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## Isolation and Characterization of a cDNA Encoding Rat Cationic Trypsinogen<sup>†</sup>

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**ABSTRACT:** A cDNA encoding rat cationic trypsinogen has been isolated by immunoscreening from a rat pancreas cDNA library. The protein encoded by this cDNA is highly basic and contains all of the structural features observed in trypsinogens. The amino acid sequence of rat cationic trypsinogen is 75% and 77% homologous to the two anionic rat trypsinogens. The homology of rat cationic trypsinogen to these anionic trypsinogens is lower than its homology to other mammalian cationic trypsinogens, suggesting that anionic and cationic trypsins probably diverged prior to the divergence of rodents and ungulates. The most unusual feature of this trypsinogen is the presence of an activation peptide containing five aspartic acid residues, in contrast to all other reported trypsinogen activation peptides which contain four acidic amino acid residues. Comparisons of cationic and anionic trypsins reveal that the majority of the charge changes occur in the C-terminal portion of the protein, which forms the substrate binding site. Several regions of conserved charge differences between cationic and anionic trypsins have been identified in this region, which may influence the rate of hydrolysis of protein substrates.

**T**he trypsins (EC 3.4.21.4) are important members of a large family of pancreatic serine proteases that share a common

catalytic mechanism and possess similar tertiary structures. These enzymes are endopeptidases which are synthesized as proenzymes by pancreatic acinar cells and secreted into the gut. The trypsins are distinguished from the other pancreatic serine proteases both by their specificity for arginine or lysine residues and by their capability to activate the other pancreatic zymogens.

Although multiple ionic forms of trypsin have been isolated from humans (Travis & Roberts, 1969; Mallory & Travis, 1973), cows (Louvard & Puigserver, 1974), rats (Brodrick et

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al., 1980), dogs (Ohlsson & Tegner, 1973), and pigs (Louvard & Puigserver, 1974), little is known concerning the possible functional significance of the different trypsins. The classically described forms of bovine and porcine trypsins are cationic proteins (Walsh & Neurath, 1964; Travis & Liener, 1965), and in these animals, the anionic forms of trypsin represent less than 10% of the total trypsin content (Louvard & Puigserver, 1974). In contrast, two anionic trypsins represent approximately 60% of the trypsin synthesized in the rat pancreas (C. Largman, unpublished results). Two rat trypsin genes have been sequenced and shown to code for the anionic trypsinogens (Craik et al., 1984). The gene for rat pancreatic trypsin I was shown to code for the major anionic form produced by the pancreas by homology to the amino acid sequence of the N-terminus of purified rat anionic trypsin (unpublished results). Cloned rat pancreatic trypsinogen II has been expressed in mammalian cells and shown to also represent an anionic form of rat trypsin (Craik et al., 1984). To date, there has not been a sequence comparison between the anionic and cationic forms of trypsin from a single species.

In the current study, we have cloned the cDNA for rat cationic trypsinogen using an expression vector and antibodies directed against rat cationic trypsin. The deduced amino acid sequence for rat cationic trypsin and the amino acid sequences of bovine and porcine cationic trypsins have been compared to those of rat anionic trypsins with regard to possible differences in structure which might result in changes in catalytic activity. In addition, comparison of these five trypsinogen sequences has facilitated an assessment of the sequence divergence of the cationic and anionic trypsinogens.

#### MATERIALS AND METHODS

**Antibody Screening of a cDNA Expression Library.** Rat cationic trypsin was purified as described by Brodrick et al. (1980). Rabbit antiserum to rat cationic trypsin was produced by a series of subcutaneous injections of rat cationic trypsin (100  $\mu$ g) in Freund's complete adjuvant as previously described (Largman et al., 1981). The IgG fractions were prepared by chromatography on protein A-Sepharose (Pharmacia, Piscataway, NJ).

A rat pancreatic cDNA library cloned into  $\lambda$ gt11 was generously supplied by J. C. Edman (UCSF). This library contains about 20 000 independent clones inserted into the unique *Eco*RI site of  $\lambda$ gt11 by the ligation of cDNA tailed with a linker sequence containing the restriction sites for *Eco*RI, *Bam*HI, and *Hind*III. The cDNA library was screened with polyclonal rabbit IgG raised against rat cationic trypsin, using  $^{125}$ I-labeled goat anti-rabbit IgG as the second antibody (Young & Davis, 1983). The goat anti-rabbit IgG was radioiodinated by using Iodogen (Pierce, Rockford, IL) as described by Salacinski et al. (1981). Preliminary tests showed that this screening system was capable of detecting 1 ng of rat cationic trypsin.

