

Supplementary Data

Supplementary Figure 1. Omit map of α -C-GalCer in mouse CD1d binding cleft.

Omit map contoured at 1 sigma. α -C-GalCer, blue; CDR1 α , purple; CDR3 α , yellow; mCD1d, grey.

Supplementary Figure 2. Differential affinity binding kinetics of V β 8.2 and V β 7 to CD1d-Ag.

Binding of increasing concentrations of V β 8.2 TCR to CD1d- α -GalCer (A) or CD1d- α -C-GalCer (B). Binding of V β 7 TCR to CD1d- α -GalCer (C) or CD1d- α -C-GalCer (D).

All results are shown as one representative experiment of two.

Supplementary Table 1

Data collection and refinement statistics

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mVα14Vβ8.2TCR-CD1d-α-C-GalCer	
Data collection	
Temperature	100K
Resolution limits (Å)	50-3.2 (3.37-3.20)
Space Group	P2 ₁ 2 ₁ 2 ₁
Cell dimensions (Å)	$a=59.17, b=86.37, c=236.40$
Total N ^o . observations	168608
N ^o . unique observations	20725
Multiplicity	8.1 (9.8)
Data completeness	100 (100)
I/ σ ₁	7.2 (2.2)
R _{p.i.m} ¹ (%)	9.8 (37.7)
Refinement statistics	
R _{factor} ² (%)	22.6
R _{free} ³ (%)	28.9
Non hydrogen atoms ⁴	
- protein	6587
- lipid	60
- other	56
Ramachandran plot	
- Most favoured	88.4
- Allowed region (%)	11.3
- Generously allowed region (%)	0.3%
B-factors (Å ²)	
- Average main chain	80.5
- Average side chain	82.0
- α -GalCer	76.1
rmsd bonds (Å)	0.007
rmsd angles (°)	1.007

$$^1 R_{p.i.m} = \sum_{hkl} [1/(N-1)]^{1/2} \sum_i |I_{hkl,i} - \langle I_{hkl} \rangle| / \sum_{hkl} \langle I_{hkl} \rangle$$

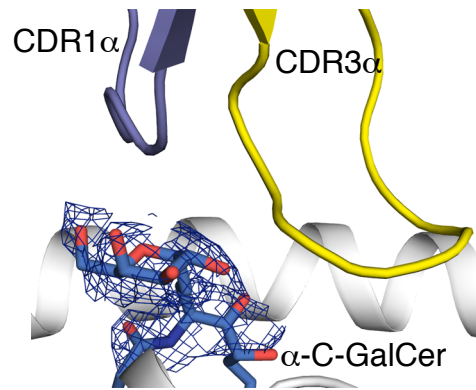
$$^2 R_{factor} = (\sum | |F_o| - |F_c| |) / (\sum |F_o|) - \text{for all data except as indicated in footnote 3.}$$

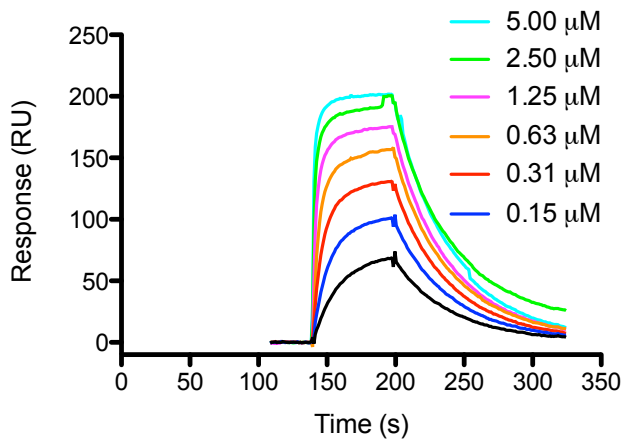
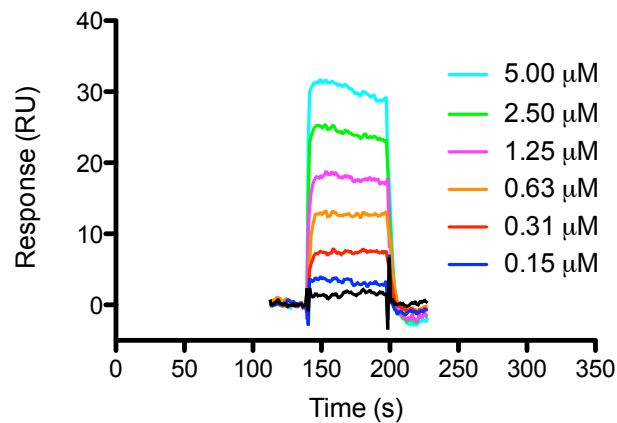
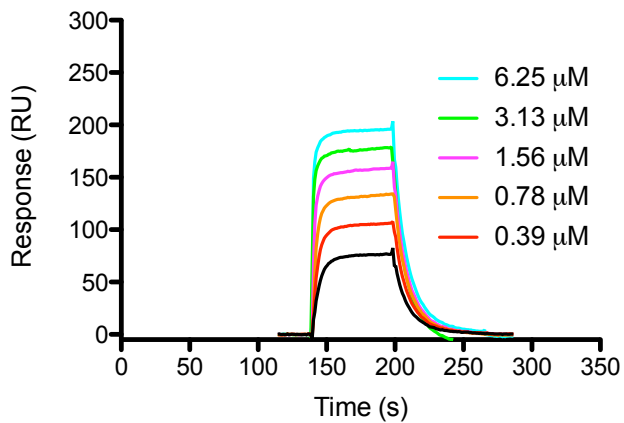
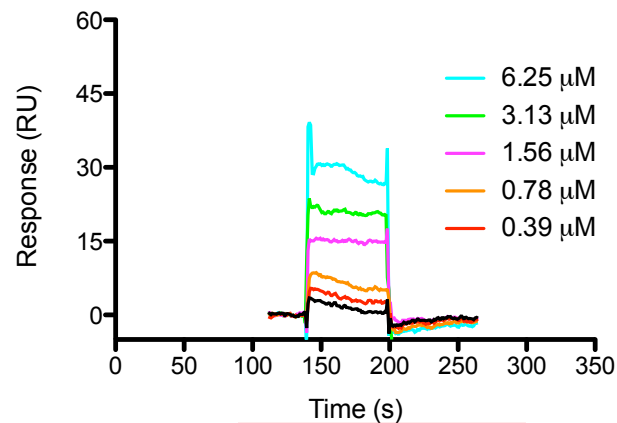
³ 5% of data was used for the R_{free} calculation

Values in parentheses refer to the highest resolution bin.

⁴The residues that could not be modelled in the structures were CD1d: residues 1-6, 300-302; β_2m : residue 1; TCR α chain: residues 1, 135-135, 209-210; TCR β chain: residues 1-2, CDR3 β loop 96-102.

SUPPLEMENTARY FIGURE 1



A**B****C****D****Supp. Fig. 2**