GalNAc-6S (Delta Di-UA2S)	$C_{14}H_{19}NO_{14}SNa_2$ (Produced as a minor component from various chondroitin sulphates by the action of chondroitinase ABC)	503.34
13E	ΔUA-GlcNAc (Delta Di-HA)	$C_{14}H_{20}NO_{11}Na$ (The only unsaturated disaccharide produced from hyaluronic acid by the action of chondroitinase ABC or AC-1)	401.3
13F	(GlcAβ1-3Glc*N*Acβ1-4)n (n=4)	Hyaluronan fragments (4mer)	
13G	(GlcAβ1-3Glc*N*Acβ1-4)n (n=8)	Hyaluronan fragment (8mer)	
13H	(GlcAβ1-3Glc*N*Acβ1-4)n (n=10)	Hyaluronan fragment (10mer)	
13I	(GlcAβ1-3Glc*N*Acβ1-4)n (n=12)	Hyaluronan fragment (12mer)	
13J	(GlcA/IdoAα/β1-4Glc*N*Acα1-4)n (n=200)	Heparin	
13K	(GlcA/IdoAβ1-3(±4/6S)Gal*N*Acβ1-4)n (n<250)	Chondroitin sulfate	
13L	((±2S)GlcA/IdoAα/b1-3(±4S)Gal*N*Acβ1-4)n (n<250)	Dermatan sulfate	
13M	(GlcA/IdoAβ1-3(±6S)Gal*N*Acβ1-4)n (n<250)	Chondroitin 6-sulfate	
13N	HA - 4 10mM		775
130	HA - 6 10mM		1155.6

13P	HA - 8 9.7mM			1534.7
14A	HA 10 7.83mM			1913.8
14B	HA-12 6.5mM			2293.4
14C	HA-14 5.6mM			2672.5
14D	HA-16 4.9mM			
14E	HA 30000 da 2.5mg/ml			
14F	HA 107000 da 2.5mg/ml			
14G	HA 190000 da 2.5 mg/ml			
14H	HA 220000 da 2.5 mg/ml			
14I	HA 1600000 da 2.5 mg/ml			
14J	Heparin sulfate 5 mg/ml			
14K	β1-3Glucan			
14L	Chondroitin disaccharide Δdi-OS, sodium salt	$C_{14}H_{20}NNaO_{11}$ (produced from various chondriotin sulfates by the action of chondriotinases ABC, AC-1 and C)		401.3
14M	ΔUA→2S-GlcN-6S	Heparin unsaturated disaccharide I-H, the major component from the action of heparinase II on de-N-sulfated heparin		541.37
14N	ΔUA→GlcN-6S	Heparin unsaturated disaccharide II-H, the major component from the action of heparinase II on de-N-sulfated heparin		439.32
14O	ΔUA→2S-GlcN	Heparin unsaturated disaccharide III-H, the major component from the action of heparinase II on de-N-sulfated heparin		439.32
14P	ΔUA→GlcN	Heparin unsaturated disaccharide iV-H is obtained from the action of heparinases on heparin		337.28
18I	GlcA	D-Glucuronic acid		194.14
TERMINAL GLUCOSE STRUCTURES				
18J	6-O-(H_2PO_4)-Glc	D-Glucose-6-phosphate		260.14
19O	Glcα1-4Glcα1-4Glc	Maltotriose		504.44
19P	Glcα1-4Glcα1-4Glcα1-4Glc	Maltotetraose		666.58
GANGLIOSIDE STRUCTURES				
17A	GalNAcβ1-4Galβ1-4Glc	asialo GM2		545.48
17B	Galβ1-3GalNAcβ1-4Galβ1-4Glc	asialo GM1		707.62

17C	Galβ1-3GalNAcβ1-4(Neu5Acα2-8Neu5Acα2-8 Neu5Acα2-3)Galβ1-4Glc	GT1c ganglioside sugar		1647.33
17D	Neu5Acα2-8Neu5Acα2-3Galβ1-3GalNAcβ1-4(Neu5Acα2-3)Galβ1-4Glc	GT1a ganglioside sugar		1647.33
17E	Galβ1-3GalNAcβ1-4(Neu5Acα2-8Neu5Acα2-3)Galβ1-4Glc	GD1b ganglioside sugar		1334.09
17F	Neu5Acα2-3Galβ1-3GalNAcβ1-4(Neu5Acα2-3)Galβ1-4Glc	GD1a Ganglioside sugar		1334.09
17G	Neu5Acα2-3Galβ1-3GalNAcβ1-4Galβ1-4Glc	GM1b ganglioside sugar		1020.86
17H	Galβ1-3GalNAcβ1-4(Neu5Acα2-3)Galβ1-4Glc	GM1a ganglioside sugar		1020.86
17I	Fucα1-2Galβ1-3GalNAcβ1-4(Neu5Acα2-3)Galβ1-4Glc	fucosyl GM1 ganglioside sugar		1168
17J	GalNAcβ1-4(Neu5Acα2-8Neu5Acα2-8Neu5Acα2-3)Galβ1-4Glc	GT2 ganglioside sugar		1485.19
17K	GalNAcβ1-4(Neu5Acα2-8Neu5Acα2-3)Galβ1-4Glc	GD2 gangliosifde sugar		1171.95
17L	GalNAcβ1-4(Neu5Acα2-3)Galβ1-4Glc	GM2 ganglioside sugar		858.72
17M	Neu5Acα2-8Neu5Acβ2-8Neu5Acα2-3Galβ1-4Glc	GT3 ganglioside sugar		1282
17N	Neu5Acα2-8Neu5Acα2-3Galβ1-4Glc	GD3 ganglioside sugar		968.76
17O	Neu5Acα2-3Galβ1-4Glc	GM3 ganglioside sugar		655.53
17P	Neu5Acα2-3Galβ1-3GalNAcβ1-4(Neu5Acα2-8Neu5Acα2-3)Galβ1-4Glc	GT1b ganglioside sugar		
COMPLEX TYPE N-GLYCANS				
19A	Galβ1-4GlcNAcβ1-2Manα1-3(Galβ1-4GlcNAcβ1-2Manα1-6Man)β1-4GlcNAcβ1-4(Fucα1-6)GlcNAc	Asialo galactosylated, fucosylated biantennary		1787.63
19B	Galβ1-4GlcNAcβ1-2(Galβ1-4GlcNAcβ1-4)Manα1-3(Galβ1-4GlcNAcβ1-2(Galβ1-4GlcNAcβ1-6)Manα1-6Man)β1-4GlcNAcβ1-4GlcNAc	Asialo, galactosylated, tetranatennary, N-linked glycan		2372.15
19C	Neu5Acα2-6Galβ1-4GlcNAcβ1-2Manα1-3(Galβ1-4GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-	Monosialo(2,6), biantennary (A1)		1932.74

	4GlcNAc		
19D	Neu5Acα2-6Galβ1-4GlcNAcβ1-2Manα1-3(Neu5Acα2-6Galβ1-4GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-4GlcNAc	Disialo (2,6) biantennary (A2)	2224
19E	Galβ1-4GlcNAcβ1-2Manα1-3(Galβ1-4GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-4GlcNAc	Asialo, galactoyslated, biantennary (NA2)	1641.49
19F	Neu5Acα2-6Galβ1-4GlcNAcβ1-2Manα1-3(Neu5Acα2-6Galβ1-4GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-4(Fucα1-6)GlcNAc	Disialo, galactosylated, fucosylated, biantennary (A2F)	2370.14
19G	Neu5Acα2-6Galβ1-4GlcNAcβ1-2(Neu5Acα2-6Galβ1-4GlcNAcβ1-4)Manα1-3(Neu5Acα2-6Galβ1-4GlcNAcβ1-2Manα1-6)Manβ1-4GlcNAcβ1-4GlcNAc	Trisialylated, galactosylated, triantennary (A3)	2880.59
19H	GlcNAcβ1-2(GlcNAcβ1-4)Manα1-3(GlcNAcβ1-2Manα1-6)GlcNAcβ1-4Manβ1-4GlcNAcβ1-4GlcNAc	Asialo, agalacto, bisected triannary (NGA3B)	1723.59

Table S3. Molecules included in the small-molecule microarray.

