

7.1 Supplemental Material

Figure A1. Sequence homologies between 3'-end of ODZ4 and NARS2. Alignments reproduced from BLAST algorithm [104].

>ref|NW_001838028.2| Homo sapiens chromosome 11 genomic contig, alternate assembly
 HuRef SCAF_1103279187758, whole genome shotgun sequence
 Length=16912879

Features flanking this part of subject sequence:

1170 bp at 5' side: [teneurin-4](#)
 80205 bp at 3' side: [probable asparaginyl-tRNA synthetase, mitochondrial precu...](#)

Score = 3943 bits (4372), Expect = 0.0
 Identities = 2188/2189 (99%), Gaps = 0/2189 (0%)
 Strand=Plus/Plus

Query 1	TCCTTCTAACAGTCCCAAAGTCCCATCTGCCTCCATGTACCAGCTGATCGCAGAGCTG	60			
Sbjct 9310615	TCCTTCTAACAGTCCCAAAGTCCCATCTGCCTCCATGTACCAGCTGATCGCAGAGCTG	9310614			
Query 61	GACTGGGGCAGGCTGGGCTTCCAGGAAATTCCTGAAGTCTGAAACAGCTTCCCTCTAG	120			
Sbjct 9310675	GACTGGGGCAGGCTGGGCTTCCAGGAAATTCCTGAAGTCTGAAACAGCTTCCCTCTAG	9310734			
Query 121	AGAAGCCCAACCAATGTGTTTTTGTAGTACAGGAAGAAGGAGGGGAAGAGCTGATGTGGT	180			
Sbjct 9310735	AGAAGCCCAACCAATGTGTTTTTGTAGTACAGGAAGAAGGAGGGGAAGAGCTGATGTGGT	9310794			
Query 181	GTGGCTGCCATATCATCAACCCACAGGAGCAGGCGAGTCCCAAGTGGTGGTCC	240			
Sbjct 9310795	GTGGCTGCCATATCATCAACCCACAGGAGCAGGCGAGTCCCAAGTGGTGGTCC	9310854			
Query 241	GTAGATCTGGGAGGCCAGGCTGGCATGATTCCTGTGAAGAACTGTGCCTGTGTGTCAGG	300			
Sbjct 9310855	GTAGATCTGGGAGGCCAGGCTGGCATGATTCCTGTGAAGAACTGTGCCTGTGTGTCAGG	9310914			
Query 301	GAGAGGCTGAGCCCTCTCAGAAGCAGGACAGCCCAACCTGAAGACAGCCCAAGCT	360			
Sbjct 9310915	GAGAGGCTGAGCCCTCTCAGAAGCAGGACAGCCCAACCTGAAGACAGCCCAAGCT	9310974			
Query 361	GAGGCAGCAGCCAGCAGGCTGGGGAGCAGTGGAGGCGAGGGGAGTCAACAGCAGAGCTG	420			
Sbjct 9310975	GAGGCAGCAGCCAGCAGGCTGGGGAGCAGTGGAGGCGAGGGGAGTCAACAGCAGAGCTG	9311034			
Query 421	GGAGCCCTTGTTCAGGATTCACATTCCTGGTTCATCCGCTAATTACCATGTGCATTAC	480			
Sbjct 9311035	GGAGCCCTTGTTCAGGATTCACATTCCTGGTTCATCCGCTAATTACCATGTGCATTAC	9311094			
Query 481	CACCTACAGGAGGCTCTGGGAGATGGGAGGGGAAGCCAAATGCTTCTTTAAGCTGGCC	540			
Sbjct 9311095	CACCTACAGGAGGCTCTGGGAGATGGGAGGGGAAGCCAAATGCTTCTTTAAGCTGGCC	9311154			
Query 541	TTCTTAGAAAATGGAACATTTTATGGGTTACATTTACATTAAGTGTGAAAATGAATTCG	600			
Sbjct 9311155	TTCTTAGAAAATGGAACATTTTATGGGTTACATTTACATTAAGTGTGAAAATGAATTCG	9311214			
Query 601	AGTCTGAGCTATTCCCGGTGAAACCTTTGTGGACTGATTAAGTCTATGGCACTCTATAG	660			
Sbjct 9311215	AGTCTGAGCTATTCCCGGTGAAACCTTTGTGGACTGATTAAGTCTATGGCACTCTATAG	9311274			
Query 661	CCTTACTCACATAGTCTTCAGAAATATACAAAGTAAATGAAACTGAGAAGTCTGACTG	720			
Sbjct 9311275	CCTTACTCACATAGTCTTCAGAAATATACAAAGTAAATGAAACTGAGAAGTCTGACTG	9311334			
Query 721	CATGAGGATCGGACAGCATGTAGTCTGGGTTCTGCCTGGCAGAGGGAGGCAACCAAAAC	780			
Sbjct 9311335	CATGAGGATCGGACAGCATGTAGTCTGGGTTCTGCCTGGCAGAGGGAGGCAACCAAAAC	9311394			
Query 781	TTCTTGGGAGAGGAGATTTGCGCTTAAAGTCAATCCCACTGGGATTAGAGGATGTGTTTC	840			
Sbjct 9311395	TTCTTGGGAGAGGAGATTTGCGCTTAAAGTCAATCCCACTGGGATTAGAGGATGTGTTTC	9311454			
Query 841	GCTAAGTCTCTTCCGTTTCCAAAAAAGCCACCTGCTGCAGCAGTGCCTTTGGC	900			
Sbjct 9311455	GCTAAGTCTCTTCCGTTTCCAAAAAAGCCACCTGCTGCAGCAGTGCCTTTGGC	9311514			
Query 901	CTGCTTGTCCACTGGTGGCCATTTGCCCTTGGATCCAGAGCTCTACTGATCAGATACAG	960			
Sbjct 9311515	CTGCTTGTCCACTGGTGGCCATTTGCCCTTGGATCCAGAGCTCTACTGATCAGATACAG	9311574			
