# **LETTERS TO NATURE**

such experiments may allow us to expand upon its catalytic versatility. 

### Methods

The crystallization and preliminary X-ray diffraction analysis of rat liver arginase has been reported previously<sup>11</sup>. Arginase crystals diffract to 2.1 Å resolution and belong to space group P3, with hexagonal unit-cell dimensions a = b = 88.5 Å, c = 106.2 Å, with one 105K trimer in the asymmetric unit. Phase determination by multiple isomorphous replacement was hindered by chronic non-isomorphism between native and heavy-atom derivative crystals, as well as non-isomorphism among native crystals themselves (the c-axis length typically ranged from 104-115 Å)<sup>11</sup>. Diffraction data were collected at room temperature on an R-AXIS IIc

Received 17 June; accepted 23 August 1996.

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image plate area detector. Data reduction was performed with MOSFLM<sup>20</sup> and CCP4<sup>21</sup>. For phasing, initial heavy-atom positions were determined in difference Patterson maps and refined with the program PHASES<sup>22</sup>. Heavy-atom binding indicated that the noncrystallographic symmetry (NCS) axis of the trimer was tilted  $\sim 9^{\circ}$  away from a normal to the *a*-*b* plane. The model was fit into an electron-density map calculated with solvent-flattened NCS-averaged phases at 3.0 Å resolution. Subsequent refinement and rebuilding of the native model was done with X-PLOR<sup>23</sup> and O<sup>24</sup>, respectively. Group B factors were refined and a bulk solvent correction was applied. In the final stages of refinement, the quality of the model was improved by gradually releasing the NCS constraints into appropriately weighted restraints as judged by  $R_{\rm free}$ . Refinement statistics are recorded in Table 1. The final protein model has excellent stereochemistry with only Gln 64 adopting a disallowed  $\phi/\phi$  conformation. This residue is located in a type II'  $\beta$ -turn between strand 2 and helix B and is characterized by clear and unambiguous electron density.

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ACKNOWLEDGEMENTS. We thank the NIH for support of this work, and R. C. Cavalli, B. S. Cooperman, F. Daghigh, G. C. Dismukes, G. Farber, C. A. Fierke, C. A. Lesburg, S. J. Lippard, W. N. Lipscomb, T. Stams, M. J. Therien and T. Widlanski for helpful discussions

CORRESPONDENCE and requests for materials should be addressed to D.W.C. (e-mail: chris@xtal. chem.upenn.edu). Atomic coordinates have been deposited in the Brookhaven Protein Data Bank with accession code 1RLA).

### ERRATUM

## **Transduction of bitter and sweet** taste by gustducin

### Gwendolyn T. Wong, Kimberley S. Gannon & Robert F. Margolskee

#### Nature 381, 796-800 (1996).

THE Nature cover relating to this letter, in the 27 June issue, did not do justice to the original image. The image has now been rescanned to emphasise the significant features (right), and the new and improved version will be available on reprints of the letter. In addition, credit should have been given in the caption to Dr Luis Ruiz-Avila. The full caption reads: "Cross section of mouse tongue epithelium demonstrating expression of the  $\alpha$  subunit of the taste-specific G protein gustducin. The centre of the image shows a foliate taste papilla containing numerous taste buds. Gustducin-positive taste receptor cells were detected by indirect immunofluorescence with a Cy3-conjugated secondary antibody. A double exposure was taken with fluorescence and differential interference contrast settings (original magnification,  $250 \times$ ). See Wong et al., page 796 and News & Views, page 737 for the effects on taste of "knocking-out" gustducin. (Image: Luis Ruiz-Avila, Mount Sinai School of Medicine, New York, NY and CIRIT, Barcelona, Spain.)"