**Primer Extension.** The 5' portion of the mRNA encoding rat cationic trypsin was sequenced by hybridizing a  $^{32}$ P-labeled oligonucleotide to rat pancreatic mRNA and extending in the presence of nucleotides and chain-terminating inhibitors (Craik et al., 1984). The reaction products were separated on a 10% polyacrylamide-urea gel. Rat pancreas RNA was extracted by using the technique of Chirgwin et al. (1979). Two rounds of chromatography of the pancreatic RNA on oligo(dT)-cellulose yielded mRNA which was subsequently used for primer extension. The priming reaction was performed as described in Craik et al. (1984), with the exception that the incubation temperature was 50 °C. The primed mRNA was redissolved in 55  $\mu$ L of 0.5 mM ethylenediaminetetraacetic

acid (EDTA) (pH 8.0) by heating to 90 °C for 2 min. Each of the extension reactions contained the following: 10  $\mu$ L of primed mRNA, four deoxynucleoside triphosphates, one di-deoxynucleoside triphosphate, and 15–20 units of avian myeloblastosis virus reverse transcriptase (Life Sciences, St. Petersburg, FL). The concentrations of the deoxynucleoside triphosphates were 800  $\mu$ M except for the one to terminated which was 100  $\mu$ M. The 2',3'-dideoxynucleoside triphosphate concentration was 200  $\mu$ M. A control reaction contained the same amount of primed mRNA and reverse transcriptase but only 500  $\mu$ M deoxynucleoside triphosphates. The extension buffer contained 50 mM tris(hydroxymethyl)aminomethane hydrochloride (Tris-HCl) (pH 8.0), 50 mM KCl, 8 mM  $\text{MgCl}_2$ , and 4 mM dithiothreitol (DTT). The extension reaction was incubated for 1 h at 42 °C. Each reaction mix was phenol extracted, ethanol precipitated, and taken up in 2  $\mu$ L of 50% formamide containing 0.05% bromophenol blue and 0.05% xylene cyanol. The tubes were then heated to 90 °C for 3 min and cooled on ice, and 2  $\mu$ L of each mixture was loaded on a 10% polyacrylamide-urea gel. The gel was run for 12 h at 1500 V, dried, and autoradiographed.

**DNA Hybridization and Dideoxy DNA Sequencing.** DNA hybridizations were performed as described in Maniatis et al. (1982). Sequencing was performed as described in Messing (1983) using the bacteriophage M13mp11 and the 17-mer sequencing primer of New England Biolabs (no. 1212, New England Biolabs, Beverly, MA). Deoxynucleotides and di-deoxynucleotides were from Pharmacia (Piscataway, NJ). The restriction enzymes were purchased from New England Biolabs (Beverly, MA) and BRL (Gaithersburg, MD). Polymerase I (Klenow) was from Boehringer Mannheim (Indianapolis, IN). DNA sequences were analyzed with computer programs supplied by Dr. H. Martinez (Biomathematics Computation Laboratory, Department of Biochemistry and Biophysics, UCSF, San Francisco, CA).

**Protein Sequencing.** A sample (10 nmol) of rat cationic trypsinogen was subjected to automatic Edman sequence analysis using a Beckman 890C automatic sequencer at the U.C. Davis Protein Structure Laboratory. Amino acid-phenylthiohydantoin (PTH) derivatives were identified by high-pressure liquid chromatography.

#### RESULTS AND DISCUSSION

**Cloning and Sequencing of the Cationic Trypsinogen cDNA.** The primary screening of the rat pancreas cDNA library with specific antibodies against rat cationic trypsin yielded 19 positive clones. Five of these were successfully purified, and two of these five had easily detectable inserts of 200–300 base pairs (bp). The largest of the two was subcloned into the *Hind*III site of M13mp11. Use of the linker with multiple restriction sites permitted subcloning with *Hind*III rather than *Eco*RI. Dideoxy sequence analysis showed that this clone extended from position 316 to position 600 (Figure 1). The DNA sequence encoded for a portion of a protein which was highly homologous to pancreatic trypsinogens and which included aspartic acid residues at amino acids 93 and 180. These two amino acid residues are homologous to the Asp-102 of the serine protease charge relay system and the Asp-189 that confers the Arg/Lys substrate specificity on trypsins.

