	Vβ8.2 TCR-mCD1d-	Vβ7 TCR-mCD1d-	Vβ11 TCR-hCD1d-α-						
	α-GalCer	α-GalCer	GalCer						
Data collection									
Temperature	100K	100K	100K						
Resolution limits (Å)	50-2.9 (3.06-2.90)	50-2.8 (2.95-2.80)	50-2.5 (2.59-2.50)						
Space Group	$P2_12_12_1$	$P2_12_12_1$	P2						
Cell dimensions (Å)	<i>a</i> =61.113, <i>b</i> =81.506,	<i>a</i> =58.229, <i>b</i> =81.913,	<i>a</i> =112.11, <i>b</i> =82.36						
	<i>c</i> = 233.451,	<i>c</i> =243.253,	<i>c</i> = <i>117.18</i> ,						
	α=β=γ=90.00°	α=β=γ=90.00°	α=90.00, β=101.3,						
			γ=90.00°						
Total N ^{o.} observations	149997	205387	195771						
N ^{o.} unique observations	26743	29526	66054						
Multiplicity	5.6 (6.0)	7.0 (5.8)	3.0 (2.7)						
Data completeness	100 (100)	99.7 (99.1)	91.1 (74.3)						
I/σ_1	11.1 (2.1)	13.7 (2.2)	10.5 (1.7)						
$R_{p.i.m}^{1}$ (%)	7.6 (31.5)	5.3 (30.4)	-						
R_{merge}^{2} (%)	-	-	8.8 (34.3)						
Refinement statistics									
$R_{factor}^{3}(\%)$	23.4	22.4	21.6						
R_{free}^{4} (%)	29.8	27.1	27.9						
Non hydrogen atoms									
- protein	6559	6528	12995						
- lipid	60	60	120						
- water	28	47	494						
- other	56	56	93						
Ramachandran plot									
- Most favoured	88.9	91.6	89.4						
- Allowed region (%)	11.1	8.3	10.1						
- Generously allowed	0.0	0.1	0.5						
region (%)									
B-factors (A ²)	10.0								
- Average main chain	48.8	44.0	42.8						
- Average side chain	49.0	44.3	42.5						
- α -GalCer	52.1	49.0	29.7						
- water	38.7	33.1	38.9						
rmsd bonds (A)	0.007	0.006	0.007						
rmsd angles (°)	1.076	1.029	1.119						

Supplementary information Supplementary Table 1 Data collection and refinement statistics

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

 $^{2} R_{merge} = \Sigma_{hkl} \Sigma_{i} \mid I_{hkl, i} - <\!\!I_{hkl}\!\!> \mid / \Sigma_{hkl} <\!\!I_{hkl}\!\!>$

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

 4 5% of data was used for the $R_{\mbox{\tiny free}}$ calculation

Values in parentheses refer to the highest resolution bin.

Supplementary radie 2 SFK data for NKT TCK interactions												
Interaction	$K_{on} (M^{-1}s^{-1})$	$K_{off}(s^{-1})$	$t_{1/2}(s)$	K _D Calc.	Chi ²	K _D obs.						
				(nm)		(nm)						
Vβ8.2 NKT-	6.40E+05	0.04	17.32	54.9	16.36	69.7						
mCD1d-α-GalCer												
Vβ8.2 NKT-	1.03E+06	0.09	7.7	84.9	7.21	93.9						
hCD1d-α-GalCer												
Vβ7 NKT- mCD1d-	4.26E+05	0.1	6.93	224	2.14	295						
α-GalCer												
Vβ7 NKT-hCD1d-	1.28E+05	0.49	1.41	3810	4.09	3420						
α-GalCer												
hNKT TCR-	3.15E+05	0.33	2.1	1060	9.15	910						
mCD1d-α-GalCer												
hNKT TCR-hCD1d-	6.27E+05	0.15	4.62	236	9.95	219						
α-GalCer												

Supplementary Table 2 SPR data for NKT TCR interactions

Supplementary Table 3 SPR data for mutant NKT TCR interactions

<u>Mutant</u>	<u>K_D (nM)</u>
Vβ7 wt	134
Vβ7 D26A	171
Vβ7 S54A	32.6
Vβ7 S56A	189
Vβ7 Y50F	520
Vβ7 E57A	225
Vβ8.2 wt	29.4
Vβ8.2 N28A	33.7
Vβ8.2 Y48F	> 1690
Vβ8.2 Y50F	377
Vβ8.2 E56A	165

Supplementary Figures

Suppl. Fig. 1. Characterisation of recombinant NKT TCRs

(A) Purified bacterially-expressed TCRs were analysed by SDS-PAGE under reducing conditions (lanes 1-4) and non-reducing conditions (lanes 5-8). Lanes 1&5 control TCR LC13, lanes 2&6 human V α 24V β 11 (NKT-15), lanes 3&7 mouse V α 14-V β 7 and lanes 4&8 mouse V α 14-V β 8.2.

