

Genetics. In the article "Isolation and characterization of a cDNA clone for the *Cat2* gene in maize and its homology with other catalases" by Leslie A. Bethards, Ronald W. Skadsen, and John G. Scandalios, which appeared in number 19, October 1987, of *Proc. Natl. Acad. Sci. USA* (84, 6830-6834), the authors request that the following corrections to the sequence (Fig. 4, p. 6832; GenBank accession no. J02976) be noted. We have resequenced the R6-67 *Cat2* clone using

overlapping deletions to avoid subcloning and find that, from nucleotide 1365 to the end (nucleotide 1714), the published sequence is that of a contaminating DNA introduced during subcloning (the correct sequence is boxed below). In addition, other very minor variations were noted in the 5' end. The complete corrected sequence is shown below. This new sequence contains two possible poly(A) consensus sequences (underlined) and a short poly(A) tail.

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1  GTACGTCGTAGCGGCTCGTCCAGCTCGCGCTCCAGCTCGCGCGCCACCGCCATG GAC CCG TAC AAG CAC CGC CCG TCG AGC GCC TTC AAC GCC CCG TAC
1  Met Asp Pro Tyr Lys His Arg Pro Ser Ser Ala Phe Asn Ala Pro Tyr
100 TGG ACC ACC AAC TCC GGC GCC CCC GTG TGG AAC AAC GAC AGC TCC CTC ACC GTA GGC GCA CGA GGT CCC ATC CTG CTG GAG GAC
17 Trp Thr Thr Asn Ser Gly Ala Pro Val Trp Asn Asn Asp Ser Ser Ser Leu Thr Val Gly Ala Arg Gly Pro Ile Leu Leu Glu Asp
184 TAC CAC TGT GAG AAG CTA GCC AAC TTC GAC CGC GAG CGC ATC CCG GAG CGC GTG GTG CAC GCG CGT GGC GCC AGC GCC AAG GGC
45 Tyr His Cys Glu Lys Leu Ala Asn Phe Asp Arg Glu Arg Ile Pro Glu Arg Val Val His Ala Arg Gly Ala Ser Ala Lys Gly
268 TTC TTC GAG GTG ACC CAC GAC ATC ACC CAC CTG ACG TGC GCC GAC TTC CTG CGC GCG CCC GGG GTG CAG ACG CCC GTC ATC GTC
73 Phe Phe Glu Val Thr His Asp Ile Thr His Thr Cys Ala Asp Phe Leu Arg Ala Pro Gly Val Gln Thr Pro Val Ile Val
352 CGC TTC TCC ACG GTC ATC CAC GAG CGC GGG AGC CCC GAG ACG CTC CGG GAC CCG CGC GGG TTC GCC GTC AAC TTC TAC ACC CGG
101 Arg Phe Ser Thr Val Ile His Glu Arg Gly Ser Pro Glu Thr Leu Arg Asp Pro Arg Gly Phe Ala Val Lys Phe Tyr Thr Arg
436 GAG GGC AAC TGG GAC CTG GTG GGC AAC AAC TTC CCC GTC TTC TTC ATC CGC GAC GGC ATC AAG TTC CCG GAC ATG GTG CAC GCG
129 Glu Gly Asn Trp Asp Leu Val Gly Asn Asn Phe Pro Val Phe Phe Ile Arg Asp Gly Ile Lys Phe Pro Asp Met Val His Ala
520 CTC AAG CCC AAC CCG CGG ACG CAC ATC CAG GAC AAC TGG CGC ATC CTC GAC TTC TTC TCG CAC CAC CCG GAG AGC CTG CAC ATG
157 Leu Lys Pro Asn Pro Arg Thr His Ile Gln Asp Asn Trp Arg Ile Leu Asp Phe Phe Ser His His Pro Glu Ser Leu His Met
604 TTC TCC TTC CTC TTC GAC GAC GTC GGC ATC CCC GCC GAC TAC CGC CAC ATG GAC GGA TCC GGG GTG CAC ACG TAC ACG CTC GTC
