

## ERRATA

*Eur. J. Hum. Genet* 1998; **6**: 291-295

**Jean-Michel Rozet et al**

Spectrum of ABCR gene mutations in autosomal recessive macular dystrophies

Due to the printing of an initial colour figure in black and white, the different phenotypic manifestations of ABCR mutations have not all been denoted properly in Figure 1 of the original article. The proper Figure 1 and accompanying legends are shown below.

*Eur. J. Hum. Genet* 1998; **6**: 413-414

**PACKAGE REVIEW**

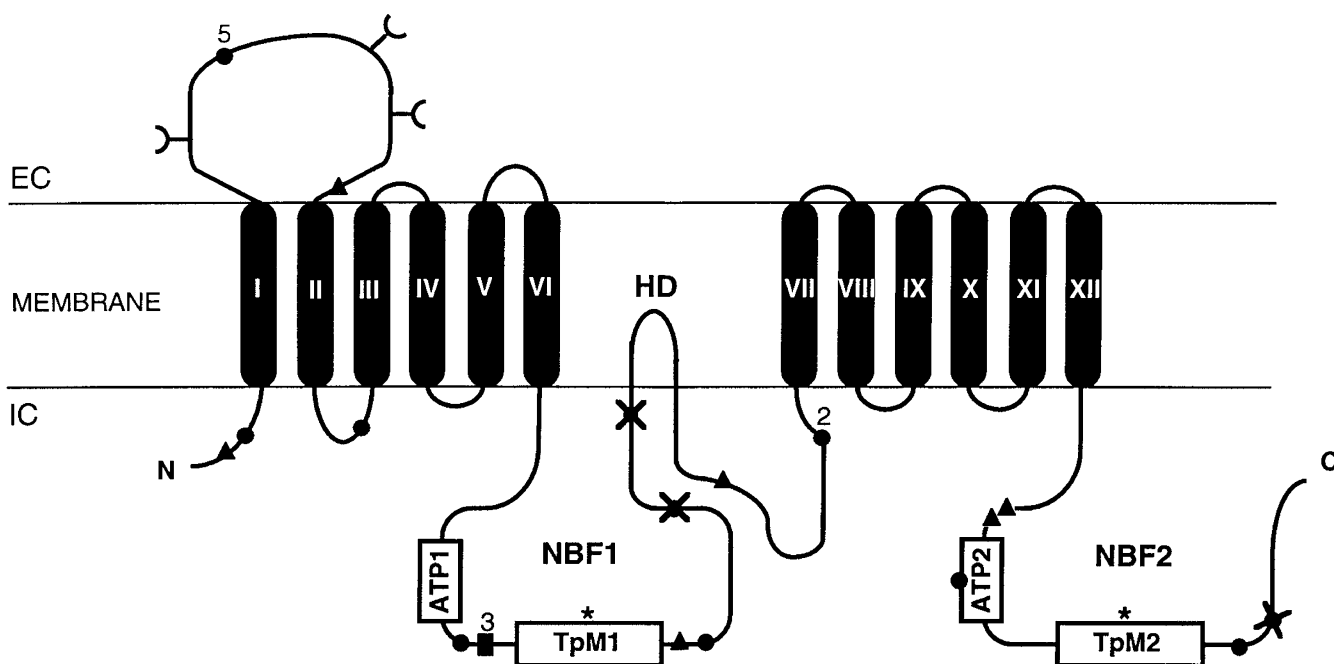
**"Jeans for Genes"**

The name of the author was incorrectly spelt in the Erratum published in 6/5. The correct name of the author is:

Ysbrand Poortman

Teacher of Biology

Vice President, European Alliance of Genetic Support Groups



**Figure 1** Predicted topology of ABCR and position of point mutations associated with STGD and FFM. EC : extracellular domain and IC: cytoplasmic domain. The 12 predicted membrane-spanning  $\alpha$ -helical segments are indicated with roman numbers.  $\gamma$  predicted N-glycosylation site. ATP1 : first ATP-binding site; ATP2 : second ATP-binding site; TpM<sub>1</sub> : first transporter signature-motif; TpM<sub>2</sub>: second transporter signature-motif; NBF1 : first nucleotide binding fold; NBF2 : second nucleotide binding fold; HD: proline rich hydrophobic domain. \*PKA-phosphorylation sites. The approximate positions of missense mutations identified in STGD, FFM and in both phenotypes are indicated by dots, triangles and a dark square, respectively.  $\times$  shows the approximate positions of nonsense mutations and  $\ddagger$  indicates that the mutation was found more than once (in n families).