NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : RBdS104E07

Lot# : 6608_B3Bd

Vector : pGCAP10

Gene	OTOP3	
RefSeq_mRNA	NM_001272005.2	2337 bp

● Plasmid DNA purification

Date :2023/02/15 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date :2023/02/16 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date :2023/02/16

DNA concentration (O.D.): 215 ng/ul

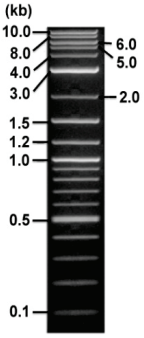
DNA	0.45 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.55 ul
Total	10 ul

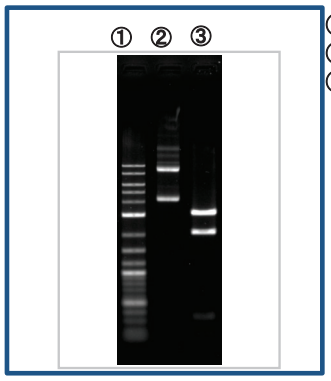
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 2.1, 0.4, 0.2 kb

Erectrophoresis : 1% agarose gel, 1x TAE Buffer

Marker : 2-Log DNA Ladder (NEB#N3200L)





①:Marker
②:uncut
③:BamHI

● Confirmation of the sequence

Date : 2026/04/22

full sequence	RBdS104E07hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/05/12

DNA (215 ng/ul)	78 ul
10x TE	67 ul
dH_2O	526 ul
Total	671 ul

● Shipping

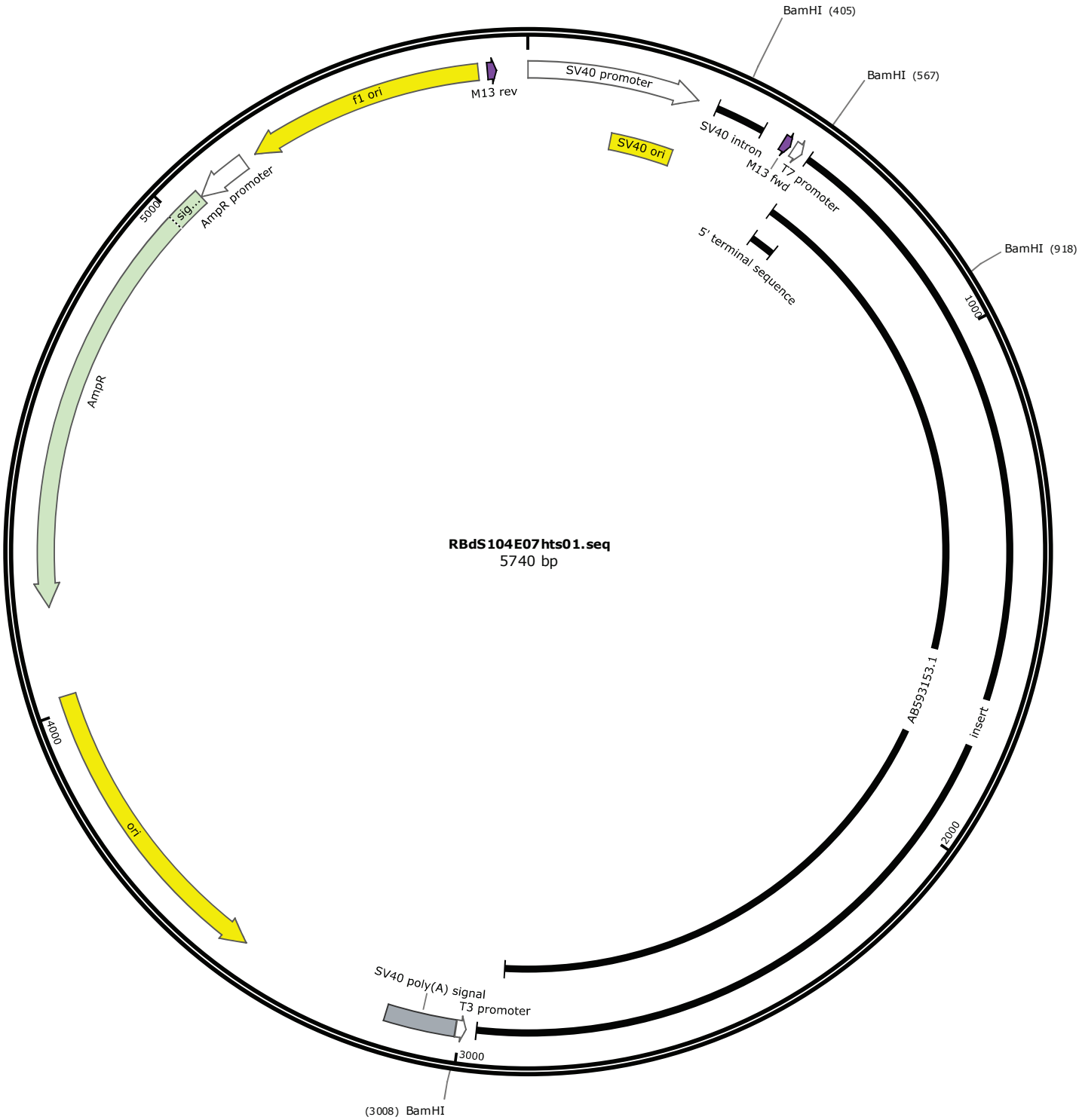
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY :

検
'26.05.12
笹沼

1 つのフィーチャーが非表示です



BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_000717:Homo sapiens carbonic anhydrase...

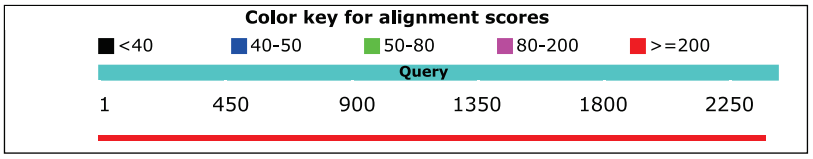
RID YGWA2Y4P114 (Expires on 04-23 14:57 pm)

Query ID	AB593153.1	**Subject ID**	lcl|Query_2941567
Description	Homo sapiens OTOP3 mRNA, complete sequence, clone: HP09106-RBdS104E07	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	2354	**Subject Length**	5740
		Program	BLASTN 2.17.0+

RBdS104E07hts01.seq

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
None provided	4348	4348	100%	0.0	100.00%	Query_2941567

Alignments

Sequence ID: Query_2941567 Length: 5740 Number of Matches: 1
Range 1: 568 to 2921

Score	Expect	Identities	Gaps	Strand	Frame
4348 bits(2354)	0.0()	2354/2354(100%)	0/2354(0%)	Plus/Plus	

