SUPPORTING INFORMATION

TABLE S1: Microbial glycan array results for FITC-labeled murine and human Langerin ECD.

Chart#	Murine (RFU)	[SEM] (RFU)	Human (RFU)	[SEM] (RFU)	Species / Origin	Type of structure /Cat.No.
313	306	34	38	23	1-2 Mannan Acetobacter methanolieus MB135	
307	-50	5	-4	12	Davanat	
305	259	315	-8	10	Escherichia coli K13	CPS
18	859	94	23	8	Escherichia coli K235 LPS	L2143
304	75	156	-21	13	Escherichia coli K5	CPS
303	17615	1165	17	11	Escherichia coli K92	CPS
32	8634	2173	73	7	Escherichia coli O106	
298	2504	550	420	46	Escherichia coli O107	PS
222	15	11	-4	5	Escherichia coli O111:B4 LPS- solution at 1 mg/mL	L5293-2ML (LPS) (Sigma)
210	317	238	1204	707	Escherichia coli O112ab	OPS
211	145	307	41	24	Escherichia coli O118	OPS
212	2	18	16	10	Escherichia coli O125	OPS
225	1005	373	-14	17	Escherichia coli O127:B8 LPS- solution at 1 mg/mL	L5668-2ML (LPS) (Sigma)
19	5039	541	6	5	Escherichia coli O128-B12 LPS	L2755
33	1056	921	183	21	Escherichia coli O130	
297	320	59	-21	28	Escherichia coli O145	LPSOH
34	201	13	38	6	Escherichia coli O148	
35	-537	323	20	9	Escherichia coli O150	
213	-68	68	12	6	Escherichia coli O151	OPS
214	10	6	46	10	Escherichia coli O168	OPS
36	522	395	496	27	Escherichia coli O180	
223	1097	483	14	24	Escherichia coli O26:B6 LPS- solution at 1 mg/mL	L5543-2ML (LPS) (Sigma)
30	52	20	20	5	Escherichia coli O29	
31	-3731	575	59	17	Escherichia coli O40	
205	161	31	163	5	Escherichia coli O49	OPS
206	10	4	-4	11	Escherichia coli O52	OPS
224	-364	221	-2	8	Escherichia coli O55:B5 LPS- solution at 1 mg/mL	L5418-2ML (LPS) (Sigma)
207	-131	54	25	7	Escherichia coli O58	OPS
208	181	149	38	16	Escherichia coli O61	LPSOH
294	282	86	209	103	Escherichia coli O71	PS
209	500	82	72	2	Escherichia coli O73	OPS
295	1041	221	265	30	Escherichia coli O85	PS
310	40	34	-33	4	Escherichia coli O86	
296	10	46	13	21	Escherichia coli O99	PS
185	-220	100	-2	2	Francisella novicida OPS	OPS
186	16	2	-9	2	Francisella tularensis OPS	OPS

311	-122	27	7	20	Galactomannan DAVANT (160102) Pro-Pharmacenti	
187	19	35	9	7	Klebsiella O1 OPS	OPS
194	191	27	82	16	Klebsiella O12 OPS	OPS
188	1001	520	67	9	Klebsiella O2a OPS	OPS
189	20	109	62	3	Klebsiella O2ac OPS	OPS
190	10	5	2	3	Klebsiella O3 OPS	OPS
191	995	576	31	4	Klebsiella O4 OPS	OPS
192	958	198	206	35	Klebsiella O5 OPS	OPS
193	420	160	248	119	Klebsiella O8 OPS	OPS
308	424	70	-12	17	Laminarin	
306	6280	416	-6	4	Neisseria meningitidis Group C	CPS
39	2004	1036	30	4	Proteus mirabilis O10 (HJ4320)	
264	8065	663	15	9	Proteus mirabilis O11 (9B-m)	PS
92	4964	1268	13	18	Proteus mirabilis O11 (PrK 24/57)	OPS
93	724	255	313	56	Proteus mirabilis O13 (PrK 26/57)	OPS
94	319	237	45	6	Proteus mirabilis O14a,14b (PrK 29/57)	OPS
95	216	47	208	43	Proteus mirabilis O16 (4652)	OPS
96	63	13	49	9	Proteus mirabilis O17 (PrK 32/57)	OPS
266	90	23	10	4	Proteus mirabilis O18 (PrK 34/57)	LPSOH
267	-229	162	152	17	Proteus mirabilis O20 (PrK 38/57)	LPSOH
174	499	245	-21	9	Proteus mirabilis O23a, 23b, 23c (CCUG 10701)	OPS
97	8033	947	10	28	Proteus mirabilis O23a,b,d (PrK 42/57)	OPS
98	1280	227	167	9	Proteus mirabilis O26 (PrK 49/57)	OPS
99	4658	333	126	14	Proteus mirabilis O27 (PrK 50/57)	OPS
100	249	305	36	11	Proteus mirabilis O28 (PrK 51/57)	OPS
101	-60	84	6	4	Proteus mirabilis O29a (PrK 52/57)	OPS
40	-181	55	25	2	Proteus mirabilis O29a, 29b (2002)	
269	1167	330	22	5	Proteus mirabilis O33 (D52)	PS
37	304	93	42	11	Proteus mirabilis O3a, 3c (G1)	
261	55	5	-29	5	Proteus mirabilis O3ab (S1959)	PS
102	43	29	51	8	Proteus mirabilis O40 (10703)	OPS
103	2259	866	-7	9	Proteus mirabilis O41 (PrK 67/57)	OPS
270	2463	1200	52	9	Proteus mirabilis O43 (PrK 69/57)	PS

