

# Nucleotide sequence of the cDNA encoding L-histidine decarboxylase derived from human basophilic leukemia cell line, KU-812-F

Kohei Yamauchi, Ruriko Sato, Yasuo Tanno, Yuichi Ohkawara, Kazutaka Maeyama<sup>1</sup>, Takehiko Watanabe<sup>1</sup>, Ken Satoh<sup>2</sup>, Miki Yoshizawa<sup>3</sup>, Shigeki Shibahara<sup>3</sup> and Tamotsu Takishima\*

First Department of Internal Medicine, <sup>1</sup>First Department of Pharmacology, <sup>2</sup>Institute of Tuberculosis and Cancer and <sup>3</sup>Department of Applied Physiology and Molecular Biology, Tohoku University, School of Medicine, Sendai 980, Japan

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Histamine is a chemical mediator released from basophils or mast cells and plays an important role in allergic reactions. The formation of histamine from L-histidine is catalyzed by L-histidine decarboxylase (HDC, EC4.1.1.22) which is localized in various tissues including brain, stomach and fetal liver as well as in basophils and mast cells (1). Recently Joseph *et al.* isolated HDC cDNA from rat fetal liver cDNA library and determined its nucleotide sequence (2). Here we present the nucleotide and deduced amino acid sequence of the cDNA coding for human HDC. A cDNA library of human basophilic leukemia cell, KU-812-F (3), was constructed in the Okayama-Berg expression vector (4) and screened with the synthetic oligonucleotides complementary to nucleotide sequence of the rat HDC cDNA (nucleotide residues 547–596 and 970–1019) (2). One clone

AGT GCG CAG GAC TGG CAA GAG GGA AGC CGG CCT GCT CCA CGC CTT TCA CGC CTT CCA CCT	60
CCT GGG TGT CCA TCT GTG AGA AGG AGC CAG ACC CCA AGG GAC ATG ATG GAG CCT GAG GAG	120
Met Met Glu Pro Glu Glu	6
TAC AGA GAG AGA CGG AGA GAG ATG GTG GAT TAC ATC TGC CAG TAC CTG AGC ACT GTG CGG	180
Tyr Arg Glu Arg Gly Arg Glu Met Val Asp Tyr Ile Cys Glu Tyr Leu Ser Thr Val Arg	26
GAG AGA CGT GTG AGC CCA GAC GTG CAG CCT GCC TAC CTG CGA CCC CAG CTG CCT GAG AGT	240
Glu Arg Arg Val Thr Pro Asp Val Glu Pro Gly Tyr Leu Arg Ala Glu Leu Pro Glu Ser	46
GCT CCT GAG GAC CCC GAC AGC TGG GAC AGC ATC TTT GGG GAC ATT GAA CGA ATC ATG ATG	300
Ala Pro Glu Asp Pro Asp Ser Trp Asp Ile Phe Gly Asp Ile Glu Arg Ile Ile Met	66
CCT GGG GTG GTA CAT TGG CAG AGC CCC CAT ATC GAC GGC TAC TAC CGA CCC CTC ACC TCT	360
