NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

Lot# : 7672_B6Je

RIKEN Clone ID : ARe33B03

Vector : pKA1U5

Gene	ITGA3	
RefSeq_mRNA	NM_002204.4	4889 bp

● Plasmid DNA purification

Date : 2026/10/19 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2026/10/20 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/10/20

DNA concentration (O.D.): 384 ng/ul

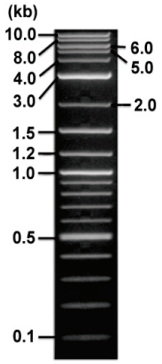
< Size of fragment expected from this clone >

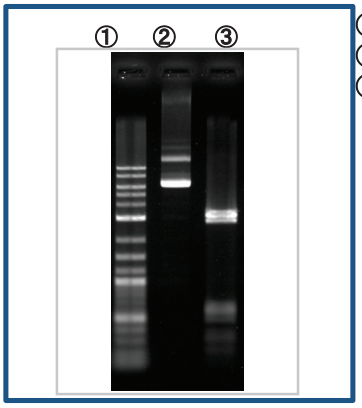
DNA	0.26	ul
Enzyme (BamHI)	1	ul
Buffer H	1	ul
dH_2O	7.74	ul
Total	10	ul

BamHI 3.1kb (vector), 2.8, 0.6, 0.5, 0.5, 0.3, 0.2, 0.1 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 : 2026/10/27

full sequence	ARe33B03hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/10/30

DNA (384 ng/ul)	84	ul
10x TE	129	ul
dH_2O	1,077	ul
Total	1,290	ul

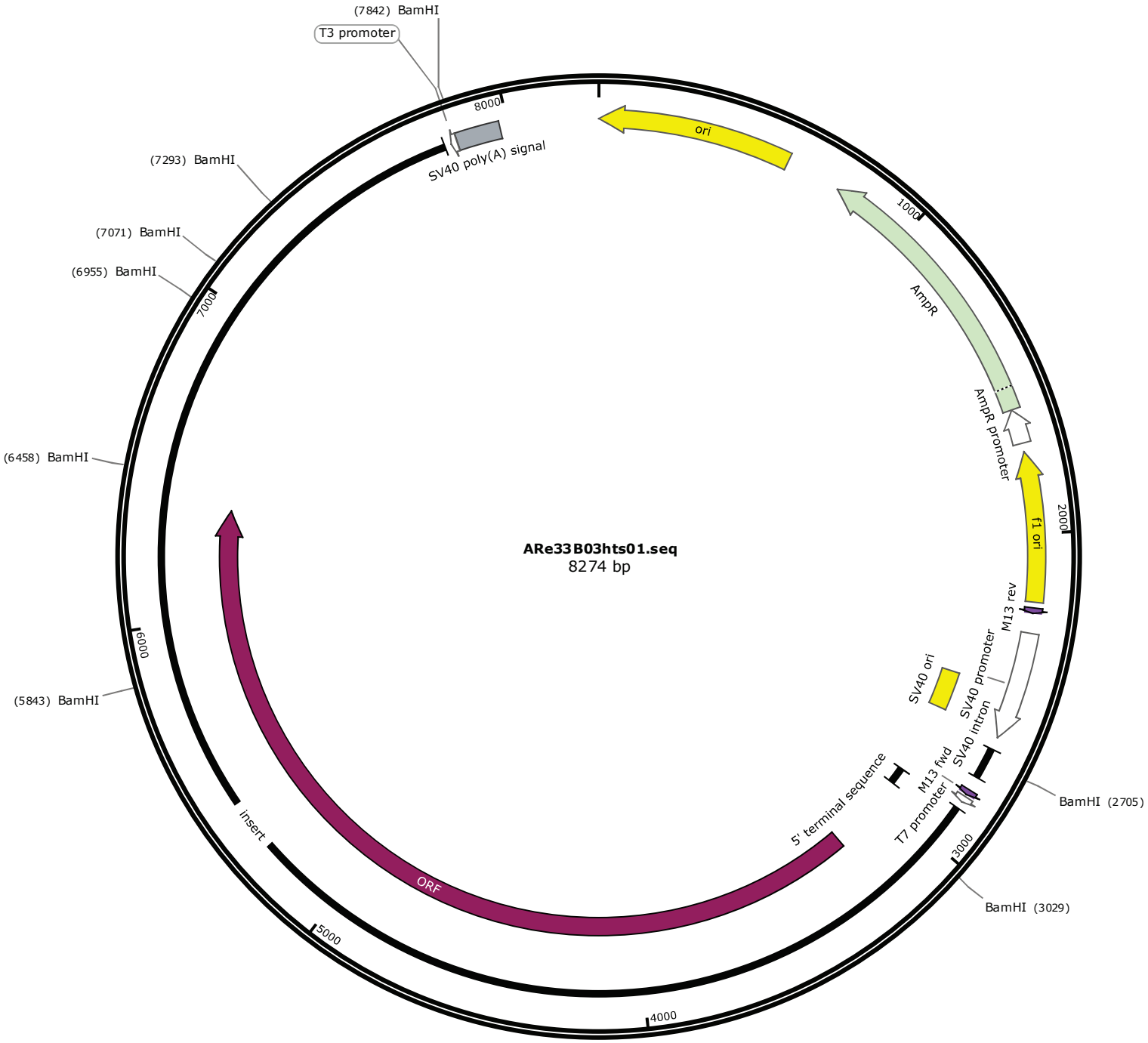
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : ___ ng/μl, Volume : ___ μl

