***NOC-mutant-12*** pr651-12 Sequence ID: Query\_19747 Length: 272

Range 1: 113 to 272 Score:291 bits (157), Expect:7e-83,

Identities:160/161(99%), Gaps:1/161(0%), Strand: Plus/Plus

Query 10 CGTTTCGCGGTGAATGTCATATTTAGAATACACGTGCGAGTTGTTTCTAACGCCGTTTAT 69

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Sbjct 113 CGTTTCGCGGTGAATGTCATATTT-GAATACACGTGCGAGTTGTTTCTAACGCCGTTTAT 171

Query 70 TTTATTTAATGATTTTTATCTAATATATAGCTTTAGAAAATATAAAATCATGCCGGCAGC 129

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Sbjct 172 TTTATTTAATGATTTTTATCTAATATATAGCTTTAGAAAATATAAAATCATGCCGGCAGC 231

Query 130 AGTGGCCACAGGTGTGCAATTCGGTGGACCGCCCAAAAACA 170

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Sbjct 232 AGTGGCCACAGGTGTGCAATTCGGTGGACCGCCCAAAAACA 272

12 fw pr651 wt >Drosophila melanogaster uncharacterized protein (CG7839), mRNA

Sequence ID: NM\_140174.5 Length: 3714

Range 1: 1 to 192

Score:346 bits (187), Expect:5e-91,

Identities:192/194(99%), Gaps:2/194(1%), Strand: Plus/Plus

Query 26 TCATATTTAGAATACACGTGCGAGTTGTTTCTAACGCCGTTTATTTTATTTAATGATTTT 85

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Sbjct 1 TCATATTT-GAATACACGTGCGAGTTGTTTCTAACGCCGTTTATTTTATTTAATGATTTT 59

Query 86 TATCTAATATATAGCTTTAGAAAATATAAAATCATGCCGGCAGCAGTGGCCACAGGTGTG 145

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Sbjct 60 TATCTAATATATAGCTTTAGAAAATATAAAATCATGCCGGCAGCAGTGGCCACAGGTGTG 119

Query 146 CAATTCGGTGGACCGCCCAAAAACAAGAAAATCGTGTTCCGACGACTCCGGCGAGGCGGT 205

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Sbjct 120 CAATTCGGTGGACCGCCCAAAAACAAGAAAATCGTGTT-CGACGACTCCGGCGAGGCGGT 178

Query 206 AGT*TAA*ACAAAACA 219

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Sbjct 179 AGTTAAACAAAACA 192

PROTEIN # 5'3' Frame 1 early stop codon

Met P A A V A T G V Q F G G P P K N K K I V F R R L R R G G S Stop

**12 rev and wt** >Drosophila melanogaster uncharacterized protein (CG7839), mRNA

Sequence ID: NM\_140174.5 Length: 3714

Range 1: 420 to 821 Score:699 bits (378), Expect:0.0,

Identities:394/402(98%), Gaps:0/402(0%), Strand: Plus/Minus

Query 68 CACATGATACCACTTCTTTTGGGACTCCTCGTCTTCATCTATTTTTGACTGATATTTGTT 127

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Sbjct 821 CACATGATACCACTTCTTTTGGGACTCCTCGTCTTCATCTATTTTTGACTGATATTTGTT 762

Query 128 GTGCTTCTTGGAAATGGAGTCCCCCAGTTCCTCATCACTGTCACCATCGGTGTCGGATAC 187

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Sbjct 761 GTGCTTTTTGGAAATGGAGTCCCCCAGTTCCTCATCACTGTCTCCATCGCTGTCGGATAC 702

Query 188 ATTTTTCCCAGCTCCATCCTCATCAAACTTGATTCGTTGGGGCTTTTTAAAGTTCTCCTT 247

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Sbjct 701 ATTTTTTCCAGCTCCATCCTCATCAAACTTGATTCGTTGGGGCTTTTTAAAGTTCTCCTT 642

Query 248 GGACTCTCCGTCATCTCCAAACTTGATTTTTTGGGACTTCTTGGTCGGTTCCGTCTTTGT 307

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Sbjct 641 GGACTCTCCGTCATCTCCAAACTTGATTTTTTGGGACTTCTTGGTCGGTTCCGTCTTTGT 582

Query 308 GTTGGAAGAATTCGCAGTTACTTCATCTTCTCCATCATCAGTGAACTTGATTTTCTGAGG 367

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Sbjct 581 GTTGGAAGAATTCGCAGTTACTTCATCTTCTCCATCATCAGTGAACTTGATTTTCTGAGG 522