Query 961	TGCTCTGCAGGCTGCTGTGGGAGGATGAGCTGAGATGGGGCTCCCACTGCGCAGGA	1020			
Sbjct 9311575	TGCTCTGCAGGCTGCTGTGGGAGGATGAGCTGAGATGGGGCTCCCACTGCGCAGGA	9311634			
Query 1021	TCATTCTGGATGAGATGAAAACAGTTTGGCTGAAGAACAAGTTTGTCTCCAGA	1080			
Sbjct 9311635	TCATTCTGGATGAGATGAAAACAGTTTGGCTGAAGAACAAGTTTGTCTCCAGA	9311694			
Query 1081	AGGGACTTACGCTCTCAAAATGTAATCTTACATACCAAGGGCCCTGGGCAAGTGTCTCC	1140			
Sbjct 9311695	AGGGACTTACGCTCTCAAAATGTAATCTTACATACCAAGGGCCCTGGGCAAGTGTCTCC	9311754			
Query 1141	TGCCAGTTGATCAGTCCCATCTCGCTGCTGCATCAGTGAAGACCTGCTGGGATGT	1200			
Query 1201	CTGCTCAGAGTCAAGGACGGCATGCGGTCCACAGGAACAGCTCCCTACGCTTCCCCCA	1260			
Sbjct 9311815	CTGCTCAGAGTCAAGGACGGCATGCGGTCCACAGGAACAGCTCCCTACGCTTCCCCCA	9311874			
Query 1261	CGCCCTGTCCCTCCTCCACAGCCCTCCCAAGGAATAGGGTGGACTTTTAGGGATCA	1320			
Sbjct 9311875	CGCCCTGTCCCTCCTCCACAGCCCTCCCAAGGAATAGGGTGGACTTTTAGGGATCA	9311934			
Query 1321	AAAACAGAATTTATGGGTgtttcattatTTTTTTCTTTCTTTCTTTTTCATAGA	1380			
Sbjct 9311935	AAAACAGAATTTATGGGTgtttcattatTTTTTTCTTTCTTTTTCATAGA	9311994			
Query 1381	gatgggtctcaatgatgtgcccagctgttctcaactcctggcctcagcagcacc	1440			
Sbjct 9311995	GATGGGTCTCAATGATGTGCCAGGCTGTCTCAACTCTGGCTCAGGCGATCCACC	9312054			
Query 1441	ttggcctcctgaagtgtgggttacaggtgtgagcactggcctgagctgagtggttg	1500			
Sbjct 9312055	TTGGCTCCTGAAGTGTGGGTACAGGTGTGAGCAGTGGCTGGAGTGTGGTGG	9312114			
Query 1501	tttctttaAAGGATCTTATATTTTTCTGTGTACATACCACAGCAGCCAGCTTCT	1560			
Sbjct 9312115	TTTTTTAAAGGATCTTATATTTTTCTGTGTACATACCACAGCAGCCAGCTTCT	9312174			
Query 1561	GTGGGGAGAGAAATGAAGATCCCGAAGCTTTAGAAAAGGATCTCAGTGTGGCAGC	1620			
Sbjct 9312175	GTGGGGAGAGAAATGAAGATCCCGAAGCTTTAGAAAAGGATCTCAGTGTGGCAGC	9312234			
Query 1621	GCAGTGTATTGCGCCTCACTGCCACATTTGGTGTCTGTTTGAAGTGTGCTTCTGCG	1680			
Sbjct 9312235	GCAGTGTATTGCGCCTCACTGCCACATTTGGTGTCTGTTTGAAGTGTGCTTCTGCG	9312294			
Query 1681	CTTGGCCCTTTTGAAGTGGTTTCATTTGGGCTGCAGGTGACTCAGTACTCCCTCTCA	1740			
Sbjct 9312295	CTTGGCCCTTTTGAAGTGGTTTCATTTGGGCTGCAGGTGACTCAGTACTCCCTCTCA	9312354			
Query 1741	AGCTGTCTCTCTGTAAGACAGCAGTCAAAACCAAGGATGAGTGTGAAGGCC	1800			
Sbjct 9312355	AGCTGTCTCTCTGTAAGACAGCAGTCAAAACCAAGGATGAGTGTGAAGGCC	9312414			
Query 1801	TAAOCTGTGCTTATGTAATAGGCTCAAGCATGACTCCCATCTGAGAGGACCGGCC	1860			
Sbjct 9312415	TAAOCTGTGCTTATGTAATAGGCTCAAGCATGACTCCCATCTGAGAGGACCGGCC	9312474			
Query 1861	TTTTGACATCAACCAAACTGTTCATTCGATAGAGTGAACAGGCTCCCTCACTG	1920			
Sbjct 9312475	TTTTGACATCAACCAAACTGTTCATTCGATAGAGTGAACAGGCTCCCTCACTG	9312534			
Query 1921	CCAGGTGTATGATCTCAGTTCCTGCTTCTCTCTACCCCGCAGCTGCCAAGTGG	1980			
Sbjct 9312535	CCAGGTGTATGATCTCAGTTCCTGCTTCTCTCTACCCCGCAGCTGCCAAGTGG	9312594			
Query 1981	TCCTACATCTCAGCCCTCTGCCACCACTTAAATAGGACTTTACTGATTTCCCAACTT	2040			
Sbjct 9312595	TCCTACATCTCAGCCCTCTGCCACCACTTAAATAGGACTTTACTGATTTCCCAACTT	9312654			
Query 2041	TGTTTTTTGTAGGATGAGATTTCCCTTTTATCCCAcccccccACAACCAACAGACAT	2100			
Sbjct 9312655	TGTTTTTTGTAGGATGAGATTTCCCTTTTATCCCAcccccccACAACCAACAGACAT	9312714			
Query 2101	TGCTGGAGGCGAGCTGGAGGAGGGGAGGCAATGCAAGTAAATGCTGTCAGCC	2160			
Sbjct 9312715	TGCTGGAGGCGAGCTGGAGGAGGGGAGGCAATGCAAGTAAATGCTGTCAGCC	9312774			
Query 2161	CTGACCTCATCTCTCAGAAATGTTGGC	2189			
Sbjct 9312775	CTGACCTCATCTCTCAGAAATGTTGGC	9312803			

