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DCTN1	1 .. 30,934	30,934 bp			gene
/note	= gene ENSG00000204843 Protein coding				
DCTN1-203	1 .. 30,931	30,931 bp			prim_transcript
/note	= primary transcript ENST00000409240				
DCTN1-212	52 .. 14,052	14,001 bp			prim_transcript
/note	= primary transcript ENST00000440727				
DCTN1-AS1-204	184 .. 6591	6408 bp			prim_transcript
/note	= primary transcript ENST00000426715 lncRNA				
DCTN1-210	221 .. 30,932	30,712 bp			prim_transcript
/note	= primary transcript ENST00000434055 Nonsense mediated decay				
DCTN1-228	222 .. 30,933	30,712 bp			prim_transcript
/note	= primary transcript ENST00000680606				
DCTN1-206	223 .. 30,930	30,708 bp			prim_transcript
/note	= primary transcript ENST00000409868				
DCTN1-208	245 .. 14,656	14,412 bp			prim_transcript
/note	= primary transcript ENST00000417090				
DCTN1-211	288 .. 14,395	14,108 bp			prim_transcript
/note	= primary transcript ENST00000437375				
DCTN1-209	308 .. 14,088	13,781 bp			prim_transcript
/note	= primary transcript ENST00000421392				
DCTN1-AS1-203	661 .. 6592	5932 bp			prim_transcript
/note	= primary transcript ENST00000418990 lncRNA				
DCTN1-AS1-201	808 .. 6564	5757 bp			prim_transcript
/note	= primary transcript ENST00000412957 lncRNA				
DCTN1-AS1-205	1423 .. 6595	5173 bp			prim_transcript
/note	= primary transcript ENST00000427343 lncRNA				
DCTN1-AS1-208	1436 .. 6395	4960 bp			prim_transcript
/note	= primary transcript ENST00000664792 lncRNA				
DCTN1-208	1461 .. 14,656	13,196 bp			CDS
▶ 4 segments	= 405 bp				
/note	= coding sequence ENSP00000402509				
/translation	= MCCLERVTLVQAYK,,TPSGSRMSAEASARPLRVGSRVEVIGKGHRGTVAAYVGATLFATGKWVGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGDTTAKTSKL 135 amino acids = 14.4 kDa				
DCTN1-AS1-207	1771 .. 6614	4844 bp			prim_transcript
/note	= primary transcript ENST00000664266 lncRNA				
DCTN1-AS1	1794 .. 6614	4821 bp			gene
/note	= gene ENSG00000237737 lncRNA				
DCTN1-AS1-206	1794 .. 6370	4577 bp			prim_transcript
/note	= primary transcript ENST00000437991 lncRNA				
DCTN1-AS1-202	3910 .. 6602	2693 bp			prim_transcript
/note	= primary transcript ENST00000416630 lncRNA				
DCTN1-213	6647 .. 13,901	7255 bp			prim_transcript
/note	= primary transcript ENST00000449655				

