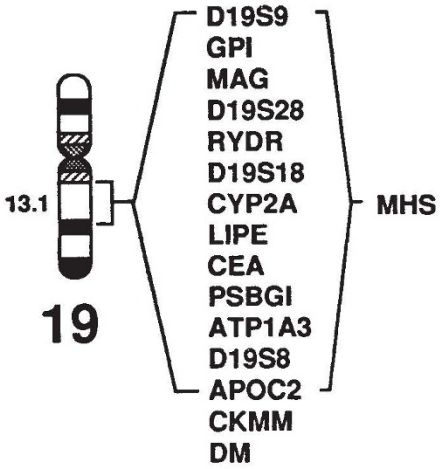

Regional localization of genes and DNA segments on chromosome 19 (see refs 8–11). Anonymous DNA segments are referred to as 'D' numbers[11]. Gene symbols: GPI, glucose phosphate isomerase; MAG, myelin-associated glycoprotein; ATP1A3, ATPase; Na^+, K^+, α3 polypeptide; RYDR, ryanodine receptor or sarcoplasmic Ca^{2+} release channel; CYP2A, cytochrome P450, subfamily IIA; LIPE, hormone sensitive lipase; CEA, carcinoembryonic antigen; PSBGI, pregnancy-specific β-1-glycoprotein 1; APOC2, apolipoprotein C-II; CKMM, creatine kinase, skeletal muscle; DM, dystrophia myotonia.

fatty acids would be produced and muscle metabolism would be disrupted. Catecholamines are significantly elevated during a hyperthermic crisis and would exacerbate the production of free fatty acids by stimulating the lipase in a potentially catastrophic metabolic spiral.

Complementary DNAs encoding the lipase in the rat have recently been described, and this gene is expressed in skeletal muscle as well as in many other tissues[8]. Mapping data from hybrid cell lines[8,9] assign the human lipase to the light-staining giemsa band 19q13.1, and indicate that this gene is flanked by the same genetic markers as the MHS gene. Therefore, the gene encoding the lipase is at, or near the chromosomal locus for the gene determining MHS (see figure).

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Homologue of TFIIS in yeast

SIR—We wish to draw attention to an interesting similarity of amino-acid sequence that we believe has been overlooked. While screening random genomic fragments from the yeast *Saccharomyces cerevisiae* we sequenced[1] a part of the gene *PPR2* which encodes a transcripitonal regulator of dihydroorotase (*URA4*). A search of the NBRF protein databank with the peptide sequence encoded by our clone revealed significant homology with only one other protein — the mouse transcription elongation factor SII (ref. 2). The search did not identify *PPR2* because this sequence was not present in the NBRF database (Release 21·0 (6·89)).

When the sequences of the 128 amino acid and *PPR2* protein and the 301 amino acid SII protein were compared, an overall identity of 40 per cent with respect to *PPR2* and a high degree of conservative amino-acid substitution was revealed (see figure). Strikingly, the two proteins share the same carboxy terminus, having 70 per cent identity in the 44 carboxy-terminal amino acids.

The activity of SII (otherwise called TFIIS[3]) is necessary for efficient RNA polymerase II transcription elongation past template-encoded pause sites, and has been described in mouse[4], *Bombyx mori*[5], bovine species[6], *Drosophila*[7] and HeLa[3] systems. The protein binds to RNA polymerase II in the absence of transcription[3,8]. The SII protein is larger than *PPR2*, but elongation-stimulating activity resides at the carboxy terminus, the very region with homology to *PPR2*.

These observations suggest that *PPR2* functions in the regulation of *URA4* expression at the level of transcriptional elongation, and also that SII may not be a general transcription factor, such as TFIIA,B,D,E and F, but instead, may regulate a specific subset of genes.

The function of the highly conserved carboxy-terminal region is at present unclear, but the absence of any obvious DNA-binding sequence suggests it may contact a component of the transcriptional machinery. A closer analysis of *PPR2* at the molecular level in yeast may be illuminating.

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```
PPR2     1 MNKVNNCDTNEAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAPLK
                        :  ||:| |   ||: : :||:|::::  |:|:|:::|  :|:::|:: ||
SII    174 EAIYQEIRNTDMKYKNRVRSRISNLKDAKNPNLRKNVLCGNIPPDLFARMTAEEMASDELK

QKIEEIAKQNLYNAQGATIERSVTDRFTCGKCKEKKVSYYQLQTRSADEPLTTFCTCEACGNRWKFS 128
:: ::::|::: : | |::: : || |||||||:|: :| |:|||||||||:||| :|::|||||||
EMRKNLTKEAIREHQMAKTGGTQTDLFTCGKCKKKNCTYTQVQTRSADEPMTTFVVCNECGNRWKFC 301
```

Amino acid alignment of yeast *PPR2* and mouse transcription elongation factor SII(TFIIS). Vertical lines indicate identity, colons conservative replacements.

Edible eyeballs from fish

SIR—We report here a simple method of vitrification of denatured proteins such as egg white or vitreous bodies of fish eyeballs which have become opaque by boiling. In vitrification, a material becomes transparent under visible light, and becomes amorphous and rigid like glass.

We vitrified denatured proteins by keeping boiled opaque egg white in a refrigerator after removal of the shell and yolk. As early as a day after refrigeration, the thin, elastic edge began to harden and become transparent. The weight was reduced by 30 per cent after 6 days (see figure), and most of it had hardened and become transparent. When the weight fell to 17 per cent of the original weight, all the egg white was perfectly hard.

The moisture from the boiled egg white evaporated in two stages (see figure). The first-stage evaporation continued until the weight was reduced to 20 per cent of the original, whereupon the second stage began, which continued until all the water in the egg white had evaporated. As these two stages are so different, the moisture lost in the first could be weakly bound to the protein, and in the second stage fairly strongly bound.

Though there have been many experiments concerning bound and free water reported[1–4], our method might reveal something new. There are known to be about 40 proteins in egg white; considering the molecular masses of the main ones[5]