7.2 List of Thesis Figures and Tables

Figure 1.1 Organization of teneurin domains.	12
Figure 1.2. Ongoing model proposed for teneurin signaling.	23
Figure 1.3. Predicted ODZ4 Mature Transcript (13.6 Kb of RefSeq, GenBank Acc.n NM_00108816)	26
Figure 2.1. Teneurin-2 expression in human cancer cell lines	35
Figure 4.1. Relative alignment of the designed primers respect to the ODZ4 transcript	44
Figure 4.2. PCR-amplification efficiency and genomic specificity of the ODZ4 primers	45
Figure 5.1. Screening of the ODZ4 Transcript in Human Cancer Cell Lines	59
Figure 5.2. ODZ4-Exon expression in different human cancer-derived cell lines.	61
Figure 5.3. ODZ4 coding-end and Splice Variants at the 5'-terminus	63
Figure 5.4. 3'-UTR region of ODZ4 Transcript derived from ovarian and breast cancer cell lines	65
Figure 5.5. The ODZ4 mRNA Is a Continuous Expressed Transcript in Human Ovarian and Breast Cancer-Derived Cell Lines	69
Figure 5.6.1. RACEs Experiments	74
Figure 5.6.2. Schematized Representation of Obtained RACE Products In Ovarian Cancer-Derived cell lines	76
Figure 5.6.3. The ODZ4 Transcript Blotting Derived From Human Breast Cancer Cell	79
Figure 6.1. ODZ4 partial-full length transcript in human ovarian and breast cancer-derived cell lines.	83
Figure 6.2. Genomic insert-sequences found in the ODZ4 mRNA derived from ovarian cancer-derived cell line (SKOV3)	86
Table 1.1. Chromosomal Location and Nomenclature for Teneurins	9
Table 1.2. Summary of Teneurin Expressions in Vertebrates.	20
Table 1.3. ODZs Gene Family and Their Predicted Characteristics in Humans	25
Table 4.1 Biological characteristics of the studied cell lines	39
Table 4.2. List of primers designed for this study and their corresponding sequences	48
Table 4.3. Expected amplicon size based on ODZ4 RefSeq transcript	49
Table 4.4. Components for the ligation reaction	50