PLOS ONE

CORRECTION

Correction: *Brucella melitensis* Methionyl-tRNA-Synthetase (MetRS), a Potential Drug Target for Brucellosis

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There is an error in the third-to-last sentence of the "BmMetRS in complex with inhibitors" section. The correct sentence is: A superposition of 4PY2 Chain B and 4MVW Chain A gives a good illustration of this (Fig 7).

There is an error in the caption for Fig 7. Please see the correct Fig 7 caption here.

Citation: Ojo KK, Ranade RM, Zhang Z, Dranow DM, Myers JB, Choi R, et al. (2016) Correction: *Brucella melitensis* Methionyl-tRNA-Synthetase (MetRS), a Potential Drug Target for Brucellosis. PLoS ONE 11(9): e0163641. doi:10.1371/journal.pone.0163641

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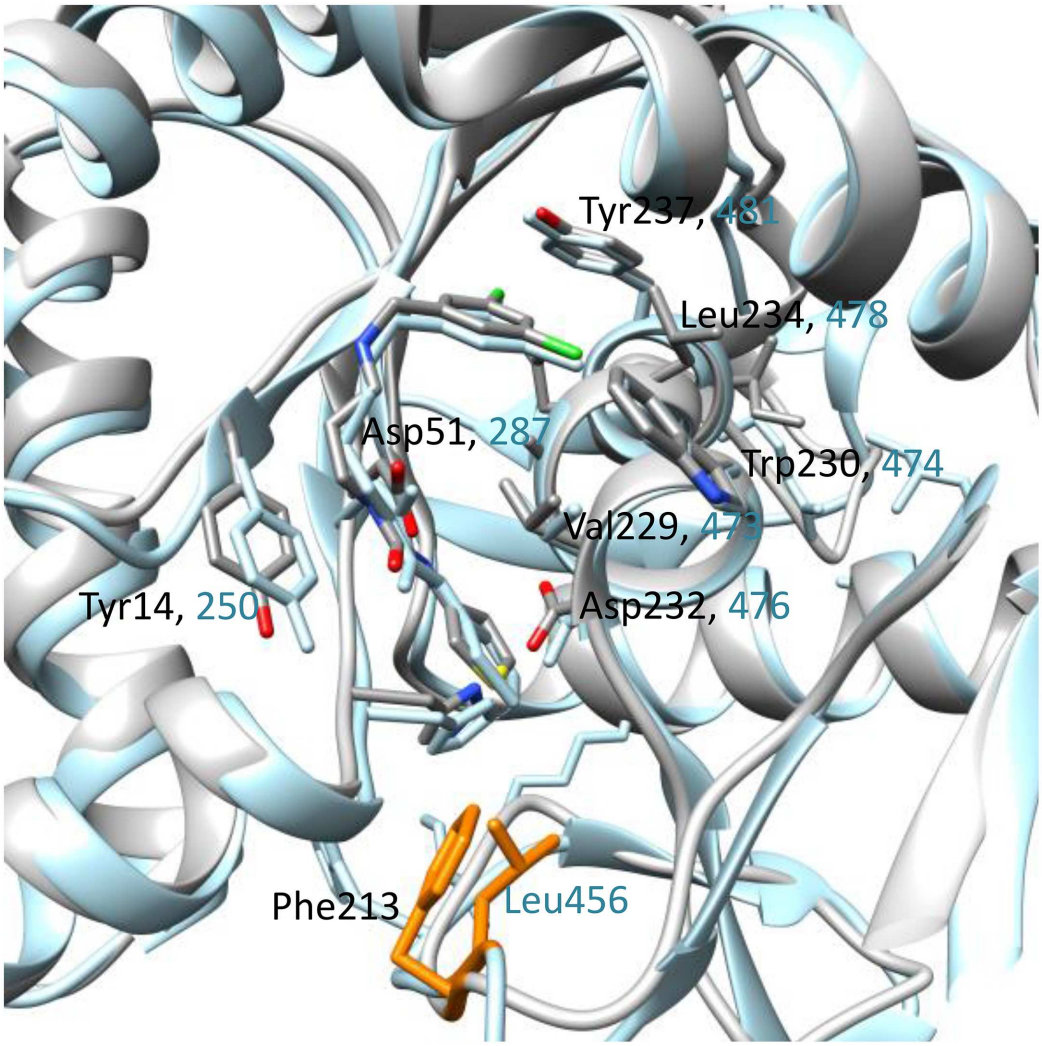

