

SUPPLEMENTARY FIGURES AND TABLES

Supplementary Figure 1: Identification of DERP6 and C3ORF75 by MS/MS. On the top, the peptide sequences and ion scores of both identified proteins are mentioned. At the bottom, DERP6 and C3ORF75 protein sequences. Sequenced peptides are highlighted in red.

Protein name	SwissProt Access number	Mass Protein (Da)	Peptide Sequences	Start - End	Mass Observed (Da)	Mr (expt) (Da)	Mr (calc) (Da)	Delta (Da)	Ion Score	Expect
Dermal papilla-derived protein 6 DERP6	Q8TE02	35219	R.EGFSDINNRL K.TEEAFPGGPLGALR.A	70 – 79 95 – 108	583.7800 707.9000	1165.5454 1413.7854	1165.5000 1413.7252	0.0455 0.0602	56 52	6.3 ^e -04 1.5 ^e -03
UPF0405 protein C3ORF75	Q0PNE2	30116	K.GMSPAVL.- + Oxidation (M) K.LTLLCDAK.T K.LGVSLT <u>M</u> AR.E + Oxidation (M) R.ATVCWELK.G R.AEGLATGFCR.D R.GQLVFLEGLK.S R.DQSFTYQYK.I K.SAVDVVFQAQK.E	260 – 266 21 – 28 68 – 76 168 – 175 210 – 219 79 – 88 240 – 248 89 – 99	690.3800 467.3000 482.3200 502.7700 541.2500 552.5800 590.3500 596.5000	689.3727 932.5854 962.6254 1003.5254 1080.4854 1103.1454 1178.6854 1190.9854	689.3418 932.5001 962.5219 1005.4953 1080.5022 1102.6386 1178.5244 1190.6295	0.0309 0.0854 0.1036 1.9699 0.0168 0.5068 0.1610 0.3559	14 45 82 7 57 66 49 96	30 0.019 3.2 ^e -06 1.7 ⁺ +02 1.8 ^e -03 1.5 ^e -04 5.6 ^e -03 1.1 ^e -07