Feature	Location	Size	Type
DCTN1-215	11,531 .. 20,445	8915 bp	prim_transcript
/note	= primary transcript ENST00000458655		
DCTN1-215	11,536 .. 20,445	8910 bp	CDS
▶ 8 segments	= 560 bp		
/note	= coding sequence ENSP00000414315		
/translation	= MLMGLLRPYILGERGTVM,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVA YV GATL FATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGD DTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSS		
186 amino acids	= 19.5 kDa		
DCTN1-201	11,733 .. 30,934	19,202 bp	prim_transcript
/note	= primary transcript ENST00000361874		
DCTN1-202	11,733 .. 30,934	19,202 bp	prim_transcript
/note	= primary transcript ENST00000394003		
DCTN1-214	11,743 .. 15,347	3605 bp	prim_transcript
/note	= primary transcript ENST00000454119		
DCTN1-226	11,777 .. 30,933	19,157 bp	prim_transcript
/note	= primary transcript ENST00000628224		
DCTN1-205	11,789 .. 30,589	18,801 bp	prim_transcript
/note	= primary transcript ENST00000409567		
DCTN1-207	11,805 .. 14,088	2284 bp	prim_transcript
/note	= primary transcript ENST00000413111		
DCTN1-201	12,051 .. 30,589	18,539 bp	CDS
▶ 31 segments	= 3822 bp		
/note	= coding sequence ENSP00000354791		
/translation	= MAQSKRHVYSR,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVA YV GATL FATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGD DTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSS		
EPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLET LRLKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRR			
LKEARK,,EAKEALEAKERYMEEMADTADA IEMATLDKEMAEERAESLQVEEALKERVDLTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQN			
ARLKDALVR,,MRDLSSEKQEHVKLQKLM EKKNQELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGA EEMVEMLTDRNLNLEEKVREL			
ETVGD,,EAMNEMNDELQENARETELELREQ LDMAGARVREAQKRVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQQEASVERQ			
QPPPETFDKIKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLLVLLMPLRLICK,,AELIRKQAQEKFELSENC SERP			
GLRGAAGEQLSFAAGLVYSLLLQATLHRYEH,,ALSQCSVDVYKKGSLY PEMS AHERSLDFLIELLHKDQLDET VNV EPLTKAIKYYQ,,HLYSIH			
LAEQPEDCTMQ LADHIK,,FTQSALDCMSVEVGR LRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDA PGIPAAALAFGPQ,,VSD			
TLLDCRKHHTVAVLQEVAAAAQ LIAPLAENEGLLVAALEELAFKASEQ,,IYGT PSSSPYECLRQSCN ILISTM NKLATAMQEGEYDAERPP			
SK,,PPPVELRAAALRAEITDAEGLGLKLEDRET VIKELKKS LKIK,,GEELSEANVRLS LLEKLD SAAKADADERIEKVQTRLEETQALLR KKEK,,EF			
EETMDALQADIDQLEAEKALQRLNSQSKRTIEGLRGP PPSGIATLVSGIAG,,GAIPGQAPGSVPGPGLVKDSP LLLQQISAMRLHISQLQHE			
NSYKGAQMKA SLA SLPPLVKA KLSHEGPGSELPA GALYRKTSQ LLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKSLSDTVEK LK			
186 amino acids	= 19.5 kDa		
DCTN1-202	12,051 .. 30,589	18,539 bp	CDS
▶ 31 segments	= 3816 bp		
/note	= coding sequence ENSP00000377571		
/translation	= MAQSKRHVYSR,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVA YV GATL FATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGD DTTAKTSKL,,APTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSS		
EPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLET LRLKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRR			
LKEARK,,EAKEALEAKERYMEEMADTADA IEMATLDKEMAEERAESLQVEEALKERVDLTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQN			
ARLKDALVR,,MRDLSSEKQEHVKLQKLM EKKNQELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGA EEMVEMLTDRNLNLEEKVREL			
ETVGD,,EAMNEMNDELQENARETELELREQ LDMAGARVREAQKRVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQQEASVERQ			
QPPPETFDKIKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPD SFLRPGGDHDCVLLVLLMPLRLICK,,AELIRKQAQEKFELSENC SERP			
GLRGAAGEQLSFAAGLVYSLLLQATLHRYEH,,ALSQCSVDVYKKGSLY PEMS AHERSLDFLIELLHKDQLDET VNV EPLTKAIKYYQ,,HLYSIH			
LAEQPEDCTMQ LADHIK,,FTQSALDCMSVEVGR LRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDA PGIPAAALAFGPQ,,VSD			
TLLDCRKHHTVAVLQEVAAAAQ LIAPLAENEGLLVAALEELAFKASEQ,,IYGT PSSSPYECLRQSCN ILISTM NKLATAMQEGEYDAERPP			
SK,,PPPVELRAAALRAEITDAEGLGLKLEDRET VIKELKKS LKIK,,GEELSEANVRLS LLEKLD SAAKADADERIEKVQTRLEETQALLR KKEK,,EFEETMDAL			
QADIDQLEAEKALQRLNSQSKRTIEGLRGP PPSGIATLVSGIAG,,EEQQR,,GAIPGQAPGSVPGPGLVKDSP LLLQQISAMRLHISQLQHEN			
SLYKGAQMKA SLA SLPPLVKA KLSHEGPGSELPA GALYRKTSQ LLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKSLSDTVEK LK			
186 amino acids	= 19.5 kDa		