272	4209	348	61	12	Proteus mirabilis O49 (PrK 75/57)	PS
262	9551	971	200	14	Proteus mirabilis O5 (PrK 12/57)	PS
41	-47	80	12	12	Proteus mirabilis O50 (TG332)	
104	-61	74	57	4	Proteus mirabilis O51 (19011)*	LPS
42	1831	427	17	15	Proteus mirabilis O54a, 54b (10704)	
273	-2	21	24	7	Proteus mirabilis O54ab (OE)	PS
43	-51	88	34	38	Proteus mirabilis O57 (TG319)	
91	63	133	56	9	Proteus mirabilis O6 (PrK 14/57)	OPS
105	5323	821	70	18	Proteus mirabilis O74 (10705, OF)	OPS
106	-145	56	-28	30	Proteus mirabilis O75 (10702, OC)	OPS
107	-68	10	28	24	Proteus mirabilis O77 (3 B-m)	OPS
38	-252	80	-1	6	Proteus mirabilis O8 (TG326)	
263	107	16	29	11	Proteus mirabilis O9 (PrK 18/57)	PS
121	153	108	-9	13	Proteus myxofaciens O60	OPS
122	4570	506	37	23	Proteus O56 (genomospecies 4)	OPS
265	220	315	36	23	Proteus penneri O17 (16)	PS
108	-39	51	46	13	Proteus penneri O31a (26)	OPS
268	203	263	56	8	Proteus penneri O31ab (28)	PS
109	-232	150	23	10	Proteus penneri O52 (15)	OPS
110	10	39	58	19	Proteus penneri O58 (12)	OPS
111	-195	30	-12	9	Proteus penneri O59 (9)	OPS
112	324	195	21	8	Proteus penneri O61 (21)	OPS
113	77	75	-15	17	Proteus penneri O62 (41)	OPS
114	166	205	33	9	Proteus penneri O63 (22)	OPS
45	64	30	-6	10	Proteus penneri O64a, 64b, 64d (39)	
115	-179	76	-11	7	Proteus penneri O64a,b,c (27)	OPS
116	-125	71	-21	4	Proteus penneri O65 (34)	OPS
46	35	7	14	9	Proteus penneri O66 (2)	
117	-8	20	43	19	Proteus penneri O67 (8)	OPS
118	-125	40	-12	27	Proteus penneri O68 (63)	OPS
47	6316	2783	30	13	Proteus penneri O69 (25)	
119	244	210	-6	12	Proteus penneri O70 (60)	OPS
48	767	283	148	12	Proteus penneri O71 (42)	
49	255	228	12	8	Proteus penneri O72a, 72b (4)	
120	294	180	50	19	Proteus penneri O73a,b (103)	OPS
274	1606	349	20	11	Proteus penneri O73ac (75)	PS
44	-2	13	12	8	Proteus penneri O8 (106)	
72	73	18	-3	7	Proteus vulgaris O1 (18984)*	LPS