DERP6

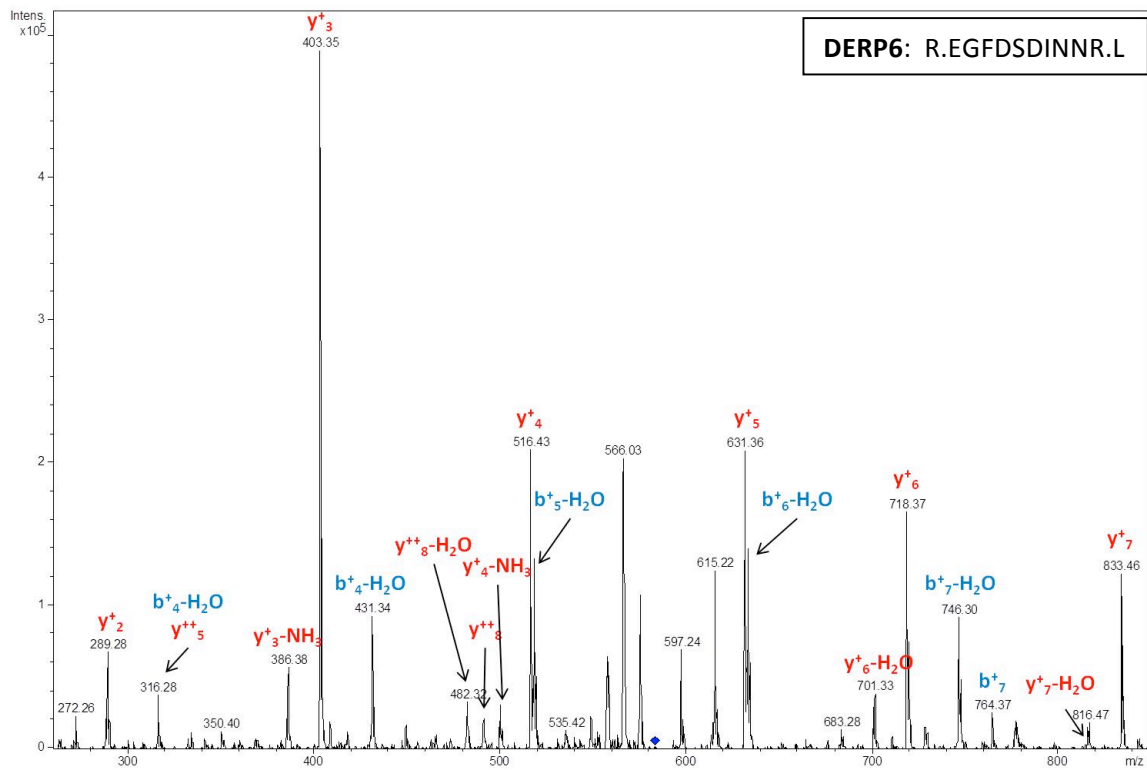
1 MTPSEGARAG TGRELEMLDS LLALGGLVLL RDSVEWEGRS LLKALVKKSA
51 LCGEQVHILG CEVSEEEFR**E GFSDINNRL** VYHDFFRDPL NWSK**TEEAFP**
101 **GGPLGALR**AM CKRTDPVPVT IALDSLWLL LRLPCTTLCQ VLHAVSHQDS
151 CPGDSSSVGK VSVLGLLHEE LHGPGVPGAL SSLAQTEVTL GGTMGQASAH
201 ILCRRPRQRP TDQTQWFSIL PDFSLDLQEG PSVESQPYS DPHIPPVDPTT
251 HLTFNHLHLSK KEREARDSLI LPFQFSSEKQ QALLRPRPGQ ATSHIFYEPD
301 AYDDLQQEDP DDDLDI

C3ORF75

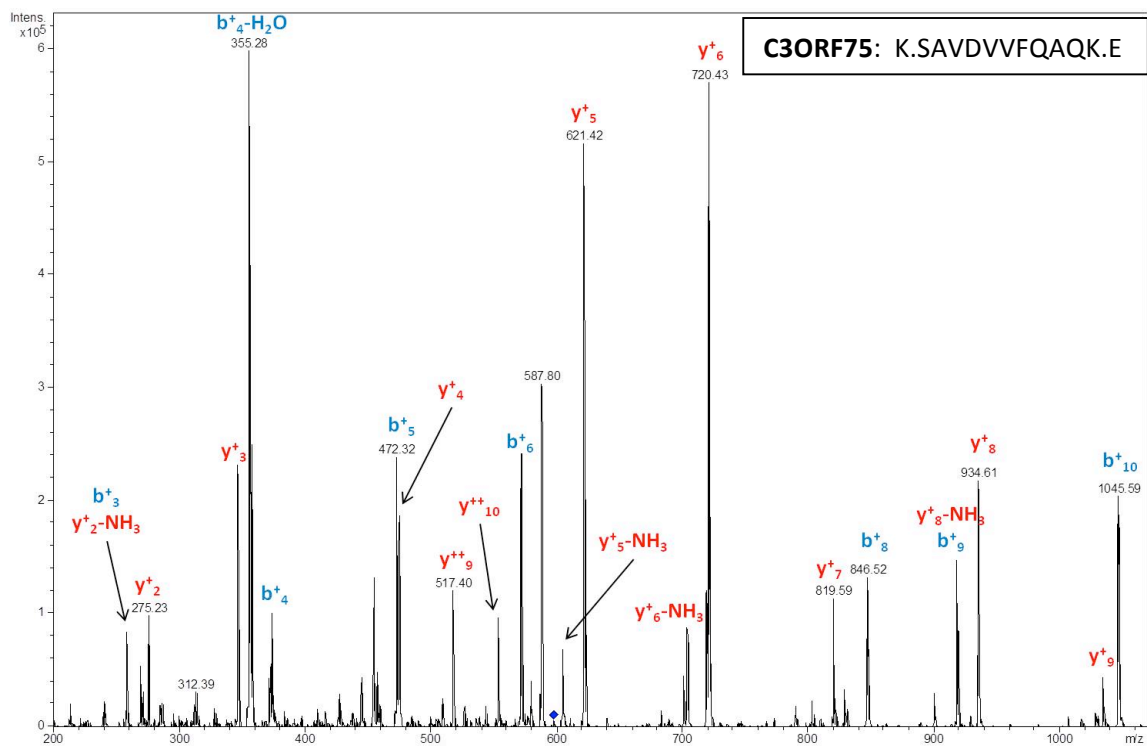
1 MFVELNLLN TTPDRAEQGK **LTLLCDAKTD** GSFLVHHFLS FYLKANCKVC
51 FVALIQSFHS YSIVGQK**LGV SLT**M**ARER****GQ** **LVFLEGLKSA** **VDVVFQAQKE**
101 PHPLQLREA NAGNLKPLFE FVREALKPV DSGEARWTYPV LLVDDLSVLL
151 SLGMGAVAVL DFIHYCR**ATV** **CWELK**GNMVV LVHDSGDAED EENDILLNGL
201 SHQSHLILR**A** **EGLATGFCRD** VHGQLRILWR RPSQPAVHRD **QSFTYQYKIQ**
251 DKSVSFFAK**G** M**SPAVL**