Pro Glu Val Val His Pro Glu His Met His Ala Ile Tyr Pro Ala Leu The Ser	86
TGG CCC TCC CTG CTA CGG GAC ATG CTG GCT GAT GGG ATC AAC TGC TTG GGA TTC ACC TGG	420
Trp Pro Ser Leu Leu Gly Asp Met Leu Ala Asp Ala Ile Asn Cys Leu Gly Phe Thr Itp	106
GCA TCC AGC CCT GGG TGT ACA GAG GAG CTG GAG ATG ATC GAC TGG TTG GCA AAA ATG	480
Ala Ser Ser Pro Ala Cys Pro Leu Glu Met Asn Val Met Asp Trp Ala Leu Lys Met	126
CTG GGA CTC CCA GAG CAC TTC TTC CAC CAC CCC ACC AGC AGC CAG GGC GGA GGC GTC CTG	540
Lau Gly Leu Pro Glu His Phe Leu His His His Pro Ser Ser Glu Gly Glu Val Lau	146
CAG CAG AGC GTC ACT GAA TCC ACT TTG ATT GGC CTG CTG GCA GCA AGG AAC AAC AAA ATC	600
Gln Glu Thr Val Ser Glu Ser Thr Ile Ala Leu Leu Ala Asp Lys Asn Lys Ile	166
CTG GAA ATG AAA ACC TGT GAG CCC GAT GCT GAT GAC TCC TCC CTA ATT GGC CGA CTC GTG	660
Lau Glu Met Lys Thr Ser Glu Pro Asp Ala Asp Glu Ser Cys Leu Asn Ala Arg Leu Val	186
GCC TAT GGG TCT GAC CAG GCT CTC TCC TCT GAA AAC GCT GGT TTG ATT TCC CTT GTG	720
Ala Tyr Ala Ser Asp Glu Ala His Ser Ser Val Glu Lys Ala Gly Leu Ile Ser Leu Val	206
AAG ATG AAA TTT CTG CCT GTC GAT GAC AAC TTC TCA CTC CGA GGG GAA CCT CTT CAG AAC	780
Lys Met Lys Phe Leu Pro Val Asp Asn Phe Ser Leu Arg Gly Glu Ala Leu Glu Lys	226
GCC ATC GAG GAA GAC AAG CAG CGG GGC TTG GTG CCC GTC TTT GTC TGT GCA ACA CTA CGG	840
Ala Ile Glu Asp Lys Glu Arg Gly Leu Val Pro Val Phe Val Cys Ala Thr Leu Glu	246
ACC ACT CGG CTC TGT CGA TCC TCA CGC CTC CGC CCC ATC TGT GGC CGT GAG	900
Thr Thr Glu Val Cys Ala Phe Asp Cys Leu Ser Glu Leu Glu Gly Pro Ile Cys Ala Arg Glu	266
GGG CTG TCG CTC CAC ATC GAT GCT GCT TAT GCA GGC ACT CCC TGC TTG CGC CCC GAG TTC	960
Gly Leu Trp Leu His Ile Cys Ala Tyr Ala Glu Thr Ala Phe Leu Cys Pro Glu Phe	286
CGG GGG TTT CTG AAC GGG ATT GAC TAT GGC GAC TCC TTC ACC TTT ATT CCT TCC AAC TAG	1020
Arg Glu Phe Leu Lys Cys Ile Glu Cys Tyr Ala Asp Ser Phe Thr Phe Asn Pro Ser Lys Trp	306
ATC ATC CTG CAT TTT GAC TGT ACT CGG TTC TTG GTC AAC GAC AAC TAC AAC CTG CAG CAG	1080
Met Met Val His Phe Asp Cys Thr Gly Phe Trp Val Lys Asp Lys Tyr Lys Leu Glu Glu	326
ACC TTC ACT GTG AAC CCC ATC TAC CTC ACC CAT GCC AAC TCA CGC GTG CCC ACC GAC TCC	1140
Thr Phe Ser Val Asn Pro Ile Tyr Leu Arg His Ala Asn Ser Glu Val Ala Thr Asp Phe	346

