

Tables

Table S1. Data collection and refinement statistics for nanobody D03.

	Nanobody D03
<u>Data collection</u>	
Space group	P65
Cell dimensions	
a, b, c (Å)	52.81 52.81 182.47
α, β, γ (°)	90 90 120
Resolution (Å)	50.00-1.76 (1.86-1.76)
Rmerge	0.103 (0.266)
I/ σ I	7.7 (1.6)
Completeness (%)	94.7 (69.5)
Redundancy	5.0 (1.7)
<u>Refinement</u>	
Resolution (Å)	44.36-1.76
No. reflections	26863
Rwork/ Rfree	0.182 / 0.204
<u>No. atoms</u>	
Protein	1997
Ligand	-
Water	133
<u>B-factors</u>	
Protein	35.55
<u>R.m.s. deviations</u>	
Bond length (Å)	0.01
Bond angles (°)	1.14

^a Values in parentheses correspond to the highest resolution shell.

^b R.m.s. deviation - Root-mean-square deviation.