Query 368 TTTATTGGCGAAGTCCGACTTTTGACCATTATGTTTATGGTTGTTTTTGGTGAAAGGTTT 427

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Sbjct 521 TTTATTGGCGAAGTCCGACTTTTGACCATTATGTTTATGGTTGTTTTTGTTGAAAGGTTT 462

Query 428 TTGATGTACTGCTTCTCCATCCTCTCCAAATTTGAATTTCTG 469

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Sbjct 461 TTGATGCACTGCTTCTCTATCCTCTCCAAATTTGATTTTCTG 420

***NOC-mutant14*** pr651-14

>Drosophila melanogaster uncharacterized protein (CG7839), mRNA

Sequence ID: NM\_140174.5 Length: 3714

Range 1: 1 to 177

Score:298 bits (161), Expect:1e-76,

Identities:172/177(97%), Gaps:2/177(1%), Strand: Plus/Plus

Query 14 TCATATTTAGATA*CACGTG*CGAGTTGTTTCTAACGCCGTTTATTTTATTTAATGATTTTT 73

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Sbjct 1 TCATATTTGAATACACGTGCGAGTTGTTTCTAACGCCGTTTATTTTATTTAATGATTTTT 60

Query 74 ATCTAATATATAGCTTTAGAAAATATAAAATCATGCCGGCAGCAGTGGCCACA-AT-TGC 131

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Sbjct 61 ATCTAATATATAGCTTTAGAAAATATAAAATCATGCCGGCAGCAGTGGCCACAGGTGTGC 120

Query 132 AATTCGGTGGACCGCCCAAAAACAAGAAAATCGTGTTCGACGACTCCGGCGAGGCGG 188

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Sbjct 121 AATTCGGTGGACCGCCCAAAAACAAGAAAATCGTGTTCGACGACTCCGGCGAGGCGG 177

# 5'3' Frame 1 wrong seq and early stop codon

Met P A A V A T I A I R W T A Q K Q E N R V R R L R R G G S Stop

**14 rev wt**

>Drosophila melanogaster uncharacterized protein (CG7839), mRNA

Sequence ID: NM\_140174.5 Length: 3714

Range 1: 473 to 821

Score:606 bits (328), Expect:4e-169,

Identities:342/349(98%), Gaps:0/349(0%), Strand: Plus/Minus

Query 68 CACATGATACCACTTCTTTTGGGACTCCTCGTCTTCATCTATTTTTGACTGATATTTGTT 127

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Sbjct 821 CACATGATACCACTTCTTTTGGGACTCCTCGTCTTCATCTATTTTTGACTGATATTTGTT 762

Query 128 GTGCTTCTTGGAAATGGAGTCCCCCAGTTCCTCATCACTGTCACCATCGGTGTCGGATAC 187

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Sbjct 761 GTGCTTTTTGGAAATGGAGTCCCCCAGTTCCTCATCACTGTCTCCATCGCTGTCGGATAC 702

Query 188 ATTTTTCCCAGCTCCATCCTCATCAAACTTGATTCGTTGGGGCTTTTTAAAGTTCTCCTT 247

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Sbjct 701 ATTTTTTCCAGCTCCATCCTCATCAAACTTGATTCGTTGGGGCTTTTTAAAGTTCTCCTT 642

Query 248 GGACTCTCCGTCATCTCCAAACTTGATTTTTTGGGACTTCTTGGTCGGTTCCGTCTTTGT 307

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Sbjct 641 GGACTCTCCGTCATCTCCAAACTTGATTTTTTGGGACTTCTTGGTCGGTTCCGTCTTTGT 582

Query 308 GTTGGAAGAATTCGCAGTTACTTCATCTTCTCCATCATCAGTGAACTTGATTTTCTGAGG 367

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Sbjct 581 GTTGGAAGAATTCGCAGTTACTTCATCTTCTCCATCATCAGTGAACTTGATTTTCTGAGG 522

Query 368 TTTATTGGCGAAGTCCGACTTTTGACCATAATGATTATGGATGTTTTTG 416

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Sbjct 521 TTTATTGGCGAAGTCCGACTTTTGACCATTATGTTTATGGTTGTTTTTG 473

results summary using https://web.expasy.org/translate/:

**ok--> mutant 14 # DNA\_sequence**

atgccggcagcagtggccacaattgcaattcggtggaccgcccaaaaacaagaaaatcgtgttcgacgactccggcgaggcggtagttaaacaa

