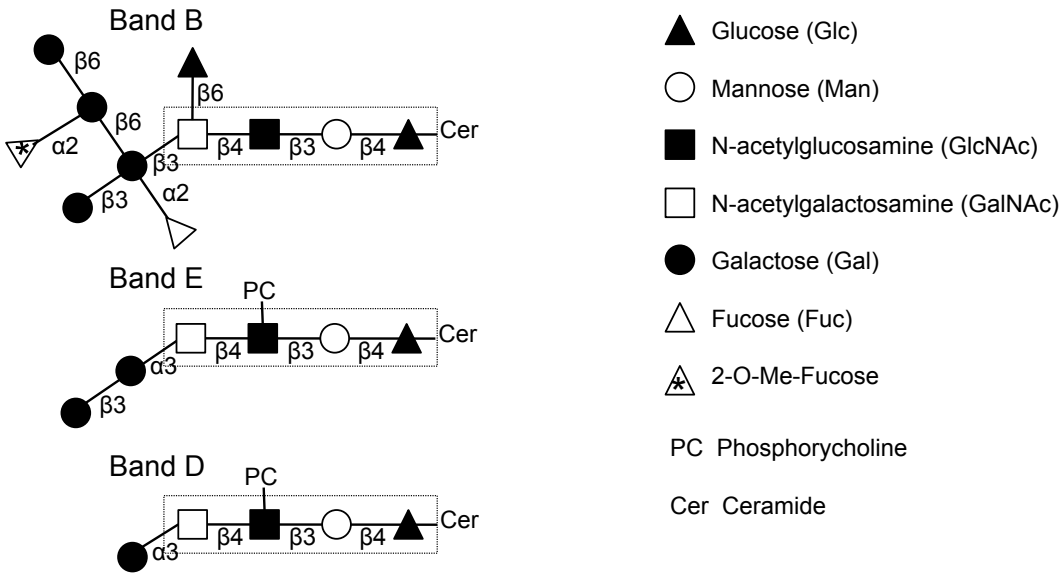

Figure S1. Glycolipid receptor of Cry5B.
Top, One of the glycolipid receptors of Cry5B, previously identified as band B (Griffitts et al., 2001). Middle, a more minimal glycan receptor of Cry5B, previously identified as band E (Griffitts et al., 2001). Bottom, glycan previously identified as band D (Griffitts et al., 2001), which is not bound by Cry5B. The arthroseries tetrasaccharide core is boxed in dotted lines.

Table S1. Data collection, phasing and refinement statistics

	Native	SeMet
Data collection		
Space group	$P6_3$	$P6_3$
Cell dimensions		
a, *b*, *c* (Å)	a=b=115.5 c=110.3	a=b=114.5 c=111.0
α, β, γ (º)	α=β=90, γ=120	α=β=90, γ=120
		Peak
Wavelength (Å)	0.97930	0.97865
Resolution (Å)	50.00-2.30 (2.34-2.30)	50.00-3.15 (3.20-3.15)
R_{merge}	15.3 (70.5)	20.6 (75.5)
I/σ_I	17.5 (3.2)	41.9 (7.3)
Completeness (%)	99.9 (100)	100 (100)
Redundancy	6.3 (6.3)	42.7 (35.9)
Refinement		
Resolution (Å)	39.9-2.3	
No. reflections	37,191	
R_{work}/ R_{free}	0.173/0.218	
No. atoms		
Protein	4,624	
Ligand/ion		
Water	481	
B-factors (Å^2)		
Protein	32.3	
Ligand/ion		
Water	33.0	
R.m.s deviations		
Bond lengths (Å)	0.008	
Bond angles (º)	1.132	

*Highest resolution shell is shown in parenthesis.