74	207	136	27	8	Proteus vulgaris O12 (PrK 25/57)	OPS
75	100	126	21	9	Proteus vulgaris O13 (8344)	OPS
76	-231	89	59	29	Proteus vulgaris O15 (PrK 30/57)	OPS
77	52	56	52	20	Proteus vulgaris O17 (PrK 33/57)	OPS
78	-253	199	30	11	Proteus vulgaris O19a (PrK 37/57)	OPS
260	2700	575	36	6	Proteus vulgaris O2 (OX2)	PS
79	7721	1653	451	47	Proteus vulgaris O21 (PrK 39/57)*	LPS
80	-41	103	30	6	Proteus vulgaris O22 (PrK 40/57)	OPS
175	-40	55	-5	5	Proteus vulgaris O24 (PrK 47/57)	LPSOH
81	-110	69	25	4	Proteus vulgaris O25 (PrK 48/57)	OPS
82	769	676	14	5	Proteus vulgaris O34 (4669)*	LPS
83	3906	2987	242	17	Proteus vulgaris O37a,b (PrK 63/57)	OPS
84	5865	719	21	8	Proteus vulgaris O37a,c (PrK 72/57)	OPS
73	-113	66	38	6	Proteus vulgaris O4 (PrK 9/57)	OPS
85	-129	113	-6	9	Proteus vulgaris O44 (PrK 67/57)	OPS
86	-23	96	-1	5	Proteus vulgaris O45 (4680)	OPS
271	-200	84	49	14	Proteus vulgaris O47 (PrK 73/57)	Not stated
87	-76	96	39	7	Proteus vulgaris O53 (TG 276-10)	OPS
88	-64	45	1	5	Proteus vulgaris O54a,54c (TG 103)	OPS
89	-71	79	11	18	Proteus vulgaris O55 (TG 155)	OPS
90	13	18	29	5	Proteus vulgaris O65 (TG 251)	OPS
275	130	78	17	5	Proteus vulgaris O76 (HSC438)	PS
136	191	248	65	16	Providencia alcalifaciens O19	LPS/NaOH
135	87	12	9	3	Providencia alcalifaciens O19	LPS
134	15	20	-57	12	Providencia alcalifaciens O19	OPS
137	-20	9	30	7	Providencia alcalifaciens O21	OPS
138	12353	876	-20	20	Providencia alcalifaciens O23	OPS
139	7	13	11	11	Providencia alcalifaciens O27	OPS
140	-7	16	26	11	Providencia alcalifaciens O29	OPS
141	225	60	62	1	Providencia alcalifaciens O30	OPS
142	18	13	-10	32	Providencia alcalifaciens O32	OPS
143	55	7	35	11	Providencia alcalifaciens O36*	LPS-NH4OH
144	33	32	11	32	Providencia alcalifaciens O39	OPS
132	4802	894	-4	22	Providencia alcalifaciens O5	OPS

133	-57	34	5	29	Providencia alcalifaciens O6*	LPS
145	163	38	-14	21	Providencia rustigianii O14	OPS
146	-74	43	-33	19	Providencia rustigianii O16	OPS
147	18	21	13	9	Providencia rustigianii O34	OPS
124	93	47	5	12	Providencia stuartii O18	OPS
125	377	375	50	15	Providencia stuartii O20*	LPS
123	1329	324	-34	25	Providencia stuartii O4	OPS
126	594	309	-3	11	Providencia stuartii O43	OPS
127	28	25	17	16	Providencia stuartii O44	OPS
128	246	22	-3	11	Providencia stuartii O47	OPS
129	221	100	4	17	Providencia stuartii O47, Core 9	OPS
1	496	426	15	6	Providencia stuartii O49	PO49 Core-linked
130	810	437	25	24	Providencia stuartii O49, Core 1	OPS
2	4887	666	56	5	Providencia stuartii O52	PO52 Core-linked
131	-2	20	0	8	Providencia stuartii O57	OPS
4	3	10	-8	1	Pseudomonas aerguinosa O1 (Fisher immunotype 4)	PO1 Core-linked
13	20	14	6	5	Pseudomonas aerguinosa O10	L8643
65	185	44	-2	6	Pseudomonas aerguinosa O10 10a,10b	IATS 10, OPS
66	3836	2153	2	22	Pseudomonas aerguinosa O10 10a,10c	IATS 19, OPS
67	5	143	15	13	Pseudomonas aerguinosa O11 11a,11b	IATS 11, OPS
68	59	11	-28	13	Pseudomonas aerguinosa O12 12	IATS 12, OPS Habs 12
6	65	39	2	4	Pseudomonas aerguinosa O13 (Sandvik serotype II)	PO13 Core-linked
69	558	302	107	12	Pseudomonas aerguinosa O13 13a,13c	IATS 14, OPS
70	136	19	-21	8	Pseudomonas aerguinosa O14 14	IATS 17,OPS Meitert X
71	425	552	16	8	Pseudomonas aerguinosa O15 15	IATS 15, OPS
50	-6	27	8	7	Pseudomonas aerguinosa O2 (2a),2d,2f	IATS 10 , OPS
5	-65	27	8	5	Pseudomonas aerguinosa O2 (Fisher immunotype 3)	PO2 Core-linked
51	329	379	10	1	Pseudomonas aerguinosa O2 2a,2b	IATS 16 OPS
52	856	692	22	8	Pseudomonas aerguinosa O2 2a,2b,2e	IATS NO, OPS
53	-41	27	14	7	Pseudomonas aerguinosa O2 2a,2d	IATS 5 OPS
54	1243	749	7	5	Pseudomonas aerguinosa O2 Immuno 7	IATS 18, OPS
55	-18	10	8	6	Pseudomonas aerguinosa O3 3a,3b	IATS NO, OPS
56	1224	646	16	5	Pseudomonas aerguinosa O3 3a,3b,3c	IATS 3, OPS
57	-45	22	25	8	Pseudomonas aerguinosa O3	IATS NO, OPS