DCTN1-205

12,051 .. 30,589

18,539 bp

CDS

▶ 28 segments = 3762 bp

/note = coding sequence [ENSP00000386843](#)

```
/translation = MAQSKRHVYSR,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVA YV GATLFATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQ
SQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGDTTAKTSKL,,PTRPASTGVAGASSLGPSPGSAAGELSSSEPSTPAQTPLAAPIIPTPVLTSP
PGAVPPLPSPSK,,EEGLRAQVRDLEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKALEAKERYME
EMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQ
EHVKLQKLMKKNQELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQ
ENARETELELREQLDMAGARVREAAQKRVEAAQETVADYQVTIKKYRQLTAHLQ,,DVNRELTNQEQEASVERQQPPPETFDKFKFAETKAHA
K,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCV L V L L L M P R L I C K ,,AELIRKQAQEKFELSENC SERPGLRGAAGEQLSFAAGLVYSL
SLLQATLHRYEH,,ALSQCSVDVYKKGSLYPMSAHERSLDFLIELLHKDQLDET V N V E P L T K A I K Y Y Q ,,HLYSIHLAEQPEDCTMQLADHIK,,FT
QSALDCMSVEVGR L R A F L Q ,,G G Q E A T D I A L L L R D L E T S C S D I R Q F C K K I R R R M P G T D A P G I P A A L A F G P Q ,,V S D T L L D C R K H L T W V V A V L Q E V A
A A A A Q L I A P L A E N E G L L V A A L E E L A F K A S E Q ,,Y G T P S S S P Y E C L R Q S C N I L I S T M N K L A T A M Q E G E Y D A E R P P S K ,,P P P V E L R A A A L R A E I T D A
E G L G L K L E D R E T V I K E L K K S L K I K ,,G E E L S E A N V R L S L L E K K L D S A A K D A D E R I E K V Q T R L E E T Q A L L R K K E K ,,E F E E T M D A L Q A D I D Q L E A E K A E L
K Q R L N S Q S K R T I E G L R G P P P S G I A T L V S G I A G ,,G A I P G Q A P G S V P G P G L V K D S P L L L Q Q I S A M R L H I S Q L Q H E N S I L K ,,G A Q M K A S L A S L P P L H V
A K L S H E G P G S E L P A G A L Y R K T S Q L L E T L N Q L S T H T H V V D I T R T S P ,,A A K S P S A Q L M E Q V A Q L K S L S D T V E K L K ,,D E V L K E T V S Q R P G A T V P T D F
A T F P S S A F L R ,,A K E E Q Q D D T V Y M G K V T F S C A A G F G Q R H R L V L T Q E Q L H Q L H S R L I S *
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DCTN1-226

12,051 .. 30,589

18,539 bp

CDS

▶ 32 segments = 3837 bp

/note = coding sequence [ENSP00000487279](#)