Supplementary Figure 2: MS/MS spectra for one of the peptides sequenced from DERP6 (A) and C3ORF75 (B).

(A)



(B)



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H.s. 1 : MTPSEGARAGTGRELEMDSLAIGGLVLRDSVEWEG..RSLKALVKKKALRGEQVHTGGCEVSEEEFREGFD.....SDINNRYVYHDFER
M.m. 1 : .....MLDSLAIGGLVLRDSVEWEG..RSLKALVKKKALRGEQVHTGGCEVSEEEFREGFD.....SDVNSRYVYHDLER
A.t. 1 : MAESIFRKLDRDGGEGELAPALTIETVASPFGLDVSGLYLLTNSSSILAGKSSSQGLVLTFFSRSPSYLQLLKQKGIIVSSSSKWRILDCYT
D.m. 1 : .....MISNLVYTKQKVIIDELNRRERAPKFIIGSLHEQOGGADTKAAPTGV.....KHAVATE
S.p. 1 : .....MSKELLNRCIRDLSPITVLRKDNLQTA..KPIINYYAKNAASRGIKVLEISYETLEKEAPEGID.CFLYATSWEKVKSLKELYE
S.c. 1 : ...MASSSHNPVILKRLRLSTESSPFIICLDSIAQTS..YKLIQEFVHQSKSKGNEYPIVYISFETVNVKPSYCT.....QFIDATQDFVHLVK

H.s. 88 : DPLNWS.KTEEAFPGGP.....LGAIRAMCKRTPVPVTTIALDSLWLLLRIPCTTLCQVLHAVSHQDSCPGDSSSVGKVS.VLGLLH...
M.m. 72 : DPLNWS.KPGEAVPEGP.....LKALRSCKRTHGVSVTIALDSLWLLCHTIPCVTLCQALHALSQQNGDPGDNSLVEQVR.VLGLLH...
A.t. 96 : DPLGIDQSSTSESESSLIKHLKCVSDLKKEFSSIEAGRELVGTGKTRFCVATDSVNEELLRHSAMPLVSGLLTDLRSHAQISSVFWSLN...
D.m. 60 : ALIDKYANNNTGSTTDS.....NSGFNVILPTLADLLCYQTPAFIFGFLNLRSDNVRRVFLWASPQHL
S.p. 82 : HISSRTQKQKQIIVMID.....TINPIINTSISSTMFPGSVLALGSIICFLTSPHKDVTLENYPSYLPCEVFLDFTSTCTVSLTGMQHLS
S.c. 86 : QIISVLPAAATQAQKH.....MVIDSDSNYISTEHTTRFLSEIASPHCFMVAIYHKDIKDNRTVI PDWNNN...YPDKITLQPMATTIVD

