ERRATA

Volume **229**, Number 1 (1996), in the article "Molecular Cloning of a Novel Rat Salt-Tolerant Protein by Functional Complementation in Yeast," by Emiko Tsuji, Yuji Tsuji, Yoshio Misumi, Atsushi Fujita, Manabu Sasaguri, Munehito Ideishi, and Kikuo Arakawa, pages 134–138: On page 136, Fig. 2 is incorrect as printed. The legend is correct as printed. For the reader's convenience, the correct Fig. 2 and its legend are printed here. The corrected, deduced amino acid sequence of the salt-tolerant protein is 547 residues, not 496 as originally stated. STP shows a high degree (80%) of peptide sequence identity to human Trip10 mRNA at the 3' end. The relevant DDBJ/EMBL/GenBank data base entry, D50557, has been revised. (The error resulted from an incorrect reading of the sequencing tracing.)

This erratum is Article No. RC977609.

$\tt TGGAGACCCGGGGCAGGAGGCGGTGGCGTCTTCCGCGGCAAGAGCAGCATGGATTGGGGTACCGAGTTGTGGGAT$	75						
M D W G T E L W D	9						
${\tt CAGTTTGAGGTGCTGGAACGCCACACACTGGGGGCTGGATCTGTTGGACAAATACGTGAAGTTCGTGAAAGAA}$	150						
Q F E V L E R H T Q W G L D L L D K Y V K F V K E	34						
CGCGTCGAGGTGGAGCAGTCTTATGCGAAGCAACTCAGGAGTCTGGTGAAAAAGTATCTTCCCAAGAGACCTGCC	225						
RVEVEQSYAKQLRSLVKKYLPKRPA	59						
AAAGATGACCCCGAAATCAAGTTTAGCCAGCAACAGTCATTTGTCCAGCTTCTCCAGGAGGTCAATGATTTTGCA	300						
K D D P E I K F S Q Q Q S F V Q L L Q E V N D F A	84						
GGCCAACGAGAGCTGGTGGCCGAGAGCCTTGGCATCCGAGTGTGTCTGGAGCTGGCTAAGTATTCACAGGAGATG	375						
GQRELVAESLGIRVCLELAKYSQEM	109						
AAGCAAGAGAGAAGATGCACTTCCAAGAAGGCCGTCGGGCCCAGCAGCAGCTGGAAAATGGCTTCAAACAGCTG	450						
K Q E R K M H F Q E G R R A Q Q Q L E N G F K Q L	134						
GAGAATAGTAAGCGAAAGTTTGAACGAGACTGTCGCGAGGCTGAGAAAGCGGCTCACACCGCAGAGCGGCTGGAC	525						
ENSKRKFERDCREAEKAAHTAERLD	159						
CAGGACATTAATGCCACCAAGGCGGATGTGGAGAAGGCCAAGCAGCAAGCCCACCTTCGGAACCACATGGCAGAA	600						
Q D I N A T K A D V E K A K Q Q A H L R N H M A E	184						
GAGAGCAAGAACGAATACGCGGCCCAGCTGCAGCGCTTCAACCGGGACCAGGCTCACTTCTACTTCTCACAGATG	675						
ESKNEYAAQLQRFNRDQAHFYFSQM	209						
CCGCAGATATTCGACAAGCTGCAGGACATGGATGAACGCCGGGCCACCCGCCTTGGGGCCGGGTATGGGCTCTTA	750						
P Q I F D K L Q D M D E R R A T R L G A G Y G L L	234						
TCTGAAGCTGAACTGCAGGTGGTTCCCATTATTGGCAAATGCTTGGAGGGCATGAAGGTGGCCGCAGAGTCCGTG	825						
S E A E L Q V V P I I G K C L E G M K V A A E S V	259						
GATGCTAAGAACGACTCGAAGGTCCTCATCGAATTACACAAGTCAGGGTTTGCCCGCCC	900						
DAKNDSKVLIELHKSGFARPGDLEF	284						
GAAGACTTCAGCCAAGTTATGAACCGAGTGCCGTCGGACAGCAGCCTGGGCACCCCAGATGGCAGGCCTGAGCTC	975						
E D F S Q V M N R V P S D S S L G T P D G R P E L	309						
CGAGCAGCTTCCAGCCGTAGTCGTGCCAAGCGTTGGCCTTTTGGGAAAAAGAACAAGACCGTGGTCACCGAAGAT	1050						
RAASSRSRAKRWPFGKKNKTVVTED	334						
TTCAGTCACCTGCCCCCGGAGCAGCAGAGAAAGCGACTCCAGCAACAGTTGGAAGAGCCGGAACCGAGAGTTGCAG	1125						
F S H L P P E Q Q R K R L Q Q Q L E E R N R E L Q	359						
AAGGAGGACCAGAGGGAGGCCCTGAAGAAGATGAAAGATGTATATGAGAAAACACCACAAATGGGGGACCCC	1200						
K E E D Q R E A L K K M K D V Y E K T P Q M G D P	384						
GCCAGCTTAGAGCCCCGCATTGCAGAGACCCTGGGCAACATTGAAAGGCTGAACGTGGAAGTGCAGAAGTATGAG	1275						
ASLEPRIAETLGNIERLNVEVQKYE	409						
GCTTGGTTGGCAGAAGCTGAAACGCGGGTCCTCAGTAACCGAGGGGACAGCCTAAGCCGTCACACTAGGCCTCCT	1350						
AWLAEAETRVLSNRGDSLSRHTRPP	434						
GATCCCCCAACTACTGCCCCACCTGATAGTAGCAGTAGCAGCAACAACAGTGGATCCCAGGATAATAAGGAGAGC	1425						
D P P T T A P P D S S S S N N S G S Q D N K E S	459						
TCAGAAGAGCCCCCTTCAGAAGAAGGCCAGGACACCCCCATCTACACTGAGTTCGATGAGGACTTTGAAGAACCT	1500						
SEEPPSEEGQDTPIYTEFDEDFEEP	484						
GCATCCCCCATCGGCCAGTGTGTGGCTATCTACCATTTTGAAGGATCCAGTGAGGGGACCGTCTCCATGTCCGAG	1575						
ASPIGQCVAIYHFEGSSEGTVSMSE	509						
${\tt GGGGAAGACCTCAGTCTGATGGAGGAAGACAAGGGTGATGGATG$	1650						
G E D L S L M E E D K G D G W T R V R R K Q G G E	534						
${\tt GGCTATGTGCCCACCTCTTACCTCCGAGTCACACTCAACTGAACCCCACTGGAGGGACGATGGGCAGGACTGTCACCTCAACTGAACCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGATCAACTGAACCCCCACTGGAGGGACGATGGGCAGGACTGTCAACTGAACTAACT$	1725						
GYVPTSYLRVTLN*	547						
GCTGCTGCTTCTGGGCCACAGGGGACTTTGCACTTTATTCCTGCCCTCGTGGCTTTTGGCTGAAACCTGTGTAAC	1800						
CTGCTGTCCCTCATCCGCCGCACCTGGCACCCCACGGACCACTTGTCTTCCCGTGTGGCTGTACATAGTTGTCAT 18							
TTCAGACCTTTCTCCCTGCCGCTCCGGTGTGGGCCAAGTTTTGTTTTATATTAAAAAGTATATAATTACAAAA 195							
AAAAAAAAAAAAA							