# 5'3' Frame 1 wrong seq and early stop codon

Met P A A V A T I A I R W T A Q K Q E N R V R R L R R G G S Stop T

Sequence ID: Query\_516791 Length: 240

Range 1: 8 to 103

Score:159 bits(86), Expect:1e-44,

Identities:93/96(97%), Gaps:2/96(2%), Strand: Plus/Plus

wt 1 ATGCCGGCAGCAGTGGCCACA-AT-TGCAATTCGGTGGACCGCCCAAAAACAAGAAAATC 58

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line14 8 ATGCCGGCAGCAGTGGCCACAGGTGTGCAATTCGGTGGACCGCCCAAAAACAAGAAAATC 67

Query 59 GTGTTCGACGACTCCGGCGAGGCGGTAGTTAAACAA 94

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Sbjct 68 GTGTTCGACGACTCCGGCGAGGCGGTAGTTAAACAA 103

**ok--> mutant 12 # DNA\_sequence**

atgccggcagcagtggccacaggtgtgcaattcggtggaccgcccaaaaacaagaaaatcgtgttccgacgactccggcgaggcggtagttaa

# 5'3' Frame 1 early stop codon

Met P A A V A T G V Q F G G P P K N K K I V F R R L R R G G S Stop

alignment

Sequence ID: Query\_45019 Length: 358

Range 1: 1 to 124

Score:200 bits(108), Expect:1e-55,

Identities:119/124(96%), Gaps:2/124(1%), Strand: Plus/Plus

wt 1 ATGCCGGCAGCAGTGGCCACAGGTGTGCAATTCGGTGGACCGCCCAAAAACAAGAAAATC 60

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line12 1 ATGCCGGCAGCAGTGGCCACAGGTGTGCAATTCGGTGGACCGCCCAAAAACAAGAAAATC 60

Query 61 GTGTT-CGACGACTCCGGCGAGGCGGTAGTTAAACAAAACAAAAAAGAGC-ACCCACAAA 118

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Sbjct 61 GTGTTCCGACGACTCCGGCGAGGCGGTAGTTAAACAAAACACACAAGAGCGACCCACAAT 120

