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letters to the editor

Comment on *CRUNCH: a phase refinement program for high-resolution macromolecular structures* by Langs, Blessing & Smith (2000)

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The February issue of the *Journal of Applied Crystallography*, in the section *Computer Programs*, contains the paper entitled *CRUNCH: a phase refinement program for high-resolution macromolecular structures*, by Langs, Blessing & Smith (2000).

We would like to point out that an earlier program system *Crunch* has been available to the scientific community for a number of years now (Abrahams & de Graaff, 1998; de Graaff, 1998; Cram *et al.*, 1999; de Gelder & de Graaff, 1999). *Crunch* has been developed for the automatic solution of difficult 'small' structures.

Without discussing the various merits and demerits of the two programs, we feel that the existence of two different programs aimed at the same or a similar group of users and bearing the same name will lead to unnecessary confusion.

We hope that Dr Langs *et al.* will address this point as soon as possible.

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Response to de Graaff & de Gelder's comment on *CRUNCH: a phase refinement program for high-resolution macromolecular structures*

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We regret that we forgot that the program name *CRUNCH* (Langs *et al.*, 2000) had been associated with the direct-methods work based on Karle–Hauptman determinants as described in the above letter by de Graaff & de Gelder (2000).

We have adopted the name *CROQUE* for future reference to our program.

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