

Article

The Secreted Protein C10orf118 Is a New Regulator of Hyaluronan Synthesis Involved in Tumour-Stroma Cross-Talk

Ilaria Caon ^{1,†}, Maria Luisa D'Angelo ^{1,†}, Barbara Bartolini ^{1,†}, Elena Caravà ¹, Arianna Parnigoni ¹, Flavia Contino ², Patrizia Cancemi ^{2,3}, Paola Moretto ¹, Nikos K. Karamanos ⁴, Alberto Passi ¹, Davide Vigetti ¹, Evgenia Karousou ^{1,*} and Manuela Viola ¹

- ¹ Department of Medicine and Surgery, University of Insubria, Via J.H. Dunant 5, 21100 Varese, Italy; i.caon@uninsubria.it (I.C.); marialuisadangelo@gmail.com (M.L.D.); bartolini.barbara@gmail.com (B.B.); e.carava@uninsubria.it (E.C.); a.parnigoni@uninsubria.it (A.P.); paola.moretto@uninsubria.it (P.M.); alberto.passi@uninsubria.it (A.P.); Davide.Vigetti@uninsubria.it (D.V.); manuela.viola@uninsubria.it (M.V.)
- ² Department of Biological Chemical and Pharmaceutical Sciences and Technologies (STEBICEF), University of Palermo, 90128 Palermo, Italy; flavia.contino@unipa.it (F.C.); patrizia.cancemi@unipa.it (P.C.)
- ³ Centro di Oncobiologia Sperimentale (C.O.B.S.), Oncology Department, La Maddalena, 90146 Palermo, Italy
- ⁴ Biochemical Analysis and Matrix Pathobiology Research Group, Laboratory of Biochemistry, Department of Chemistry, University of Patras, 26110 Patras, Greece; n.k.karamanos@upatras.gr
- * Correspondence: jenny.karousou@uninsubria.it
- † These authors contributed equally to this work.

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Supplementary

A

{MATRIX} Mascot Search Results

Protein View

Match to: Q7Z3E2|CJ118_HUMAN Score: 36 Expect: 4.5
 Uncharacterized protein C10orf118 - Homo sapiens (Human)

Nominal mass (M_r): **104307**; Calculated pI value: 5.94
 NCBI BLAST search of Q7Z3E2|CJ118_HUMAN against nr
 Unformatted [sequence string](#) for pasting into other applications

Taxonomy: [Homo sapiens](#)

Fixed modifications: Carbamidomethyl (C)
 Variable modifications: Oxidation (M)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Number of mass values searched: 17
 Number of mass values matched: 8
 Sequence Coverage: 11%