In order to isolate a full-length cDNA, the cDNA fragment was isolated, labeled with  $^{32}$ P by nick translation, and employed to probe the full library. Approximately 5% of the phage in the cDNA library hybridized to this sequence under stringent conditions. An 800 bp clone was isolated, subcloned into M13mp11, and sequenced. This clone contained an open reading frame extending from position 49 (amino acid 2) to

```

-15      -10      -1  1      10
met lys ala leu ile phe leu ala phe leu gly ala ala val ala leu pro leu asp asp asp asp asp lys ile val gly gly tyr thr
1 ATG AAG GGC TTA ATT TTC CTT GCT TTC CTT GGA GCT GCT GTT GCT CTC OCT CTG GAT GAT GAT GAT GAC AAG ATT GTT GGA GGC TAC ACC

      20      30      40
cys gln lys asn ser leu pro tyr gln val ser leu asn ala gly tyr his phe cys gly gly ser leu ile asn ser gln trp val val
91 TGC CAG AAG AAT TCT CTC CCA TAC CAG GTG TCT CTG AAT GCT GGC TAC CAT TTT TGT GGA GGC TOC CTC ATC AAT TOC CAG TGG GTT GTT

      50      60      70
ser ala ala his cys tyr lys ser arg ile gln val arg leu gly glu his asn ile asp val val glu gly gly glu gln phe ile asp
181 TCA GGC GCT CAC TGC TAC AAA TOC CGA ATT CAG GTG CGC CTG GGA GAA CAC AAC ATT GAT GTC GTT GAG GGT GGT GAG CAA TTC ATT GAT

      80      90      100
ala ala lys ile ile arg his pro ser tyr asn ala asn thr phe asp asn asp ile met leu ile lys leu asn ser pro ala thr leu
271 GCA GCT AAA ATC ATC CGC CAC CCC AGT TAT AAT GCA AAC ACC TTT TTT GAC AAT GAT ATT ATT TTG ATT AAG CTG AAT TCA OCT GGC ACC CTC

      110      120      130
asn ser arg val ser thr val ser leu pro arg ser cys gly ser ser gly thr lys cys leu val ser gly trp gly asn thr leu ser
361 AAT TCT CGA GTG TOC ACT GTC TCT CTG CCA AGA TCT TGT GGA TCA TCT GGT ACT AAG TGC CTT GTG TCT GGC TGG GGC AAC ACC CTG AGC

      140      150      160
ser gly thr asn tyr pro ser leu leu gln cys leu asp ala pro val leu ser asp ser ser cys lys ser ser tyr pro gly lys ile
451 TCT GGC ACG AAC TAC OCT TCA CTG CTT CAG TGT CTT GAT GCC OCT GTC CTC TCT GAC AGT TCT TGC AAA AGT TCT TAC CCA GGC AAG ATC

      170      180      190
thr ser asn met phe cys leu gly phe leu glu gly gly lys asp ser cys gln gly asp ser gly gly pro val val cys asn gly gln
541 ACT AGC AAC ATG TTC TGT CTG GGC TTT CTG GAG GGC GGA AAG GAC TOC TGC CAG GGT GAC TCT GGT GGC OCT GTA GTC TGC AAT GGC CAG

      200      210      220
leu gln gly val val ser trp gly tyr gly cys ala gln lys gly lys pro gly val tyr thr lys val cys asn tyr val asn trp ile
631 CTC CAG GGT GTT GTT TOC TGG GGT TAT GGC TGT GCT CAG AAA GGA AAA OCT GGT GTC TAT ACC AAG GTA TGC AAC TAC GTG AAC TGG ATT

      230      232
gln gln thr val ala ala asn STOP
721 CAG CAG ACC GTC GCT GGC AAC TAA AAGCCTTTTATGTCCTTTATCTTTGTAGTCAATCCACCTTCCTTTGTATGCCCCAAGTCATTCTCACAAGAAAAACA

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FIGURE 1: Nucleotide sequence and the deduced amino acid sequence of rat cationic trypsinogen. The underlined amino acids correspond to His-57, Asp-102, Asp-189, Ser-195, Gly-216, and Gly-226 (chymotrypsin numbering system). The predicted prepeptide consists of amino acid residues -15 to -1. Residue 1 is the first residue of the zymogen.

position 741 (Figure 1). The deduced sequence of the N-terminal 19 amino acids was identical with that found for purified rat cationic trypsinogen (amino acids 2-20). It continued for 80 bp beyond the 3' end of the coding region but did not include a polyadenylation site. Although this clone contained the coding information for the active enzyme and activation peptide, the 5' terminus was incomplete and lacked the signal sequence found in other pancreatic secretory proteins (Watson, 1984).

In an attempt to isolate the 5' terminus, six independent clones of rat cationic trypsinogen were isolated by using a 73 bp 5' fragment from the "full-length" clone. These clones were subcloned into M13mp11 using *EcoRI* and sequenced. Two of these clones extended to position 5, lacking only the methionine codon and the first base of the lysine codon.