Features:

```
Query  1    GATCCGCTCAGCGCCCGCAGTCGGTGGTTAGCCCACGGCGATGCCTCTCCCGGCCTCAGC  60
Sbjct  568  ............................................................  627

Query  61   CCCTGCTGAGGCTACACCCATGCCTTCTTCAGAAGCACAGGAGACTGAAGCAGCCCCGGA  120
Sbjct  628  ............................................................  687

Query  121  GAAGGAGAACCGAGTGGATGTGGGGGCCGAGGAGAGAGCGGCCGCCACCCGGCCCCAGCA  180
Sbjct  688  ............................................................  747

Query  181  GAAGTCCTGGCTGGTGAGGCATTTCTCTCTGCTGCTGCGGCGGGACCGGCAGGCCCAGAA  240
Sbjct  748  ............................................................  807

Query  241  GGCTGGACAACTCTTCTCGGGGCTCCTGGCCCTGAATGTGGTGTTCCTGGGTGGCGCCTT  300
Sbjct  808  ............................................................  867

Query  301  CATCTGCAGCATGATCTTCAACAAGGTGGCCGTCACTCTGGGTGACGTGTGGATCCTGCT  360
Sbjct  868  ............................................................  927

Query  361  GGCCACGCTGAAGGTCCTCTCCCTGCTTTGGCTTCTCTACTATGTGGCAAGCACCACCCG  420
Sbjct  928  ............................................................  987
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Query  421   CCAACCACACGCCGTGCTCTACCAAGATCCCCACGCGGGGCCCCTCTGGGTGCGGGGTTC  480
Sbjct  988   ............................................................  1047

Query  481   CCTAGTGCTCTTCGGCAGCTGCACCTTCTGCCTCAACATCTTCCGAGTGGGCTACGATGT  540
Sbjct  1048  ............................................................  1107

Query  541   GAGCCACATCCGCTGCAAGTCACAGCTGGACCTTGTCTTCCCTGTCATCGAGATGGTCTT  600
Sbjct  1108  ............................................................  1167

Query  601   CATCGGCGTCCAGACCTGGGTGCTCTGGAAACACTGCAAAGACTGTGTTCGGGTCCAGAC  660
Sbjct  1168  ............................................................  1227

Query  661   CAACTTCACTAGGTGTGGCCTGATGCTGACCCTGGCCACAAAACCTGCTGCTGTGGGTTC  720
Sbjct  1228  ............................................................  1287

Query  721   TGGCCGTTACCAATGACTCCATGCACCGAGAGATCGAAGCTGAGCTTGGCATCCTCATGG  780
Sbjct  1288  ............................................................  1347

Query  781   AAAAATCCACAGGCAATGAGACCAACACCTGTCTGTGCCTCAATGCCACCGCGTGTGAAG  840
Sbjct  1348  ............................................................  1407

Query  841   CTTTCCGGAGAGGCTTCCTGATGCTCTACCCCTTCAGCACTGAGTACTGCCTCATCTGCT  900
Sbjct  1408  ............................................................  1467

Query  901   GTGCTGTGCTGTTTGTCATGTGGAAGAACGTGGGCCGCCACGTGGCACCCCACATGGGTG  960
Sbjct  1468  ............................................................  1527

Query  961   CCCACCCTGCCACCGCACCCTTCCACCTGCACGGGGCCATCTTCGGGCCGCTGCTGGGCC  1020
Sbjct  1528  ............................................................  1587

Query  1021  TGCTGGTGCTGCTGGCAGGTGTGTGCGTCTTTGTGCTCTTCCAAATCGAGGCCAGTGGCC  1080
Sbjct  1588  ............................................................  1647

Query  1081  CTGCCATTGCTTGCCAGTACTTCACCCTCTACTATGCCTTCTATGTGGCTGTGCTGCCCA  1140
Sbjct  1648  ............................................................  1707

Query  1141  CCATGAGTCTGGCGTGCCTGGCAGGCACAGCCATACACGGGCTGGAGGAGAGAGAGCTGG  1200
Sbjct  1708  ............................................................  1767

Query  1201  ACACGGTCAAGAACCCTACCCGCAGCCTGGATGTGGTGCTGCTAATGGGTGCTGCACTGG  1260
Sbjct  1768  ............................................................  1827

Query  1261  GCCAGATGGGCATCGCCTATTTCTCCATCGTGGCCATTGTGGCCAAGCGCCCGCATGAGC  1320
Sbjct  1828  ............................................................  1887

Query  1321  TGCTCAACCGCCTCATCCTGGCCTACTCGCTGCTGCTCATCCTGCAGCACATCGCTCAGA  1380
Sbjct  1888  ............................................................  1947

Query  1381  ACCTCTTCATCATCGAGGGCCTGCACCGGCGCCCACTCTGGGAGACAGTTCCCGAGGGCC  1440
Sbjct  1948  ............................................................  2007

Query  1441  TGGCAGGAAAGCAGGAGGCTGAGCCTCCCCGCAGAGGCTCCTTGCTGGAGCTGGGCCAGG  1500
Sbjct  2008  ............................................................  2067

Query  1501  GCCTGCAGCGGGCCTCACTGGCCTACATCCACTCCTACAGCCACCTCAACTGGAAGCGGA  1560
Sbjct  2068  ............................................................  2127

Query  1561  GGGCACTCAAGGAGATCTCACTCTTCCTCATCCTCTGCAATATCACACTGTGGATGATGC  1620
Sbjct  2128  ............................................................  2187

Query  1621  CTGCATTTGGCATACACCCGGAGTTTGAGAACGGGCTAGAAAAGGATTTCTACGGCTACC  1680
Sbjct  2188  ............................................................  2247

Query  1681  AGATATGGTTCGCCATCGTCAACTTCGGCCTGCCTCTGGGGGTCTTCTACCGCATGCACT  1740
Sbjct  2248  ............................................................  2307

Query  1741  CTGTGGGAGGCCTGGTGGAGGTCTACCTGGGGGCCTGAGGCTGCCCACCCCCGGCAGAAC  1800
Sbjct  2308  ............................................................  2367

Query  1801  CTCGAAGTGCCAAGGTGGGGAAGATGGTAGCCCAGAGTCTCTGAGCAGATGCCTCATTCT  1860
Sbjct  2368  ............................................................  2427

Query  1861  GAGGTGCCGAGACCAGCCTGAGGCTCTCAAGGCCTCCTGCTCCCCAGAGCCTCACTGAAG  1920
Sbjct  2428  ............................................................  2487

Query  1921  GGGAGGGCACTGCCTAGAGCCAGAGGCCAACAGCAGGGGCCTGGACACTGAGCTTCTGAT  1980
Sbjct  2488  ............................................................  2547

Query  1981  GCCCACGGCCAGGCCTGGGCACATGCCTGCCCCCTGCCTTCCCACCACGATCCGCAAGCC  2040
Sbjct  2548  ............................................................  2607

Query  2041  AAGGGTGCACCCCAGGAGGCTGGCAGGGGCCCCCTCACGGCTACTCTGTGGGAGGGTCAG  2100
Sbjct  2608  ............................................................  2667

Query  2101  ACCTACATGACTGAGTCTGGGGAGCTTGGCGAGGGGCACCCCTCTCCAGCCAGGACTCAG  2160
Sbjct  2668  ............................................................  2727

Query  2161  GGGTCTGCCCCCTGCTGCGAGAAGAGCACCTGGTCCAAGTGTGGCTCTGGACATCCTCAG  2220
Sbjct  2728  ............................................................  2787

Query  2221  AGCTCAGAGCTCCGAGCTAGGAGGCCAGCTCCTCTCCCCACACACCTGTCTCCTAATGAG  2280
Sbjct  2788  ............................................................  2847

Query  2281  CTCATTCATTGGCTGCCAGGCAGGGTTCAACAGCTCTCTCCTGCCGCATAAACCCTATTT  2340
Sbjct  2848  ............................................................  2907

Query  2341  GTTTGATGGATTGC  2354
Sbjct  2908  ..............  2921
```