Ligands	Short name	Molecular weight
alanine	Ala	89.09 g/mol
arginine	Arg	174.2 g/mol
cysteine	Cys	121.16 g/mol
glutamine	GluA	146.14 g/mol
proline	Pro	115.13 g/mol
tryptophane	Tryp	204.23 g/mol
α-ketoglutarate	a-keto	146.11 g/mol
aspartate	Asp	133.11 g/mol
asparagine	Asn	132.12 g/mol
glutamate	Glu	147.13 g/mol
glycine	Gly	75.07 g/mol
isoleucine	Iso	131.17 g/mol
serine	Ser	105.09 g/mol
valine	Val	117.151 g/mol
purine	Pur	120.11 g/mol
leucine	Leu	131.17 g/mol
methionine	Met	149.21 g/mol
threonine	Thr	119.1192 g/mol
malic acid	Malic	134.0874 g/mol
glucosamine	GlucA	179.17 g/mol
lysine	Lys	146.19 g/mol
phenylalanine	Phe	165.19 g/mol
tryrosine	Try	181.19 g/mol
fumarate	Fum	116.07 g/mol
thiamine	Thia	265.355 g/mol
succinate	Suc	118.09 g/mol

Table S4. Complex glycan structures recognized by Tlp10.

Number	Spacer form of saccharide
MONOSACCHARIDES	
6	GalNAcβ-sp3
22	GlcNAcβ-sp4
48	Neu5Acα-sp3
20	Rhaα-sp3
3	Galβ-sp3
16	Manα-sp3
49	Neu5Acα-sp9
DISACCHARIDES	
73	Fucα1-4GlcNAcβ-sp3
78	Galα1-3GalNAcα-sp3
100	Galβ1-6Galβ-sp4
115	GlcNAcβ1-4GlcNAcβ-Asn
168	GMDP-Lys
72	Fucα1-3GlcNAcβ-sp3
87	Galβ1-3Galβ-sp3
84	Galβ1-2Galβ-sp3
93	Galβ1-4Glcβ-sp4
104	GalNAcβ1-3Galβ-sp3
120	Manα1-3Manβ-sp4
149	GlcNAcβ1-4(6-O-Su)GlcNAcβ-sp2
151	6-O-Su-Galβ1-3GalNAcα-sp3
171	Neu5Acα2-3GalNAcα-sp3
TRISACCHARIDES	
233	Le^a
293	Neu5Acα2-3Galβ1-4Glcβ-sp3
241	$(Glcα1-6)_3β$-sp4
252	GlcNAcβ1-4GlcNAcβ1-4GlcNAcβ-sp4
254	Galβ1-3(GlcNAcβ1-6)GalNAcα-sp3
250	GlcNAcβ1-3Galβ1-4GlcNAcβ-sp3
Glycosaminoglycans - high and low molecular weight	
12G	ΔUA-2S-GlcNS-6S
12D	Neocarrahexaose-41, 3, 5-tri-O-sulphate (Na+)
14F	HA 107000 da 2.5mg/ml
Fucosylated glycans	
7E	Lacto-N-difucohexaose II
19M	Galβ1-3(Fucα1-4)GlcNAcβ1-3Gal
Ganglioside structures	
17I	fucosyl GM1 ganglioside sugar
1H	Lacto-N-neotetraose
Mannosyl containing glycans	
5E	Manα1-4Man
	Terminal galactose
2G	iso-Lacto-N-octaose (iLNO)
18N	Galβ1-6Gal

Table S5. Chemotaxis responses of WT and mutant *C. jejuni* strains. Nutrient depleted chemotaxis assays and µ-slide chemotaxis assays. Chemotaxis assays were performed using the indicated ligands as test compounds. The universal attractant mucin was used a positive control. The *C. jejuni* non-motile mutant (81116*ΔflaA/flaB*) and PBS were used as negative controls. Data (Log 10 CFU/mL) are from three technical replicates and are representative of three independent experiments (*n* = 3).

Nutrient-depleted chemotaxis assay							
Ligands	*C. jejuni* 11168-O WT		*Δtlp10*^{LBD}		*Δtlp10* ^{LBD}c		81116 *ΔflaA/flaB*
	2 mM	5 mM	2 mM	5 mM	2 mM	5 mM	2 mM
mucin	5.8± 0.56	6.2± 0.68	5.8± 0.76	6± 0.9	5.7± 0.64	5.9± 0.32	0
arginine	3.6± 0.56	3.1± 0.3	4.6± 0.31	4.9± 0.57	3.4± 0.54	3.8± 0.77	0
aspartate	5.6± 0.75	5.8± 0.9	3.3± 0.52	3.8± 0.21	4.7± 0.67	5.3± 0.51	0
isoleucine	5.7± 0.42	6.2± 0.6	3.5± 0.5	4.2± 0.32	4.9± 0.69	5.2± 0.24	0
thiamine	3.9±0.19	4.1±0.3	4.6±0.24	4.9±0.37	3.8±0.59	3.2±0.16	0
purine	4.7± 0.67	4.2± 0.1	4.5± 0.66	4.8± 0.28	5.6± 0.75	5.7± 0.36	0
malate	5.8± 0.51	6.1± 0.42	4.4± 0.45	4.2± 0.19	5.2± 0.72	5.9± 0.24	0
fumarate	5.7± 0.76	5.5± 0.3	3.6± 0.56	3.9± 0.85	4.2± 0.63	4.8± 0.11	0
α-ketoglutarate	4.7± 0.68	4.9± 0.57	4.3± 0.64	4.2± 0.45	4.7± 0.67	4.8± 0.14	0
galactose	4.6± 0.45	4.6± 0.2	5.6± 0.25	5.9± 0.17	4.5± 0.55	4.8± 0.11	0
mannose	3.9± 0.25	3.4± 0.16	3.08±0.33	3.2± 0.28	3.7± 0.59	3.8± 0.25	0
rhamnose	3.3± 1.07	3.6± 0.49	3.2± 0.28	3.5± 0.39	3.6± 0.08	3.9± 0.27	0
fucose	5.8± 0.66	5.9± 0.43	3.8± 0.68	3.1± 0.32	4.5± 0.71	5.3± 0.42	0
PBS	0	0	0	0	0	0	0
µ-slide chemotaxis assay							
Ligands	*C. jejuni* 11168-O WT		*Δtlp10*^{LBD}		*Δtlp10* ^{LBD}c		81116*ΔflaA/flaB*
galactose	3.3± 0.16		4.09± 0.34		3.6± 0.44		0
mannose	3.7± 0.21		3.3± 0.17		3.4± 0.02		0
rhamnose	3.4± 0.24		3.08± 0.06		3.5± 0.69		0
fucose	4.9± 0.41		3.6± 0.65		4.3± 0.28		0
sialic acid	2.3± 0.28		2.7± 0.14		2.4± 0.05		0

*Log 10 colony-forming units per mL (Log 10 CFU/mL).