The final portion of the sequence was determined by primer extension. A 30-mer primer extending from position 46 to 75 was synthesized. This particular sequence was selected because it was the most different from the anionic mRNAs in this highly conserved region, having four mismatches between the anionic trypsinogens and this primer, one of which was at the 3' end of the primer, as well as a deletion of 3 bp. This should have ensured that the mRNA for cationic trypsinogen was the only sequence primed (Reyes & Wallace, 1984). However, although there was a major pattern corresponding to cationic trypsin, minor patterns coding for the two anionic trypsins could be detected. Fortunately, the portion of the sequence that was unknown for cationic trypsin is shared by all three sequences and is thus unambiguous (results not shown).

**Sequence Homology to Other Trypsin-like Proteases.** The sequence of rat cationic trypsinogen contains all of the major structural features common to trypsinogens (Figure 2). In addition to the obligatory Asp-189 and the catalytic triad of His-57, Asp-102, and Ser-195 (chymotrypsin numbering system; Hartley, 1970), rat cationic trypsinogen contains the following conserved features: an activation peptide containing a poly(aspartic acid) sequence as described below; and the six

conserved disulfide bonds found in other rat trypsinogens. In addition, residues 199 and 200 of rat cationic trypsinogen are valines, as are the homologous residues in cow, pig, sheep, turkey, spiny dogfish, and rat anionic trypsins. This feature is unlike trypsin-like enzymes including rat pancreatic kallikrein (Leu-Val) (Swift et al., 1982), human kidney kallikrein (Leu-Met) (Baker & Shine, 1985), adipsin (Leu-Val) (Cook et al., 1985), and hanakah factor (Leu-Leu) (Gershenfield & Weissman, 1986).

The N-terminal sequence is similar to those of other trypsinogens (Figure 3). All trypsinogens have a polyanionic cluster immediately preceding the activation cleavage position (Lys-15/Ile-16), with the possible exception of human cationic trypsinogen which is reported by Brodrick et al. (1978) to contain an Asp-Lys activation peptide. Rat cationic trypsinogen is unique in having five negatively charged residues in a row compared to the four acidic residues reported for most other trypsins (Stroud et al., 1978). The initial few residues which immediately precede the polyanionic sequence in the activation peptides are notable in that they seem to generally consist of either a single valine residue (cow and turkey) or three residues of which one is proline [pig, sheep, all rat trypsinogens, and the human trypsinogens reported by Guy et al. (1978)].

The signal peptide sequence follows the usual pattern of a charged residue in the first few residues followed by regions of hydrophobic residues and small, uncharged amino acids. It is of interest that the signal peptides of both anionic trypsinogen II and cationic trypsinogen have a basic amino acid immediately after the methionine whereas the signal peptide of anionic trypsinogen I has a serine at that position (Figure 2). Although the presence of a charged amino acid is more typical (Watson, 1984), anionic trypsinogen I is the most abundant of the three proteins.

Rat cationic trypsinogen shows a high degree of overall homology with the two rat anionic trypsinogens. At the DNA level, rat cationic trypsinogen is 76% and 75% homologous to

[illegible]

**Charge Distribution.** The most obvious difference between the rat trypsins is their difference in overall net charge. The

	8	9	10	11	11A	12	13	14	15
RCT	Leu	Pro	Leu	Asp	Asp	Asp	Asp	Asp	Lys
AN1	Phe	Pro	Leu	Glu	—	Asp	Asp	Asp	Lys