Fig 7. A superposition of *Bm*MetRS (PDB ID 4PY2 Chain B) and *Tb*MetRS (PDB ID 4MVW Chain) bound to compound 1433. A key difference is the interaction of *Bm*MetRS Phe213 which is functionally equivalent to Leu456 in *Tb*MetRS but led to different protein geometry. The *Tb*MetRS structure is shown in blue and the 2 different residues in orange.

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Additionally, in Table 2, the "PDB code" value for "1433" should read "4PY2". Please view the corrected Table 2 here.

Table 2. Data collection and model refinement statistics.

Crystal	SeMet	1312	1415	1433
PDB code	4DLP	5K0S	5K0T	4PY2
Data collection				
Space Group	P 1 21 1	P 1	P 1	P 1
Cell dimensions				
a, *b*, *c* (Å)	116.25, 77.62, 116.27	45.27, 99.74, 104.63	45.16, 99.65, 104.30	45.01, 99.48, 104.00
A, β, γ (˚)	90, 119.67, 90	110.58, 87.63, 99.91	110.46, 88.09, 99.72	110.47, 87.24, 99.99
Resolution range (Å)	50.00–2.65 (2.72–2.65)	50.00–2.40 (2.46–2.40)	50.00–2.60 (2.67–2.60)	50.00–2.15 (2.21–2.15)
No. of unique reflections	52379	63652	49660	88924
R_{merge} (%)[a]	7.1 (48.6)	6.4 (52.5)	7.5 (47.0)	6.6 (53.6)
Redudancy [a]	3.7 (3.7)	2.4 (2.4)	2.4 (2.4)	3.9 (4.0)
Completeness (%)[a]	99.3 (99.5)	96.3 (85.2)	96.0 (97.5)	98.2 (97.3)
I/σI[a]	15.21 (2.63)	11.43 (2.13)	10.12 (2.07)	15.76 (2.73)
Refinement				
Resolution range	50.00–2.65 (2.72–2.65)	50.00–2.40 (2.46–2.40)	50.00–2.60 (2.67–2.60)	50.00–2.15 (2.21–2.15)
No. of protein atoms	10934	11469	11189	11480
No. of water molecules	88	219	169	135
R_{cryst} (%)	19.7	21.0	25.6	17.8
R_{free} (%)	23.7	25.6	28.6	21.1
Root-mean-square deviations from ideal stereochemistry				
Bond lengths (Å)	0.012	0.003	0.008	0.011
Bond angles (˚)	1.421	0.577	1.183	1.384
Mean B factor (all atoms) ($Å^2$)	48.25	43.29	49.76	35.98
Ramachandran plot				
Favored region (%)	96.87	98.77	98.67	97.43
Allowed regions (%)	3.13	1.23	1.33	2.57
Outlier regions (%)	0.00	0.00	0.00	0.00
Clashscore	2.3	2.5	0.46	0.79
Molprobity Score	1.18	1.15	0.74	0.75

doi:10.1371/journal.pone.0163641.t001

Reference

1. Ojo KK, Ranade RM, Zhang Z, Dranow DM, Myers JB, Choi R, et al. (2016) *Brucella melitensis* Methionyl-tRNA-Synthetase (MetRS), a Potential Drug Target for Brucellosis. PLoS ONE 11(8): e0160350. doi: 10.1371/journal.pone.0160350 PMID: 27500735