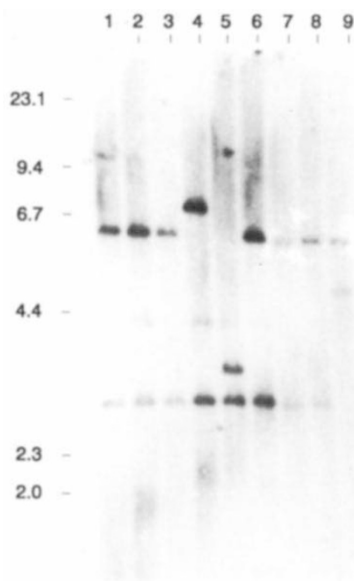


**The gene involved in X-linked agammaglobulinaemia is a member of the src family of protein-tyrosine kinases**

D. Vetriche et al.

*Nature* **361**, 226–233 (1993).

In Fig. 2b of this article, the sizing of DNA fragments was incorrect. The corrected sizes are shown below, together with the appropriately amended section of the legend to Fig. 2c.



Section D (which represents the 5' end of the *atk* cDNA sequence) detected 0.7, 1.7, 1.8, 2.5 and 6.2 kb *Msp*I fragments in normal genomic DNA; in patient E, no 6.2 or 2.5 kb *Msp*I fragments were observed; a novel 7.2 kb band was seen. cDNA 6G11 (which does not extend to the 5' terminus of the *atk* gene) hybridized to 0.7, 1.0, 3.0, 4.3 and 6.2 kb *Msp*I fragments in normal individuals and also detected the abnormality in patient E. Section C detected no *Msp*I abnormalities in patient E. Section C detected 1.0, 1.7, 3.0 and 4.3 kb *Msp*I fragments in normal DNA; the 3.0 kb fragment was absent in patient D, but a novel 1.2 kb band was observed. Section D did not detect any abnormalities in patient D.

## Atomic structure and chemistry of human serum albumin

X. M. He &amp; D. C. Carter

*Nature* **358**, 209–215 (1992)

WE failed to recognize the following typographical error in the proofs of this research article. In Table 1, page 211, the unit cell constant for the *b* axis of the recombinant crystal form should have been 88.3 Å instead of 38.3 Å. A statement in Fig. 4 should

read that Lys 199 and His 242 are located at the 'top' of Fig. 4a, not the 'bottom'. In addition, we incorrectly referenced an earlier publication on recombinant albumin (ref. 25). The appropriate reference should be: Sleep, D., Belfield, G. P. & Goodey, A. R. *Biotechnology* **8**, 42-46 (1990). □

# Mutations in Cu/Zn superoxide dismutase gene are associated with familial amyotrophic lateral sclerosis

Daniel R. Rosen et al.

*Nature* **362**, 59–62 (1993)

FIGURE 1c in this letter shows a comparison of amino-acid sequences for exon 2 of SOD-1, but incorrectly positions the residue numbers and the mutations on the sequences. The corrected panel is shown here.

EXON 2

	FALS				N				P				R				
human	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
cow	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
pig	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
mouse	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
swordfish	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
<i>Drosophila</i>	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
<i>Oncocercus</i>	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
tomato	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
spinach	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L
<i>S. cerevisiae</i>	N	L	L	L	R	V	L	L	R	L	L	L	R	L	L	L	L

Also, in Table 3, the base-pair change for family 9967C should read GGC→CGC. □

## A single amino acid of the cholecystikinin-B/gastrin receptor determines specificity for non-peptide antagonists

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Edward W. McBride<sup>\*</sup>, Suzanne M. Quinn<sup>\*</sup>  
& Alan S. Kopin<sup>\*‡</sup>**

*Nature* **362**, 348–350 (1993)

WE have noted an error in our numbering of amino acids in this letter. The valine in transmembrane domain VI that confers antagonist affinity to the human receptor was erroneously numbered as 319. The correct numbering should be human valine 349. In addition, the numbering of three of the canine mutants shown in Fig. 2 is incorrect:  $^{316}\text{G}$  should be  $^{322}\text{G}$ ,  $^{321}\text{Y}$  should be  $^{327}\text{Y}$ , and  $^{360}\text{SS}$  should be  $^{366}\text{SS}$ . The relative positions of the human and canine amino-acid sequences shown in Figs 2 and 4 are correct; the numbering error therefore does not affect any of our conclusions.  $\square$