AN2	Phe	Pro	Val	Asp	—	Asp	Asp	Asp	Lys
PCT	Phe	Pro	Tyr	Asp	—	Asp	Asp	Asp	Lys
ST	Phe	Pro	Tyr	Asp	—	Asp	Asp	Asp	Lys
HT1	Ala	Pro	Phe	Asp	—	Asp	Asp	Asp	Lys
HT2	Ala	Pro	Phe	Asp	—	Asp	Asp	Asp	Lys
TT			Val	Asp	—	Asp	Asp	Asp	Lys
BCT			Val	Asp	—	Asp	Asp	Asp	Lys
HCT								Asp	Lys

FIGURE 3: Activation peptides for a number of trypsinogens. Abbreviations: RCT, rat cationic trypsinogen; AN1, rat anionic trypsinogen I; AN2, rat anionic trypsinogen II; PCT, porcine cationic trypsin; ST, sheep trypsinogen; HT1, human trypsinogen I; HT2, human trypsinogen II; TT, turkey trypsinogen; BCT, bovine cationic trypsinogen; HCT, human cationic trypsinogen. Sequences are from the following: AN1 and AN2, Craik et al. (1984); PCT, Hermanson et al. (1973); ST, Dayhoff (1969); HT1 and HT2, Guy et al. (1978); TT, Kishida & Liener (1968); BCT, Hartley (1970); and HCT, Brodrick et al. (1978).

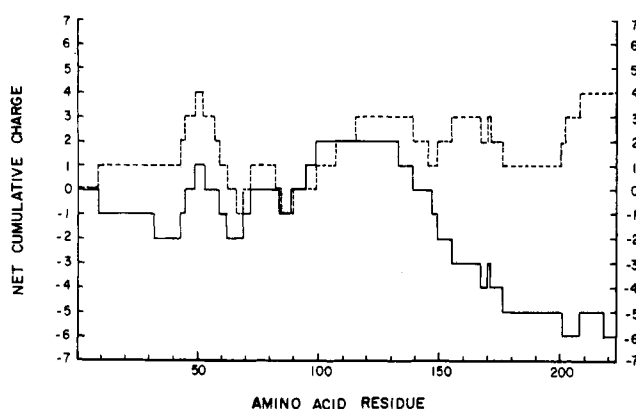


FIGURE 4: Net cumulative charge of rat cationic trypsin (dotted line) and rat anionic trypsin I (solid line). The net cumulative charge is summed, starting at Ile-16, over the whole active trypsin sequence. For the sake of clarity, the other trypsins were not included in this figure. These two profiles are representative of the cationic and anionic trypsins, respectively.

cumulative net charge is shown for rat anionic trypsin I and rat cationic trypsin in Figure 4. These two patterns are representative of those seen for other anionic and cationic molecules. Rat cationic trypsin has a net charge of +4 whereas both anionic trypsins have a net charge of -6. This is as would be expected on the basis of their isoelectric points (anionic = 5.3, cationic = 8.5; C. Largman et al., unpublished results). One intriguing point is that the cumulative net charges of the three rat trypsins, bovine cationic trypsin, and porcine cationic trypsin are all within one charge of each other in the region from amino acids 16 to 165 and most of the charge difference is located in the C-terminal 78 residues of the trypsin molecule (Figure 4). It should be noted that the substrate binding site is formed by the residues in this C-terminal part of trypsin.

If one assumes that differences in charge are functionally important, then they should be conserved among cationic trypsins and occur in regions of the molecule that are involved in either binding specificity or catalysis. When one compares the charge differences between the rat anionic trypsins and rat, porcine, and bovine cationic trypsin, there are several substitutions that are shared in all cationic trypsins. Two amino acid clusters, residues 167-169 and 222-224 (Figure 2), which are adjacent to each other in the tertiary structure of active trypsins show consistent charge changes between anionic and cationic trypsins. The net charge difference between cationic and anionic trypsins is 3+ at residues 167-169

and 3+ at residues 222-224, resulting in an overall net change of 6 charges. In addition, at residues 166, 170, and 221A, which flank these two regions, there is a pattern of substitution of nonpolar residues in anionic trypsins for polar residues in cationic trypsins. While this region is not known to be critical to the activity of the enzyme, it should be noted that amino acids 222-224 are adjacent to the binding pocket. In addition to the changes noted above, there are consistent charge changes at residues 49 (Asp to Ser) and at position 113 (Lys to Thr) that result in net charge changes of 1+ and 1-, respectively. However, both of these changes are distant from the active site and do not appear to be of obvious functional significance.