					3a,3d	
3	344	247	5	2	Pseudomonas aerguinosa O4 (Habs serotype 4)	PO4 Core-linked
58	-78	272	22	5	Pseudomonas aerguinosa O4 4a,4c	IATS NO, OPS
59	-4	10	16	6	Pseudomonas aerguinosa O6 6a	IATS 6, OPS
60	517	105	74	12	Pseudomonas aerguinosa O6 6a,6c	IATS NO, OPS
61	166	160	15	13	Pseudomonas aerguinosa O6 Immuno 1	IATS NO, OPS
8	120	66	11	5	Pseudomonas aerguinosa O6a (Habs serotype6, fraction IIa)	PO6a Core-linked-O-unit
9	0	50	-3	2	Pseudomonas aerguinosa O6a (Habs serotype6, fraction IIb)	PO6a unsubstituted core
62	824	140	16	9	Pseudomonas aerguinosa O7 7a,7b,7c	IATS 7,LPS
63	867	801	24	10	Pseudomonas aerguinosa O7 7a,7b,7d	IATS 8,LPS
64	34	63	21	4	Pseudomonas aerguinosa O7 7a,7d	IATS NO, LPS
7	44	44	24	3	Pseudomonas aerguinosa O9 (9a, 9b, 9d)	PO9 Core-linked
20	24	17	21	3	Salmonella enterica abortus equi LPS	L5886
299	227	128	101	8	Salmonella enterica O17	PS
300	463	53	127	5	Salmonella enterica O28	PS
301	169	42	41	31	Salmonella enterica O47	PS
302	44	30	28	14	Salmonella enterica O55	PS
15	-44	37	-6	6	Salmonella enteritidis dodeca saccharide	1262
22	308	86	53	31	Salmonella enteritidis LPS	L2012
14	11	3	-3	4	Salmonella typhimurium dodeca saccharide	4809
16	551	266	114	36	Salmonella typhimurium LPS	L2262
10	168	66	214	23	Salmonella typhimurium SL 11881 (Re mut)	LPS-L9516
12	243	37	30	3	Salmonella typhimurium SL 684 (Rc mut)	LPS-L5891
11	677	237	31	7	Salmonella typhimurium TV 119 (Ra mut)	LPS-L6016
21	150	120	23	20	Salmonella typhosa LPS	L2387
17	66	30	20	14	Serratia marcescens LPS	L6136
25	5598	1474	29	13	Shigella bodyii type10	
23	25	8	138	50	Shigella bodyii type2	
24	181	48	36	9	Shigella bodyii type4	
195	78	32	48	4	Shigella boydii type 1	LPSOH
199	-49	67	142	88	Shigella boydii type 11	OPS
200	105	15	66	12	Shigella boydii type 12	OPS
292	6238	981	532	164	Shigella boydii type 13	LPSOH
293	129	11	83	12	Shigella boydii type 14	LPSOH
201	86	68	13	6	Shigella boydii type 15	OPS

