Table 1. Crystallographic statistics of Reelin R5-6

Data collection and reduction	
Space group	$P2_1$
Unit cell dimensions a, b, c (Å)	61.01, 70.95, 94.77
β (deg)	93.61
Resolution range (Å)	47.29-2.00 (2.07-2.00)
Completeness (%)	99.9 (99.9)
Redundancy	4.1 (4.1)
R_{merge} (%)	7.5 (32.5)
$\langle I/\sigma(I)\rangle$	21.8 (4.0)
Refinement	
R_{work} (%)	17.9
R_{free} (%)*	21.9
Non-H atoms	6185
Protein (No. residues)	5581 (705)
Water	500
Acetate	3
Oligosaccharide	95
Ca^{2+}	4
Zn^{2+}	2
R.m.s.d from ideal values	
Bond lengths (Å)	0.009
Bond angles (deg)	1.16
Mean *B*-factor for protein atoms (Å^2)	
Main chain	26.82
Side chain	27.57
Ramachandran plot (%)	
Most favored	84.9
Additionally allowed	14.4
Generously allowed	0.7
Disallowed	0

* R_{free} is the *R*-factor for 5% of the reflections excluded from the refinement.