H.s. 169 : EELHGGPVGALSSLAQTEVTLGGTMGOASAHILCRRPRORPTDQOWFSTLPDFSLDLQEGPSVESQPYSDPHIPPVDPTT.....
M.m. 153 : EELHGGPVGALNTLAQTEVTLGSKVDQTSASILCRRPQQRATYQTWFFSVLPDFSLTLHEGLPLRSELHPDHHTTQVDPTA.....
A.t. 187 : TDLHQEKVTNALEYSTMKANLEPLCPSSDGQRNALENLFSVHQDFGKGRFHVRFKLRKGRVVRVMSEYHVDQSGINFSPISVDTVIAATKSLI
D.m. 126 : QDPHADIYLAGCEYLAELVLRLESDKLLSLIRKPGGGVSNRRYSCEVSKTQFKVTPLDGGPLPAGASPKQSPPEAEQTTEPAS.....
S.p. 168 : VEHDAKMRSLNPLPELQDDKLIISLLGNCETAIVLHVFEFRKSGR..ITKESCVLKNKLEPYTPFEETARGPEPADNQIDEN.....
S.c. 171 : IDVVLGTIDTEEVSELENEFRIPRGLNNDIPQLRLVNRKRSGRSLEYDFIVNSNTHEYELLSTTKQEESSSSNGLETPEMLQG.....

H.s. 251 : .HLTFNLHLSKREAREARDSLTLPPQFSSEKQALLRP.....RPGQATSHFYEPAFDDVLP..EDPDDLDI
M.m. 235 : .HLTFNLHLSKREAREARDSLTLPPQFSSEKQKALLHP.....VPSRTTGHFYEPAFDDVLP..EDPDDLDI
A.t. 282 : PKVQFNLCSEKREVEKVVLPFPHQDDGKSNEIYDGRSLVDGKIETTPLSMELQTDVVS SGGKSEIYFRISDDEHPDSDPDDLDI
D.m. 209 : .SIFKIEDEDEVLARNAITLPEYERTSEFSE.....GNITTYTPEADDFDE..EDPDDLDI
S.p. 251 : .VSEFNLVSEKREKRDVLEPYFSAQMVGSOHKSS.....FVDECTIYHAIEADDFDE..EDPDDLDI
S.c. 255 : .LTFNLGTSNRKRLAKDQVALPFLAQSEFGQ.....GCATVYVEYKDDYDE..EDPDDDFP.

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Supplementary Figure 3: Multiple sequence alignment of DERP6/ELP5 and its homologues from other species using ClustalW2 (1). *H.s.*, *Homo sapiens*; *M.m.*, *Mus musculus*; *A.t.*, *Arabidopsis thaliana*; *D.m.*, *Drosophila melanogaster*; *S.p.*, *Schizosaccharomyces pombe*; *S.c.*, *Saccharomyces cerevisiae*. 60% conserved residues are shaded in light gray, 80% conserved residues are shaded in dark gray and identical residues are shaded in black. Similarity groups' option is enabled. Homology between human DERP6/ELP5 and *S. cerevisiae* Elp5 is 15% identical and 29% similar. Homology comparison of different homologues ranges from 8% identical/25% similar (*A. thaliana* and *S. cerevisiae*) to 71% identical/80% similar (*H. sapiens* and *M. musculus*).