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BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_001272005:Homo sapiens otopetrin 3 (OTOP3),...

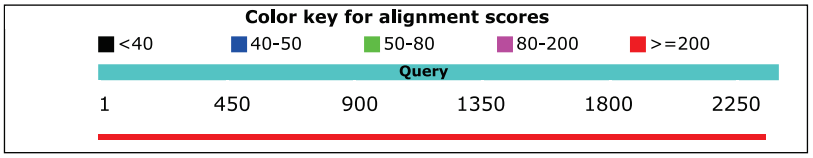
RID YGNAVMTE114 (Expires on 04-23 12:58 pm)

Query ID NM_001272005.2
Description Homo sapiens otopetrin 3 (OTOP3), transcript variant 2, mRNA
Molecule type nucleic acid
Query Length 2337

Subject ID AB593153.1
Description Homo sapiens OTOP3 mRNA, complete sequence, clone: HP09106-RBdS104E07
See details
Molecule type nucleic acid
Subject Length 2354
Program BLASTN 2.17.0+

Graphic Summary

Distribution of the top 1 Blast Hits on 1 subject sequences



Dot Matrix View

Descriptions

Sequences producing significant alignments:

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Homo sapiens OTOP3 mRNA, complete sequence, clone: HP09106-RBdS104E07	4272	4272	100%	0.0	99.66%	AB593153.1

Alignments

Homo sapiens OTOP3 mRNA, complete sequence, clone: HP09106-RBdS104E07
Sequence ID: **AB593153.1** Length: 2354 Number of Matches: 1
Range 1: 17 to 2354

