

loop at the end of the helix. On the basis of comparison of existing structures, it may be very difficult, if not impossible, to differentiate between insertions that occurred in loops, as opposed to insertions that originally occurred in helices but were propagated into neighbouring loops. □

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ERRATUM

Evolution and environment in the Hominoidea

Peter Andrews

Nature **360**, 641–646 (1992)

IN this Review Article, in the figure in Box 4 on page 644, the labels 'Orang' and 'Human' in the diagram labelled "Classification at family, subfamily and tribe level of the Hominoidea" were inadvertently transposed.

CORRECTIONS

Molecular and genetic damage in humans from environmental pollution in Poland

Frederica P. Perera, Kari Hemminki, Ewa Gryzbowska, Grazyna Motykiewicz, Jadwiga Michalska, Regina M. Santella, Tie-Lan Young, Christopher Dickey, Paul Brandt-Rauf, Immaculata DeVivo, William Blaner, Wei-Yann Tsai & Mieczyslaw Chorazy

Nature **360**, 256–258 (1992)

IN Table 1 on page 257, the *P* values for the comparisons of PAH-DNA adducts between the 'Exposed winter' (EW) to 'Control summer' (CS) and 'Exposed summer' (ES) to CS are reversed. The correct *P* value for the comparison of EW to CS is 0.012 and that for the comparison of ES to CS is 0.078, as expected from the means in the table. The correct *P* values further strengthen the finding of an effect of air pollution on DNA adducts.

Cloning and characterization of a gene that regulates cell adhesion

W. E. Pullman & W. F. Bodmer

Nature **356**, 529–532 (1992)

SHOWN below is a revision of the nucleotide sequence and inferred amino acid sequence for a cellular adhesion regulatory molecule, the gene for which is now known as CMAR (CAR in this letter). The authors acknowledge helpful information received from Drs Alejandro Aruffo and Po-Ying Chan of Bristol-Myers Squibb, Pharmaceutical Research Institute, Seattle, USA, and H. Durbin (ICRF) in making this correction.

CMAR

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GCATGGAACACTTCGAGTTCACAGGGTTATAGACAGTCGTTCCAGTGTGG      51
CTGAGGCCACCCAGGCGACAGAGCATTCAGACTCCAAACAGACCCCTGT      102
TCATGCCGACGCTTGACGACCGCCAGTTCCTGTGGCTCCCTCGGAATG      153
      _ _ _ _ _ M _ _ _ _ _
      _ _ _ _ _
CTAAGGGGATCGGACATGAAAGGACCCCTGTGAGCCGATTGTCTTATCTCCA      204
L R G S D M K G P C E P I V L S P
      _ _ _ _ _
GGGGCCCTGTATCCAGTCACTCATCAATGGGGCCAGTCAGGCCAGGCA      255
A A L S S S S L I N G A S Q A Q A
      _ _ _ _ _
CTGGGCTCCGGAGACTCACCACTGCCCCCTGTCGCATGTGGACTGGTGC      306
L G S G G L T T A P C C H V D W C
      _ _ _ _ _
AAGTTGAGGACTTCTTGTGGTCTAGTCACGACAGTGTGGGGATGCC      357
K L R T S C W S S H A C S V G D A
      _ _ _ _ _
TTGGTTTTACTGCTCTGAGATTGTTGAGATACCTTACTAATAAAGTGTG      408
L V F T A L R I V E I L Y
      _ _ _ _ _
TAGTTGGAAAAA          429
      _ _ _ _ _ myristoylation site
      _ _ _ _ _ tyrosine phosphorylation site
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