Reference:

1. Larkin, M. A., Blackshields, G., Brown, N. P., Chenna, R., McGettigan, P. A., McWilliam, H., Valentin, F., Wallace, I. M., Wilm, A., Lopez, R., Thompson, J. D., Gibson, T. J., and Higgins, D. G. (2007) *Bioinformatics* **23**, 2947-2948

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H.s. 1 : --MFVLENNLNTTPDRAEQ-----GKTLTCD-AKDGSEFLVHFFLS-FYTKANCK--VCFVALIQSFSHYSIVGQKLCVSLTMAERERGQLVE
M.m. 1 : --MFPELNNLSTTPDKTEQ-----GTTLTCD-AKDGSEFLVHFFLS-FYTKANCK--VCFVALIQSFSHYNIVGQKLCVSLTAARDRGQLVE
A.t. 1 : --MDRSLNLLDLALGFDEQLAIPSPLNKGVILLEDCEVEISGSEFLVHQLMK-RVLSNSSDALIFLAFARPFSHYDRILRNLGCNLIATHKSNRLVE
D.m. 1 : ----MATSVLLACGLNEQKLP-----GEVHHSSESNVDGSEFLTSCVVG-QRDRISNAG-TLLVCLQHHYQHYFNAGMRLCYNTNIFQG-KTLGV
S.p. 1 : -----MSSHEHLRPIEPE-----FSITLLGTRELPVTFHFHYLY-HALKAKES--TCEITFSKTLDEHAISMRWEMDITKTKN--FFE
S.c. 1 : MSSVQRQDLVIFSDQSVLPAHFFQDSNSHNFFITHQSCIQPLMFINALVETHVLTGSPSSLNESSSSMLPSSSTRSHAVLASFIHEQNYFTNSLNKLIK

H.s. 84 : EGLKSAVDVVFQAQKEPHPLQFLREANAGNLKPLFEFVREALKPVDSGEARWTPVLLVDD-----LSVLLSLTGMG--AVAVDFTHYCRATVCWE
M.m. 84 : EGLKSSVEVLFHSQDEPHPLQFLREAGTGNLQSLTYFTIQDTLKPADSEESPWKYPVLLVDD-----LSVLLSLTGVG--AVAVDFMQYCRATVCCE
A.t. 94 : FD-----MLMVKCSDGDQ-----MEDNVSAAVAKLFREIQETVRKLOSVTS--GNITVMVDD-----MSLLEIATTGNSNDHVLDFLHYC-HTSSE
D.m. 83 : ID-----VLSDMAGEGLASKWLTNTEGQTLTEQLVEDIRAQVESNYANRNSYTVLTDN-----LSITLFGAS-----KIQVQQFCQDLAALG
S.p. 78 : IDG----FSMLFAPISKPS----KVOAPEKKNHFKSVFAPVTCQVEENDEEFENSITITED-----IDLIQ-----STHAFDSTKIQQAITELR
S.c. 98 : IP-----SNNYNVLDLSDFIVNIHNKPRDKLISDVLAKFSAAIQNNPTDITVITIQPELILSLVSGITCSELNNKFTPLLRQCKVITIV

H.s. 174 : LKGNMVLVHDSGDAEEDNDILLNGSHQSHITRAEGLATGFCRDVHGQLRLLWRRPSQP----AVHRDQSFTYQYKIQDKSVSPEAKGMSPAVL
M.m. 174 : LKGNVVALVHDTGATDEGNDTLLNGSHQSHILRAEGLATGFCRDVHGQLSLWRRPSPS----TAQRAQSLTYQYKIQDNKVSPEAKGMSPAVL
A.t. 172 : SNCSLVITNHEDIYASMERPAFLIQVCLADVVIKAEPLASGLANVHGQLTVLNKGISNSG--RGSSRNKLNQFCRIRKENGIDYEPCCRS---
D.m. 161 : KEREKLVITKLSNS--DIYQLTDNNVAKLGQVRIQVLRIRKSGVFRVVDGRLTHERVLDEGN---YACEETRKEVLYKQVNDRNKVKVAPGEIGVKV
S.p. 154 : -KCFSRVIVNVTLGAPLPQKSLGSSIGHMATRCHSCRPLRSGSARRITCELRHRSRMNHFRSGICETPEDDDKELLYEITTEAGAKVYSKQVTLQL
S.c. 185 : SNSDIFNIDEYDASVHPSNLQNFYKSSFIKSMNINLNLPLRTGFAKDVITGSLHVCRGGAPIATS-NTSLHVVENEVYLNKEKSTKLYR-----

