PLOS ONE

CORRECTION

Correction: The Crystal Structure and Small-Angle X-Ray Analysis of CsdL/TcdA Reveal a New tRNA Binding Motif in the MoeB/E1 Superfamily

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There are multiple errors in Table 1. Please see the corrected Table 1 here.

There is an error in the last sentence of the "TcdA crystallization, structure determination and refinement" subsection of the Materials and Methods. The correct sentence is: A data set for the AMP complex was collected to 1.80-Å resolution at the PROXIMA 2A beamline (Synchrotron SOLEIL, Paris, France). All the data sets were integrated with XDS [26] and scaled with Aimless [27] from the CCP4 suite of programs [28] (Table 1).

There are errors in the fifth and sixth sentences of the "Crystal structure of TcdA" subsection of the Results and Discussion. The correct sentences are: To shed light onto the structural basis for the tRNA binding and ct^6A synthetic properties of TcdA-ATP, we determined the crystal structure of *E. coli* TcdA (Table 1 and Fig 2) loaded with ATP to 1.77 Å resolution (R/R_{free} values of 0.141/0.183) (Fig 3A) and AMP to 1.80 Å resolution (R/R_{free}values of 0.139/0.176) (Fig 3B). The asymmetric unit contained four TcdA chains arranged in two independent dimers, with a solvent content of 39%.

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Table 1. Crystallographic data processing and refinement statistics.

PDB code	TcdA-ATP 4D79	TcdA-AMP 4D7A
Data collection		
Wavelength (Å)	0.9795	0.9801
Resolution range (Å)	41.13–1.77 (1.83–1.77)	41.14–1.80 (1.86–1.80)
Space group	*P* 1 21 1	*P* 1 21 1
Unit cell dimensions		
a, *b*, *c* (Å)	65.3, 96.7, 82.8	65.7, 97.2, 83.2
β (°), α = γ = 90°	90, 111.2, 90	90, 111.6, 90
Total reflections	312,887 (11,351)	351,361 (33,129)
Unique reflections	89,883 (5907)	87,219 (8261)
Multiplicity	3.5 (1.9)	4.0 (4.0)
Completeness (%)	95.96 (63.90)	97.14 (92.68)
Mean *I*/σ(*I*)	18.97 (3.75)	19.93 (4.05)
Wilson B-factor	23.95	21.59
R-merge	0.08388 (0.663)	0.04687 (0.412)
R-meas[a]	0.09797	0.05407
CC1/2[b]	0.995 (0.556)	0.999 (0.0.875)
CC*[c]	0.999 (0.846)	1.000 (0.966)
Refinement		
R-work	0.1416 (0.2994)	0.1396 (0.1839)
R-free	0.1833 (0.3236)	0.1768 (0.2350)
# non-H atoms	8167	8064
# Protein atoms	7484	7411
# Ligand atoms	172	46
# Water	511	607
Protein residues	996	974
RMS(bonds) (Å)	0.011	0.007
RMS(angles) (°)	1.430	1.01
Ramachandran analysis		
Favored/Allowed/Outlier (%)	98.0/2.0/0.0	98.0/2.0/0.0
Clashscore	1.88	1.93
Average *B*-factor (Å^2)	34.40	32.10
Protein	33.60	31.50
Ligands	60.80	49.70
Solvent	38.00	37.20

[a]Rmeas = Σ_{hkl} $(n/n-1)^{1/2}$ Σ_i $|I_i(hkl)-<I(hkl)>|$ / $\Sigma\Sigma_i$ $I_i(hkl)$; where i is the ith measurement of reflection (hkl) and <I(hkl)> is the average over symmetry related observations of a unique reflection (hkl).

[b]CC1/2 is the Pearson correlation coefficient calculated between two random half data sets.

[c]CC* is the CC of the full data set against the true intensities, estimated from CC* = [2 CC1/2/(1+CC1/2)]$^{1/2}$.

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Reference

1. López-Estepa M, Ardá A, Savko M, Round A, Shepard WE, Bruix M, et al. (2015) The Crystal Structure and Small-Angle X-Ray Analysis of CsdL/TcdA Reveal a New tRNA Binding Motif in the MoeB/E1 Superfamily. PLoS ONE 10(4): e0118606. doi: 10.1371/journal.pone.0118606 PMID: 25897750