pseudo-free CC of the unambiguous solution were 67%, 93% and 70.0%, respectively, compared to 38%, 84% and 54.6% for the enantiomorph. The unambiguous solution was then analysed to decide which of the 11 sites corresponded to the 10 Se sites of RNase Z. Non-crystallographic symmetry (NCS) operations from 11 heavy atom sites were found automatically using FINDNCS[22,26]. This results in one NCS for a maximum of 8 matching pairs. The 8 Se positions were refined and phasing was performed with CNS[13]. The resulting phases were extended to 2.2 Å using the CNS density modification procedure. These phases were used to begin automatic model building and refinement using warpNtrace[27] and the peak data set with a resolution of 2.1 Å. The resulting ARP model contained 69.4% of the dimer's backbone atoms and 47.5% of the RNase Z sequence. The R_{factor} and R_{free} values for the refinement at this step were 27.1% and 34.1%, respectively.

The initial model provided by ARP was completed and adjusted with the program O[28], first with the solvent-flattened MAD map, then with the combined model and experimental phases (as calculated by CNS). Refinement was performed using CNS and the peak data set at 2.1 Å resolution. Standard protocols of structure refinement with experimental phases (Hendrickson–Lattman coefficients from MAD phasing), including energy minimization, both before and after simulated annealing (using torsion angle dynamics), bulk solvent correction and anisotropic B-factors (applies the isotropic component of the correction to the model and the anisotropic component to the observed data) were used. Each round of refinement was alternated with a round of manual refitting using the cross-validated, sigma-A weighted, phase combined $2F_o-F_c$ and F_o-F_c maps. Progress in the model refinement was evaluated by decrease in the free R-factor.

The current model includes 566 residues (1–158, 197–307 for the A subunit, and 1–236, 247–307 for the B subunit), two Zn^{2+} ions, a phosphate ion and 176 water molecules. Residues 159–196 of the A subunit and 237–246 of the B subunit were not visible in the electronic density maps, and are omitted in the final molecular model. Superposition of 518 α-carbon atoms from the A and B subunits (residues 1–158, 197–236 and 247–307) results in an r.m.s.d. of 1.76 Å.

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corrigendum

The yeast Rat1 exonuclease promotes transcription termination by RNA polymerase II

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In this Letter to *Nature*, reference 5 should be: Connelly, S. & Manley, J. L. A functional mRNA polyadenylation signal is required for transcription termination by RNA polymerase II. *Genes Dev.* **2,** 440–452 (1988). □