APPROVED BY : 検 '26.10.30 笹沼

http://dna.brc.riken.jp/index.html


(7842) BamHI
T3 promoter
8000
SV40 poly(A) signal
ori
(7293) BamHI
(7071) BamHI
(6955) BamHI
7000
1000
AmpR
AmpR promoter
(6458) BamHI
2000
f1 ori
M13 rev
SV40 ori
SV40 promoter
SV40 intron
6000
(5843) BamHI
M13 fwd
T7 promoter
5' terminal sequence
BamHI (2705)
3000
insert
ORF
BamHI (3029)
5000
4000
ARe33B03hts01.seq
8274 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_014236:Homo sapiens glyceronephosphate...

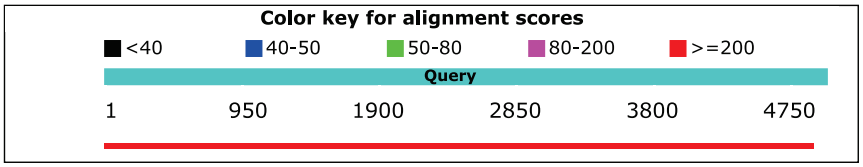
RID E0DXCSBX114 (Expires on 10-28 13:33 pm)

Query ID	NM_002204.4	**Subject ID**	lcl|Query_799759
Description	Homo sapiens integrin subunit alpha 3 (ITGA3), mRNA	**Description**	None
Molecule type	nucleic acid		See details
Query Length	4889	**Molecule type**	dna
		Subject Length	8274
		Program	BLASTN 2.17.0+

ARe33B03hts01.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	8997	8997	100%	0.0	99.90%	Query_799759

Alignments

Sequence ID: Query_799759 Length: 8274 Number of Matches: 1
Range 1: 2883 to 7769

Score	Expect	Identities	Gaps	Strand	Frame
8997 bits(4872)	0.0()	4882/4887(99%)	0/4887(0%)	Plus/Plus	

Features:

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Query          1     AGATCCGCCGCGAAGCCGGGATCGAAGGCGACAGCGCGGCCAAGGGGGCGCGGCCGGGAC  60
Sbjct          2883  ............................................................  2942

Query          61    AAGCTGGGGGCCGGTTGCCCGGGGCAGGGACGGCGGCGACCCGGCCGCTGGGGAGGCAGG  120
Sbjct          2943  ............................................................  3002