Table S6. Illustration of A-B-A competition SPR analysis of WT Tlp10^{LBD}. The table shows where a cumulative response is observed when a second analyte (B) is flown across the bound protein while the first analyte (A) is present. The experimental value (value determinant) is actual response units (RU) values calculated from competition SPR data. The theoretical value (mathematical prediction) is response units (RU) values based on math theory. For each pair of ligands, binding was categorized as independent, shared, or preferential shared. All response data were normalised to 100Da molecular weight for each analyte, allowing direct comparison of responses. The data represent mean values (±SD) of three replicates in three independent experiments (n = 3).

Ligand (A)	Response units (RU± SD)	Ligand (B)	Response units (RU± SD)	Experimental RU (RU B +A ±SD)	Experimental RU (RU A + B ±SD)	Theoretical RU (Independent)	Theoretical RU (Shared)	Binding Status (B +A)	Binding Status (A+B)
arginine	**1.18 ±0.20**								
	+	fumarate	3.07 ±0.30	2.1 ±0.21	2.86 ±0.26	4.24	2.12	**Shared**	**Shared**
	+	α-ketoglutarate	2.16 ±0.24	1.53 ±0.22	1.28 ±0.23	3.33	1.67	**Shared**	**Shared**
	+	malate	3.26 ±0.6	4.7 ±0.2	4.31 ±0.2	4.44	2.22	**Independent**	**Independent**
	+	isoleucine	2.25 ±0.2	1.6 ±0.1	2.19 ±0.1	3.43	1.71	**Shared**	**Shared**
	+	thiamine	3.00 ±0.1	4.39 ±0.1	2.3 ±0.1	4.17	2.09	**Independent**	**Shared**
	+	purine	2.41 ±0.2	2 ±0.2	2.62 ±0.2	3.58	1.79	**Shared**	**Shared**
	+	aspartate	2.14 ±0.2	2.25 ±0.2	2.64 ±0.1	3.32	1.66	**Shared**	**Shared**
	+	galactose	1.25 ±0.2	3.08 ±0.1	2.96 ±0.09	2.43	1.21	**Independent**	**Independent**
	+	mannose	1.53 ±0.2	1.61 ±0.1	2.23 ±0.2	2.7	1.35	**Shared**	**Shared**
	+	rhamno	1.68	2.1	2.99	2.85	1.43	**Shared**	**Indepe**

		se	±0.1	±0.1	±0.1				**ndent**
	+	fucose	2.77 ±0.1	2.39 ±0.1	3.81 ±0.2	3.95	1.97	**Shared**	**Indepe ndent**
	+	Sialic acid	0.79 ±0.02	1.22 ±0. 6	1.53 ±0.06	1.97	0.98	**Shared**	**Shared**
mala te	**3.3 ±0.65 2**								
	+	fumarat e	3.06 ±0.33	6.27 ±0.25	5.636 ±0.28	6.330	3.165	**Indepe ndent**	**Shared**
	+	α-ketoglut arate	2.2 ±0.24	4.1 ±0.27	4.7 ±0.16	5.4	2.709	**Shared**	**Shared**
	+	isoleuci ne	2.24± 0.21	4.562±0. 21	4.788±0. 11	5.512	2.756	**Shared**	**Shared**
	+	thiamin e	2.99 ±0.13	4.381 ±0.18	6.484±0. 16	6.259	3.129	**Shared**	**Indepe ndent**
	+	purine	2.406 ±0.29	4.839 ±0.3	5.390 ±0.27	5.669	2.834	**Indepe ndent**	**Indepe ndent**
	+	aspartat e	2.141 ±0.26	4.229 ±0.65	3.93 ±0.5	5.404	2.702	**Indepe ndent**	**Shared**
	+	galactos e	1.24 ±0.19 6	2.972 ±0.214	4.188 ±0.039	4.512	2.256	**Shared**	**Prefere ntial Shared**
	+	mannos e	1.526 ±0.14 1	3.787 ±0.225	4.360 ±0.136	4.789	2.395	**Shared**	**Prefere ntial Shared**
	+	rhamno se	1.675 ±0.21	4.325 ±0.15	4.526 ±0.17	4.938	2.469	**Shared**	**Shared**
	+	fucose	2.772 ±0.25	3.588 ±0.080	4.929 ±0.188	6.034	3.017	**Shared**	**Shared**
	+	Sialic acid	0.792 ±0.01	2.639 ±0.018	2.471 ±0.059	4.055	2.027	**Shared**	**Shared**

Table S7. Illustration of A-B-A competition SPR analysis of Tlp10^{LBD}Y70A. The table shows where a cumulative response is observed when a second analyte (B) is flown across the bound protein while the first analyte (A) is present. The experimental value (value determinant) is actual response units (RU) values calculated from competition SPR data. The theoretical value (mathematical prediction) is response units (RU) values based on math theory. For each pair of ligands, binding was categorized as independent, shared, or preferential shared. All response data was normalised 100Da molecular weight for each analyte allowing direct comparison of responses. The data represents as mean values (±SD) of three replicates of three independent experiments (n = 3).

Ligand (A)	**Response units (RU ±s.d)**	**Ligand (B)**	**Response units (RU ±s.d)**	**Experimental RU (RU $^{B+A}$ ±s.d)**	**Experimental RU (RU $^{A+B}$ ±s.d)**	**Theoretical RU (Independent)**	**Theoretical RU (Shared)**	**Binding Status (B+A)**	**Binding Status (A+B)**
arginine	1.09 ±0.3								
	+	fumarate	4.00 ±0.4	2.65 ±0.3	3.51 ±0.2	5.09	2.54	Shared	Shared
	+	α-ketoglutarate	1.37 ±0.2	1.19 ±0.3	1.25 ±0.1	2.46	1.23	Shared	Shared
	+	malate	2.16 ±0.13	3.49 ±0.5	3.43 ±0.6	3.25	1.62	Independent	Independent
	+	isoleucine	3.30 ±0.4	2.54 ±0.3	3.32 ±0.1	4.39	2.19	Shared	Shared
	+	thiamine	1.83 ±0.2	2.91 ±0.2	1.3 ±0.2	2.92	1.46	Independent	Shared
	+	purine	3.41 ±0.4	3.64 ±0.8	3.88 ±0.3	4.50	2.25	Shared	Shared
	+	aspartate	2.18 ±0.4	2.47 ±0.3	1.50 ±0.2	3.27	1.63	Shared	Shared
	+	galactose	1.72 ±0.3	3.95 ±0.2	2.43 ±0.3	2.81	1.41	Independent	Independent
	+	mannose	1.78 ±0.3	2.20 ±0.3	1.69 ±0.3	2.87	1.43	Shared	Shared
	+	rhamnos	2.74	1.89	1.66	3.83	1.92	Shared	Shared

		e	±0.3	±0.3	±0.2				
	+	fucose	2.31 ±0.2	1.89 ±0.1	3.37 ±0.2	3.41	1.70	Shared	Shared
	+	Sialic acid	0.82 ±0.1	2.03 ±0.2	1.13 ±0.2	1.91	0.95	Independent	Shared
malate	2.16 ±0.13								
	+	fumarate	3.997 ±0.4	5.7 ±0.89	5.4 ±0.49	6.15	3.076	Shared	Shared
	+	α-ketoglutarate	1.35 ±0.2	3.1 ±0.22	3.3 ±0.62	3.52	1.76	Shared	Shared
	+	isoleucine	3.2 ±0.4	4.2 ±0.3	4.8 ±0.53	5.45	2.72	Shared	Shared
	+	thiamine	1.9 ±0.2	2.35 ±0.38	4.13 ±0.66	3.98	1.99	Shared	Independent
	+	purine	3.4 ±0.4	3.36 ±0.38	4.21 ±0.31	5.56	2.78	Shared	Shared
	+	aspartate	2.2 ±0.4	2.92 ±0.45	4.01 ±0.45	4.33	2.16	Shared	Shared
	+	galactose	1.7 ±0.3	3.2 ±0.52	2.03 ±0.16	3.87	1.93	Shared	Shared
	+	mannose	1.7 ±0.5	3.8 ±0.43	3.1 ±0.74	3.93	1.96	Shared	Shared
	+	rhamnose	2.74 ±0.3	4.05 ±0.19	3.3 ±0.23	4.89	2.44	Shared	Shared
	+	fucose	2.3 ±0.2	4.1 ±0.46	3.2 ±0.51	4.47	2.23	Shared	Shared
	+	Sialic acid	0.8 ±0.1	2.8 ±0.32	1.9 ±0.17	2.97	1.48	Shared	Shared