202	431	244	75	33	Shigella boydii type 16	OPS
203	14	17	-8	5	Shigella boydii type 17	OPS
204	47	16	97	46	Shigella boydii type 18	OPS
196	42	21	19	7	Shigella boydii type 3	OPS
197	26	3	14	2	Shigella boydii type 5	OPS
289	1455	485	30	9	Shigella boydii type 6	PS
290	1035	387	140	16	Shigella boydii type 7	PS
291	34	21	93	10	Shigella boydii type 8	PS
198	155	42	8	3	Shigella boydii type 9	OPS
28	-25	29	-2	3	Shigella dysennteriae type 11	
29	1163	975	274	60	Shigella dysennteriae type 13	
26	328	103	28	5	Shigella dysennteriae type 3	
27	31	10	4	4	Shigella dysennteriae type 8 (batch 12)	
288	491	254	232	80	Shigella dysenteriae type 1	PS
215	437	184	34	3	Shigella dysenteriae type 2	LPSOH
216	14	7	18	14	Shigella dysenteriae type 4	OPS
217	21	4	56	8	Shigella dysenteriae type 5	OPS
218	-81	108	39	12	Shigella dysenteriae type 6 SR-strain	SR-strain
219	-3	9	19	6	Shigella dysenteriae type 7	OPS
220	-1088	878	-8	11	Shigella dysenteriae type 8 (Russian)	OPS
221	323	312	14	7	Shigella dysenteriae type 9	OPS
276	580	534	37	5	Shigella flexneri type 1a	PS
277	205	25	602	51	Shigella flexneri type 1b	PS
278	-70	46	-29	5	Shigella flexneri type 2a	PS
279	132	8	452	67	Shigella flexneri type 2b	PS
280	79	32	200	13	Shigella flexneri type 3a	PS
281	1420	320	1190	74	Shigella flexneri type 3b	PS
282	357	112	149	42	Shigella flexneri type 4a	PS
283	1144	141	1493	114	Shigella flexneri type 4b	PS
284	519	215	195	8	Shigella flexneri type 5b	PS
286	2005	1599	147	66	Shigella flexneri type 6	PS
285	682	74	2029	303	Shigella flexneri type 6a	PS
287	131	49	197	39	Shigella flexneri type X	PS
226	7605	3760	29	7	Streptococcus pneumoniae type 1 (Danish type 1)	161-X // Capsular PS
233	97	171	-11	12	Streptococcus pneumoniae type 12 (Danish type 12F)	193-X// Capsular PS
234	-14	4	43	8	Streptococcus pneumoniae type 14 (Danish type 14)	197-X// Capsular PS
235	-69	58	-8	10	Streptococcus pneumoniae type 17 (Danish type 17F)	201-X// Capsular PS
236	3	21	-8	3	Streptococcus pneumoniae type 19 (Danish type 19F)	205-X// Capsular PS
227	-188	117	9	17	Streptococcus pneumoniae type 2 (Danish type 2)	165-X// Capsular PS
237	-47	94	6	4	Streptococcus pneumoniae type 20 (Danish type 20)	209-X// Capsular PS

238	-44	50	15	5	Streptococcus pneumoniae type 22 (Danish type 22F)	213-X// Capsular PS
239	7610	3930	12	5	Streptococcus pneumoniae type 23 (Danish type 23F)	217-X// Capsular PS
240	51802	794	1123	333	Streptococcus pneumoniae type 26 (Danish type 6B)	225-X// Capsular PS
228	4197	1970	1	6	Streptococcus pneumoniae type 3 (Danish type 3)	169-X// Capsular PS
241	-36	5	27	7	Streptococcus pneumoniae type 34 (Danish type 10A)	229-X// Capsular PS
229	-44	127	-3	16	Streptococcus pneumoniae type 4 (Danish type 4)	173-X// Capsular PS
242	-119	175	4	5	Streptococcus pneumoniae type 43 (Danish type 11A)	233-X// Capsular PS
230	490	588	-25	7	Streptococcus pneumoniae type 5 (Danish type 5)	177-X// Capsular PS
243	-28	39	19	10	Streptococcus pneumoniae type 51 (Danish type 7F)	237-X// Capsular PS
244	-397	202	1	13	Streptococcus pneumoniae type 54 (Danish type 15B)	241-X// Capsular PS
245	-27	6	18	19	Streptococcus pneumoniae type 56 (Danish type 18C)	245-X// Capsular PS
246	7824	1874	-1	7	Streptococcus pneumoniae type 57 (Danish type 19A)	249-X// Capsular PS
247	-37	32	-10	4	Streptococcus pneumoniae type 68 (Danish type 9V)	253-X// Capsular PS
248	-32	32	86	13	Streptococcus pneumoniae type 70 (Danish type 33F)	257-X// Capsular PS
231	-97	76	4	15	Streptococcus pneumoniae type 8 (Danish type 8)	185-X// Capsular PS
232	20	8	14	9	Streptococcus pneumoniae type 9 (Danish type 9N)	189-X// Capsular PS
309	12264	3236	14535	771	Yeast Mannan	
312	19942	737	20693	265	Yeast Mannan Sigma M-3640	
153	98	32	-8	4	Yersinia pestis 1146-25	Core oligo saccharide
177	217	102	223	32	Yersinia pestis 260(11)-37C-186	LPS
178	76	41	239	7	Yersinia pestis 260(11)-37C-187	LPS
179	54	52	64	16	Yersinia pestis 260(11)-37C-416	LPS
180	466	158	159	51	Yersinia pestis 260(11)-37C-417	LPS
183	239	246	5	24	Yersinia pestis I-2377-25C	OS
184	312	167	145	9	Yersinia pestis I-2377-37C	LPS
249	1337	452	38	19	Yersinia pestis KM218-6C	OS
176	43	99	398	21	Yersinia pestis KM260(11)-6C	LPS
252	982	308	153	28	Yersinia pestis KM260(11)-wabC/waaL	OS
251	-93	90	15	12	Yersinia pestis KM260(11)-wabD/waaL	OS
250	-68	58	7	10	Yersinia pestis KM260(11)-yjhW-6C	OS

181	-18	3	31	4	Yersinia pestis P-1680-25C	OS	
182	103	203	89	38	Yersinia pestis P-1680-37C	LPS	
156	152	54	421	75	Yersinia pestis, 0KM218-37	LPS	
152	-54	46	155	24	Yersinia pestis, 1146-25	LPS	
154	870	110	128	4	Yersinia pestis, 1146-37	LPS	
155	142	78	45	20	Yersinia pestis, 1146-37	Core saccharide	oligo
172	702	122	15	25	Yersinia pestis, 11M-25	LPS	
173	-48	88	24	7	Yersinia pestis, 11M-37	LPS	
171	8	3	26	8	Yersinia pestis, KIMD1-25	Core saccharide	oligo
170	616	122	-17	8	Yersinia pestis, KIMD1-37	Core saccharide	oligo
159	83	146	7	7	Yersinia pestis, KM218-25	Core saccharide	oligo
158	16	53	1361	598	Yersinia pestis, KM218-25	LPS	
157	15	15	18	2	Yersinia pestis, KM218-37	Core saccharide	oligo
162	475	178	3275	1102	Yersinia pestis, KM260(11)-Δ0186	LPS	
163	35	16	-9	9	Yersinia pestis, KM260(11)-Δ0186	Core saccharide	oligo
149	7	22	24	14	Yersinia pestis, KM260(11)-Δ0187	Core saccharide	oligo
148	378	72	452	43	Yersinia pestis, KM260(11)-Δ0187	LPS	
161	109	40	26	23	Yersinia pestis, KM260(11)-ΔpmrF	Core saccharide	oligo
160	1460	308	575	82	Yersinia pestis, KM260(11)-ΔpmrF	LPS	
150	755	300	91	28	Yersinia pestis, KM260(11)-Δrfe	LPS	
151	-7	18	-62	11	Yersinia pestis, KM260(11)-Δrfe	Core saccharide	oligo
166	186	85	174	59	Yersinia pestis, KM260(11)-ΔwaaL	LPS	
165	-32	21	-5	9	Yersinia pestis, KM260(11)-ΔwaaQ	Core saccharide	oligo
164	164	146	577	200	Yersinia pestis, KM260(11)-ΔwaaQ	LPS	
167	141	44	390	34	Yersinia pestis, KM260(11)-25	LPS	
168	105	13	33	22	Yersinia pestis, KM260(11)-25	Core saccharide	oligo
169	108	109	-13	6	Yersinia pestis, KM260(11)-37	Core saccharide	oligo
254	112	53	1	5	Yersinia pseudotuberculosis 85pCad-20C	OS	
253	-71	70	-10	13	Yersinia pseudotuberculosis 85pCad-37C	OS	
255	13011	3710	6265	1156	Yersinia pseudotuberculosis O:2a	PS	
256	456	176	134	8	Yersinia pseudotuberculosis O:2a-dhmA	PS	

257	421	116	2	6	Yersinia O:2c	pseudotuberculosis	PS
258	5731	784	380	62	Yersinia O:3	pseudotuberculosis	PS
259	456	30	225	19	Yersinia O:4b	pseudotuberculosis	PS

FIGURE S1: STD built up curves for **1** interacting with murine and human Langerin, respectively. Curves were fitted according to (35).

