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ERRATUM**The 1.7 Å Crystal Structure of the Apo Form of the Soluble Quinoprotein Glucose Dehydrogenase from *Acinetobacter calcoaceticus* Reveals a Novel Internal Conserved Sequence Repeat**

**Arthur Oubrie, Henriëtte J. Rozeboom, Kor H. Kalk
Johannis A. Duine and Bauke W. Dijkstra
J. Mol. Biol. (1999) 289, 319–333**

It is regretted that an error occurred in the above paper. In the Abstract and Results and Discussion sections the free R -factor value was listed as 0.8% instead of 20.8%. The corrected sentences are given below.

The first sentence of the abstract should read:

The crystal structure of a dimeric apo form of the soluble quinoprotein glucose dehydrogenase (s-GDH) from *Acinetobacter calcoaceticus* has been solved by multiple isomorphous replacement followed by density modification, and was subsequently refined at 1.72 Å resolution to a final crystallographic R -factor of 16.5% and free R -factor of 20.8%.

The first sentence of the 'Refinement and quality of the model' section in the Results and Discussion should read:

Final crystallographic (R_{crys}) and free (R_{free} ; Brünger, 1992) R -factor values of 16.5% and 20.8%, respectively, were obtained for data from 20.0 to 1.72 Å resolution (no σ cut-off).