Table S8. Illustration of A-B-A competition SPR analysis of Tlp10^{LBD}Y115A. The table shows where a cumulative response is observed when a second analyte (B) is flown across the bound protein while the first analyte (A) is present. The experimental value (value determinant) is actual response units (RU) values calculated from competition SPR data. The theoretical value (mathematical prediction) is response units (RU) values based on math theory. For each pair of ligands, binding was categorized as independent, shared, or preferential shared. All response data was normalised 100Da molecular weight for each analyte allowing direct comparison of responses. The data represents as mean values (±s.d) of three replicates of three independent experiments (n = 3).

Ligand (A)	**Response units (RU±s.d)**	**Ligand (B)**	**Response units (RU±s.d)**	**Experimental RU (RU^{B+A} ±s.d)**	**Experimental RU (RU^{A+B} ±s.d)**	**Theoretical RU (Independent)**	**Theoretical RU (Shared)**	**Binding Status (B+A)**	**Binding Status (A+B)**
arginine	1.18 ±0.1								
	+	fumarate	2.71 ±0.1	3 ±0.1	3.07 ±0.1	3.89	1.95	Shared	Shared
	+	α-ketoglutarate	1.81 ±0.1	1.78 ±0.1	1.97 ±0.1	2.99	1.5	Shared	Shared
	+	malate	3.64 ±0.8	4.25 ±0.1	4.51 ±0.1	4.81	2.41	Shared	Shared
	+	isoleucine	2.33 ± 0.1	2.59 ±0.1	2.78 ±0.1	3.51	1.75	Shared	Shared
	+	thiamine	3.49 ±0.08	5.39 ±0.1	3.12 ±0.1	4.66	2.33	Independent	Preferential Shared
	+	purine	2.37 ±0.1	2.75 ±0.1	3.23 ±0.1	3.55	1.77	Shared	Shared
	+	aspartate	2.14 ±0.1	2.9 ±0.1	2.96 ±0.1	3.32	1.66	Shared	Shared
	+	galactose	1.36 ±0.1	3.7 ±0.1	3.53 ±0.1	2.54	1.27	Independent	Independent
	+	mannose	1.47 ±0.1	2.23 ±0.1	2.46 ±0.1	2.65	1.32	Preferential Shared	Preferential Shared
	+	rhamnose	1.98 ±0.1	2.93 ±0.1	3.58 ±0.2	3.16	1.58	Preferential Shared	Independent

	+	fucose	2.59 ±0.1	3.22 ±0.1	4.17 ±0.15	3.77	1.88	Preferential Shared	Independent
	+	Sialic acid	0.86 ±0.07	1.76 ±0.09	1.95 ±0.05	2.03	1.02	Preferential Shared	preferential Shared
malate	3.64 ±0.8								
	+	fumarate	3.067 ±0.18	5.23 ±0.16	4.67 ±0.16	6.7	3.3	Shared	Shared
	+	α-ketoglutarate	1.81 ±0.14	3.53 ±0.15	3.818 ±0.15	5.44	2.72	Shared	Shared
	+	isoleucine	2.24 ±0.21	3.73 ±0.15	3.95 ±0.15	5.88	2.94	Shared	Shared
	+	thiamine	2.99 ±0.079	5.77 ±0.15	9.8 ±0.15	6.63	3.31	Shared	Independent
	+	purine	2.4 ±0.29	4.2 ±0.16	4.91 ±0.16	6.04	3.02	Shared	Shared
	+	aspartate	2.14 ±0.26	3.85 ±0.15	3.48 ±0.15	5.77	2.88	Shared	Shared
	+	galactose	1.24 ±0.19	2.97 ±0.13	3.99 ±0.13	4.88	2.44	Shared	Shared
	+	mannose	1.47 ±0.11	3.4 ±0.13	3.97 ±0.13	5.1	2.55	Shared	Shared
	+	rhamnose	1.67 ±0.21	3.78 ±0.14	3.99 ±0.14	5.31	2.65	Shared	Shared
	+	fucose	2.77 ±0.21	3.25 ±0.14	4.45 ±0.14	6.4	3.2	Shared	Shared
	+	Sialic acid	0.79 ±0.01	2.41 ±0.09	2.37 ±0.09	4.42	2.21	Shared	Shared

Table S9. Illustration of A-B-A competition SPR analysis of Tlp10^{LBD}Y120A. The table shows where a cumulative response is observed when a second analyte (B) is flown across the bound protein while the first analyte (A) is present. The experimental value (value determinant) is actual response units (RU) values calculated from competition SPR data. The theoretical value (mathematical prediction) is response units (RU) values based on math theory. For each pair of ligands, binding was categorized as independent, shared, or preferential shared. All response data was normalised 100Da molecular weight for each analyte allowing direct comparison of responses. The data represents as mean values (±s.d) of three replicates of three independent experiments (n = 3).

Ligand (A)	**Response units (RU±s.d)**	**Ligand (B)**	**Response units (RU±s.d)**	**Experimental RU (RU^{B+A} ±s.d)**	**Experimental RU (RU^{A+B} ±s.d)**	**Theoretical RU (Independent)**	**Theoretical RU (Shared)**	**Binding Status (B +A)**	**Binding Status (A+B)**
arginine	1.00 ±0.06								
	+	fumarate	2.63 ±0.1	3.27 ±0.1	3 ±0.15	3.63	1.82	Shared	Shared
	+	α-ketoglutarate	1.75 ±0.1	1.72 ±0.1	1.97 ±0.04	2.75	1.37	Shared	Shared
	+	malate	3.08 ±0.08	3.80 ±0.06	4.12 ±0.06	4.08	2.04	Shared	Independent
	+	isoleucine	2.33 ±0.2	2.59 ± 0.09	2.46 ±0.1	3.33	1.66	Shared	Shared
	+	thiamine	2.96 ±0.09	4.62 ±0.07	2.93 ±0.1	3.96	1.98	Independent	Shared
	+	purine	2.62 ±0.06	3.09 ±0.1	3.23 ±0.07	3.63	1.81	Shared	Shared
	+	aspartate	2.22 ±0.1	3.16 ±0.10	2.96 ±0.05	3.22	1.61	Shared	Shared
	+	galactose	1.58 ±0.04	3.53 ±0.04	3.25 ±0.06	2.59	1.29	Independent	Independent
	+	mannose	1.69 ±0.07	2.57 ±0.1	2.23 ±0.08	2.7	1.35	Shared	Shared
	+	rhamnose	2.28 ±0.04	3.34 ±0.1	2.99 ±0.09	3.29	1.64	Independent	Shared