Matched peptides shown in Bold Red

```

1 MSETDHIAS TSSDKNVGKTP ELKEDSCNLF SGNESKLEN ESKLLSLNTD
51 KTLCPNEHN NRIEAQENYI PDHGGGEDSC AKTDTGSENS EQIANFPSPGN
101 FAKHISK TNE TEQKVTQILV ELRSSTFPES ANEKTYSESP YDTCCTKFKFI
151 SKIKSVSASE DLLEEIESEL LSTFAEHRV PNGMNGEHA LVLFEKCVQD
201 KYLQQEHIK KLIKENKKHQ ELFVVICSEK DNLREELKRR TETEKQHMNT
251 IKQLESRIEE LNKEVKASRD QLIAQDVTA NAVQQLHKEM AQRMEQANKK
301 CEEARQEKEA MVMKYVRGEK ESLDLRKEKE TLEKLRDAN KELEKNTNKI
351 KQLSQEKGR L HQLYETKEGE TTRLIREIDK LKEDINSHVI KVKWAQNKLK
401 AEMDSHKETK DKLKETTTKL TOAKEEADQI RKNCDMIKT YQSESEIKSN
451 ELDAKLRVTK GELEKQMQEK SDQLEMHHAK IKELEDLKR TFKEGMDELRT
501 LRTKVKCLE D ERLRTEDELS KYKEIINRQK AEIQNLLDKV KTADQLQEQL
551 QRKQEIENL KEEVESLNSL INDLQKDIEG SRKRESELLL FTERLTSKNA
601 QLQSESNLQ SQFDKVSCE SQLSQCEQM KQTNINLESR LLKEEELRKE
651 EVQTLQAELA CRQTEVKALS TQVEELKDEL VTQRRKHASS IKDLTKQLQQ
701 ARRLKLDQVES GSYDKEVSSM GSRSSSSGSL NARSSAEDRS PENTGSSVAV
751 DNFPQVDKAM LIERIVRLQK AHARKNEKIE FMEDHIKQLV EEIRKTKII
801 QSYILREESG TSSSEASDFN KVHLRRGGI MASLYTSHPA DNGLTLELSL
851 EINRRLQAVL EDTLLKNITL KENLQTLGTE IERLIKHQHE LEQRTKKT
  
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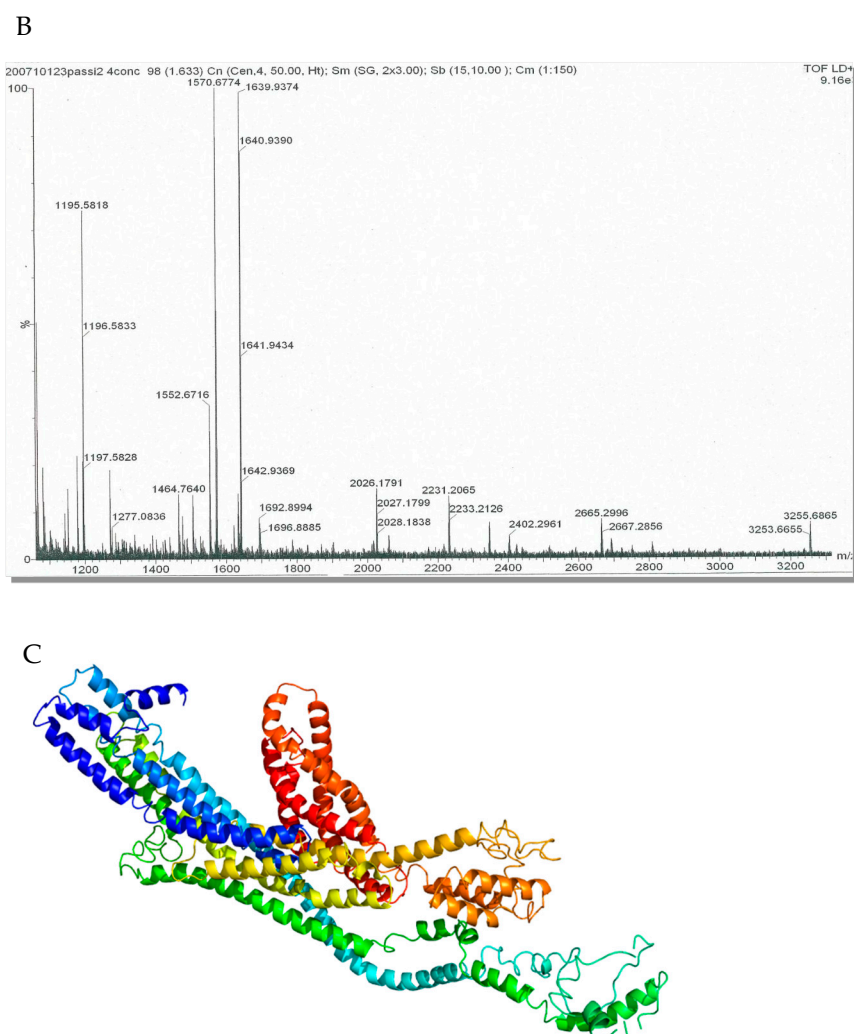


Figure S1. (A) MALDI-TOF spectrum of peptides obtained from SDS-PAGE band excised and analysed as reported in Materials and Methods. (B) MASCOT Search results of the peptides matching the human uncharacterized protein c10orf118. (C) Prediction of the protein 3D-structure by Phyre2 program, showing the presence of many alpha-helix as secondary structures.