Query          121   AAGATAGACCCACGGATCTTAGGAAGGGATCCGAGAGCGCAGCTGTGAAACTGGCTGGGG  180
Sbjct          3003  ............................................................  3062

Query          181   CTGGGGGCACGAAACCGATCAGCGCTACGGAGCGCAGCGGCCGGCGGGTTCCAGTGTCCT  240
Sbjct          3063  ............................................................  3122

Query          241   CCGGCGGCGCGGGGAGCAGGTGAACAGGTCCTCACGCCCAGCTCCGCGCCCTCACGCGCT  300
Sbjct          3123  ............................................................  3182

CDS:integrin alpha-3 1                                  M  G  P  G  P  S  R  A  P  R
Query          301   CTcgccgggaccccgcttccgctggcagccatgggccccggccccagccgcgcgccccgc  360
Sbjct          3183  ............................................................  3242

CDS:integrin alpha-3 11     A  P  R  L  M  L  C  A  L  A  L  M  V  A  A  G  G  C  V  V
Query          361   gccccacgccTGATGCTCTGTGCGCTCGCCTTGATGGTGGCGGCCGGCGGCTGCGTCGTC  420
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Sbjct                3243  ..........................................................  3302

CDS:integrin alpha-3   31    S  A  F  N  L  D  T  R  F  L  V  V  K  F  A  G  N  P  G  S
Query                421   TCCGCCTTCAACCTGGATACCCGATTCCTGGTAGTGAAGGAGGCCGGGAACCCGGGCAGC  480
Sbjct                3303  ..........................................................  3362

CDS:integrin alpha-3   51    L  F  G  Y  S  V  A  L  H  R  Q  T  E  R  Q  Q  R  Y  L  L
Query                481   CTCTTCGGCTACTCGGTCGCCCTCCATCGGCAGACAGAGCGGCAGCAGCGCTACCTGCTC  540
Sbjct                3363  ..........................................................  3422

CDS:integrin alpha-3   71    L  A  G  A  P  R  E  L  A  V  P  D  G  Y  T  N  R  T  G  A
Query                541   CTGGCTGGTGCCCCCCGGGAGCTCGCTGTGCCCGATGGCTACACCAACCGGACTGGTGCT  600
Sbjct                3423  ..........................................................  3482

CDS:integrin alpha-3   91    V  Y  L  C  P  L  T  A  H  K  D  D  C  E  R  M  N  I  T  V
Query                601   GTGTACCTGTGCCCACTCACTGCCCACAAGGATGACTGTGAGCGGATGAACATCACAGTG  660
Sbjct                3483  ..........................................................  3542

CDS:integrin alpha-3   111   K  N  D  P  G  H  H  I  I  E  D  M  W  L  G  V  T  V  A  S
Query                661   AAAAATGACCCTGGCCATCACATTATTGAGGACATGTGGCTTGGAGTGACTGTGGCCAGC  720
Sbjct                3543  ..........................................................  3602

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Query                721   CAGGGCCCTGCAGGCAGAGTTCTGGTCTGTGCCCACCGCTACACCCAGGTGCTGTGGTCA  780
Sbjct                3603  ..........................................................  3662

CDS:integrin alpha-3   151   G  S  E  D  Q  R  R  M  V  G  K  C  Y  V  R  G  N  D  L  E
Query                781   GGGTCAGAAGACCAGCGGCGCATGGTGGGCAAGTGCTACGTGCGAGGCAATGACCTAGAG  840
Sbjct                3663  ..........................................................  3722

CDS:integrin alpha-3   171   L  D  S  S  D  D  W  Q  T  Y  H  N  E  M  C  N  S  N  T  D
Query                841   CTGGACTCCAGTGATGACTGGCAGACCTACCACAACGAGATGTGCAATAGCAACACAGAC  900
Sbjct                3723  ..........................................................  3782