Two cDNAs which apparently code for human trypsinogens have recently been sequenced (Emi et al., 1986). These clones, which are 89% homologous, have not been conclusively identified as coding for either anionic or cationic trypsinogens, and we have chosen to not include them in the discussion of the sequence differences between anionic and cationic trypsins. However, it is of interest that these two sequences do not follow the pattern of the other trypsins, in that both proteins resemble the anionic trypsins at residues 165-170 but the cationic trypsins at residues 221A-224.

**Residues Important for Substrate Binding.** Although other members of the serine protease family have an extended substrate binding region which spans up to seven amino acids (Nakajima et al., 1979; Thompson & Blout, 1973; Harper et al., 1984; Baumann et al., 1973), the specificity of trypsins is usually thought to be dominated by the selectivity of the P<sub>1</sub> position with little influence of secondary binding sites. However, small variations in hydrolysis rates of synthetic peptides varying in the P<sub>2</sub> and P<sub>3</sub> positions have been observed (Tanaka et al., 1983), implying the presence of an extended binding site for trypsin. Furthermore, X-ray crystallographic studies of trypsin-protein inhibitor complexes reveal numerous interactions which have been interpreted as an extended binding region (Bolognesi et al., 1982). These studies have led to identification of several residues which appear to be involved in the interaction of trypsin with Japanese Quail ovomucoid protease inhibitor (Papamokos et al., 1982), pancreatic secretory trypsin inhibitor (Bolognesi et al., 1982), pancreatic trypsin inhibitor (Janin & Chothia, 1976), or soybean trypsin inhibitor (Janin & Chothia, 1976). The amino acid residues of trypsin that appear to be in close contact with one or more of these inhibitors are underlined in Figure 2. Of these 23 residues, 9 are polymorphic in the trypsins listed in Figure 2. The sequence of one region (residues 96-99) is quite variable among the trypsins and appears to be partially conserved within the cationic trypsins. This suggests that the interaction of cationic and anionic trypsins with these inhibitors may be different due to charge and steric bulk changes in this region. In addition to this particular difference, there are changes at residues 39, 149, 151, 175, and 217 that could also affect substrate binding. If these interactions are analogous to the interactions of trypsin with its protein substrates, then it would be reasonable to hypothesize that changes at these residues may affect substrate specificity.

Another amino acid which may be important for substrate specificity is Phe-99. In kallikreins, a tyrosine is usually present at this position and is thought to form a hydrophobic sandwich with Trp-215, resulting in an increased affinity for peptides such as Phe-Arg-X (Swift et al., 1982). The Phe-99 in rat cationic trypsin is also capable of forming a sandwich structure with Trp-215 and the substrate aromatic ring. Anionic rat trypsins, as well as bovine and porcine cationic trypsin, contain a leucine at this position. This difference suggests that rat

cationic trypsin should exhibit a higher affinity for Phe-Arg substrates.

Comparisons of the selectivity of anionic or cationic trypsins toward peptide or protein substrates have not been reported, but our results suggest the hypothesis that some of the amino acid differences between anionic and cationic trypsins, particularly residues 165–170, 221A–224, and 96–99, might result in preferential hydrolysis of protein substrates as the result of secondary binding site interactions. Such a hypothesis could be tested by constructing hybrid trypsins containing portions of the anionic and cationic enzymes. This could be most easily done with the rat trypsins, since the respective cDNAs share a considerable number of homologous restriction sites.

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