## Structural homology between the human *fur* gene product and the subtilisin-like protease encoded by yeast *KEX2*

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In previous studies, we have described a human genomic DNA fragment of about 21 kbp which was found immediately upstream of the fes/fps proto-oncogene and contained genetic sequences of a new gene that we called fur (1). Now we present the complete nucleotide sequence of the fur coding sequences and the deduced amino acid sequence of the fur product furin. From computer analysis it appeared that the deduced furin sequence exhibited a striking homology to the subtilisin-type serine protease encoded by the KEX2 gene of yeast Saccharomyces cerevisiae (2). In the subtilisin-like domain (underlined with a solid line) structural similarity is also found with the catalytic domains of the subtilisins thermitase (3) and subtilisin BPN' (4). The potential transmembrane domain is underlined with a broken line. These observations suggests that furin is a prime candidate for a mammalian precursor protein processing enzyme.

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200150	
GCGGGGAAGCAGCAGCGGCCAGGATGAATCCCAGGTGCTCTGGAGCTGGATGGTGAAGGTCGGCACTCTTCACCCTCCCGAGCCCTGCCCC	STCTCG
-100 -50 -50 -50 -50 -50 -50 -50 -50 -50 -	-1 cccccc
1	
ATGGAGCTGÁGGCCCTGGTTGCTATGGGTGGTAGCAGCAGCAGCAGCTTGGTCCTGCTAGCAGCTGATGCTCAGGGCCAGAAGGTCTTCACCAACACTGGGCTGGGCCATCI M E L R P W L L W V V A A T G T L V L L A A D A Q G Q K V F T N T W A V R I	P G
150 COCCCAGOGOGOCCANCACATOCOCACCAGOAGCATOCOTTCCTCAACCTOCGCCAGATCTTCGGGGACTATTACCACTTCTCTGCATCCAGGGATCACGAAGCGGTCCCTGTGG G P A V A N S V A R K N G F L N L G Q I P G D Y Y H F M N R G V T K R S L S	
290 COCCCCCCCCCCCCCCCACCCCCCACCCCCACCCCCACCCCC	CCTCAG P Q
A50 CAGTGGTACCTGTGTCACTCACCGGGACCTGAATGGAAGGCGGCCCCGGGCCTAGGGCTACCACGGCGACGCCTTGCATCTCACTTCTGACGGTGGCATCGAGAGG M Y L S G V T Q R D L N V K A A M A Q G Y T G N G I V V S I L D D G I E K	
500 550 CCGGACTTGGCAGGCAATTATGATGCCAGGCCAGTTTTGATGTCAATGACCAGGACCCTGACCCCCGACCTCGGTACACACAGATGAATGA	
P D L A G N Y D P G A S F D V N D Q D P D P Q P R Y T Q M N D N R H G T R C	A C
GANGTOCOCTOCOGTOCCAACAACOGTOTCTGTGTGTGGGTGTGCCTACAACCCCCCCATTGGAGGGGTGCCAATGCTGGATGCCGAGTGACAATGCACTGGAGGCACCCC EVAAVANNGVCGVGVAYNARIGGVCGVRVALDGCCCCATTGGAGGGGTGACAATGCAGTGAACCAATGCAGTGAACCAATCCATGGAGGCACCCC	
750	_
COCCTORACCCCARCHICATCHICACATCTACACTOCCACCTOCCCCCCAGGATCACCOCCAGATCACCCCCACTCCCCACCACCACCACCACCACCACCACC	
850 900 950	
COCCCAGGGGGCTCCATCTTTGTCTGGCCTCGGGGAACGGGGCCGGGAACATGACAGCTGCAACTGCAGCGCTACACCAACAGTATCTACACCTGTCCATCAGC G R G G L G S I P V W A S G N G G R E H D S C N C D G Y T N S I Y T L S I S	
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ACCCACTTTOCCAACCTOCCTTGCTACACCAGCCCTCCTCCTCCACACTGGCCCACCTACCACCTACCAGAATCAGAAACCAGAATCCTGACGACTGACT	
1100 ACCOGNICTERCACCOCCACTCACCCCCCTTAGCAGCCCOCATCATTGCTCTCACCCCGAGCCCAATAAGAACCTCACACGCCGACATGCAACCCCGTGGTAT TESHTOTSASAPLAAGIIALLTLEANKWLTWRDWQHLVV	1200 CAGACC Q T
1250 TCGAACCCACCCACCTCAATGCCAACCACTGCCCCCACACGCCCCACACGCCCCACCACCTCATATGCCTACGCCTTCATGCCCACGCCCACGCCCCCCCC	
1350 1400	
TOGACCACATOGOCCCCCAOCGGAAGTCCATCATCATCCACATCCTCACCCAOCCCAAAGCATCCOGGAAGCCCTCGGAAGCCCTCGAAGCCCTCACCCGGAAGCCCTCACCCGGAAGCCCTCACCCGGAAGCCCTCACCCGGAAGCCCTCACCCGGAAGCCCTCACCCGGAAGCCCTCACCCGGAAGCCCCTCACCACCCAAACCACCACACACA	
1450 1550 ATCACTCOGCTGCACCCCTCCACCCCCCCCCCCCCCCCCC	
	K F
1600 CATGACTACTCCCCAGATGGGTTTAATGACTGGGGATCTAGGACTCTCTGGGGATGAGGATGGGGTCTAAGGATTGAAAACACCAGCGAACCCAAC H D Y S A D G F N D W A F N T T N S W D E D P S G E W V L E I E N T S E A M	
1700 1750 GOGACCCTGACCHAGTICACCTCGTACTCTATOGCACCOCCCTGACGOCCTGCCCGTACCTCCAGGACCATGCACCTCAAGGACCCTCAACGTCCAGGACCCTGACGTCCAGGACCCTGACGTCCAGGACCCTGACGTCCAGGACCCTGACGTCCAGGACCCTGACGTCCAGGACCCTGACGACCAGGACCTGACGACCAGGACCTGACGACCAGGACCTGACGACGACGACGACGACGACGACGACGACGACGACGACG	1800 TGCGAG
1850 - 1900 GAMAGGOTTTCTCCCTCCACCAGAMAGACTATGTCCTCACCACTCCCCCCCCAMAGTCCTCGATACCACCTATACCACCGAGAMATGACGTGGGAGACCATCCCGCCC E G F S L H Q K S C V Q H C P P G F A P Q V L D T N T S T E N D V E T I R A	AGCGTC S V
1950 TOCCCCCCCTCCCACCCCTACTOTCCACATTCCCCCACCACCCCCCCTCTCCACCTCCCCTCACCTCCCCCC	AGCCAG S Q
2050 ACCACCGGGGGTCCCCCCCAACCACCACCCCCCCCACCCTCCCCCCCAACCCCCC	GGCCTC G_L
2200 ACTCCCCCTTCATCCTCCTCCTCATCTTCCTCTCTCTCT	
. 2300	4180
GOCCTOCCCCTGAACCCTGGAGGAGGAGTCCCCGTCTGACTCAGAAGAGGACGACGGCCGGAGAGGACCCCCTTTATCAAAGACCAGACCCCCTCTGA G L P P E A W Q E E C P S D S E E D E G R G E R T A F I K D Q S A L *	-100

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