CDS:integrin alpha-3   191   Y  L  E  T  G  M  C  Q  L  G  T  S  G  G  F  T  Q  N  T  V
Query                901   TACCTGGAGACGGGCATGTGCCAGCTGGGCACCAGCGGTGGCTTCACCCAGAACACTGTG  960
Sbjct                3783  ..........................................................  3842

CDS:integrin alpha-3   211   Y  F  G  A  P  G  A  Y  N  W  K  G  N  S  Y  M  I  Q  R  K
Query                961   TACTTCGGCGCCCCCGGTGCCTACAACTGGAAAGGAAACAGCTACATGATTCAGCGCAAG  1020
Sbjct                3843  ..........................................................  3902

CDS:integrin alpha-3   231   E  W  D  L  S  E  Y  S  Y  K  D  P  E  D  Q  G  N  L  Y  I
Query                1021  GAGTGGGACTTATCTGAGTATAGTTACAAGGACCCAGAGGACCAAGGAAACCTCTATATT  1080
Sbjct                3903  ..........................................................  3962

CDS:integrin alpha-3   251   G  Y  T  M  Q  V  G  S  F  I  L  H  P  K  N  I  T  I  V  T
Query                1081  GGGTACACGATGCAGGTAGGCAGCTTCATCCTGCACCCCAAAAACATCACCATTGTGACA  1140
Sbjct                3963  ..........................................................  4022

CDS:integrin alpha-3   271   G  A  P  R  H  R  H  M  G  A  V  F  L  L  S  Q  E  A  G  G
Query                1141  GGTGCCCCACGGCACCGACATATGGGCGCGGTGTTCTTGCTGAGCCAGGAGGCAGGCGGA  1200
Sbjct                4023  ..........................................................  4082

CDS:integrin alpha-3   291   D  L  R  R  R  Q  V  L  E  G  S  Q  V  G  A  Y  F  G  S  A
Query                1201  GACCTGCGGAGGAGGCAGGTGCTGGAGGGCTCGCAGGTGGGCGCCTATTTTGGCAGCGCC  1260
Sbjct                4083  ..........................................................  4142

CDS:integrin alpha-3   311    I  A  L  A  D  L  N  N  D  G  W  Q  D  L  L  V  G  A  P  Y
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Query                1261  ATTGCCCTGGCAGACCTGAACAATGATGGGTGGCAGGACCTCCTGGTGGGCGCCCCCTAC  1320
Sbjct                4143  ..........................................................  4202

CDS:integrin alpha-3   331   Y  F  E  R  K  E  E  V  G  G  A  I  Y  V  F  M  N  Q  A  G
Query                1321  TACTTCGAGAGGAAAGAGGAAGTAGGGGGTGCCATCTATGTCTTCATGAACCAGGCGGGA  1380
Sbjct                4203  .....T.....................................................  4262

CDS:integrin alpha-3   351   T  S  F  P  A  H  P  S  L  L  L  H  G  P  S  G  S  A  F  G
Query                1381  ACCTCCTTCCCTGCTCACCCCTCACTCCTTCTTCATGGCCCCAGTGGCTCTGCCTTTGGT  1440
Sbjct                4263  ..........................................................  4322

CDS:integrin alpha-3   371   L  S  V  A  S  I  G  D  I  N  Q  D  G  F  Q  D  I  A  V  G
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Sbjct                4323  ..........................................................  4382

CDS:integrin alpha-3   391   A  P  F  E  G  L  G  K  V  Y  I  Y  H  S  S  S  K  G  L  L
Query                1501  GCTCCGTTTGAAGGCTTGGGCAAAGTGTACATCTATCACAGTAGCTCTAAGGGGCTCCTT  1560
Sbjct                4383  ..........................................................C  4442

CDS:integrin alpha-3   411   R  Q  P  Q  Q  V  I  H  G  E  K  L  G  L  P  G  L  A  T  F
Query                1561  AGACAGCCCCAGCAGGTAATCCATGGAGAGAAGCTGGGACTGCCTGGGTTGGCCACCTTC  1620
Sbjct                4443  ..........................................................  4502