	+	fucose	2.53 ±0.1	3.34 ±0.09	3.81 ±0.04	3.57	1.86	Shared	Independent
	+	Sialic acid	0.99 ±0.1	1.96 ±0.1	1.53 ±0.09	1.99	1	Independent	Shared
malate	3.08 ±0.08								
	+	fumarate	2.62 ±0.061	4.517 ±0.085	4.03 ±0.144	5.7	2.852	Shared	Shared
	+	α-ketoglutarate	1.74 ±0.048	3.1 ±0.133	3.17 ±0.076	4.8	2.411	Shared	Shared
	+	isoleucine	2.32 ±0.137	3.05 ±0.158	3.2 ±0.140	5.4	2.701	Shared	Shared
	+	thiamine	2.95 ±0.040	3.18 ±0.053	5.28 ±0.155	6	3.017	Shared	Shared
	+	purine	2.62 ±0.059	3.89 ±0.118	4.36 ±0.056	5.7	2.849	Shared	Shared
	+	aspartate	2.21 ±0.173	3.63 ±0.139	3.18 ±0.079	5.3	2.646	Shared	Shared
	+	galactose	1.58 ±0.03	2.97 ±0.045	3.34 ±0.045	4.7	2.329	Shared	Shared
	+	mannose	1.69 ±0.03	3.02 ±0.14	3.4 ±0.095	4.8	2.385	Shared	Shared
	+	rhamnose	2.28 ±0.04	3.52 ±0.1	3.58 ±0.047	5.4	2.680	Shared	Shared
	+	fucose	2.52 ±0.14	3.118 ±0.15	3.722 ±0.1	5.6	2.802	Shared	Shared
	+	Sialic acid	0.98 ±0.09	2.18 ±0.04	2.12 ±0.24	4.1	2.031	Shared	Shared

Table S10. Illustration of A-B-A competition SPR analysis of Tlp10^{LBD}H193A. The table shows where a cumulative response is observed when a second analyte (B) is flown across the bound protein while the first analyte (A) is present. The experimental value (value determinant) is actual response units (RU) values calculated from competition SPR data. The theoretical value (mathematical prediction) is response units (RU) values based on math theory. For each pair of ligands, binding was categorized as independent, shared, or preferential shared. All response data was normalised 100Da molecular weight for each analyte allowing direct comparison of responses. The data represents as mean values (±s.d) of three replicates of three independent experiments (n = 3).

Ligand (A)	**Response units (RU± s.d)**	**Ligand (B)**	**Response units (RU± s.d)**	**Experimental RU (RU^{B+A} ±s.d)**	**Experimental RU (RU^{A+B} ±s.d)**	**Theoretical RU (Independent)**	**Theoretical RU (Shared)**	**Binding Status (B +A)**	**Binding Status (A+B)**
arginine	1.52 ±0.3								
	+	fumarate	3.56 ±0.3	2.55 ±0.2	3.41 ±0.2	5.08	2.54	**Shared**	**Preferential Shared**
	+	α-ketoglutarate	2.02 ±0.1	1.4 ±0.16	1.47 ±0.1	3.54	1.77	**Shared**	**Shared**
	+	malate	3.26 ±0.1	4.99 ±0.2	4.80 ±0.2	4.78	2.39	**Independent**	**Independent**
	+	isoleucine	3.18 ±0.2	2.96 ±0.5	3.88 ±0.04	4.7	2.35	**Preferential Shared**	**Preferential Shared**
	+	thiamine	2.89 ±0.1	4.69 ±0.1	2.30 ±0.1	4.41	2.2	**Independent**	**Preferential Shared**
	+	purine	2.54 ±0.2	3.01 ±0.2	3.07 ±0.1	4.06	2.03	**Preferential Shared**	**Preferential Shared**
	+	aspartate	2.29 ±0.2	2.44 ±0.2	1.59 ±0.2	3.81	1.91	**Preferential Shared**	**Shared**
	+	galactose	1.80 ±0.2	3.81 ±0.2	3.51 ±0.3	3.33	1.66	**Independent**	**Independent**
	+	mannose	1.86 ±0.2	2.23 ±0.4	1.78 ±0.4	3.38	1.69	**Preferential Shared**	**Preferential Shared**

	+	rhamnose	2.83 ±0.20	1.98 ±0.2	4.74 ±0.4	4.35	2.18	**Shared**	**Independent**
	+	fucose	2.35 ±0.22	1.98 ±0.2	3.99 ±0.1	3.87	1.93	**Shared**	**Independent**
	+	Sialic acid	0.69 ±0.1	2.03 ±0.1	1.19 ±0.1	2.21	1.11	**Preferential Shared**	**Preferential Shared**
malate	3.64 ±0.8								
	+	fumarate	3.56 ±0.3	5.5 ±0.85	5.03 ±0.14	6.82	3.41	**Shared**	**Shared**
	+	α-ketoglutarate	2.02 ±0.1	4.1 ±0.13	4.6 ±0.3	5.28	2.64	**Shared**	**Shared**
	+	isoleucine	3.18 ±0.4	5 ±0.18	5.9 ±0.14	6.44	3.22	**Shared**	**Shared**
	+	thiamine	2.89 ±0.5	3.17 ±0.53	6.28 ±0.15	6.14	3.07	**Shared**	**Shared**
	+	purine	2.54 ±0.21	3.8 ±0.11	4.3 ±0.5	5.79	2.89	**Shared**	**Shared**
	+	aspartate	2.29 ±0.3	4.6 ±0.13	5.2 ±0.79	5.55	2.77	**Shared**	**Shared**
	+	galactose	1.80 ±0.2	2.972 ±0.4	3.341 ±0.5	5.06	2.53	**Shared**	**Shared**
	+	mannose	1.86 ±0.2	3 ±0.14	4.4 ±0.9	5.12	2.56	**Shared**	**Shared**
	+	rhamnose	2.83 ±0.20	4.5 ±0.101	4.8 ±0.047	6.09	3.04	**Shared**	**Shared**
	+	fucose	2.35 ±0.22	3.118 ±0.154	5.22 ±0.1	5.6	2.8	**Shared**	**Shared**
	+	Sialic acid	0.69 ±0.1	2.18 ±0.41	2.2 ±0.24	3.95	1.97	**Shared**	**Shared**

Table S11. Analysis of protein-protein interactions with Tlp10^{sig} using the yeast two-hybrid system. The following *C. jejuni* chemotaxis proteins/domains were analysed for interactions with the Tlp10 signalling domain (Tlp10^{sig}): CheA, CheW, CheV, the CheW-like domain of CheV (CheV^{dW}), CheY, the signalling domain of Tlp1 (Tlp1^{sig}), the signalling domain common to Tlps 2, 3, and 4 (Tlp234^{sig}) and the signalling domain of Tlp7 (Tlp7^{sig}) (described in detail in Table S12).

AD-Tlp10^{sig} with:		**BD-Tlp10^{sig} with:**	
BD-CheA	-	AD-CheA	-
BD-CheW	-	AD-CheW	+
BD-CheV	+++	AD-CheV	+++
BD-CheV^{dW}	+++	AD-CheV^{dW}	+++
BD-CheY	-	AD-CheY	-
BD-Tlp10^{sig}	++	AD-Tlp10^{sig}	++
BD-Tlp1^{sig}	+	AD-Tlp1^{sig}	+
BD-Tlp234^{sig}	+	AD-Tlp234^{sig}	+
BD-Tlp7^{sig}	+	AD-Tlp7^{sig}	-

*Protein-protein interactions of Tlp10^{sig} fused to the GAL-4 activation domain (AD- Tlp10^{sig}) and GAL-4 binding domain (BD- Tlp10^{sig}) were analysed with selected chemotaxis proteins and individual domains fused to the GAL-4 DNA binding domain (BD) and GAL-4 activation domain (AD), respectively. Co-transformation of AD-CheW and BD-CheA was used as a positive control when testing for interactions, with a result of +++.