Score	Expect	Identities	Gaps	Strand	Frame
4272 bits(2313)	0.0()	2330/2338(99%)	1/2338(0%)	Plus/Plus	

Features:

```
CDS:proton channel O  1                              M  P  L  P  A  S  A  P  A  E  A  T
Query                 1    GCAGTCGGTGGTTAGCCCACGGCGATGCCTCTCCCGGCCTCAGCCCCTGCTGAGGCTACA  60
Sbjct                 17   ............................................................  76

CDS:proton channel O  13    P  M  P  S  S  E  A  Q  E  T  E  A  A  P  E  K  E  N  R  V
Query                 61   CCCATGCCTTCTTCAGAAGCACAGGAGACTGAAGCAGCCCCGGAGAAGGAGAACCGAGTG  120
Sbjct                 77   ............................................................  136

CDS:proton channel O  33    D  V  G  A  E  E  R  A  A  A  T  R  P  R  Q  K  S  W  L  V
Query                 121  GATGTGGGGGCCGAGGAGAGAGCGGCCGCCACCCGGCCCCGGCAGAAGTCCTGGCTGGTG  180
Sbjct                 137  ...........................................A................  196

CDS:proton channel O  53    R  H  F  S  L  L  L  R  R  D  R  Q  A  Q  K  A  G  Q  L  F
Query                 181  AGGCATTTCTCTCTGCTGCTGCGGCGGGACCGGCAGGCCCAGAAGGCTGGACAACTCTTC  240
Sbjct                 197  ............................................................  256

CDS:proton channel O  73    S  G  L  L  A  L  N  V  V  F  L  G  G  A  F  I  C  S  M  I
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161 G>A (R46Q)

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Query                241  TCGGGGCTCCTGGCCCTGAATGTGGTGTTCCTGGGTGGCGCCTTCATCTGCAGCATGATC  300
Sbjct                257  ............................................................  316

CDS:proton channel O  93    F  N  K  V  A  V  T  L  G  D  V  W  I  L  L  A  T  L  K  V
Query                301  TTCAACAAGGTGGCCGTCACTCTGGGTGACGTGTGGATCCTGCTGGCCACGCTGAAGGTC  360
Sbjct                317  ............................................................  376

CDS:proton channel O  113   L  S  L  L  W  L  L  Y  Y  V  A  S  T  T  R  R  P  H  A  V
Query                361  CTCTCCCTGCTTTGGCTTCTCTACTATGTGGCAAGCACCACCCGCCGACCACACGCCGTG  420
Sbjct                377  ...........................................A................  436

CDS:proton channel O  133   L  Y  Q  D  P  H  A  G  P  L  W  V  R  G  S  L  V  L  F  G
Query                421  CTCTACCAAGATCCCCACGCGGGGCCCCTCTGGGTGCGGGGTTCCCTAGTGCTCTTCGGC  480
Sbjct                437  ............................................................  496

CDS:proton channel O  153   S  C  T  F  C  L  N  I  F  R  V  G  Y  D  V  S  H  I  R  C
Query                481  AGCTGCACCTTCTGCCTCAACATCTTCCGAGTGGGCTACGATGTGAGCCACATCCGCTGC  540
Sbjct                497  ............................................................  556

CDS:proton channel O  173   K  S  Q  L  D  L  V  F  S  V  I  E  M  V  F  I  G  V  Q  T
Query                541  AAGTCACAGCTGGACCTTGTCTTCTCTGTCATCGAGATGGTCTTCATCGGCGTCCAGACC  600
Sbjct                557  ..........C.................................................  616

CDS:proton channel O  193   W  V  L  W  K  H  C  K  D  C  V  R  V  Q  T  N  F  T  R  C
Query                601  TGGGTGCTCTGGAAACACTGCAAAGACTGTGTTCGGGTCCAGACCAACTTCACTAGGTGT  660
Sbjct                617  ............................................................  676

CDS:proton channel O  213   G  L  M  L  T  L  A  T  N  L  L  L  W  V  L  A  V  T  N  D
Query                661  GGCCTGATGCTGACCCTGGCCAC-AAACCTGCTGCTGTGGGTTCTGGCCGTTACCAATGA  719