CDS:integrin alpha-3   431   G  Y  S  L  S  G  Q  M  D  V  D  E  N  F  Y  P  D  L  L  V
Query                1621  GGCTATTCCCTCAGTGGGCAGATGGATGTGGATGAGAACTTCTACCCAGACCTTCTAGTG  1680
Sbjct                4503  ..........................................................  4562

CDS:integrin alpha-3   451   G  S  L  S  D  H  I  V  L  L  R  A  R  P  V  I  N  I  V  H
Query                1681  GGAAGCCTGTCAGACCACATTGTGCTGCTGCGGGCCCGGCCCGTCATCAACATCGTCCAC  1740
Sbjct                4563  ..........................................................  4622

CDS:integrin alpha-3   471   K  T  L  V  P  R  P  A  V  L  D  P  A  L  C  T  A  T  S  C
Query                1741  AAGACCTTGGTGCCCAGGCCAGCTGTGCTGGACCCTGCACTTTGCACGGCCACCTCTTGT  1800
Sbjct                4623  ..........................................................  4682

CDS:integrin alpha-3   491   V  Q  V  E  L  C  F  A  Y  N  Q  S  A  G  N  P  N  Y  R  R
Query                1801  GTGCAAGTGGAGCTGTGCTTTGCTTACAACCAGAGTGCCGGGAACCCCAACTACAGGCGA  1860
Sbjct                4683  ..........................................................  4742

CDS:integrin alpha-3   511   N  I  T  L  A  Y  T  L  E  A  D  R  D  R  R  P  P  R  L  R
Query                1861  AACATCACCCTGGCCTACACTCTGGAGGCTGACAGGGACCGCCGGCCGCCCCGGCTCCGC  1920
Sbjct                4743  ..........................................................  4802

CDS:integrin alpha-3   531   F  A  G  S  E  S  A  V  F  H  G  F  F  S  M  P  E  M  R  C
Query                1921  TTTGCCGGCAGTGAGTCCGCTGTCTTCCACGGCTTCTTCTCCATGCCCGAGATGCGCTGC  1980
Sbjct                4803  ..........................................................  4862

CDS:integrin alpha-3   551   Q  K  L  E  L  L  L  M  D  N  L  R  D  K  L  R  P  I  I  I
Query                1981  CAGAAGCTGGAGCTGCTCCTGATGGACAACCTCCGTGACAAACTCCGCCCCATCATCATC  2040
Sbjct                4863  ..........................................................  4922

CDS:integrin alpha-3   571   S  M  N  Y  S  L  P  L  R  M  P  D  R  P  R  L  G  L  R  S
Query                2041  TCCATGAACTACTCTTTACCTTTGCGGATGCCCGATCGCCCCCGGCTGGGGCTGCGGTCC  2100
Sbjct                4923  ..........................................................  4982

CDS:integrin alpha-3   591   L  D  A  Y  P  I  L  N  Q  A  Q  A  L  E  N  H  T  E  V  Q
Query                2101  CTGGACGCCTACCCGATCCTCAACCAGGCACAGGCTCTGGAGAACCACACTGAGGTCCAG  2160
Sbjct                4983  ..........................................................  5042
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1326 C>T

1560 T>C

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CDS:integrin alpha-3  611   F  Q  K  E  C  G  P  D  N  K  C  E  S  N  L  Q  M  R  A  A
Query                 2161  TTCCAGAAGGAGTGCGGGCCTGACAACAAGTGTGAGAGCAACTTGCAGATGCGGGCAGCC  2220
Sbjct                 5043  ............................................................  5102

CDS:integrin alpha-3  631   F  V  S  E  Q  Q  Q  K  L  S  R  L  Q  Y  S  R  D  V  R  K
Query                 2221  TTCGTGTCAGAGCAGCAGCAGAAGCTGAGCAGGCTCCAGTACAGCAGAGACGTCCGGAAA  2280
Sbjct                 5103  ............................................................  5162

