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Author Correction: A shape-shifting redox foldase contributes to *Proteus mirabilis* copper resistance

Emily J. Furlong¹, Alvin W. Lo^{2,3}, Fabian Kurth^{1,6}, Lakshmanane Premkumar^{1,2,7}, Makrina Totsika^{2,3,8}, Maud E.S. Achard^{2,3,9}, Maria A. Halili¹, Begoña Heras⁴, Andrew E. Whitten^{1,10}, Hassanul G. Choudhury^{1,11}, Mark A. Schembri^{2,3} & Jennifer L. Martin^{1,5}

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This Article contains errors in Fig. 1, Table 1 and the Methods section. In panel c, the labels for PmScsC and EcDsbC in the upper two curves are interchanged. In Table 1 and the Methods section entitled ‘Extended structure’, the space group of the extended PmScsC structure is incorrectly referred to as H3₂ and should read H32. Correct versions of Fig. 1 and Table 1 are presented below; the errors have not been corrected in the Article.

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¹Institute for Molecular Bioscience, University of Queensland, St. Lucia, QLD 4072, Australia. ²School of Chemistry and Molecular Biosciences, University of Queensland, St. Lucia, QLD 4072, Australia. ³Australian Infectious Diseases Research Centre, University of Queensland, St. Lucia, QLD 4072, Australia. ⁴La Trobe Institute for Molecular Science, La Trobe University, Bundoora, VIC 3068, Australia. ⁵Griffith Institute for Drug Discovery, Griffith University, Nathan, QLD 4111, Australia. ⁶Present address: Bristol-Myers Squibb, Arnulfstraße 29, 80636 Munich, Germany. ⁷Present address: Department of Microbiology and Immunology, School of Medicine, University of North Carolina, Chapel Hill, NC 27514, USA. ⁸Present address: Institute of Health and Biomedical Innovation, School of Biomedical Sciences, Queensland University of Technology, Kelvin Grove, QLD 4059, Australia. ⁹Present address: School of Human Movement and Nutrition Sciences, University of Queensland, St. Lucia, QLD 4072, Australia. ¹⁰Present address: Australian Centre for Neutron Scattering, Australian Nuclear Science and Technology Organization, Lucas Heights, New South Wales 2234, Australia. ¹¹Present address: Cello Health Consulting, Farnham Surrey GU9 7DN, UK. Correspondence and requests for materials should be addressed to A.E.W. (email: awh@ansto.gov.au) or to M.A.S. (email: m.schembri@uq.edu.au) or to J.L.M. (email: jlm@griffith.edu.au)

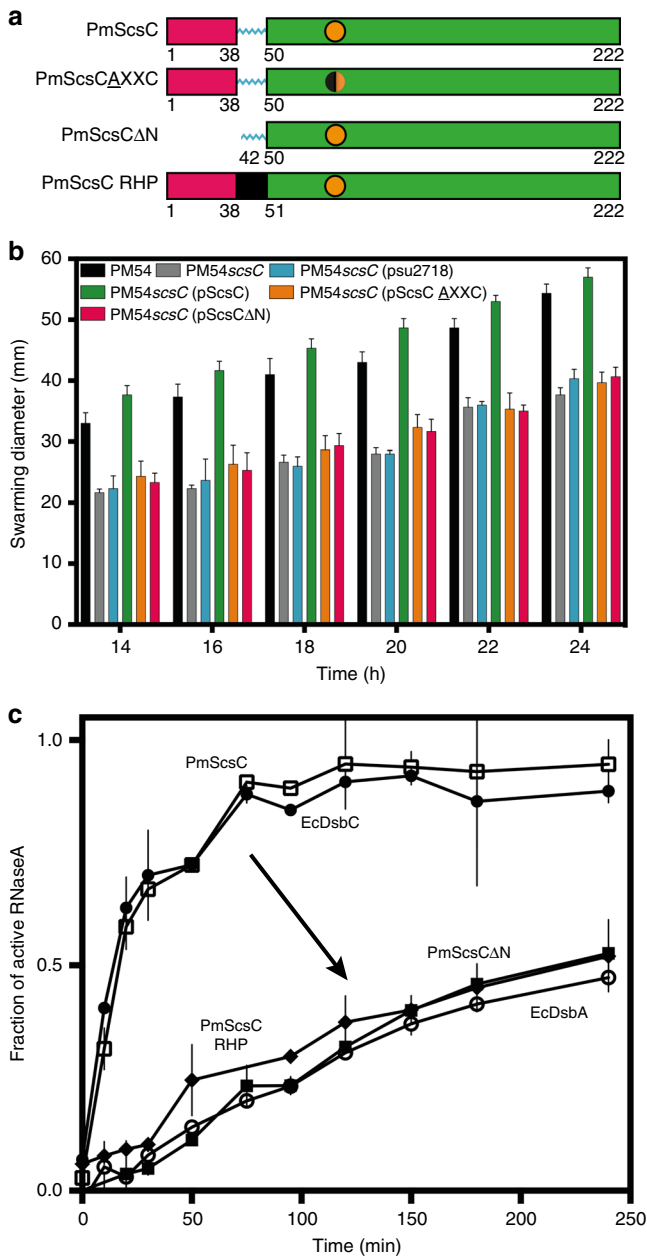


Table 1 PmScsC crystal structure statistics

| | Compact (4XVW) | Transitional (5IDR) | Extended (5ID4) |
|---|------------------------|-------------------------|-------------------------|
| <i>Data collection</i> | | | |
| Space group | P2 ₁ | I4 | H32 |
| Cell dimensions | | | |
| <i>a</i> , <i>b</i> , <i>c</i> (Å) | 137.5, 163.9, 181.9 | 193.1, 193.1, 105.8 | 86.7, 86.7, 330.9 |
| α , β , γ (°) | 90, 90, 90 | 90, 90, 90 | 90, 90, 120 |
| Resolution (Å) | 91.15–2.60 (2.74–2.60) | 136.51–2.56 (2.57–2.56) | 110.29–2.92 (2.93–2.92) |
| <i>R</i> _{merge} | 0.072 (0.617) | 0.083 (0.741) | 0.059 (0.625) |
| <i>I</i> / σ | 11.0 (2.0) | 14.9 (2.2) | 14.2 (2.8) |
| Completeness (%) | 98.6 (95.4) | 99.4 (100.0) | 99.2 (100.0) |
| Redundancy | 3.8 (3.7) | 4.1 (4.1) | 4.1 (4.2) |
| <i>Refinement</i> | | | |
| Resolution (Å) | 91.15–2.60 | 42.82–2.56 | 40.36–2.92 |
| No. of reflections | 243,409 | 62,069 | 10,652 |
| <i>R</i> _{work} / <i>R</i> _{free} (%) | 24.8/28.2 | 17.1/22.2 | 25.1/26.3 |
| No. of atoms | | | |
| Protein | 40,850 | 10,262 | 1720 |
| Ligand/ion | NA | NA | NA |
| Water | 281 | 82 | 0 |
| <i>B</i> factors (Å ²) | | | |
| Protein | 59.7 | 50.6 | 122.2 |
| Ligand/ion | NA | NA | NA |
| Water | 41.5 | 43.0 | NA |
| <i>RMS deviations</i> | | | |
| Bond length (Å) | 0.006 | 0.008 | 0.010 |
| Bond angles (°) | 1.21 | 1.05 | 1.17 |

Single crystals were used to collect each dataset. Values for highest resolution shell are shown in parentheses

Fig. 1