Using more than 801 296 small-molecule crystal structures to aid in protein structure refinement and analysis. Addendum

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An addendum to the *Introduction* of Cole *et al.* [(2017), *Acta Cryst.* D**73**, 234–239] is made to recognize the work of Bricogne, Smart and others in the development of methods to make use of Cambridge Structural Database data in protein structure solution.

In the *Introduction* to Cole *et al.* (2017) a short resume of example areas where *Mogul* (Bruno *et al.*, 2004) has been used was given. Two contributions in this area (*BUSTER* and *GRADE*; Smart *et al.*, 2011) were the pioneering works where *Mogul* was applied to protein crystallography, and so should also have been recognised.

References

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