CDS:integrin alpha-3  651   L  L  L  S  I  N  V  T  N  T  R  T  S  E  R  S  G  E  D  A
Query                 2281  TTGCTCCTGAGCATCAACGTGACGAACACCCGGACCTCGGAGCGCTCCGGGGAGGACGCC  2340
Sbjct                 5163  ............................................................  5222

CDS:integrin alpha-3  671   H  E  A  L  L  T  L  V  V  P  P  A  L  L  L  S  S  V  R  P
Query                 2341  CACGAGGCGCTGCTCACCCTGGTGGTGCCTCCCGCCCTGCTGCTGTCCTCAGTGCGcccc  2400
Sbjct                 5223  ............................................................  5282

CDS:integrin alpha-3  691   P  G  A  C  Q  A  N  E  T  I  F  C  E  L  G  N  P  F  K  R
Query                 2401  cccGGGGCCTGCCAAGCTAATGAGACCATCTTTTGCGAGCTGGGGAACCCCTTCAAACGG  2460
Sbjct                 5283  ............................................................  5342

CDS:integrin alpha-3  711   N  Q  R  M  E  L  L  I  A  F  E  V  I  G  V  T  L  H  T  R
Query                 2461  AACCAGAGGATGGAGCTGCTCATCGCCTTTGAGGTCATCGGGGTGACCCTGCACACAAGG  2520
Sbjct                 5343  ..........................A.................................  5402

CDS:integrin alpha-3  731   D  L  Q  V  Q  L  Q  L  S  T  S  S  H  Q  D  N  L  W  P  M
Query                 2521  GACCTTCAGGTGCAGCTGCAGCTCTCCACGTCGAGTCACCAGGACAACCTGTGGCCCATG  2580
Sbjct                 5403  ............................................................  5462

CDS:integrin alpha-3  751   I  L  T  L  L  V  D  Y  T  L  Q  T  S  L  S  M  V  N  H  R
Query                 2581  ATCCTCACTCTGCTGGTGGACTATACACTCCAGACCTCGCTTAGCATGGTAAATCACCGG  2640
Sbjct                 5463  ............................................................  5522

CDS:integrin alpha-3  771   L  Q  S  F  F  G  G  T  V  M  G  E  S  G  M  K  T  V  E  D
Query                 2641  CTACAAAGCTTCTTTGGGGGGACAGTGATGGGTGAGTCTGGCATGAAAACTGTGGAGGAT  2700
Sbjct                 5523  ............................................................  5582

CDS:integrin alpha-3  791   V  G  S  P  L  K  Y  E  F  Q  V  G  P  M  G  E  G  L  V  G
Query                 2701  GTAGGAAGCCCCCTCAAGTATGAATTCCAGGTGGGCCCAATGGGGGAGGGGCTGGTGGGC  2760
Sbjct                 5583  ............................................................  5642

CDS:integrin alpha-3  811   L  G  T  L  V  L  G  L  E  W  P  Y  F  V  S  N  G  K  W  L
Query                 2761  CTGGGGACCCTGGTCCTAGGTCTGGAGTGGCCCTACGAAGTCAGCAATGGCAAGTGGCTG  2820
Sbjct                 5643  ............................................................  5702

CDS:integrin alpha-3  831   L  Y  P  T  E  I  T  V  H  G  N  G  S  W  P  C  R  P  P  G
Query                 2821  CTGTATCCCACGGAGATCACCGTCCATGGCAATGGGTCCTGGCCCTGCCGACCACCTGGA  2880
Sbjct                 5703  ............................................................  5762

CDS:integrin alpha-3  851   D  L  I  N  P  L  N  L  T  L  S  D  P  G  D  R  P  S  S  P
Query                 2881  GACCTTATCAACCCTCTCAACCTCACTCTTTCTGACCCTGGGGACAGGCCATCATCCCCA  2940
Sbjct                 5763  ............................................................  5822

CDS:integrin alpha-3  871   Q  R  R  R  R  Q  L  D  P  G  G  G  Q  G  P  P  P  V  T  L
Query                 2941  CAGCGCAGGCGGCGACAGCTGGATCCAGGGGGAGGCCAGGGCCCCCCACCTGTCACTCTG  3000
Sbjct                 5823  ............................................................  5882