185 Phe Ser Phe Leu Phe Asp Asp Val Gly Ile Pro Ala Asp Tyr Arg His Met Asp Gly Ser Gly Val His Thr Tyr Thr Leu Val
688 AGC CGC GCC GGC ACC GTC ACC TAC GTC AAG TTC CAC TGG CGC CCC ACC TGC GGC GTG CGC TCG CTG ATG GAC GAC GAG GCC GTC
213 Ser Arg Ala Gly Thr Val Thr Tyr Val Lys Phe His Trp Arg Pro Thr Cys Gly Val Arg Ser Leu Met Asp Asp Glu Ala Val
772 CGT TGC GGC GCC AAC CAC AGC CAC GCC ACC AAG GAC CTC ACG GAC GCC ATC GCG GCG GGG AAC TTC CCC GAG TGG ACG CTC TAC
214 Arg Cys Gly Ala His Ser His Ala Thr Lys Asp Leu Thr Asp Ala Ile Ala Ala Gly Asn Phe Pro Glu Trp Thr Leu His Met
856 ATC CAG ACC ATG GAC CCC GAG ATG GAA GAC CGC CTC GAC GAC CTG GAC CCG CTG GAC GTG ACC AAG ACG TGG CCC GAG GAC CGG
269 Ile Gln Thr Met Asp Pro Glu Met Glu Asp Arg Leu Asp Asp Leu Asp Pro Leu Asp Val Thr Lys Thr Trp Pro Glu Asp Arg
940 TTC CCG CTG CAG CCC GTG GGC CGC CTG GTG CTC AAC CGC AAC ATC GAC AAC TTC TTC GCG GAG AAC GAG CAG CTG GCC TTC TGC
297 Phe Pro Leu Gln Pro Val Gly Arg Leu Val Leu Asn Arg Asn Ile Asp Asn Phe Phe Ala Glu Asn Glu Gln Leu Ala Phe Cys
1024 CCG GGC CTC ATC GTC CCT GGT ATC TAC TAC TCC GAC GAC AAG CTG CTG CAG ACC AGG ATC TTC TCC TAC TCC GAC ACG CAG CGC
325 Pro Gly Leu Ile Val Pro Gly Ile Tyr Tyr Ser Asp Asp Lys Leu Leu Gln Thr Arg Ile Phe Ser Tyr Ser Asp Thr Gln Met
1108 CAC CGC CTC GGC CCC AAC TAC CTG CTG CTA CCG GCC AAC GCG CCC AAG TGC GCA CAC CAC AAC AAC CAC TAC GAC GGA TCC ATG
353 His Arg Leu Gly Pro Asn Tyr Leu Leu Leu Pro Ala Asn Ala Pro Lys Cys Ala His His Asn Asn His Tyr Asp Gly Ser Met
1192 AAC TTC ATG CAC CGC CAC GAG GAG GTC GAC TAC TTC CCC TCC AGG TAC GAC GCC GTC AGG AAC GCG CCG AGG TAC CCG ATC CCG
381 Asn Phe Met His Arg His Glu Glu Val Asp Tyr Phe Pro Ser Arg Tyr Asp Ala Val Arg Asn Ala Pro Arg Tyr Pro Ile Pro
1276 ACC GCC CAC ATC GCC GGC CGC CGA GAG AAG ACT GTG ATT AGC AAG GAG AAC AAC TTC AAG CAG CCC GGG GAG AGG TAC CGC GCG
409 Thr Ala His Ile Ala Gly Arg Arg Glu Lys Thr Val Ile Ser Lys Glu Asn Asn Phe Lys Gln Pro Gly Glu Arg Tyr Arg Ala
1360 ATG GAC CCA GCA AGG CAA GAG CGG TTC ATA ACC AGA TGG GTC GAC GCG CTC TCC GAC CCC CGC CTC ACC CAC GAG ATC AGG ACC
437 Met Asp Pro Ala Arg Gln Glu Arg Phe Ile Thr Arg Trp Val Asp Ala Leu Ser Asp Pro Arg Leu Thr His Glu Ile Arg Thr
1444 ATC TGG CTC TCC AAC TGG TCT CAG GCC GAC AGG TCT CTG GGC CAG AAG CTC GCG AGC CGC CTC AGC GCC AAG CCG Arg ATG TAA
465 Ile Trp Leu Ser Asn Trp Ser Gln Ala Asp Arg Ser Leu Gly Lys Leu Ala Ser Arg Leu Ser Arg Ser Met ---
1528 GATCAACCAGACAAGGGCGCCGCGGGGAGGACGGAGCTCTCTGTCCTCGTCGTCATCATCATACGCATGGAACCAAGACAAATTACTCTAGCAGACTAGCACGG
1639 GTACTGAATCGCGTTTCCGCTGATCCTTTCCCTAGTTTGTGTTTTCGCCCCGGATAAAGGCTGCTAGCTTGGTTGTATAATGGGTGGCTGTGCCAGAACTCTTGC
1750 ACTCTTCCAGATGCCCGAATAATAATATTCCTTTTTCCAAAAA

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