+++: cream, dense growth of > 75% of co-transformants observed on high stringency media and intermediate stringency media (strong interaction).

++: creamy pink, moderate growth for 50% - 75% of co-transformants observed on high stringency media and intermediate stringency media (medium interaction).

+: creamy pink, light growth for up to 50% of co-transformants observed on high stringency media and/or intermediate stringency media (weak interaction).

-: no growth of co-transformants observed.

Table S12. Fusion proteins for yeast two-hybrid experiments. The indicted chemotaxis proteins from *C. jejuni* NCTC11168-O were expressed as fusions to the GAL-4 activation domain (AD) and to the DNA-binding domain (BD) using pGADT7 and pGBKT7, respectively.

***C. jejuni* NCTC11168 chemotaxis protein/domain**	**Description of protein/domain**
$Tlp1^{sig}$	Residues 501 - 684 of Tlp1 (Cj1506c) encompassing the cytoplasmic signalling domain
$Tlp2(3, 4)^{sig}$	Residues 513 – 659 of Tlp 2 (Cj0144), residues 517 – 662 of Tlp 3 (Cj1564) and residues 520 – 665 of Tlp 4 (Cj0262c) encompassing the cytoplasmic signalling domain, these residues are identical in Tlps2, 3 and 4
$Tlp7^{sig}$	Residues 31 – 224 of Tlp7 (Cj0951c) encompassing the cytoplasmic signalling domain
$Tlp10^{sig}$	Residues 377 – 592 of Tlp10 (Cj0019c) encompassing the cytoplasmic signalling domain
CheA	Cj0284c, the full length CheA homologue
CheW	Cj0283c, the full length CheW homologue
CheV	Cj0285c, the full length CheV homologue
$CheV^{dW}$	Residues 1-166 of CheV (Cj0285c) encompassing the CheW-like domain
CheY	Cj1118c, the full length CheY homologue

Table S13. Microbial strains and plasmids used in this study.

Strain/Plasmid	Description	Reference/source
Bacterial strains/ plasmids		
C. jejuni NCTC11168	Genome sequenced strain of *C. jejuni* 11168	63
C. jejuni 11168-O	Original clinical isolate of *C. jejuni* 11168	(Skirrow, 1977)
*C. jejuni*11168-O Δ*tlp10*^{LBD}*::aphA3*	Isogenic mutant of *tlp10*	This study
*C. jejuni*11168-O Δ*tlp10*^{LBD} *::aphA3 Ωcj0046:: Km*	Complemented *tlp10* mutant in *C. jejuni* 11168-O*Δtlp10:: Km*	This study
C. jejuni 81116Δ*flaA*$^{-}$*/flaB*$^{-}$	Isogenic mutant of *flaA/flaB*	J.M. Ketley
E. coli DH5α	F$^{–}$, ø80d*lacZ*ΔM15, Δ(*lacZYA-argF*)U169, *deo*R, *recA*1, *endA*1, *hsdR*17(rK$^{–}$, mK^{+}), *phoA*, *supE*44, λ–, *thi*-1, *gyrA*96, *relA*1	15
E. coli BL21(DE3)	F^{-} *ompT hsdS*$_B$ (r$_B^{-}$ m$_B^{-}$) *gal dcm* (DE3)	Novagen
E. coli BL21(DE3)pLysS	F^{-} *ompT hsdS*$_B$ (r$_B^{-}$ m$_B^{-}$) *gal dcm* (DE3) pLysS (Cm^{R})	Novagen
pGEM-T Easy	Cloning vector	Promega
Yeast strains		
S.cerevisiae AH109	*MATa, trp1-901, leu2-3, 112, ura3-52, his3-200, gal4Δ, gal80Δ, LYS2::GAL1*$_{UAS}$*-GAL1*$_{TATA}$*-HIS3, GAL2*$_{UAS}$*-GAL2*$_{TATA}$*-ADE2, URA3::MEL1*$_{UAS}$*-MEL1*$_{TATA}$*-lacZ*	Clontech
Cloning intermediates		
pGEMXScheA	*cheA* (Cj0284**)** cloned into pGEM-T Easy with flanking *Xma*I/*Sal*I restriction endonuclease recognition	12

	sites, Amp^R	
pGEMNBcheW	*cheW* (Cj0283c**)** cloned into pGEM-T Easy with flanking *Not*I/*Bgl*II restriction endonuclease recognition sites, Amp^R	12
pGEMNBcheA	*cheA* (Cj0284**)** cloned into pGEM-T Easy with flanking *Not*I/*Bgl*II restriction endonuclease recognition sites, Amp^R	12
pGEMNBcheV	*cheV* (Cj0285c) cloned into pGEM-T Easy with flanking *Not*I/*Bam*HI restriction endonuclease recognition sites, Amp^R	12
pGEMEBtlp1	DNA sequence encoding residues 501-684 of *Tlp1* (Cj1506c) cloned into pGEM-T Easy with flanking *Eco*RI/*Bam*HI restriction endonuclease recognition sites, Amp^R	12
pGEMEBtlp2(3, 4)	DNA sequence encoding residues 513 – 659 of *Tlp 2* (Cj0144), residues 517 – 662 of *Tlp 3* (Cj1564) and residues 520 – 665 of *Tlp 4* (Cj0262c) cloned into pGEM-T Easy with flanking *Eco*RI/*Bam*HI restriction endonuclease recognition sites, Amp^R	13
pGEMEBtlp7	DNA sequence encoding residues 31 – 224 of *Tlp7* (Cj0951c) cloned into pGEM-T Easy with flanking *Eco*RI/*Bam*HI restriction endonuclease recognition sites, Amp^R	This study
pGEMXBtlp10	DNA sequence encoding residues 377 – 592 of *Tlp10* (Cj0019c) cloned into pGEM-T Easy with flanking *Xma*I/*Bam*HI restriction endonuclease recognition sites, Amp^R	This study

pGEMNdeBcheV	*cheV* (Cj0285c) cloned into pGEM-T Easy with flanking *Nde*I/*Bam*HI restriction endonuclease recognition sites, Amp^R	12
pGEMNdeBcheW	*cheW* (Cj0283c**)** cloned into pGEM-T Easy with flanking *Nde*I/*Bgl*II restriction endonuclease recognition sites, Amp^R	12
pGEMNBtlp1	DNA sequence encoding residues 501-684 of *Tlp1* (Cj1506c) cloned into pGEM-T Easy with flanking *Nde*I/*Bam*HI restriction endonuclease recognition sites, Amp^R	12
pGEMBScheV	*cheV* (Cj0285c) cloned into pGEM-T Easy with flanking *Bam*HI/*Sal*I restriction endonuclease recognition sites, Amp^R	12
pGEMBXcheW	*cheW* (Cj0283c**)** cloned into pGEM-T Easy with flanking *BamH*I/*Xho*I restriction endonuclease recognition sites, Amp^R	12
pGEMBEtlp1	DNA sequence encoding residues 501-684 of *Tlp1* (Cj1506c) cloned into pGEM-T Easy with flanking *Bam*HI/*Eco*RI restriction endonuclease recognition sites, Amp^R	12
Yeast two-hybrid plasmids		
pGADT7	GAL-4 activation domain expression vector	Clontech
pGBKT7	GAL-4 DNA binding domain expression vector	Clontech
pGADT7-T	Allows expression of the SV40 large T-antigen as a fusion to the GAL-4 AD	Clontech