ATC CAC TGG CAG ATC CCC CTG ACC CGA CGC TTT CGC TCT GTT AAA CTC TGG TTC GTG ATT	1200
Met His Trp Gin Ile Pro Leu Ser Arg Arg Phe Arg Ser Val Lys Leu Trp Phe Val Ile	366
CGG TCC TTC GGG GTG AGG AAT CTT CAA CGA CAT GTC AGA CAT GCT ACT GAA ATG GCT AAA	1260
Arg Ser Phe Gly Val Lys Asn Leu Gin Ala His Val Arg His Gly Thr Glu Met Ala Lys	386
TAT TTT GAA TCT CTG GTC AGA AAC GAC CCT CTC TTT GAA ATT OCT GGC AAC AGG CAC CTT	1320
Tyr Phe Glu Ser Leu Val Arg Asn Asp Pro Ser Phe Glu Ile Pro Ala Lys Arg His Leu	406
GCG CTG GTG GTT TTT CGT CTA AAC GGT CCT ATT TGT CTC AGC ACA GAA ATT GTG TTA AAC GAA	1380
Gly Leu Val Val Phe Arg Leu Lys Pro Asp Asn Cys Leu Thr Glu Asp Val Leu Lys Glu	426
ATA GCT AAA GCT GGC CGT CTC TTC CTC ATC CCG GGC ACT ATC CAG GAC AAC TTA ATC ATC	1440
Ile Ala Lys Ala Cys Arg Leu Leu Ile Asp Ala Thr Ile Glu Asp Lys Leu Ile Ile	446
GCT TTC ACT GTG ACA TCC CAG TTT ACC ACT AGG GAT GAC CTC AGA GAC TGC TGG ATT CTC	1500
Arg Phe Thr Val Thr Ser Gin Phe Thr Thr Arg Asp Asp Ile Leu Arg Asp Trp Asn Leu	466
ATT CGA GAT GCT CCC ACT CTC ATC CTC AGT CAG GAC CAG TGC ACT TCC CAA CGC ACC CCT CGG	1560
Ile Arg Asp Ala Thr Leu Ile Asn Cys Ser Gin His Cys Thr Ser Gin Pro Ser Pro Arg	486
GTT GGG AAC CTC ATC TCC CAA ATC AGG GGT GGC AGA GGC TGG GCC TGT GGA ACC TCC CTT	1620
Val Gly Asn Leu Ile Ser Glu Ile Arg Cys Glu Ala Arg Ala Trp Ala Cys Gly Thr Ser Leu	506
CAG TCT GTC AGT GGC GCA GGA GAT GAT CCA GTC CAG GGC AGG AAC ATC ATC AAC CAG CCT	1680
Gin Ser Val Ser Gly Ile Arg Asp Pro Val Gin Ile Arg Lys Ile Ile Lys Glu Pro	526
CAG CGT GTG GCA CGC CCT CCC ATC ATG AAA AGG GAA ATT CCT CTC CAT CTT GAA ACC CTG CTG	1740
Gly Ile Arg Val Gly Pro Asp Lys Arg Glu Asn Cys Leu His Leu Glu Thr Leu Leu	546
GAC CGA CCA GTT GAT GAC TGC TTT TCA GAA GAG CGC CGC CAA GAT GCC ACC AAC CAC AAC TGC TCC	1800
Asp Pro Val Asp Asp Cys Phe Ser Glu Glu Ala Pro Asp Ala Thr Lys His Lys Leu Ser	566
TCC TTC CTG TTC AGT TAC TTG TCT GTC ACT AAC AGG AAC ACC GTG CGG CCT TCC CTC ACT	1860
Ser Phe Leu Phe Ser Tyr Leu Ser Val Glu Thr Lys Lys Leu Thr Val Arg Ser Leu Ser	586
TGC AAC AGT GTG CCA GTG ACT GCT CAG AAC CCA CTG CCC ACA GAG GGC CCT TGT GTG AAC ATT	1920
Cys Asn Ser Val Pro Val Ser Ala Glu Lys Pro Leu Pro Thr Glu Ala Ser Val Lys Asn	606
GCG GGC TCC TCC ACC AGC ATA ACT TTT TCA AGC ATT CCT CCA GAA GAC ATG ATG ATC CTC ACT	1980
Gly Cys Ser Ser Arg Val Ile Phe Ser Asp Arg Phe Pro Glu Asp Met Met Not Met Leu Lys	626
AAA AGT GGC TCC AAA AAC CTC TAC TCC ACC AGC GTC CGC CCT TGT CCT GAA TGC ACC	2040
Ser Thr Ala Phe Lys Leu Ile Ser Tyr Pro Val Ser Val Pro Ser Phe Pro Glu Cys Ser	640
TCT CAA TGT GGA CTC CAG CTG CCC TGT TGC CCT CTG CAG GCC ATG ATT GCA CAG CCC	2100
Ser Gin Cys Gly Leu Glu Pro Leu Pro Cys Cys Pro Leu Glu Ala Met Val ***	663
CTT CAG CAG ACT CTC AGG ATA TAC TAC AGC GAC TCT GTG AAC CCC TCA CAA TTG TAT GCC	2160
AAC TTT GTG TGC TTA TGT GTC GAT GCA TTT TTC TTG GGG CGA GTT CAT AAT TTT ATT CAA	2220
ATT CTC ATC CGG CCT CAT GAC CCA CAA TAG CAT ACA AAC GAA GAC TTT AAC CCA GCA TGA	2280
TCC AGA TGG GTT CAT CAG CCT GAT GCG GAG GGT AGA CAG GCA GCT TCT	2340
GTC GTT CAG CTC GTG ACA TGA TAT ATA ACA CAG AAA TAA ATT ATG CTT GTG CCT GAA AAA	2400

pTN-2, containing an insert of 2.4 kb, is confirmed to encode human HDC by transient expression of HDC activity in COS cells (data not shown). Human HDC consists of 662 amino acid residues ( $M_r$  74,178) and shares 85% homology in amino acid sequence with rat HDC.

## REFERENCES

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\* To whom correspondence should be addressed