(B) The structural integrity of the constant domains of the recombinant soluble TCRs were assessed by using the conformationally-specific mAb, 12H8 in an ELISA. Plate bound TCRs, LC13 (positive control), human V α 24V β 11 NKT-15 TCR, mouse V α 14V β 7 TCR, mouse V α 14V β 8.2 TCR or irrelevant HLA B8-FLR (negative control) were treated with graded amounts of 12H8. 12H8-reactivity is shown as absorbance at 492nm on the vertical axis and concentration of 12H8 (µg/ml) is indicated on the horizontal axis.

Suppl. Fig. 2 Shift in the position of the galactose head group of α -GalCer in mCD1d when ligated to the mouse NKT TCR. Mouse NKT TCR CDR1 α , purple; CDR3 α , yellow; mCD1d in ternary complex, grey; α -GalCer in ternary complex, magenta; mCD1d in binary complex, pink; α -GalCer in binary complex, green.

Suppl. Fig. 3 Sequence alignments between mouse and human NKT TCRs

Suppl. Fig. 4 Comparison of mouse NKT TCR-mCD1d-α-GalCer with human NKT TCR-hCD1d-α-GalCer. Parallel docking mode of the human and mouse NKT-TCR onto CD1d-α-GalCer. (**A**) Superposition of mouse Vα14-Vβ8.2 NKT TCR-mCD1d-α-GalCer and human Vα24-Vβ11 NKT TCR-hCD1d-α-GalCer. mTCR α-chain, cyan; mTCR β-chain, green; α-GalCer in mouse complex, magenta; mCD1d heterodimer, grey; hTCR α-chain, salmon; hTCR β-chain, yellow; α-GalCer in human complex, marine; hCD1d heterodimer, palegreen; (**B**) Superposition of mouse Vα14-Vβ7 NKT TCR-mCD1d-α-GalCer and human Vα24-Vβ11 NKT TCR-hCD1d-α-GalCer. mTCR β-chain, blue. mTCR α-chain, α-GalCer in mouse and human complex, mCD1d, hTCR and hCD1d colour coding as in **A**.



12H8 µg/ml

Supplementary Figure 2



Supplementary Figure 3

	CDR1b					CDR2b																			
	26	27	2	28	29	30	3	1			48	49	9 5	50	51	52	53	3 5	4	55	56				
Mouse Vb8.2	т	Ν	N	1	н	Ν	Ν				Y	S	Y	Ζ	G	А	G	S		т	Е				
Mouse Vb7	D	М	S	5	н	Е	т				I	S	У	ζ	D	v	D	S		N	S				
Human Vb11	т	М	G	5	н	D	Κ				Y	S	У	ζ	G	v	Ν	S		т	Е				
	CDR	Bb																							
Mouse Vb8.2	92 C	93 A	94 S	95 G	96 D	97 A	98 G	99 G	100 N	101 Y	102 A	103 E	Q	F	F	G	Ρ	G	т	R	L	т	v	L	117
Mouse Vb7	С	A	S	S	S	т	G	L	D	Т	Q	Y	F	G	P	G	Т	R	L	L	V	L	-		
Human VDII	C	A	5	5	G	Г	R	D	R	G	Г	Y	Е	Q	ĭ	F.	G	Р	G	т	R	Г	т	v	т
	CDR1a						CD	DR2a																	
	26	27	2	28	29	30	3	1			49	50) 5	51	52	53	54	ł							
Mouse Val4	v	т	F)	D	Ν	Н				L	V	Γ)	Q	Κ	D								
Human Va24	v	S	F)	F	S	Ν				М	т	E	r	S	Е	Ν								
	CDR	Ba																							
Mouse Val4	90 C	91 V	92 V	93 G	94 D	95 R	96 G	97 S	98 A	99 т.	100 G	103 R	104 T.	105 н	106 F	107 G	108 A	109 G	110 T	111	112 T.	113 T	114 V	115 T	116 P
Human Va24	C	v	v	S	D	R	G	S	т	L	G	R	L	Y	F	G	R	G	T	õ	L	T	v	Ŵ	P

Supplementary Figure 4