```
/translation = MAQSKRHVYSR,,TPSGSRMSAEASARPLRVGSRVEVIGKGRGTVA YV GATLFATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQ
SQ,,IQVFEDGADTTSPETPDSSASKVLKR,,EGDTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSLGPSPGSAAGELSSS
EPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEGLRAQVRDLEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRR
LKEARK,,EAKALEAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQN
ARLKDALVR,,MRDLSSEKQEHVKLQKLMKKNQELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTDRNLNLEEKVRELRE
ETVGD L ,,EAMNEMNDELQENARETELELREQLDMAGARVREAAQKRVEAAQETVADYQVTIKKYRQLTAHLQ,,DVNRELTNQEQEASVERQQ
PPPETFDFKFKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCV L V L L L M P R L I C K ,,AELIRKQAQEKFELSENC SERP
GLRGAAGEQLSFAAGLVYSL S L L Q A T L H R Y E H ,,A L S Q C S V D V Y K K G S L Y P M S A H E R S L D F L I E L L H K D Q L D E T V N V E P L T K A I K Y Y Q ,,HLYSIH
LAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGR L R A F L Q ,,G G Q E A T D I A L L L R D L E T S C S D I R Q F C K K I R R R M P G T D A P G I P A A L A F G P Q ,,V S D
T L L D C R K H L T W V V A V L Q E V A A A A Q L I A P L A E N E G L L V A A L E E L A F K A S E Q ,,Y G T P S S S P Y E C L R Q S C N I L I S T M N K L A T A M Q E G E Y D A E R P P
S K ,,P P P V E L R A A A L R A E I T D A E G L G L K L E D R E T V I K E L K K S L K I K ,,G E E L S E A N V R L S L L E K K L D S A A K D A D E R I E K V Q T R L E E T Q A L L R K K E K ,,E F
E E T M D A L Q A D I D Q L E A E K A E L K Q R L N S Q S K R T I E G L R G P P P S G I A T L V S G I A G ,,E E Q R R ,,G A I P G Q A P G S V P G P G L V K D S P L L L Q Q I S A M R L H I
S Q L H N S I L K S A Q M K A S L A S L P P L H V A K L S H E G P G S E L P A G A L Y R K T S Q L L E T L N Q L S T H T H V V D I T R T S P ,,A A K S P S A Q L M E Q V A Q L K S L S
D T V E K L K ,,D E V L K E T V S Q R P G A T V P T D F A T F P S S A F L R ,,A K E E Q Q D D T V Y M G K V T F S C A A G F G Q R H R L V L T Q E Q L H Q L H S R L I S *
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DCTN1-203

13,861 .. 30,589

16,729 bp

CDS

▶ 27 segments = 3711 bp

/note = coding sequence [ENSP00000386406](#)

```
/translation = MSAEASARPLRVGSRVEVIGKGRGTVA YV GATLFATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPET
DSSASKVLKR,,EGDTTAKTSKL,,PTRPASTGVAGASSLGPSPGSAAGELSSSEPSTPAQTPLAAPIIPTPVLTSPGAVPPLPSPSK,,EEGLRA
QVRDLEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKALEAKERYMEEMADTADAIEMATLDKEMA
EERAESLQQEVEALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMKKNQELEVVR
QQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARV
EAQKRVEAAQETVADYQVTIKKYRQLTAHLQ,,DVNRELTNQEQEASVERQQPPPETFDKFKFAETKAHAK,,AIEMELRQMEVAQANRHMSL
LTA F M P D S F L R P G G D H D C V L V L L L M P R L I C K ,,AELIRKQAQEKFELSENC SERPGLRGAAGEQLSFAAGLVYSL S L L Q A T L H R Y E H ,,A L S Q C S V D
V Y K K V G S L Y P M S A H E R S L D F L I E L L H K D Q L D E T V N V E P L T K A I K Y Y Q ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGR L R A F L Q ,,
G G Q E A T D I A L L L R D L E T S C S D I R Q F C K K I R R R M P G T D A P G I P A A L A F G P Q ,,V S D T L L D C R K H L T W V V A V L Q E V A A A A Q L I A P L A E N E G L L V A A
L E E L A F K A S E Q ,,Y G T P S S S P Y E C L R Q S C N I L I S T M N K L A T A M Q E G E Y D A E R P P S K ,,P P P V E L R A A A L R A E I T D A E G L G L K L E D R E T V I K E L K K S L K
I K ,,G E E L S E A N V R L S L L E K K L D S A A K D A D E R I E K V Q T R L E E T Q A L L R K K E K ,,E F E E T M D A L Q A D I D Q L E A E K A E L K Q R L N S Q S K R T I E G L R G P P P S
G I A T L V S G I A G ,,G A I P G Q A P G S V P G P G L V K D S P L L L Q Q I S A M R L H I S Q L Q H E N S I L K ,,G A Q M K A S L A S L P P L H V A K L S H E G P G S E L P A G A L Y R K T
S Q L L E T L N Q L S T H T H V V D I T R T S P ,,A A K S P S A Q L M E Q V A Q L K S L S D T V E K L K ,,D E V L K E T V S Q R P G A T V P T D F A T F P S S A F L R ,,A K E E Q Q D D T V
Y M G K V T F S C A A G F G Q R H R L V L T Q E Q L H Q L H S R L I S *
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DCTN1-206

13,861 .. 30,589

16,729 bp

CDS

▶ 30 segments = 3771 bp

/note = coding sequence [ENSP00000387327](#)