FIGURE S2: STD built up curves for (A) **2** and (B) **3** interacting with human and murine Langerin respectively. Curves were fitted according to (35).

FIGURE S3: Multiple sequence alignment of 28 mammalian Langerin sequences found in the UniProtKB. Alignment was performed using CLUSTAL Omega (1.2.1) (42). Color-coded according to conservation (black identical, grey – similar) for residues with at least 80% identity using Sequence manipulation suite (45).

FIGURE S3: Multiple sequence alignment of 27 mammalian asialoglycoprotein sequences found in the UniProtKB. Alignment was performed using CLUSTAL Omega (1.2.1) (42). Color-coded according to conservation (black identical, grey – similar) for residues with at least 80% identity using Sequence manipulation suite (45).

Figure S1

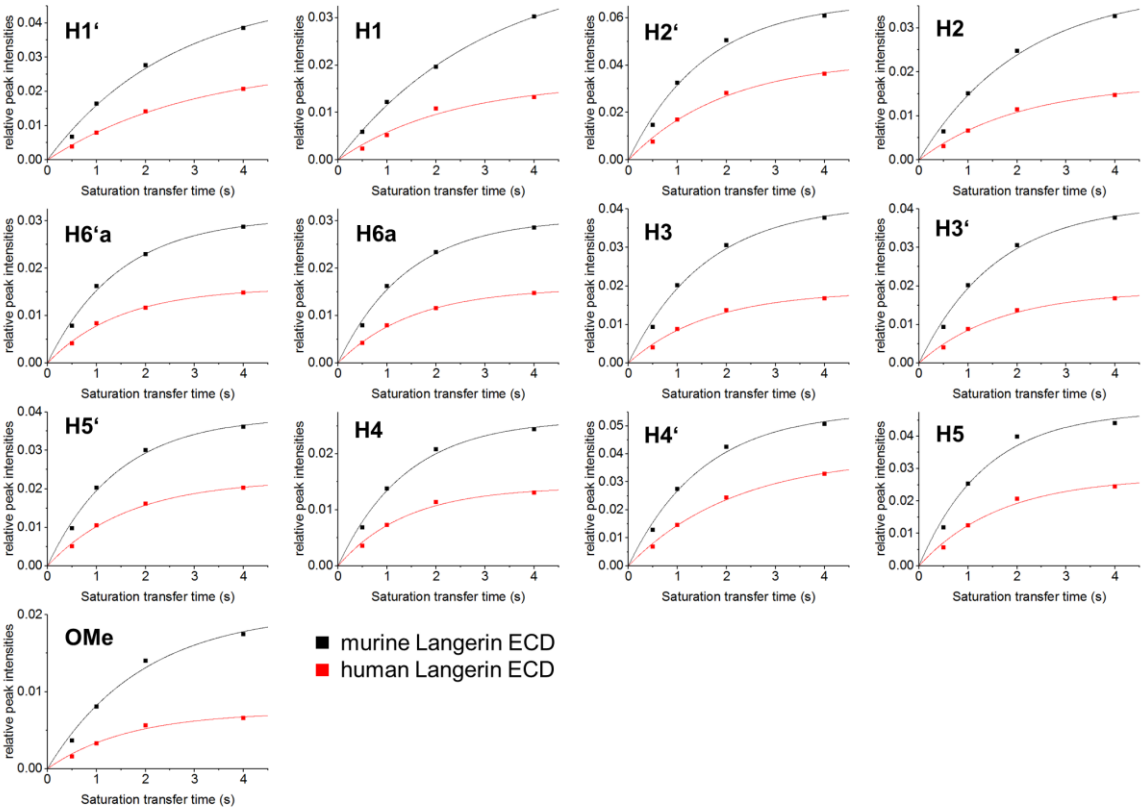

H1‘
H1
H2‘
H2
H6‘a
H6a
H3
H3‘
H5‘
H4
H4‘
H5
OMe
relative peak intensities
Saturation transfer time (s)
murine Langerin ECD
human Langerin ECD

