Corrigenda

A novel serine kinase activated by rac1/ CDC42Hs-dependent autophosphorylation is related to PAK65 and STE20

George A.Martin, Gideon Bollag, Frank McCormick and Arie Abo

The EMBO Journal, **14**, 1970–1978, 1995

In the above paper, the first 12 amino acids of hPAK65 and the 5′ untranslated region should be eliminated from the reported sequence. The correct N terminus of hPAK65 should be read as the following:

1 M S D N G E L E D K P P A P P V R M S S T I F
S T G G K D P 30

Except for three amino acids, the corrected hPAK65 sequence is identical to hPAK2, which was submitted to the database by J.Chernoff, accession number HSU24153. The above changes will also be made to the database.

NMR solution structure of a double-stranded RNA-binding domain from *Drosophila* staufen protein reveals homology to the N-terminal domain of ribosomal protein S5

Mark Bycroft, Stefan Grünert, Alexey G.Murzin, Mark Procter and Daniel St Johnston

The EMBO Journal, **14**, 3563–3571, 1995

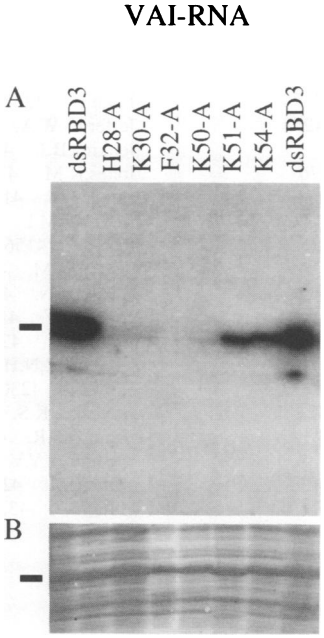

Figure 5A. Due to a contamination of the peptides containing the H28-A and K30-A mutations with the wild type domain, we erroneously reported that these two peptides had no effect on RNA binding. Upon repetition of the experiment with the pure peptides, we observe negligible RNA binding activity for these peptides, comparable with the level seen for the peptide containing mutation K50-A. A revised Figure 5A is shown above. Although we originally reported that loop 2, which contains these mutations, does not contribute significantly to the interaction of the domain with dsRNA, these results indicate that this loop is involved in RNA binding. Even though this is in contrast to our initial report, the revised result is in better agreement with the proposed model for the interaction of the dsRBD with RNA shown in Figure 5C. Therefore no essential conclusions of our original report are affected. We apologize for any inconvenience caused.