pGBKT7-53	Allows expression of the murine p53 protein as a fusion to the GAL-4 DNA-BD, used as positive control when co- transformed with pGADT7-T	Clontech
pGBKT7-Lam	Allows expression of the human lamin C protein as a fusion to the GAL-4 DNA-BD, used as a negative control when co-transformed with pGADT7-T	Clontech
pADcheW	*cheW* cloned into pGADT7, Amp^R	12
pADcheA	*cheA* cloned into pGADT7, Amp^R	12
pADcheY	*cheY* cloned into pGADT7, Amp^R	12
pADcheV	*cheV* cloned into pGADT7, Amp^R	12
pADcheV^{dW}	DNA sequence encoding the *CheW*-like domain of *CheV* cloned into pGADT7, Amp^R	12
pADtlp1^{sig}	DNA sequence encoding residues 501-684 of *Tlp1* cloned into pGADT7, Amp^R	12
pADtlp234^{sig}	DNA sequence encoding residues 513 – 659 of *Tlp 2* (Cj0144), residues 517 – 662 of *Tlp 3* (Cj1564) and residues 520 – 665 of *Tlp 4* (Cj0262c) cloned into pGADT7, Amp^R	13
pADtlp7^{sig}	DNA sequence encoding residues 31 – 224 of *Tlp7* cloned into pGADT7, Amp^R	This study
pADtlp10^{sig}	DNA sequence encoding residues 377 – 592 of *Tlp10* cloned into pGADT7, Amp^R	This study
pBKcheW	*cheW* cloned into pGBKT7, Km^R	12
pBKcheA	*cheA* cloned into pGBKT7, Km^R	12

pBKcheY	*cheY* cloned into pGBKT7, Km^R	12
pBKcheV	*cheV* cloned into pGBKT7, Km^R	12
pBKcheV^{dW}	DNA sequence encoding the *CheW*-like domain of *CheV* cloned into pGBKT7, Km^R	12
pBKtlp1^{sig}	DNA sequence encoding residues 501-684 of *Tlp1* cloned into pGBKT7, Km^R	12
pBKtlp234^{sig}	DNA sequence encoding residues 513 – 659 of *Tlp 2* (Cj0144), residues 517 – 662 of *Tlp 3* (Cj1564) and residues 520 – 665 of *Tlp 4* (Cj0262c) cloned into pGBKT7, Km^R	13
pBKtlp7^{sig}	DNA sequence encoding residues 31 – 224 of *Tlp7* cloned into pGBKT7, Km^R	This study
pBKtlp10^{sig}	DNA sequence encoding residues 377 – 592 of *Tlp10* cloned into pGBKT7, Km^R	This study
Mutagenesis		

pET-19b	His-tag expression vector	Novagen
pGU0708	*Tlp10* ^{LBD} wildtype cloned into pET-19b	This study
pGU0709	*Tlp10* ^{LBD} Y70A	This study
pGU07010	*Tlp10* ^{LBD} Y115A	This study
pGU07011	*Tlp10* ^{LBD} Y120A	This study
pGU07012	*Tlp10* ^{LBD}H193A	This study
pGU0816	*Tlp10* cloned into pGEM-T easy	This study
pGU0817	Δ*tlp10*^{LBD}::*Cm*^{R} cloned into pGEM-T easy	This study
pGU0818	*Tlp10* cloned into pKp*fdx*A vector (*p*Kp*fdx*A cj0046:: *tlp10)*	This study
pAV35	Chloramphenicol resistant	65
pK46	*C. jejuni cj0046* pseudogene integration vector; Km^{R}	13

Table S14. DNA primers used in this study.

Primer name	Sequence 5'-3'	Restriction Site	Reference
Mutagenesis of *tlp10*			
TLP10 ^{LBD}.F	CATATGAACTATTCTTCATCTAAAGATAATAA	*Nde*I	This study
TLP10 ^{LBD} -R	CTCGAGTTATTTAAATAAATTAGATTGTTCTATAGT	*Xho*I	This study
TLP10 LBD Y70A-F	TTATCAACGCTGATCCAAGTGTTCA	-	This study
TLP10 LBD Y70A -R	AACACTTGGATCAGCGTTGATAAAA	-	This study
TLP10 LBD Y115A-F	TTTAAATCCGCAGCTTCCATAGCAGTA	-	This study
TLP10 LBD Y115A-R	TACTGCTATGGAAGCTGCGGATTTAAA	-	This study
TLP10 LBD Y120A-F	TCCATAGCAGTAGCTTCAAAACTTTAT	-	This study
TLP10 LBD Y120A-R	ATAAAGTTTTGAAGCTACTGCTATGGA	-	This study
TLP10 LBDH193A-F	CTTTTTTTAAAAGCTTATAACATGAT	-	This study
TLP10 LBDH193A-R	ATCATGTTATAAGCTTTTAAAAAAAG	-	This study
TLP10 Mut-F	CCCGGGATGACAAATAAAAAAAGTTCATTTTTG	*SmaI*	This study
TLP10 Mut-R	GAGCTCTTACTGAAAGCTACTTAATTTTTCGG	*SacI*	This study
TLP10 inv-F	GAAGATCTGCGCTAATTTAGCTAGCAAAGAAGC	*Bgl*II	This study
TLP10 inv-R	GAAGATCTTCAGTTGAAAGAACGCTTAACATAG	*Bgl*II	This study
TLP10Comp-F	AGGCGTCTCACATGACAAATAAAAAAAG	*Bsm*BI	This study
TLP10Comp-R	GACCATGGTTACTGAAAGCTACTTAATT	*NcoI*	This study
CAT F NW	GAAGATCTGATTGAAAAGTGGATAGATTTATG	*Bgl*II	This study
CAT R NW	GAAGATCTATTTTTCGATTGGCGCGCCTGAGGG	*Bgl*II	This study
Topo Kan F	ATGATTGAACAAGATGGATTGC		This study
Topo Kan R	TCAGAAGAACTCGTCAAGAAGG		This study
pK46 Kan F	AATGGCTAAAATGAGAATATC		This study

pK46 Kan R	AAACAATTCATCCAGTAAAAT		This study
Sequencing			
T7	TAATACGACTCACTATAG		pET-19b (Novagen)
Cj0046F	CACTACCCAATTGAAAATCTAAG		This study
Cj0046R	GTGAGTTAATGCCATCATAAC		This study
Cloning			
tlp7^{sig}EcoRIF	GAATTCTCAACAGTATCTCAAAATGAAA	EcoRI	This study
tlp7^{sig}BamHIR	GGATCCAAATTTGAAATTGGTTAAGTCC	BamHI	This study
tlp10^{si}XmaIIF	CCCGGGGGAAAATATGCAAGATATGCACA	XmaII	This study
tlp10^{sig}BamHIR	GGATCCACTGAAAGCTACTTAATTTTTC	BamHI	This study

Table S15. MIRAGE glycan and small-molecule arrays for Tlp10. Supplementary glycan microarray document based on MIRAGE guidelines DOI: 10.1093/glycob/cww118.