Sbjct                677  ..........A.................................................  736

CDS:proton channel O  233   S  M  H  R  E  I  E  A  E  L  G  I  L  M  E  K  S  T  G  N
Query                720  CTCCATGCACCGAGAGATCGAAGCTGAGCTTGGCATCCTCATGGAAAAATCCACAGGCAA  779
Sbjct                737  ............................................................  796

CDS:proton channel O  253   E  T  N  T  C  L  C  L  N  A  T  A  C  E  A  F  R  R  G  F
Query                780  TGAGACCAACACCTGTCTGTGCCTCAATGCCACCGCGTGTGAAGCTTTCCGGAGAGGCTT  839
Sbjct                797  ............................................................  856

CDS:proton channel O  273   L  M  L  Y  P  F  S  T  E  Y  C  L  I  C  C  A  V  L  F  V
Query                840  CCTGATGCTCTACCCCTTCAGCACTGAGTACTGCCTCATCTGCTGTGCTGTGCTGTTTGT  899
Sbjct                857  ............................................................  916

CDS:proton channel O  293   M  W  K  N  V  G  R  H  V  A  P  H  M  G  A  H  P  A  T  A
Query                900  CATGTGGAAGAACGTGGGCCGCCACGTGGCACCCCACATGGGTGCCCACCCTGCCACCGC  959
Sbjct                917  ............................................................  976

CDS:proton channel O  313   P  F  H  L  H  G  A  I  F  G  P  L  L  G  L  L  V  L  L  A
Query                960  ACCCTTCCACCTGCACGGGGCCATCTTCGGGCCGCTGCTGGGCCTGCTGGTGCTGCTGGC  1019
Sbjct                977  ............................................................  1036

CDS:proton channel O  333   G  V  C  V  F  V  L  F  Q  I  E  A  S  G  P  A  I  A  C  Q
Query                1020 AGGTGTGTGCGTCTTTGTGCTCTTCCAAATCGAGGCCAGTGGCCCTGCCATTGCTTGCCA  1079
Sbjct                1037 ............................................................  1096

CDS:proton channel O  353   Y  F  T  L  Y  Y  A  F  Y  V  A  V  L  P  T  M  S  L  A  C
Query                1080 GTACTTCACCCTCTACTATGCCTTCTATGTGGCTGTGCTGCCCACCATGAGTCTGGCGTG  1139
Sbjct                1097 ............................................................  1156
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407 G>A (R128Q)

565 T>C (S181P)

683_684 ins A

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CDS:proton channel O  373   L  A  G  T  A  I  H  G  L  E  E  R  E  L  D  T  V  K  N  P
Query                1140 CCTGGCGGGCACAGCCATACACGGGCTGGAGGAGAGAGAGCTGGACACGGTCAAGAACCC  1199
Sbjct                1157 ......A.....................................................  1216

CDS:proton channel O  393   T  R  S  L  D  V  V  L  L  M  G  A  A  L  G  Q  M  G  I  A
Query                1200 TACCCGCAGCCTGGATGTGGTGCTGCTAATGGGTGCTGCACTGGGCCAGATGGGCATCGC  1259
Sbjct                1217 ............................................................  1276

CDS:proton channel O  413   Y  F  S  I  V  A  I  V  A  K  R  P  H  E  L  L  N  R  L  I
Query                1260 CTATTTCTCCATCGTGGCCATTGTGGCCAAGCGCCCGCATGAGCTGCTCAACCGCCTCAT  1319
Sbjct                1277 ............................................................  1336

CDS:proton channel O  433   L  A  Y  S  L  L  L  I  L  Q  H  I  A  Q  N  L  F  I  I  E
Query                1320 CCTGGCCTACTCGCTGCTGCTCATCCTGCAGCACATCGCTCAGAACCTCTTCATCATCGA  1379
Sbjct                1337 ............................................................  1396

CDS:proton channel O  453   G  L  H  R  R  P  L  W  E  T  V  P  E  G  L  A  G  K  Q  E