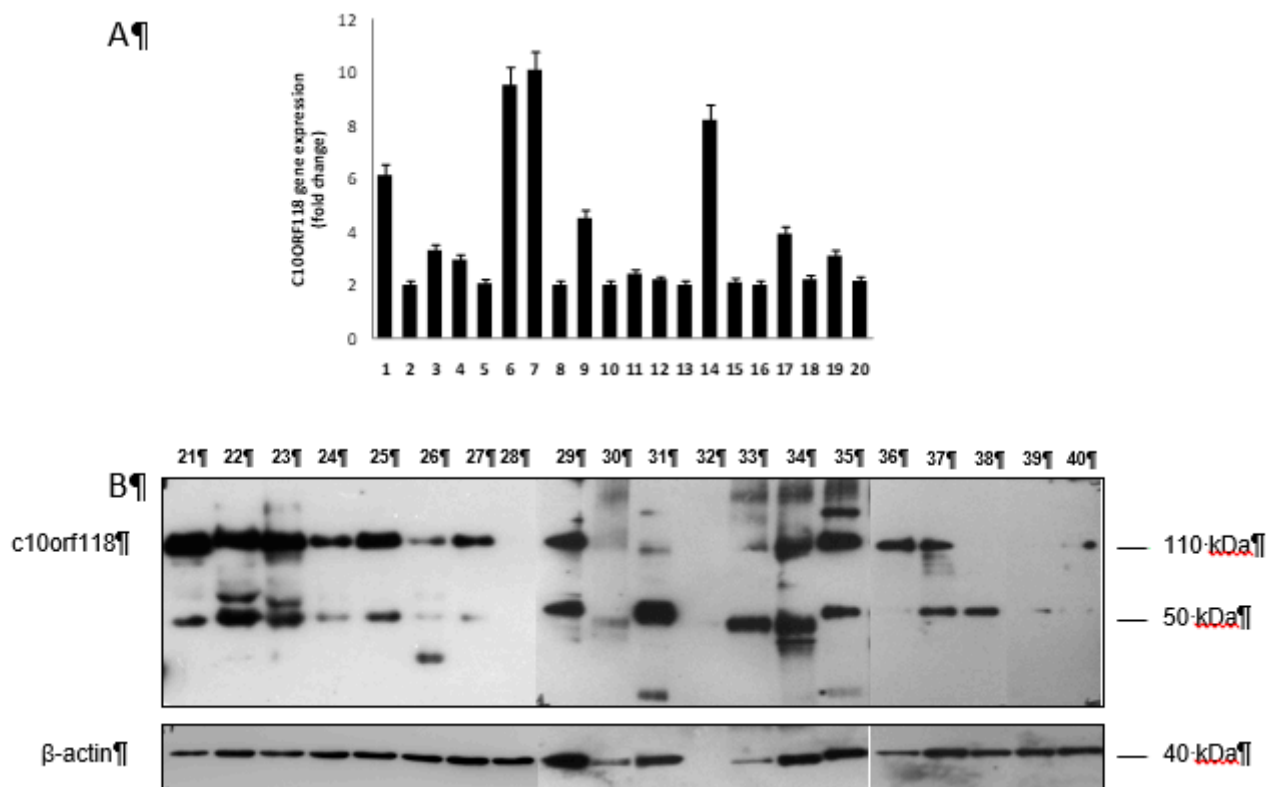


Figure S2. A. RT-PCR analysis of the c10orf118 gene expression in 20 tissue specimens from breast cancer patients; B. western blot analysis of the c10orf118 protein expression in 20 tissue specimens from breast cancer patients.

Table S1. Information of different gene variants and protein isoforms of c10orf118, according to Ensembl bioinformatics program.

Name	Transcript ID	bp	Protein	Translation ID	Biotype
CCDC186-006	ENST00000369287	7245	898aa	ENSP00000358293	Protein coding
CCDC186-003	ENST00000369285	2035	211aa	ENSP00000358291	Protein coding
CCDC186-002	ENST00000369286	1928	211aa	ENSP00000358292	Protein coding
CCDC186-001	ENST00000428953	1576	436aa	ENSP00000415344	Protein coding
CCDC186-004	ENST00000497592	661	No protein	-	Processed transcript
CCDC186-005	ENST00000490661	477	No protein	-	Retained intron

Table S2. Cellular localization of c10orf118 predicted by ComPPI computational program (<http://comppi.linkgroup.hu/>).

Major Localization	Minor Localization	Localization Score	Experiment Type	Source Database
Cytosol	Cytoplasm (GO:0005737)	0.91	Predicted: pTarget method	LOCATE
Cytosol	Cytoplasm (GO:0005737)	0.91	Predicted: PAML algorithm	PA-GOSUB
Nucleus	Nucleus (GO:0005634)	0.7	Predicted: SVM decision tree	eSLDB
Secretory-pathway	Golgi apparatus (GO:0005794)	0.94	Predicted: PAML algorithm	PA-GOSUB
Secretory-pathway	Golgi apparatus (GO:0005794)	0.94	Experimental: annotated protein expression (APE)	The Human Protein Atlas