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Supplementary Figure 4: Multiple sequence alignment of C3ORF75/ELP6 and its homologues from other species using ClustalW2 (1). *H.s.*, *Homo sapiens*; *M.m.*, *Mus musculus*; *A.t.*, *Arabidopsis thaliana*; *D.m.*, *Drosophila melanogaster*; *S.p.*, *Schizosaccharomyces pombe*; *S.c.*, *Saccharomyces cerevisiae*. 60% conserved residues are shaded in light gray, 80% conserved residues are shaded in dark gray and identical residues are shaded in black. Similarity groups' option is enabled. Homology between human C3ORF75/ELP6 and *S. cerevisiae* Elp6 is 9% identical and 25% similar. Homology comparison of different homologues ranges from 8% identical/26% similar (*M. musculus* and *S. cerevisiae*) to 80% identical/90% similar (*H. sapiens* and *M. musculus*).

Reference:

1. Larkin, M. A., Blackshields, G., Brown, N. P., Chenna, R., McGettigan, P. A., McWilliam, H., Valentin, F., Wallace, I. M., Wilm, A., Lopez, R., Thompson, J. D., Gibson, T. J., and Higgins, D. G. (2007) *Bioinformatics* **23**, 2947-2948

Supplementary Table 1: shRNA sequences used in this study

shRNA species	and	Tracking number	Sequence
Ctrl		SHC002	non-mammalian sequence
Elp1#1 mus musculus		TRCN0000088775	CGCTGAGTGAAGTGGTACAAA
Elp1#2 mus musculus		TRCN0000088773	CCTCAGTTCCTGTTGTTTCATA
Elp3#1 mus musculus		TRCN0000039309	CGGAGAGATTATGTTGCCAAT
Elp3#2 mus musculus		TRCN0000039311	GCACAAGAAATTATTACCGAA
Elp5#1 mus musculus		TRCN0000192282	CCTTGTCCTTTGTTACTTTGT
Elp5#2 mus musculus		TRCN0000189577	CCCTGTGTTACACTCTGTCAA
ELP5 homo sapiens		TRCN0000130483	GCCCAGAACCATCTTTCTATT
Elp6#1 mus musculus		TRCN0000267114	CTTCTACCTGAAAGCTAATTG
Elp6#2 mus musculus		TRCN0000267116	TGTCCAGTCCTTCAGCCATTA

Supplementary Table 2: Oligonucleotide sequences used to assess mRNA expression through qRT-PCR analysis

Name species	and	Forward primer	Reverse primer
GAPDH mus musculus		TGATGACATCAAGAAGGT GGTGAAG	TCCTTGGAGGCCATGTAGGCCAT
ELP3 mus musculus		AGGACCTGACTCCGATTTTG	CTCTCATGGAAGTTGGCTCA
ELP5#1 mus musculus		CATTGCCCTTGACTCTCTCA	CAGAGCATGTAGGGCTTGAC
ELP5#2 mus musculus		GTCTCCTGAAGGCTCTTATC	TCTGAAGAGGTCATGGTAAAC
ELP6#1 mus musculus		CCGGA ACTCAACAACCTTCT	AGCGTCACAGAGGAGAGTCA
ELP6#2 mus musculus		GTCTGCTTTGTGGCACTTGT	AGAGGACTTGAGACCCTCCA