Query                1380 GGGCCTGCACCGGCGCCCACTCTGGGAGACAGTTCCCGAGGGCCTGGCAGGAAAGCAGGA  1439
Sbjct                1397 ............................................................  1456

CDS:proton channel O  473   A  E  P  P  R  R  G  S  L  L  E  L  G  Q  G  L  Q  R  A  S
Query                1440 GGCTGAGCCTCCCCGCAGAGGCTCCTTGCTGGAGCTGGGCCAGGGCCTGCAGCGGGCCTC  1499
Sbjct                1457 ............................................................  1516

CDS:proton channel O  493   L  A  Y  I  H  S  Y  S  H  L  N  W  K  R  R  A  L  K  E  I
Query                1500 ACTGGCCTACATCCACTCCTACAGCCACCTCAACTGGAAGCGGAGGGCACTCAAGGAGAT  1559
Sbjct                1517 ............................................................  1576

CDS:proton channel O  513   S  L  F  L  I  L  C  N  I  T  L  W  M  M  P  A  F  G  I  H
Query                1560 CTCACTCTTCCTCATCCTCTGCAATATCACACTGTGGATGATGCCTGCATTTGGCATACA  1619
Sbjct                1577 ............................................................  1636

CDS:proton channel O  533   P  E  F  E  N  G  L  E  K  D  F  Y  G  Y  Q  I  W  F  A  I
Query                1620 CCCGGAGTTTGAGAACGGGCTAGAAAAGGATTTCTACGGCTACCAGATATGGTTCGCCAT  1679
Sbjct                1637 ............................................................  1696

CDS:proton channel O  553   V  N  F  G  L  P  L  G  V  F  Y  R  M  H  S  V  G  G  L  V
Query                1680 CGTCAACTTCGGCCTGCCTCTGGGGGTCTTCTACCGCATGCACTCTGTGGGAGGCCTGGT  1739
Sbjct                1697 ............................................................  1756

CDS:proton channel O  573   E  V  Y  L  G  A
Query                1740 GGAGGTCTACCTGGGGGCCTGAGGCTGCCCACCCCCGGCAGAACCTCGAAGTGCCAAGGT  1799
Sbjct                1757 ............................................................  1816

Query                1800 GGGGAAGATGGTAGCCCAGAGTCTCTGAGCAGATGCCTCATTCTGAGGTGCCGAGACCAG  1859
Sbjct                1817 ............................................................  1876

Query                1860 CCTGAGGCTCTCAAGGCCTCCTGCTCCCCAGAGCCTCACTGAAGGGGAGGGCACTGCCTA  1919
Sbjct                1877 ............................................................  1936

Query                1920 GAGCCAGAGGCCAACAGCAGGGGCCTGGACACTGAGCTTCTGATGCCCACGGCCAGGCCT  1979
Sbjct                1937 ............................................................  1996

Query                1980 GGGCACATGCCTGCCCCCTGCCTTCCCACCACGATCCGCAAGCCAAGGGTGCACCCCAGG  2039
Sbjct                1997 ............................................................  2056

Query                2040 AGGCTGGCAGGGGCCCCCTCACGGCTACTCTGTGGGAGGGTCAGACCTACATGACCGAGT  2099
Sbjct                2057 ..........................................................T.  2116
```

1146 G>A

```
Query  2100  CTGGGGAGCTTGGCGAGGGGCACCCCTCTCCAGCCAGGACTCAGAGGTCTGCCCCCTGCT  2159
Sbjct  2117  ..........................................G.................  2176

Query  2160  GCGAGAAGAGCACCTGGTCCAAGTGTGGCTCTGGACATCCTCAGAGCTCAGAGCTCCGAG  2219
Sbjct  2177  ............................................................  2236

Query  2220  CTAGGAGGCCAGCTCCTCTCCCCACACACCTGTCTCCTAATGAGCTCATTCATTGGCTGC  2279
Sbjct  2237  ............................................................  2296

Query  2280  CAGGCAGGGTTCAACAGCTCTCTCCTGCCGCATAAACCCTATTTGTTTAATGGATTGC  2337
Sbjct  2297  ..................................................G.........  2354
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