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Errors in Genome Reviews

It is becoming clear (*1*) that the advent of the genome sequencing era is accompanied by the propagation of erroneous functional annotations in an increasing number of cases. The sudden availability of an enormous amount of information has raised the probability that review articles may contain erroneous annotations. It often appears that the transfer of functional assignments either from (i) annotations or (ii) additional sequence information are not carefully checked in the reviews that follow.

As an example of the first case, the assignment for the *Methanoccus jannaschii* ORF MJ1228, originally correctly characterized as the archaeal eIF-5A (*2*), was subsequently miscopied as eIF-5 in two more recent reviews (*3, 4*). An eIF-5 homolog has not been found in Archaea thus far (*5*).

As an example of the second case, the tentative annotations of certain archaeal ORFs as eIF-2B alpha and delta (*2*), the best available predictions at that time, have proliferated in a review that followed (*4*), without reference to more recent literature. With new sequence information (*6*), it has been possible to show that these archaeal ORFs belong to a different subfamily named aIF-2B I and II (*7*).

These annotation errors engender ill-derived conclusions. The authors who are writing reviews based on genomic data should use extreme caution copying the information and should confirm the results they intend to cite.

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