

The Crystal Structure of Human CD1d with and without α -Galactosylceramide Bound

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The glycolipid α -galactosylceramide binds with high affinity to CD1d and stimulates NKT cells. Here we report the crystal structure of human CD1d in complex with synthetic α -galactosylceramide at 3.2 Å resolution. The structure reveals a tightly fit lipid in the CD1d hydrophobic binding groove, with the sphingosine chain bound in the C' pocket and the longer acyl chain anchored in the A' pocket. Pocket volumes and hydrogen bonds to the glycolipid head group optimize α -galactosylceramide binding to CD1d. The structure of CD1d without lipid is also presented which shows a more open conformation of the binding groove than is seen in lipid-bound CD1d, suggesting a dual conformation of CD1d in which the "open" conformation is more able to load lipids than the lipid-bound "closed" conformation.

Keywords: humanCD1d, empty MHC class I-like protein, α -Galactosylceramide