Figure S2

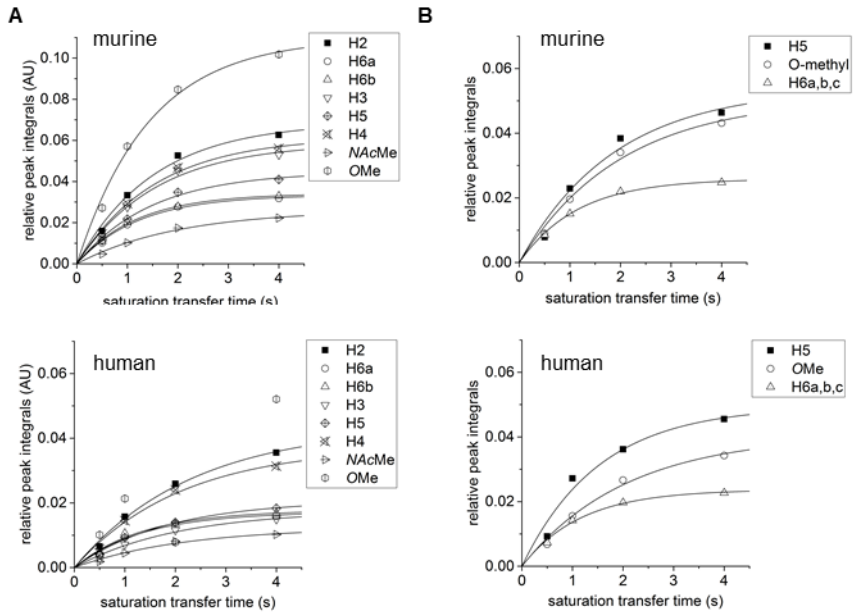

A
murine
relative peak integrals (AU)
saturation transfer time (s)
H2
H6a
H6b
H3
H5
H4
NAcMe
OMe
human
relative peak integrals (AU)
saturation transfer time (s)
H2
H6a
H6b
H3
H5
H4
NAcMe
OMe
B
murine
relative peak integrals
saturation transfer time (s)
H5
O-methyl
H6a,b,c
human
relative peak integrals
saturation transfer time (s)
H5
OMe
H6a,b,c

Figure S3

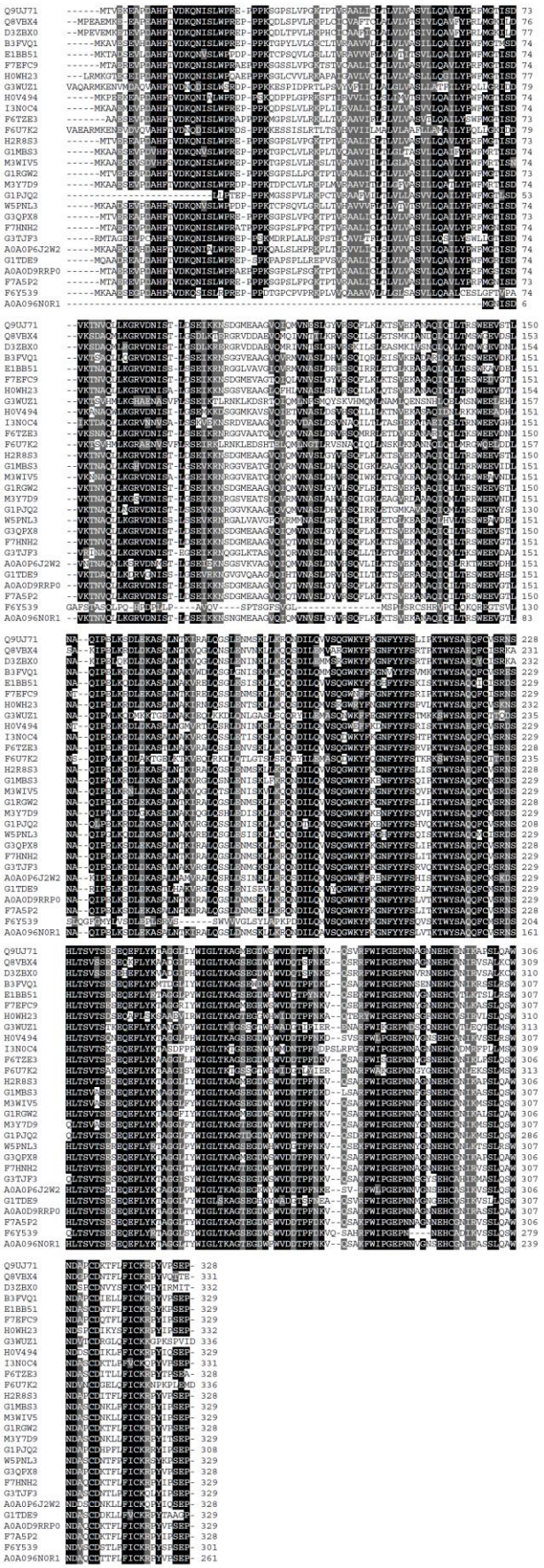


Figure S4