```
/translation = MSAEASARPLRVGSRVEVIGKGRGTVA YV GATLFATGKWWGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPET
DSSASKVLKR,,EGDTTAKTSKL,,RGLKPKK,,APTARK,,TTTRRPK,,PTRPASTGVAGASSLGPSPGSAAGELSSSEPSTPAQTPLAAPIIPTPV
LTSPGAVPPLPSPSK,,EEGLRAQVRDLEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKALEAKERY
MEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDELTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEK
QEHVKLQKLMKKNQELEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQ
ENARETELELREQLDMAGARVREAAQKRVEAAQETVADYQVTIKKYRQLTAHLQ,,DVNRELTNQEQEASVERQQPPPETFDKFKFAETKAHA
K,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCV L V L L L M P R L I C K ,,AELIRKQAQEKFELSENC SERPGLRGAAGEQLSFAAGLVY
S L L L Q A T L H R Y E H ,,A L S Q C S V D V Y K K V G S L Y P M S A H E R S L D F L I E L L H K D Q L D E T V N V E P L T K A I K Y Y Q ,,HLYSIHLAEQPEDCTMQLADHIK,,
F T Q S A L D C M S V E V G R L R A F L Q ,,G G Q E A T D I A L L L R D L E T S C S D I R Q F C K K I R R R M P G T D A P G I P A A L A F G P Q ,,V S D T L L D C R K H L T W V V A V L Q E V A
A A A A Q L I A P L A E N E G L L V A A L E E L A F K A S E Q ,,Y G T P S S S P Y E C L R Q S C N I L I S T M N K L A T A M Q E G E Y D A E R P P S K ,,P P P V E L R A A A L R A E I T
D A E G L G L K L E D R E T V I K E L K K S L K I K ,,G E E L S E A N V R L S L L E K K L D S A A K D A D E R I E K V Q T R L E E T Q A L L R K K E K ,,E F E E T M D A L Q A D I D Q L E A E K
A E L K Q R L N S Q S K R T I E G L R G P P P S G I A T L V S G I A G ,,G A I P G Q A P G S V P G P G L V K D S P L L L Q Q I S A M R L H I S Q L Q H E N S I L K ,,G A Q M K A S L A S L P P
L H V A K L S H E G P G S E L P A G A L Y R K T S Q L L E T L N Q L S T H T H V V D I T R T S P ,,A A K S P S A Q L M E Q V A Q L K S L S D T V E K L K ,,D E V L K E T V S Q R P G A T V P
T D F A T F P S S A F L R ,,A K E E Q Q D D T V Y M G K V T F S C A A G F G Q R H R L V L T Q E Q L H Q L H S R L I S *
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Feature	Location	Size	Type
DCTN1-228	13,861 .. 30,589	16,729 bp	CDS
▶ 31 segments = 3786 bp			
/note	= coding sequence ENSP00000505612		
/translation	= MSAEASARPLRVGSRVEVIGKGHRGTVA YV GATLFATGKWVGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETP DSSASKVLKR,,EGDTTAKTSKL,,RGLKPKK,,APTARK,,TTRRPK,,PTRPASTGVA GASSSLGPSGSA SAGELSSSEPSTPAQTPLAAPIIPTPV LTSPGAVPPLPSPSK,,EEEGLRAQVRDLEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEKARK,,EAKALEAKERY MEEMADTADAIEMATLDKEMAEERAESLQQEVEALKERVDLTTDLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEK QEHVKKLQKLMKKNQEEVVRQQRERLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTRNLNLEEKVRELRETVGDL,,EAMNEMNDELQ ENARETELELREQ LDMAGARVREARQKRVEAAQETVADYQQTIKKYRQLTAHLQ,,DVNRELTNQEQASVERQQQPPPETDFKIKFAETKAHA K,,AIEMELRQMEVAQANRHMSLLTAFMPDSFLRPGGDHDCVLLVLLMPRLICK,,AELIRKQAQEKFELSENC SERPGLRGAAGEQLSFAAGLVY SLSLLQATLHRYEH,,ALSQCSVDVYKKGSLYPMSAHERSLDFLIELLHKDQLDET VNVPELTKAIKYYQ,,HLYSIHLAEQPEDCTMQ LADHIK,, FTQSA LDCMSVEVGRRLRAFLQ,,GGQEATDIALLLRDLETSCSDIRQFCKKIRRRMPGT DAPGIPAAALAFGPQ,,VSDTL LDCRKHLLTWWVAVLQE VAAAAAQ LIAPLAENEGLLVA ALEELAFKASEQ,,YGT PSSSPYECLRQSCNII LSTMNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEIT DAEGLGLKLEDRETVIKELKSLKIK,,GEELSEANVRLSLEKLDKSAAKDADERIEKVQTRLEETQALLRKKEK,,EFEETMDALQADIDQLEAEK AELKQRLNSQSKRTIEGLRGGPPSGIATLVSGIAG,,EEQQR,,GAIPGQAPGSVPGPLVKDSPLLLQ QISAMRLHISQLQHENSILK,,GAQMKA S265LPHHVAIKLSHEGSSRDEA GALYRKTSQLLETLNQLSTHTHVVDITRTSP,,AAKSPSAQLMEQVAQLKLSLDTVEKLL,,DEVLKETVSQR PGATVPTDFATFPSSAFLR,,AKEEQDDTVYMGKVTFSCAAGFGORHRLVLTQEQ LHLHLSRLIS*		
DCTN1-214	13,861 .. 15,347	1487 bp	CDS
▶ 4 segments = 364 bp			
/note	= coding sequence ENSP00000404038		
/translation	= MSAEASARPLRVGSRVEVIGKGHRGTVA YV GATLFATGKWVGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTTSPETP DSSASKVLKR,,EGDTTAKTSKL,,RGLKPKK 121 amino acids = 12.9 kDa		
DCTN1-211	13,861 .. 14,395	535 bp	CDS
▶ 2 segments = 262 bp			
/note	= coding sequence ENSP00000395312		
/translation	= MSAEASARPLRVGSRVEVIGKGHRGTVA YV GATLFATGKWVGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ,,IQVFEDGADTT 87 amino acids = 9.3 kDa		
DCTN1-207	13,861 .. 14,088	228 bp	CDS
/note	= coding sequence ENSP00000413268		
/translation	= MSAEASARPLRVGSRVEVIGKGHRGTVA YV GATLFATGKWVGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ 76 amino acids = 8.1 kDa		
DCTN1-209	13,861 .. 14,088	228 bp	CDS
/note	= coding sequence ENSP00000409363		
/translation	= MSAEASARPLRVGSRVEVIGKGHRGTVA YV GATLFATGKWVGVILDEAKGKNDGTVQGRKYFTCDEGHGIFVRQSQ 76 amino acids = 8.1 kDa		
DCTN1-212	13,861 .. 14,052	192 bp	CDS
/note	= coding sequence ENSP00000400059		
/translation	= MSAEASARPLRVGSRVEVIGKGHRGTVA YV GATLFATGKWVGVILDEAKGKNDGTVQGRKYFTC 64 amino acids = 6.8 kDa		
DCTN1-213	13,861 .. 13,901	41 bp	CDS
/note	= coding sequence ENSP00000407484		
/translation	= MSAEASARPLRVG 13 amino acids = 1.3 kDa		
✓ Donor Template SNV -> REV	13,956 .. 14,055	100 bp	misc_feature
✓ Protospacer Sequence	13,974 .. 13,993	20 bp	misc_feature
✓ SNV	13,984 .. 13,984	1 bp	misc_feature
/note	= REV = G SNV = A		
✓ PAM	13,994 .. 13,996	3 bp	misc_feature
DCTN1-204	17,353 .. 30,931	13,579 bp	prim_transcript
/note	= primary transcript ENST00000409438		
DCTN1-227	17,353 .. 30,931	13,579 bp	prim_transcript
/note	= primary transcript ENST00000633691		
DCTN1-220	17,393 .. 20,731	3339 bp	prim_transcript
/note	= primary transcript ENST00000477966 Retained intron		