CDS:integrin alpha-3  891   A  A  A  K  K  A  K  S  E  T  V  L  T  C  A  T  G  R  A  H
Query                 3001  GCTGCTGCCAAAAAAGCCAAGTCTGAGACTGTGCTGACCTGTGCCACAGGGCGTGCCCAC  3060
Sbjct                 5883  ............................................................  5942
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2485 G>A (A719T)

```
CDS:integrin alpha-3  911   C  V  W  L  E  C  P  I  P  D  A  P  V  V  T  N  V  T  V  K
Query                 3061  TGTGTGTGGCTAGAGTGCCCCATCCCTGATGCCCCCGTTGTCACCAACGTGACTGTGAAG  3120
Sbjct                 5943  ............................................................  6002

CDS:integrin alpha-3  931   A  R  V  W  N  S  T  F  I  E  D  Y  R  D  F  D  R  V  R  V
Query                 3121  GCACGAGTGTGGAACAGCACCTTCATCGAGGATTACAGAGACTTTGACCGAGTCCGGGTA  3180
Sbjct                 6003  ............................................................  6062

CDS:integrin alpha-3  951   N  G  W  A  T  L  F  L  R  T  S  I  P  T  I  N  M  E  N  K
Query                 3181  AATGGCTGGGCTACCCTATTCCTCCGAACCAGCATCCCCACCATCAACATGGAGAACAAG  3240
Sbjct                 6063  ............................................................  6122

CDS:integrin alpha-3  971   T  T  W  F  S  V  D  I  D  S  E  L  V  E  E  L  P  A  E  I
Query                 3241  ACCACGTGGTTCTCTGTGGACATTGACTCGGAGCTGGTGGAGGAGCTGCCGGCCGAAATC  3300
Sbjct                 6123  ............................................................  6182

CDS:integrin alpha-3  991   E  L  W  L  V  L  V  A  V  G  A  G  L  L  L  L  G  L  I  I
Query                 3301  GAgctgtggctggtgctggtggccgtgggtgcagggctgctgctgctggggctgATCATC  3360
Sbjct                 6183  ............................................................  6242

CDS:integrin alpha-3  1011  L  L  L  W  K  C  G  F  F  K  R  A  R  T  R  A  L  Y  E  A
Query                 3361  CTCCTGCTGTGGAAGTGCGGCTTCTTCAAGCGAGCCCGCACTCGCGCCCTGTATGAAGCT  3420
Sbjct                 6243  ............................................................  6302

CDS:integrin alpha-3  1031  K  R  Q  K  A  E  M  K  S  Q  P  S  F  T  F  R  L  T  D  D
Query                 3421  AAGAGGCAGAAGGCGGAGATGAAGAGCCAGCCGTCAGAGACAGAGAGGCTGACCGACGAC  3480
Sbjct                 6303  ............................................................  6362

CDS:integrin alpha-3  1051  Y
Query                 3481  TACTGAGGGGGCAGccccccgccccGGCCCACCTGGTGTGACTTCTTTAAGCGGACCCG  3540
Sbjct                 6363  ............................................................  6422

Query                 3541  CTATTATCAGATCATGCCCAAGTACCACGCAGTGCGGATCCGGGAGGAGGAGCGCTACCC  3600
Sbjct                 6423  ............................................................  6482

Query                 3601  ACCTCCAGGGAGCACCCTGCCCACCAAGAAGCACTGGGTGACCAGCTGGCAGACTCGGGA  3660
Sbjct                 6483  ............................................................  6542

Query                 3661  CCAATACTACTGACGtcctccctgatcccacccccctcctcccccagtgtcccctTTCTTC  3720
Sbjct                 6543  ............................................................  6602

Query                 3721  CTATTTATCATAAGTTATGCCTCTGACAGTCCACAGGGGCCACCACCTTTGGCTGGTAGC  3780
Sbjct                 6603  ............................................................  6662

