

The Drosophila PROS-29 gene is a new member of the PROS-gene family

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The proteasome (MCP) is a high molecular weight multicatalytic proteinase consisting of about 15–20 non-identical subunits with molecular weights between 22–35 kDa (reviewed by Rivett, 1). So far two Drosophila (2, 3) and one rat (4) proteasome subunit have been cloned. These PROS-genes are highly homologous and belong to an evolutionarily conserved gene family (3). The proteasome subunits show strong similarities between their N-terminal halves while the C-terminal part is less conserved (3). The PROS-29 cDNA was isolated by screening a λgt11 embryonic cDNA library with a synthetic oligonucleotide comprising the sequence between bp 118–143 of the PROS-28.1 cDNA (3). This sequence (underlined) is highly conserved between the isolated PROS-genes. Under reduced hybridization conditions we isolated 37 positive clones. 12 of them represented the PROS-35 and PROS-28.1 cDNAs. From the remaining 25 clones 3 were identical and analysed further. The deduced molecular weight of the PROS-29 protein product is 29.4 kDa, the calculated IP 7.89. In 2-dimensional electrophoresis the PROS-29 in vitro translation product comigrates with the 28 kDa proteasome subunit of IP 7.8 (5). In agreement with previous data on the PROS-genes the deduced aa sequence possesses strong sequence homologies with the N-terminal halves of the 35 kDa and the 28 kDa no. 1 proteasome subunits (50% identity between aa 2–30). The C-terminal part of the three proteasome subunits shows a reduced sequence conservation. By aa sequence comparison of the three Drosophila proteasome subunits three boxes [PROS-box I, II, III] of high sequence conservation can be identified (boxed in the figure). The consensus sequences for the PROS-boxes are: [I] QVEYAMEAV; [II] AGLTADARVL; [III] GRRPFGVSLL.

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001 GGCAACCCTACACTGAATGACAAGTAAATTCTGTTCGTTTTGCAAAATAAACTTGTAAATTGGTATATTCCTTAGCAATGGCGCGCCGCTATGATT
001                                                                                   M  A  R  R  Y  D
097 CCCGCACCACGATCTTCTCGCCGGAGGGCCGTTTGTACCAGGTGGAGTACGCCATGGAGGCCATCTCGCACGCCGGAACCTGCCTGGGAATCCTCG
007 S  R  T  T  I  F  S  P  E  G  R  L  Y  Q  V  E  Y  A  M  E  A  I  S  H  A  G  T  C  L  G  I  L
193 CCGAGGACGGCATCCTGTTGGCAGCCGAGTGCCGCAGCACAAACAAATTGCTGGACAGCGCCATTCCTTCGGAAAAGATCTATCGCCGTAACGACA
039 A  E  D  G  I  L  L  A  A  E  C  R  S  T  H  K  L  L  D  S  A  I  P  S  E  K  I  Y  R  R  N  D
289 ACATGGTCTGTTCGGTGGCTGGCATCACCTCCGATGCCAATGTGCTGACCTCAGAACTGCGTCTGATTGCCCAGCGTTACCAGTTCAGCTACGGCG
071 N  M  V  C  S  V  A  G  I  T  S  D  A  N  V  L  T  S  E  L  R  L  I  A  Q  R  Y  Q  F  S  Y  G
385 AGGTGATTCCCTGCGAGCAGCTGGTGTCGCACCTCTGCGACATCAAACAGGCGTACACTCAGTACGGCGGAAAGCGTCCCTTCGGCGTCTCGCTGC
103 E  V  I  P  C  E  Q  L  V  S  H  L  C  D  I  K  Q  A  Y  T  Q  Y  G  G  K  R  P  F  G  V  S  L
481 TCTACATGGGATGGGACAACAAGTACGGCTACCAACTGTACCAGTCGGATCCCAGCGGCAACTACGGCGGATGGAAGGCCACTTGTATTGGCAACA
135 L  Y  M  G  W  D  N  K  Y  G  Y  Q  L  Y  Q  S  G  P  S  G  N  Y  G  G  W  K  A  T  C  I  G  N
577 ACTTCGGTGCCGCGATCTCCATGCTGAAGCAGGAGCTGGCCGATAAGGAGAACGTGAAGCTGACGCTGGCGGACGCCAAGGATTTGGCCATCAAGG
167 N  F  G  A  A  I  S  M  L  K  Q  E  L  A  D  K  E  N  V  K  L  T  L  A  D  A  K  D  L  A  I  K
673 TACTGAGCATGACCCTGGACACCACCAAGCTGACCCCGGAGAAGGTGGAGATGGCCACGCTGCAGCGTGTGGACAATAAGACCGTATACAGTGTCC
199 V  L  S  M  T  L  D  T  T  K  L  T  P  E  K  V  E  M  A  T  L  Q  R  V  D  N  K  T  V  Y  S  V
769 TGGAGAAACCCGATGTGGAGAAGCTGATCGAGAAGTACACAAAGGTACAGGCGGAGGCCGAGGCTGCCAAGAAGGAGAAGCAAGCGAAGCAGCCGA
231 L  E  K  P  D  V  E  K  L  I  E  K  Y  T  K  V  Q  A  E  A  E  A  A  K  K  E  K  Q  A  K  Q  P
865 CCAAGTAATCCCAAGGATGCATTATTATTGATTAAGGGTCTATCCTGATTTTTGTAACCGATCC
263 T  K
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