Query 119 GGCC 122

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Sbjct 121 GGCC 124

original sequences

**3278 cDNA SD02424**

TTTGAATACACGTGCGAGTTGTTTCTAACGCCGTTTATTTTATTTAATGATTTTTATCTAATATATAGCTTTAGAAAATA

TAAAATCATGCCGGCAGCAGTGGCCACAGGTGTGCAATTCGGTGGACCGCCCAAAAACAAGAAAATCGTGTTCGACGACT

CCGGCGAGGCGGTAGTTAAACAAAACAAAAAAGAGCACCCACAAAGGCCAAAATTTGAAGGGAAGGAACAGGTGAAAAAG

CCGCAGAAAATTAAGTTTGGAGAGGATGGAAAAGCGAAAGGTGCCAAGTCTTTTAAGAAGAACCACCAAAAGCCGGATTT

TGCCAACAAACCACAGAGAATAAAGTTCGGCGATGATGGAGAGCAAGAAGCTCCGAAGTCGTTCAACCAAAATCATAAAA

ATGGACCAAAACCACAGAAAATCAAATTTGGAGAGGATGGAGAAGCAGTACATCAAAAACCTTTCACCAAAAACAACCAT

AAACATAATGGTCAAAAGTCGGACTTCGCCAATAAACCTCAGAAAATCAAGTTCACTGATGATGGAGAAGATGAAGTAAC

TGCGAATTCTTCCAACACAAAGACGGAACCGACCAAGAAGTCCCAAAAAATCAAGTTTGGAGATGACGGAGAGTCCAAGG

AGAACTTTAAAAAGCCCCAACGAATCAAGTTTGATGAGGATGGAGCTGGGAAAAATGTATCCGACACCGATGGTGACAGT

GATGAGGAACTGGGGGACTCCATTTCCAAGAAGCACAACAAATATCAGTCAAAAATAGATGAAGACGAGGAGTCCCAAAA

GAAGTGGTATCATGTGCATCCTGACTATCCGTCCACCGATGAGGTGCTGGACATGAAGGAGAACGATCAGCTGGAGCTGT

ACAATCTCTGCAAGAATTCCTTCGAGGCGGAGAAGATAACTTTTAATAAACGTAATCCCTCGGATGCTCGCTGGTTGCAA

ACCGCTTTGCACAAGGGTACTGCAAAGGATCGGGCCAATGCGGGCGCCCTTCTGGTGACGAGCAATCCACTGGGCAATTT

GGAAGCATTGAGCACTTTAATTGGCTTCTGCAAGATCTCCAACAAGGCCAGCAATGATGTGATTGCAGTGCTCACGGATT

TGTGGCAGGAGGTGCTGCTCCCGCCAAACAGAAAACTCCTGGCGGTGCACACACGTGGTGCTGATTGGAAAAAGCTGAAG

AAGGATGAGAATTTGCGCAACGAACAGAAGCGCCGCATTTACGCGTACTGGCATTTTGAGAGCGAATTAAAGGATCAGTA

CCACGAGTTCTTGAAGAACGTTATGCAGGGCCTGCAGACTGGACAGGAACACAATAAGAACTCCTCTATTGTGTCAGCAG

CCAGGCTGTTGGCCTATGCTCCCGAAAAGGAGCAGCTGCTGCTAACCATGCTGGTAAACAAACTGGGCGATCCCATCGCC

AAGATTGCCTCCAAGGCGTTGCATCACCTCAGCGAGGTGGCCCAGAAACATCCGAACATGTGCGGTGTTATTGTTGCCGA

AGCGGAGAAGCTACTTTTCCGTAACAATATTTCCGAGCGAGCGCAGCACTTTGCACTGTGCTTCCTCTCCAGCATCGCAC

CCTCTGGCCGGCCCGAAGTCTGCACCAAGTTGGTCAACATATGCTTTGCCCTCTTCAAGGTTCTCGTGCAGAAGGGAGCC

GTCAATAATAGAACCATGCAGGCCATACTGCGATGCTTGCAAAAGGCTATCGTGGAGGCTAAGCCGGCAAAGGATAGCAA

TGGGGAATTACTCACCAAGGAAATGCAGGACACCATTTATCGATTGGTCCACTTGGCAGACATTAGGGTCGCTGTACAGA

CTCTCGGCCTGCTGCTGCAATTGGTTGCAGTAAAAACTGAGAAATCGGATCGGTTTTATAATGCTTTGTATGTAAAGCTG

CTGGATCTGAACCTAATTAATGTGGGTAGCAAAACGGCGGCTCATCTACTGCATATTGTACATCGTGCCATCCACATCGA

CAACCATGTGGCCAGGGCCCAGGCATTCGTGAAGCGTCTGCTGCAGTTGACCCTATACGCTCCACCGCACATTGCAGCTG

GTTGTTTAATCGTCATCCACAAGTTGCTGCGCATGCGCCGTGAGCTAATTGGCGGCACTGGAGCTTCTGAGGAAGTGGAG

GAAGGTTCCAAAGTTGTTCTACCAATCAGTGCGGATCTGGACAAGTTCGGTAGCGACGATGAGGAGGTCTACGAGGATGT

TAAAGATGAGGCAGATGATACTAAGGACTCCAGTCCATTGGAGGAGAAGGCAGACAATGATGTTAAGTCAAGTGCATCAT

CCTGGCATCATGCCCGTGTGGCTGCCACAGAGGCCAAGGTGCGGGATATTGATTCCTGCAAGTACGATCCGTACCATCGA

GTGCCCGCTTTTGCAGGAGCCGCATATGCACTCCGCCACGAACTGTTGTTGCTGCGGCAACACTACCATCCCACCGTTCA