Feature	Location	Size	Type
DCTN1-204	17,736 .. 30,589	12,854 bp	CDS
▶ 26 segments = 3420 bp			
/note	= coding sequence ENSP00000387270		
/translation	= MMRQAPTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSSEPSTPAQTPLAAPIIPTPVLTPSGAVPPLPSPSK,,EEEGLRAQVRD LEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKAELEAKERYMEEMADTADAIEMATLDKEMAERA ESLQQEVEALKERVDELTTDLLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMKKNQLELVVRQRE RLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARVREAQK RVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQEQASVERQQQPPPETFDFKIKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAF MPDSFLRPGGDHDCVLLVLLMPRLICK,,AELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYSLSLQLATLHRYEH,,ALSQCSVDVYKK VGSLYPEMSAHERSLDFIELLHKDQLDDEVNVEPLTKAIKYYQ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGRRAFLQ,,GGQE ATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAAALAFGPQ,,VSDTLLDCRKHLTVVAVLQEVAAAAAQLIAPLAENEGLLVALEELA FKASEQ,,IYGTSSSPYECLRQSCNLISTMNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKSKLKIK,,GE ELSEANVRLSLEKLDKSAKADADERIEKVQTRLEETQALLRKKEK,,EFEETMDALQADIDQLEAEKALQRLNSQSKRTIEGLRGGPPSGIATL VSGIAG,,GAIPGQAPGSVPGPLVKDPSLLLQISAMRLHISQLQHENSILK,,GAQMKA SLASLPPLHVAKLSHEGPGSELPA GALYRKTSQLL ETVQAHHTHTHYVDITRSPKDAKSPSAQLMEQVAQLKLSLSDTVEKLG,,DEV LKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQQDDTVYMGK VTFSCAAGFGQRHRLVLTQEQLHQLHSRLIS*		
DCTN1-227	17,736 .. 30,589	12,854 bp	CDS
▶ 27 segments = 3435 bp			
/note	= coding sequence ENSP00000487724		
/translation	= MMRQAPTARK,,TTTRRPK,,PTRPASTGVAGASSSLGPGSGSASAGELSSSEPSTPAQTPLAAPIIPTPVLTPSGAVPPLPSPSK,,EEEGLRAQVRD LEEKLETLRKRAEDKAKLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLEARK,,EAKAELEAKERYMEEMADTADAIEMATLDKEMAERA ESLQQEVEALKERVDELTTDLLEILKAEIEEK,,GSDGAASSYQLKQLEEQNARLKDALVR,,MRDLSSEKQEHVKLQKLMKKNQLELVVRQRE RLQEELSQAESTIDELKEQ,,VDAALGAEEMVEMLTDRNLNLEEKVRELRETVGDL,,EAMNEMNDELQENARETELELREQLDMAGARVREAQK RVEAAQETVADYQQTICKYRQLTAHLQ,,DVNRELTNQEQASVERQQQPPPETFDFKIKFAETKAHAK,,AIEMELRQMEVAQANRHMSLLTAF MPDSFLRPGGDHDCVLLVLLMPRLICK,,AELIRKQAQEKFELSENCSERPGLRGAAGEQLSFAAGLVYSLSLQLATLHRYEH,,ALSQCSVDVYKK VGSLYPEMSAHERSLDFIELLHKDQLDDEVNVEPLTKAIKYYQ,,HLYSIHLAEQPEDCTMQLADHIK,,FTQSALDCMSVEVGRRAFLQ,,GGQE ATDIALLLRDLETSCSDIRQFCKKIRRRMPGTDAPGIPAAALAFGPQ,,VSDTLLDCRKHLTVVAVLQEVAAAAAQLIAPLAENEGLLVALEELA