Correction

Correction: Identification of a New Epitope in uPAR as a Target for the Cancer Therapeutic Monoclonal Antibody ATN-658, a Structural Homolog of the uPAR Binding Integrin CD11b (α M)

The *PLOS ONE* Staff

There are 2 errors in Table 1. The following PDB codes are missing: 4K23 for ATN-658 Fab and 4K24 for ATN-658-uPAR-ATF-SMB. Please see below for a corrected version.

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Table 1. Statistics of X-ray data collection and structural model refinement.

Crystals	ATN 658 Fab	ATN-658-uPAR-ATF-SMB
X-ray source	APS SER-CAT beamline 22-ID	BNL x29
Temperature (K)	100	100
Resolution range	31.45-1.60 (1.64-1.60) ^a	26.90- 4.50 (4.66-4.50) ^a
Wavelength (Å)	1.04	1.04
Space group	P12 ₁ 1	H32
Cell parameters (Å)	37.31, 132.30, 46.83	164.65, 164.659, 391.582
Unique reflections	49312 (4021)	12451 (1221)
Rmerge (%) ^b	0.094 (0.290)	0.139 (0.841)
Completeness (%)	85.7(70.0)	99.7(100.0)
Average I/σ	9.2 (4.65)	16.14 (2.03)
Data redundancy	3.0 (2.6)	4.4 (4.5)
Model refinement:		
R-factor/Rfree (%)	19.8/24.6	20.7/29.3
Overall B-factors (Å ²)	23.0	61.436
Protein B-factors (Å ²)	21.3	259.694
Solvent B-factors (Å ²)	39.4	
R.m.s.d. from ideal bond length (Å)	0.012	0.013
R.m.s.d. from ideal bond angles (°)	1.407	2.018
Ramachandran plot, % residues in regions:		
favored	93.8	84.5
allowed	5.7	13.7
outlier	0.5	1.8
PDB ID	4K23	4K24

^aNumbers in the parentheses are for the highest resolution shells; ^b $R_{\text{merge}} = \sum h \sum |I_i(h) - \langle I(h) \rangle| / \sum h \sum I_i(h)$, where $\langle I(h) \rangle$ is the mean intensity of reflection h .
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References

1. Xu X, Cai Y, Wei Y, Donate F, Juarez J, et al. (2004) Identification of a New Epitope in uPAR as a Target for the Cancer Therapeutic Monoclonal Antibody ATN-658, a Structural Homolog of the uPAR Binding Integrin CD11b (αM). PLoS ONE 9(1): e85349. doi:10.1371/journal.pone.0085349