Table S1. Data Collection and Refinement Statistics, Related to Figures 1 and 2

	C5b6[a]	C5b6[b]
Data collection		
Space group	$I2_12_12_1$	$I2_12_12_1$
Cell dimensions		
a, *b*, *c* (Å)	154.2, 230.8, 270.0	154.2, 230.8, 270.0
α, β, γ (°)	90.0, 90.0, 90.0	90.0, 90.0, 90.0
Resolution (Å)	50.0-3.5 (3.83-3.50)[c]	50.0-3.8 (4.25-3.80)
R_{merge}	0.159 (1.043)	0.126 (0.464)
R_{pim}	0.143 (0.946)	0.113 (0.418)
$I / \sigma I$	4.8 (1.1)	5.9 (2.3)
Mn (*I*) CC[d]	0.986 (0.302)	0.989 (0.709)
Completeness (%)	98.0 (97.2)	98.3 (97.6)
Redundancy	3.0 (3.0)	3.0 (3.0)
Refinement		
Resolution (Å)[d]	50.0-3.5 (*a**=4.2, *b**=3.8, *c**=3.5)	
No. reflections	59017	
R_{work} / R_{free}	25.6/27.0	
No. atoms	19028	
Protein	18928	
Glycans	99	
Ions	1	
B-factors (Å^2)		
Protein	157	
R.m.s. deviations		
Bond lengths (Å)	0.007	
Bond angles (°)	1.04	

[a]Data statistics for all data between 50 and 3.5Å.

[b]Data statistics for data between 50 and 3.8Å, based on an overall half-dataset correlation coefficient > 0.5

[c]Values in parentheses are for highest-resolution shell.

[d]The data included is based upon a half-dataset correlation coefficient > 0.5

Table S2. Rigid Body Changes in the C5 to C5b Transition, Related to Figure 1D

	C5->C5b		C3->C3b	
	Translation (Å)	Rotation (°)	Translation (Å)	Rotation (°)
MG3	3	44	4	15
MG7	11	38	8	36
MG8	19	57	23	61
CUB	38	36	40	37
TED	45	132	66	104
C345C	32	141	5	8

The structure of C5b was compared to that of C5 (Fredslund et al., 2008) (PDB code: 3CU7). First, the structures were superimposed on the β-chain. After that, all domains of C5 were individually superimposed on the corresponding domains of the C5b model. Those showing major rearrangements are depicted in the table. As a comparison, the same procedure was also performed for the C3 to C3b transition using for C3 (Janssen et al., 2005) (PDB code: 2A73), and for C3b (Janssen et al., 2006) (PDB code: 2I07). All calculations were done using the program Superpose from the CCP4 suite (1994).

Table S3. Rigid Body Changes in C6 upon Binding to C5b, Related to Figure 1F

	C6->(C5b)C6	
	Translation (Å)	Rotation (°)
CCP1	28	95
CCP2	83	71
FIMACs	153	108

The structure of C5b bound C6 was compared to that of free C6 (Aleshin et al., 2012) (PDB code: 3T5O). First, the structures were superimposed on the MACPF core. After that, the other domains of C6 were individually superimposed on the corresponding domains of the C5bC6 model. Those showing major rearrangements are depicted in the table. All calculations were done using the program Superpose from the CCP4 suite (1994).