FIG. 2. Nucleotide and deduced amino acid sequences of salt-tolerant protein (STP). The deduced amino acid sequence is shown in the single-letter code below the nucleotide sequence. Nucleotides and amino acids are numbered on the right. The stop codon is indicated by an asterisk. Double underlining denotes a nucleotide sequence that shows partial homology to the nucleotide sequence of human thyroid receptor-interacting protein 10 (Trip 10).

Volume **236**, Number 2 (1997), in Article No. RC976952, "Biotin Synthase, a New Member of the Family of Enzymes Which Uses S-Adenosylmethionine as a Source of Deoxyadenosyl Radical," by Dominique Guianvarc'h, Dominique Florentin, Bernadette Tse Sum Bui, Frederic Nunzi, and Andrée Marquet, pages 402–406: Due to a compositor's error, Table 1 on page 404 contained two errors. In column 3, lines 3 and 7 should read "Minus DTB" instead of "Minus DTP." For the reader's convenience, the correct Table 1 is printed here.

This erratum is Article No. RC977611.

TABLE 1

AdoMet Cleavage in the Presence of Biotin Synthase of Bacillus sphaericus and Escherichia coli with Deazaflavin

Entry	Strain	Reaction mixture	Biotin (nmol)	5'-Deoxyadenosine (nmol)	5'-Deoxyadenosine (entry 1 minus entry 2)/Biotin	Methionine (nmol)	Methionine (entry 1 minus entry 2)/Biotin
1	B. sphaericus	Complete	0.3	1.18 ± 0.13^{b}	2.9^a	1.61 ± 0.42^{c}	3.1
2	•	Minus DTB	0	0.31 ± 0.13^{b}	_	0.69 ± 0.29^{c}	_
3		Minus enzyme	0	0^{b}	_	0.4 ± 0.22^{c}	_
4		Inactivateď enzyme	0	0^d	_	ND	_
5	E. coli	Complete	0.3	2.1 ± 0.25^{e}	2.9	ND	_
6		Minus DTB	0	1.25 ± 0.25^{e}	_	ND	_
7		Minus enzyme	0	0^{e}	_	ND	_

Note. The reaction mixture is described under Materials and Methods. As the production of biotin varied up to 2-fold between the different sets of experiments, all the data were normalized to correspond to the formation of 0.3 nmol of biotin. ND, not determined.

Volume **237**, Number 3 (1997), in Article No. RC977089, "Insulin-like Growth Factor Binding Protein-3 Induces Apoptosis in MCF7 Breast Cancer Cells," by Tara Nickerson, Hung Huynh, and Michael Pollak, pages 690–693: On page 693, under References, References 7 and 25 are incorrect as printed. For the reader's convenience, the correct references are printed here.

This erratum is Article No. RC977610.

^a The enzyme used was after the Co(II)-chelating sepharose step since we checked that the results were the same as with the pure enzyme. Data represent the mean \pm SD of:

^b 10 independent experiments

^c 3 independent experiments

^d 2 independent experiments, biotin synthase was boiled for 20 minutes

^e 2 independent experiments

Dudek, H., Datta, S. R., Franke, T. F., Birnbaum, M. J., Yao, R., Cooper, G. M., Segal, R. A., Kaplan, D. R., and Greenberg, M. E. (1997) Science 275, 661–665.

^{25.} Levine, A. J. (1997) Cell 88, 323-331.