Computer modeling of agrin G3 domain structure — The structural models were built by using the homology modeling function of Swiss-PdbViewer V3.7 b2 [1]. The crystal structure of αL2LG5 (PDB code: 1DYKA) was selected as the template and the sequence alignment of AgG3 and αL2LG5 was adjusted according to their secondary structures (see below for sequence alignment, [2]). The modeling request was submitted to Swiss-Model server and the modeling results were presented by PdbViewer.

```
L2Lg5       -------SGTYFDGTGFAKAVGGFKVG------------LDLLVEFEFRTTRPTGVLLGI
AgG3  1757 EFPVGDLETLAFDGRTYIEYLNAVIESELTNEIPAEKALQSNHFELSLRTEATQGLVLWI

L2Lg5       -------SGTYFDGTGFAKAVGGFKVG------------LDLLVEFEFRTTRPTGVLLGI
AgG3  1824 GKAAERADYMALAIVDGHLQLSYDLGSQPVVLRSTV----KVNTNRWLRIRAHREHREGS

L2LG5       LVVD-GNQVDAQSPNSASTSADTNDPVFVGGFPG--GLNQFGLTTNIRFRGCIRSLKLTK
AgG3  1880 LQVGNEAPVTGSSP-LGATQLDTDGALWLGGLQKLPVGQALPKAYGTGFVGCLRDVVVG-
```

References

[1] Guex, N. and Peitsch, M.C. (1997). SWISS-MODEL and the Swiss-PdbViewer: an environment for comparative protein modeling. Electrophoresis 18, 2714-23.

[2] Hohenester, E., Tisi, D., Talts, J.F. and Timpl, R. (1999). The crystal structure of a laminin G-like module reveals the molecular basis of alpha-dystroglycan binding to laminins, perlecan, and agrin. Molecular Cell 4, 783-92.