Query                 3781  AGCAGGCTCAGGCACATACACCTCGTCAAGAGCATGCACATGCTGTCTGGCCCTGGGGAT  3840
Sbjct                 6663  ............................................................  6722

Query                 3841  CTTCCCACAGGAGGGCCAGCGCTGTGGACCTTACAACGCCGAGTGCACTGCATTCCTGTG  3900
Sbjct                 6723  ............................................................  6782

Query                 3901  CCCTAGATGCACGTGGGGCCCACTGCTCGTGGACTGTGCTGGTGCATCACGGATGGTGCA  3960
Sbjct                 6783  ............................................................  6842

Query                 3961  TGGGCTCGCCGTGTCTCAGCCTCTGCCAGCGCCAAAACAAGCCAAAGAGCCTCCCACCAG  4020
Sbjct                 6843  ............................................................  6902

Query                 4021  AGCCGGGAGGAAAAGGCCCCTGCAATGTGGTGACACCTCCCCCTTTCACACTGGATCCAT  4080
Sbjct                 6903  ...T........................................................  6962
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Query  4081  CTTGAGCCACAGTCACTGGATTGACTTTGCTGTCAAAACTACTGACAGGGAGCAGCCCCC  4140
Sbjct  6963  ............................................................  7022

Query  4141  GGGCCGCTGGCTGGTGGGCCCCCAATGACACCCATGCCAGAGAGGTGGGGATCCTGCCTA  4200
Sbjct  7023  ............................................................  7082

Query  4201  AGGTTGTCTACGGGGGCACTTGGAGGACCTGGCGTGCTCAGACCCAACAGCAAAGGAACT  4260
Sbjct  7083  ............................................................  7142

Query  4261  AGAAAGAAGGACCCAGAACGGCTTGCTTTCCTGCATCTCTGTGAAGCCTCTCTCCTTGGC  4320
Sbjct  7143  ............................................................  7202

Query  4321  CACAGACTGAACTCGCAGGGAATGCAGCAGGAAGGAACAAAGACAGGCAAACGGCAACGT  4380
Sbjct  7203  .....................G......................................  7262

Query  4381  AGCCTGGGCTCACTGTGCTGGGGCACGGCGGGATCCTCCACAGAGAGGAGGGGACCAATT  4440
Sbjct  7263  ............................................................  7322

Query  4441  CTGGACAGACAGATGTTGGGAGGATACAGAGGAGATGCCACTTCTCACTCACCACTACCA  4500
Sbjct  7323  ............................................................  7382

Query  4501  GCCAGCCTCAGAAGGCCCCAGAGAGACCCTGCAAGACCACGGAGGGAGCGACACTTGAAT  4560
Sbjct  7383  ............................................................  7442

Query  4561  GTAGAATAGGCAGGGGGCCCTGCCCCACCCCATCCAGCCAGACCCCACGCTGACCATGCG  4620
Sbjct  7443  ............................................................  7502

Query  4621  TCAGGGGCCTAGAGGTGGAGTTCTTAGCTATCCTTGGCTTTCAGAGCCAGCCTGGCTCTG  4680
Sbjct  7503  ............................................................  7562

Query  4681  CCCCCTCCCCCATGGGCTGTGTCCTAAGGCCCATTTGAGAAGCTGAGGCTAGTTCCAGAA  4740
Sbjct  7563  ............................................................  7622

Query  4741  AACCTCTCCTGACCCCTGCCTGTTGGCAGGCCCACTCCCCAGCCCCAGCCCCTTCCATGG  4800
Sbjct  7623  ............................................................  7682

Query  4801  TACTGTAGCAGGGGAATTCCCTCCCCCTCCTTGTGCCTTCTTTGTATATAGGCTTCTCAC  4860
Sbjct  7683  ............................................................  7742

Query  4861  GGCGACCAATAAACAGCTCCCAGTTTG  4887
Sbjct  7743  ...........................  7769
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