

- abolish ability of human eRF1 to trigger peptidyl-tRNA hydrolysis. *RNA* 5, 1014–1020 (1999).
- Zavialov, A. V., Mora, L., Buckingham, R. H. & Ehrenberg, M. Release of peptide promoted by the GGQ-motif of class I release factors regulates the GTPase activity of RF3. *Mol. Cell* (in the press).
 - Song, H. *et al.* The crystal structure of human eukaryotic release factor eRF1-mechanism of stop codon recognition and peptidyl-tRNA hydrolysis. *Cell* 100, 311–321 (2000).
 - Vestergaard, B. *et al.* Bacterial polypeptide release factor RF2 is structurally distinct from eukaryotic eRF1. *Mol. Cell* 8, 1375–1382 (2001).
 - Freistrotter, D. V., Pavlov, M. Y., MacDougall, J., Buckingham, R. H. & Ehrenberg, M. Release factor RF3 in *E. coli* accelerates the dissociation of release factors RF1 and RF2 from the ribosome in a GTP dependent manner. *EMBO J.* 16, 4126–4133 (1997).
 - Zavialov, A. V., Buckingham, R. H. & Ehrenberg, M. A Posttermination ribosomal complex is the guanine nucleotide exchange factor for peptide release factor RF3. *Cell* 107, 115–124 (2001).
 - van Heel, M. *et al.* Single-particle electron cryo-microscopy: towards atomic resolution. *Q. Rev. Biophys.* 33, 307–369 (2000).
 - Yusupov, M. M. *et al.* Crystal structure of the ribosome at 5.5 Å resolution. *Science* 292, 883–896 (2001).
 - Moffat, J. G. & Tate, W. P. A single proteolytic cleavage in release factor 2 stabilizes ribosome binding and abolishes peptidyl-tRNA hydrolysis activity. *J. Biol. Chem.* 269, 18899–18903 (1994).
 - Tin, O. F. *et al.* Proteolytic fragmentation of polypeptide release factor 1 of *Thermus thermophilus* and crystallization of the stable fragments. *Biochimie* 82, 765–772 (2000).
 - Kastner, B., Trotman, C. N. & Tate, W. P. Localization of the release factor-2 binding site on 70 S ribosomes by immuno-electron microscopy. *J. Mol. Biol.* 212, 241–245 (1990).
 - Wilson, K. S., Ito, K., Noller, H. F. & Nakamura, Y. Functional sites of interaction between release factor RF1 and the ribosome. *Nature Struct. Biol.* 7, 866–870 (2000).
 - Xu, W., Pagel, F. T. & Murgola, E. J. Mutations in the GTPase center of *Escherichia coli* 23S rRNA indicate release factor 2-interactive sites. *J. Bacteriol.* 184, 1200–1203 (2002).
 - Wimberly, B. T., Guymon, R., McCutcheon, J. P., White, S. W. & Ramakrishnan, V. A detailed view of a ribosomal active site: the structure of the L11-rRNA complex. *Cell* 97, 491–502 (1999).
 - Conn, G. L., Draper, D. E., Lattman, E. E. & Gittis, A. G. Crystal structure of a conserved ribosomal protein-rRNA complex. *Science* 284, 1171–1174 (1999).
 - Yusupova, G. Z., Yusupov, M. M., Cate, J. H. & Noller, H. F. The path of messenger RNA through the ribosome. *Cell* 106, 233–241 (2001).
 - Uno, M., Ito, K. & Nakamura, Y. Polypeptide release at sense and noncognate stop codons by localized charge-exchange alterations in translational release factors. *Proc. Natl Acad. Sci. USA* 99, 1819–1824 (2002).
 - Nissen, P. *et al.* Crystal structure of the ternary complex of Phe-tRNA^{Phe}, EF-Tu, and a GTP analog. *Science* 270, 1464–1472 (1995).
 - Ito, K., Ebihara, K., Uno, M. & Nakamura, Y. Conserved motifs in prokaryotic and eukaryotic polypeptide release factors: tRNA-protein mimicry hypothesis. *Proc. Natl Acad. Sci. USA* 93, 5443–5448 (1996).
 - Bertram, G., Bell, H. A., Ritchie, D. W., Fullerton, G. & Stansfield, I. Terminating eukaryote translation: domain 1 of release factor eRF1 functions in stop codon recognition. *RNA* 6, 1236–1247 (2000).
 - Frolova, L. Y., Seit-Nebi, A. & Kisselev, L. L. Highly conserved NIKS tetrapeptide is functionally essential in eukaryotic translation termination factor eRF1. *RNA* 8, 129–136 (2002).
 - Inagaki, Y., Blouin, C., Doolittle, W. F. & Roger, A. J. Convergence and constraint in eukaryotic release factor 1 (eRF1) domain 1: the evolution of stop codon specificity. *Nucleic Acids Res.* 30, 532–544 (2002).
 - Merkulova, T. I., Frolova, L. Y., Lazar, M., Camonis, J. & Kisselev, L. L. C-terminal domains of human translation termination factors eRF1 and eRF3 mediate their in vivo interaction. *FEBS Lett.* 443, 41–47 (1999).
 - Jelenc, P. C. & Kurland, C. G. Nucleotide triphosphate regeneration decreases the frequency of translation errors. *Proc. Natl Acad. Sci. USA* 76, 3174–3178 (1979).
 - Harauz, G. & van Heel, M. Exact filters for general geometry three-dimensional reconstruction. *Optik* 73, 146–156 (1986).
 - Jones, T. A., Zou, J. Y., Cowan, S. W. & Kjeldgaard, M. Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Crystallogr. A* 47, 110–119 (1991).
 - Evans, S. V. Setor: Hardware lighted three-dimensional solid model representations of macromolecules. *J. Mol. Graphics* 11, 134–138 (1993).