Classification	Guidelines
1. Sample: Glycan Binding Sample	
Description of Sample	Sample names: Tlp10 protein Origin: *Campylobacter jejuni* 11168*;* produced as a recombinant His -tagged protein in *E. coli*. Method of preparation: The preparation of Tlp10 is explained in the Materials and Methods section: Expression and purification of the periplasmic domain of tlp10.
Sample modifications	Sample is a His Tagged protein containing only the periplasmic receptor domain of the full length Tlp10 transmembrane protein.
Assay protocol	Please see *Materials and Methods: Identification of ligand binding potential of Tlp10 by glycan and small molecule arrays.* Proteins were complexed with mouse anti-his antibody, with secondary and tertiary AlexaFluor555 antibodies (rabbit anti-mouse, goat anti-rabbit) at a molar ratio of 4:2:1. The protein/antibody complex was incubated on ice for 10 mins prior to placing on the array. Arrays were performed with 1 µg of complexed protein incubated on the array for 20 min. Arrays were then washed 3 times in Array PBS (PBS + 2mM $MgCl_2$ + 2mM $CaCl_2$) then dried by centrifugation for 3 min at 300 x *g*. Scanning was performed using ProScanArray and analyzed using ScanArray Express. Yes/no binding was determined by six positive replicate spots in three replicate experiments. Positive binding was determined by spots being significantly greater than negative control spots by two-tailed *t* test.
2.1 Glycan Library	
Glycan description for defined glycans	Glycans in this study are listed in Table S2 and is a published library in doi: 10.1371/journal.pntd.0004120.
Glycan description for undefined glycans	N/A.
Glycan modifications	Glycans were prepared in one of two ways for printing: 1. Glycans (with IDs in number/letter format; e.g. 1A, 4C, 7K) were sourced commercially from Dextra Laboratories, Elicityl and Carbosythn and were made into glycoamines using the protocol published in Day et al 2009 (doi: 10.1371/journal.pone.0004927). 2. Glycans (with IDs in number only format) were obtained from Prof Nicolai Bovin and were modified with spacers as per DOI: 10.1073/pnas.0407902101. The library of these glycans was first published in DOI: 10.1016/j.molimm.2009.06.010

2.2 Small molecule Library	
Sample description for defined compounds	Compounds printed in the amino acid/small molecule array for this study are listed in Table S3.
3. Printing Surface; e.g., Microarray Slide	
Description of surface	Epoxy activated glass microarray slides.
Manufacturer	ArrayIt SuperEpoxy 3 (SME3).
Custom preparation of surface	N/A.
Non-covalent Immobilisation	N/A.
4. Arrayer (Printer)	
Description of Arrayer	**Glycan array:** SpotBot® Extreme Protein Microarray Spotter (ArrayIt, California, USA). **Small molecule array:** ArrayJet Argus Marathon non-contact printer.
Dispensing mechanism	**Glycan array:** Contact printing using 946NS6 pins with a 6 pin in a 3 columns x 2 rows configuration. **Small molecule array:** Non-contact jet printing
Glycan and small molecule deposition	**Glycan array:** Approximately 1.8 nl per spot is printed according to manufactures guidelines. Glycan were at 500 µM in 50:50 DMF:DMSO. **Small molecule array:** Approximately 320 nl per spot is printed according to manufactures guidelines. Samples were at 1000 µM in PBS with 2% glycerol
Printing conditions	**Glycan array:** Array were printed with dehumidification at a maximum humidity of 60% relative humidity (Standard laboratory starting humidity of 75-90%) at 22ºC. Glycans were left to react with the slide for at least 8 hours after the print was completed. **Small molecule array:** Array were printed with dehumidification at a maximum humidity of 60% relative humidity (Standard laboratory starting humidity of 75-90%) at 22ºC. Samples were left to react with the slide for at least 15 hours after the print was completed.
5.1 Glycan array with "Map"	
Array layout	The array consists of a single array of glycans split between 6 pins (3 columns x 2 rows) with 4500µm row and column spacing. Each pin printed a 20 columns x 16 rows with 200µm spot spacing (centre to centre) with a minimum spot size of 100µm. Each sample is printed in quadruplicate with each of the 6 print areas including at least three negative control samples (print solution only) and two positive control samples consisting of one sample of fluoroscienamine and one sample of a mixture of rabbit anti-mouse antibody labeled with Alexa 555 and Alexa 647. Positive controls provide proof of successful immobilization of the amine reagents and provides for orientation for analysis. The antibodies also can provide

	controls for secondary antibodies used in experiments (if applicable).
Glycan identification and quality control	Arrays are quality controlled by a range of measures. 1. Each printed array is post print scanned to confirm deposition of the glycans on the array surface prior to neutralization of the remaining slide surface. 2. Post neutralized slides are scanned again to monitor for remaining autofluorescence. 3. Slides are assayed with fluorescently labeled lectins: WGA-Texas Red (EY Laboratories) and ConA-FITC (EY Laboratories).
5.2 Small molecule array with "Map"	
Array layout	The array consists of triplicate sub-arrays of amino acids and small moleucles (24 rows x 10 columns) with 400µm spot spacing (centre to centre) with a minimum spot size of 100µm. Each sample is printed six times, with each of the 3 sub-arrays including at least six negative control samples (print solution only) and a positive control samples consisting of one a mixture of rabbit anti-mouse antibody labeled with Alexa 555 and Alexa 647. Positive controls provide proof of successful immobilization of the amine reagents and provides for orientation for analysis.
Sample identification and quality control	Arrays are quality controlled by a range of measures. 1. Each printed array is post print scanned to confirm deposition of the samples on the array surface prior to neutralization of the remaining slide surface. 2. Post neutralized slides are scanned again to monitor for remaining autofluorescence.
6. Detector and Data Processing	
Scanning hardware	ProScanArray (Lasers: 488 nM, 532 nM with two filter sets for analysis at 532 and 595 nM), 635 nM) scanner.
Scanner settings	Scanning resolution: 10µM Laser channel: 532nM operating 595nM excitation / 625nM emission filter set. PMT: 20% gain Scan powers: Low laser power.
Image analysis software	ScanArray Express.
Data processing	Data was exported as a CSV file and exported to Microsoft Excel.
7. Glycan Microarray Data Presentation	
Data presentation	Glycan array: Data is presented as yes/no binding in Table S4. The full list of glycans is shown in Table S2.
8. Interpretation and Conclusion from Microarray Data	
Data interpretation	**Glycan arrays:** We only use glycan arrays as a yes/no binding tool. Due to this we look only at binding that is unambiguously above background vs lack of binding above background. Average background + 3x standard deviation of the background of 20 sets of 4 spots of DMF:DMSO only spots is applied to determine if binding observed is significantly above background. Only spots with values equal to or greater than this value were considered as binding from data of any tested slide. These values are slide dependent. **Small molecule arrays:** We only use amino acid arrays as a yes/no binding tool. Due to this we look only at binding that is unambiguously above background vs lack of binding above background. Average background + 3x standard deviation of the background of 6 spots of PBS + 2% glycerol only spots is applied to determine if binding observed is significantly above

	background. Only spots with values equal to or greater than this value were considered as binding from data of any tested slide. These values are slide dependent.
Conclusions	Tlp10 was found to bind to a wide range of molecules on both array types indicating a broad ligand specificity for chemotaxis.

Movie S1. *C. jejuni* migrate toward the attractant isoleucine. Live imaging of fluorescently labelled *C. jejuni* 11168-O WT and *Δtlp10* migrating from the left chamber towards 10mM isoleucine in the right chamber in a μ-Slide Chemotaxis apparatus.

Movie S2. Migration of *C. jejuni* toward the attractant isoleucine is reduced by addition of the repellent arginine. Live imaging of fluorescently labelled *C. jejuni* 11168-O WT and *Δtlp10* migrating from the left chamber of a μ-Slide apparatus towards 10mM isoleucine in the right chamber followed by the introduction of 10 mM arginine into right chamber at the 20s time point.

Movie S3. PBS control for the effect of arginine on the migration of WT *C. jejuni* toward isoleucine. Live imaging of fluorescently labelled *C. jejuni* 11168-O WT from the left chamber of μ-Slide followed by introduction of PBS into the right chamber.

Data File S1. Proteins included in DAHL domain MSA. List of DAHL domain-containing proteins, their domain architectures and taxonomic distribution. This is provided as an Excel file.