Table 2. Data collection and refinement statistics.						
	cAb-lys3*	**D2-L19†**	**cAb-Lys2†**	**D3-L11**	**D2-L29**	**D2-L24**
Space group	C 2	$P2_12_12_1$	$P2_12_12_1$	$P2_1$	$P4_32_12$	I4
a/b/c, Å	128.2/72.8/38.7	51.5/53.4/104.5	50.0/68.4/72.1	43.9/49.9/57.0	114.1/114.1/35.7	114.8/114.8/33.3
$\alpha/\beta/\gamma$, °	90/106.94/90	90/90/90	90/90/90	90/92.1/90	90/90/90	90/90/90
Data statistics						
Resolution, Å	100.0-2.1	30.0-1.85	27.0-1.4	17.0-1.6	81.7-2.0	17.0-1.5
R merge	0.15	0.077	0.065	0.087	0.056	0.061
Completeness, %	99.8	98.4	99.0	99.5	99.8	99.9
I/σ	11.5	23.2	22.9	11.0	26.2	10.5
Highest resolution shell, Å	2.18-2.1	1.92-1.85	1.45-1.40	1.66-1.60	2.07-2.0	1.55-1.50
R factor	0.432	0.251	0.371	0.354	0.425	0.353
Completeness, %	99.8	91.4	96.8	98.8	100.0	99.5
I/σ	3.48	7.15	3.35	2.5	4.5	3.0
Refinement statistics						
Number of reflections	19935	24895	48908	29781	16470	35086
Number of reflections in free set	1810	1254	2475	1536	830	1762
R	0.18	0.17	0.22	0.20	0.22	0.21
R_{free}	0.20	0.20	0.24	0.23	0.24	0.23
Ramachandran Plot						
Most favored regions, %	88.6	92.2	89.2	89.6	84.4	90.1
Additionally allowed, %	10.9	7.8	10.8	10.0	14.6	9.9
Generously allowed regions, %	0.5	0	0	0.5	0	0
Disallowed regions, %	0	0	0	0	0	0
RMS deviations						
Rms deviation bond lengths, Å	0.017	0.0075	0.0044	0.0092	0.0059	0.0096
Rms deviation bond angles, °	1.760	1.414	1.296	1.683	1.360	1.604

* Decanniere K., Transue T.R., Desmyter A., Maes D., Muyldermans S. & and Wyns L. (2001) *J. Mol. Biol.* **313**, 473-478. (PDB ID code: 1JTT)

† De Genst, E., Silence, K., Ghahroudi, M. A., Decanniere, K., Loris, R., Kinne, J., Wyns, L. & Muyldermans, S. (2005) *J. Biol. Chem.* **280**, 14114-14121. (PDB ID codes: 1RJC and 1RI8)