Supplementary Information accompanies the paper on *Nature's* website (♦ <http://www.nature.com>). A stereo representation of figure 3 and the FSC plot to assess the resolution of the reconstruction are provided.

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Competing interests statement The authors declare competing financial interests: details accompany the paper on *Nature's* website (♦ <http://www.nature.com/nature>).

Correspondence and requests for materials should be addressed to M.v.H. (e-mail: m.vanheel@ic.ac.uk). The atomic coordinates of the *E. coli* RF2 structure fitted into the cryo-EM map have been deposited in the Protein Data Bank (e-mail: <http://www.rcsb.org>) with the accession code 1ML5. The cryo-EM map has been deposited in the 3D EM data base (e-mail: http://www.ebi.ac.uk/msd/MSDProjects/IIMS3D_EM.html) with the accession code EMD-1005.

corrigenda

The genome sequence of *Schizosaccharomyces pombe*

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In this Article, the author Andreas Düsterhöft was mistakenly omitted: his name and affiliation (footnote 6) should have been inserted between M. Fuchs and C. Fritzc in the author list. In addition, the name of L. Cerutti (in the last line of the author list) was misspelled. On p874 in the penultimate sentence of the 'Intergene regions' section, "tamendly oriented genes" should read "divergently oriented genes." □

Probing the free-energy surface for protein folding with single-molecule fluorescence spectroscopy

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The upper limit on the polypeptide reconfiguration time (τ_0) was inadvertently calculated using $(\sigma_{app} - \sigma_0)^2$, instead of $(\sigma_{app}^2 - \sigma_0^2)$, as given in the formula in the text (page 745, right column). The correct upper limit is therefore 0.2 ms. This results in a lower limit on the free energy barrier (Δ) of $2k_B T$, corresponding to an activation entropy of $+3k_B$ (page 746, right column), and an upper limit on the pre-exponential factor ($2\pi\tau_0$) of 1 ms. This mistake does not affect any of the conclusions. We thank Taekjip Ha for bringing it to our attention. □