GGTCTTCGCCGAACAGATTCTTCAGCAATCACGCATTGATTACTATGGTGATCCGCTCAGAGATTTCGGTCTGCCACACT

TTTTGGAACGTTTCGCCTTTAAGAATCCGAAAAAGCTGGAAGCTTCACAAGCAGCGGAAAATGCTACCGTGGCACACAAG

CGATACATGGCTCACGGAGCGCGAGGAAGACCAGTGAAATCGCTGACCAAGGCCAACTGTACCGAGGACGAGATGTTCAT

CTTCAACTTCTTGGAGCATAAACGCAGACAGGCGGAAATTGTGGCGCAGAACAAAAAGCAGAAGGAGATCAAGAAGGACG

CCGCAGAAGAGGGAGATGATGGCGAGGCTGGAGAGGAATACCTGAAGGAGGGCGAAGTAGATGACGATGAGTTCGAGGCC

TATTTGGATGGATATTTCGGCAAGAAGTTCAAGGAAGGTGTCGACGAAGAGCAAGATGAAGAGGAGCTGAACTTCCTGCA

GGAGCTGGGTGGCGAGATAAAGAAGGATAAGTCCAAGGATAAGAAAAAGAAGAAGCAGTCCGACAAGGCGGAAGATGAAA

TGGACGATATTGATGACGACTGGGGTGATGACGACTTGGCAGAAGATGAATATGATGAAATTGAGGGCGAAGATCAGTCC

GATGATGAAACGGGCTCGATTGATTTGCAGCCACTTGATGACGACGACGATGATGATGATGATGACGATGAGGGCTCGAT

TTCAGAAGGCGGCCCTGGCGACAGTGATTCAAGCGATGCTCCTGAGAGTCCAGACGAAGAGGATGACGACGACGAAGATG

CACCACCGAGATCCAAAAAATCCCGCAAAGACTCCACCGACATGGTGGGAGGACGAAGCTTTGCCAAAACACTCAAACAG

AGTCACGATATGTCCTCTCTGTTTGCTGCCGCCGATGACTTCTCTTCGCTGCTGGAGGAGACGGCCAAGGTAAAGGGTCA

GGGAACCAGCAATGCCGTCTTTAACAAGGACAAGTCCTCCGACAAACAATTGAAATGGGAAGAAAACCGACGATCGAACT

CCAAATCCTACAAGGGCAAGAAGTTCGCCGGCAAACCAGCGGCCAAAGGCGGTAGACCACAGAAAGCGGGCAAGAAACGA

AAACACTAAACTAAACTCGATTATCAAACTCTACTCCATTTAAGTGGTTGTAAAGTTGTAAATATCTAAACGAAAGATTA

AAACCAATTTCTATTAAAGTTAGTGGAAAAAAAAAAAAAAAAAAAAAA

protein

1 MPAAVATGVQ FGGPPKNKKI VFDDSGEAVV KQNKKEHPQR PKFEGKEQVK KPQKIKFGED

61 GKAKGAKSFN KNHQKPDFAN KPQRIKFGDD GEQVASKSFN QNHKNGPKPQ KIKFGEDREA

121 VHQKPFNKNN HKHNGQKSDF ANKPQKIKFT DDGEDEVTAN SSNTKTEPTK KSQKIKFGDD

181 GESKENFKKP QRIKFDEDGA GKNVSDSDGD SDEELGDSIS KKHNKYQSKI DEDEESQKKW

241 YHVHPDYPST DEVLDMKEND QLELYNLCKN SFEAEKITFN KRNPSDARWL QTALHKGTAK

301 DRANAGALLV TSNPLGNLEA LSTLIGFCKI SNKASNDVIA VLTDLWQEVL LPPNRKLLAV

361 HTRGADWKKL KKDENLRNEQ KRRIYAYWHF ESELKDQYHE FLKNVMQGLQ TGQEHNKNSS

421 IVSAARLLAY APEKEQLLLT MLVNKLGDPI AKIASKALHH LSEVAQKHPN MCGVIVAEAE

481 KLLFRNNISE RAQHFALCFL SSIAPSGRPE VCTKLVNICF ALFKVLVQKG AVNNRTMQAI

541 LRCLQKAIVE AKPAKDSNGE LLTKEMQDTI YRLVHLADIR VAVQTLGLLL QLVAVKTEKS

601 DRFYNALYVK LLDLNLINVG SKTAAHLLHI VHRAIHIDNH VARAQAFVKR LLQLTLYAPP

661 HIAAGCLIVI HKLLRMRREL IGGTGASEEV EEGSKVVLPI SADLDKFGSD DEEVYEDVKD

721 EADDTKDSNP LEEKADNDVK SSASSWHHAR VAATEAKVRD IDSCKYDPYH RVPAFAGAAY

781 ALRHELLLLR QHYHPTVQVF AEQILQQSRI DYYGDPLRDF GLPHFLERFA FKNPKKLEAS

841 QAAENATVAH KRYMAHGARG RPVKSLTKAN CTEDEMFIFN FLEHKRRQAE IVAQNKKQKE

901 IKKDAAEEGD DGEAGEEYLK EGEVDDDEFE AYLDGYFGKK FKEGVDEEQD EEELNFLQEL

961 GGEIKKDKSK DKKKKKQSDK AEDEMDDIDD DWGDDDLAED EDDEIEGEDQ SDDETGSIDL

1021 QPLDDDDDDD DDDDDEGSIS EGGPGDSDSS DAPESPDEED DDDEDAPPRS KKSRKDSTDM

1081 VGGRSFAKTL KQSHDMSSLF AAADDFSSLL EETAKVKGQG TSNAVFNKDK SSDKQLKWEE

1141 NRRSNSKSYK GKKFAGKPAA KGGRPQKAGK KRKH