FKASEQ,,IYGTSSSPYECLRQSCNLISTMNKLATAMQEGEYDAERPPSK,,PPPVELRAAALRAEITDAEGLGLKLEDRETVIKELKSKLKIK,,GE ELSEANVRLSLEKLDKSAKADADERIEKVQTRLEETQALLRKKEK,,EFEETMDALQADIDQLEAEKALQRLNSQSKRTIEGLRGGPPSGIATL VSGIAG,,EEQQR,,GAIPGQAPGSVPGPLVKDPSLLLQISAMRLHISQLQHENSILK,,GAQMKA SLASLPPLHVAKLSHEGPGSELPA GALYR KTSPKHTHTHYVDITRSPKDAKSPSAQLMEQVAQLKLSLSDTVEKLG,,DEV LKETVSQRPGATVPTDFATFPSSAFLR,,AKEEQQDD TVYMGKVT FSCAAGFGQRHRLVLTQEQLHQLHSRLIS*		
DCTN1-217	18,706 .. 21,082	2377 bp	prim_transcript
/note	= primary transcript ENST00000463583 protein_coding_CDS_not_defined		
DCTN1-216	18,873 .. 20,413	1541 bp	prim_transcript
/note	= primary transcript ENST00000462813 Retained intron		
DCTN1-218	20,046 .. 30,929	10,884 bp	prim_transcript
/note	= primary transcript ENST00000466110 Retained intron		
DCTN1-219	20,193 .. 21,109	917 bp	prim_transcript
/note	= primary transcript ENST00000470351 Retained intron		
DCTN1-225	22,693 .. 30,933	8241 bp	prim_transcript
/note	= primary transcript ENST00000497666 protein_coding_CDS_not_defined		
DCTN1-223	24,075 .. 26,116	2042 bp	prim_transcript
/note	= primary transcript ENST00000495643 protein_coding_CDS_not_defined		
DCTN1-224	25,894 .. 26,631	738 bp	prim_transcript
/note	= primary transcript ENST00000495895 Retained intron		
DCTN1-221	27,187 .. 30,933	3747 bp	prim_transcript
/note	= primary transcript ENST00000491465 Retained intron		
/note	= gene ENSG00000264324 Protein coding		
/note	= primary transcript ENST00000451608 Nonsense mediated decay		
DCTN1-222	29,159 .. 30,037	879 bp	prim_transcript
/note	= primary transcript ENST00000492717 Retained intron		

Primer	Length	Binding Sites	Tm	Date Added
✓ PCR Forward /sequence = GCCTGGTCTAAACTGAGTTATTTGC 44% GC / 7663.0 Da	25-mer	13,474 .. 13,498	58°C	Jan 20, 2023
✓ Sanger Sequencing /sequence = TCCCGTGTAGAGGTGATTGG 55% GC / 6204.1 Da	20-mer	13,900 .. 13,919	58°C	Jan 20, 2023
✓ Donor Template SNV -> REV /sequence = ATCACAAAGTGAAGTACTTCCTGCCTTGAACAGTTCCATCATTTTTGCCCTTTGCTTCATCCAGAATCACGCCTACCCATTTGCCAGTGG 40% GC / 13015.9 Da	100-mer	13,956 .. 14,055	76°C	Jan 20, 2023
✓ gRNA Protospacer /sequence = CAAATGGGTAAGCGTGATTC 45% GC / 6181.1 Da	20-mer	13,974 .. 13,993	47°C	Jan 20, 2023
✓ PCR Reverse /sequence = GGGAAGTAGTATCTGCTCCATCTTC 48% GC / 7648.0 Da	25-mer	14,374 .. 14,398	58°C	Jan 20, 2023