NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN Clone ID : RBdS007F07

Lot# : 6608_B6K5

Vector : pGCAP10

Gene	PPARGC1B	
RefSeq_mRNA	NM_133263.4	10569 bp

● Plasmid DNA purification

Date : 2026/11/09 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 2026/11/10 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 2026/11/10

DNA concentration (O.D.): 394 ng/ul

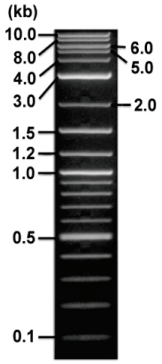
DNA	0.25 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.75 ul
Total	10 ul

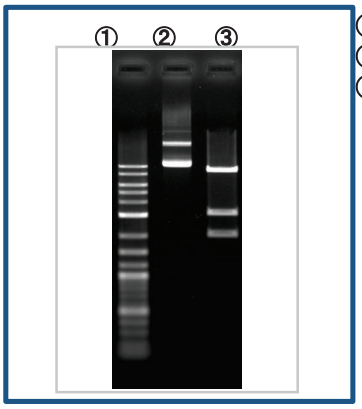
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 8.7, 2.1 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 : 2026/11/12

full sequence	RBdS007F07hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/11/17

DNA (394 ng/ul)	86 ul
10x TE	136 ul
dH_2O	1,134 ul
Total	1,355 ul

● Shipping

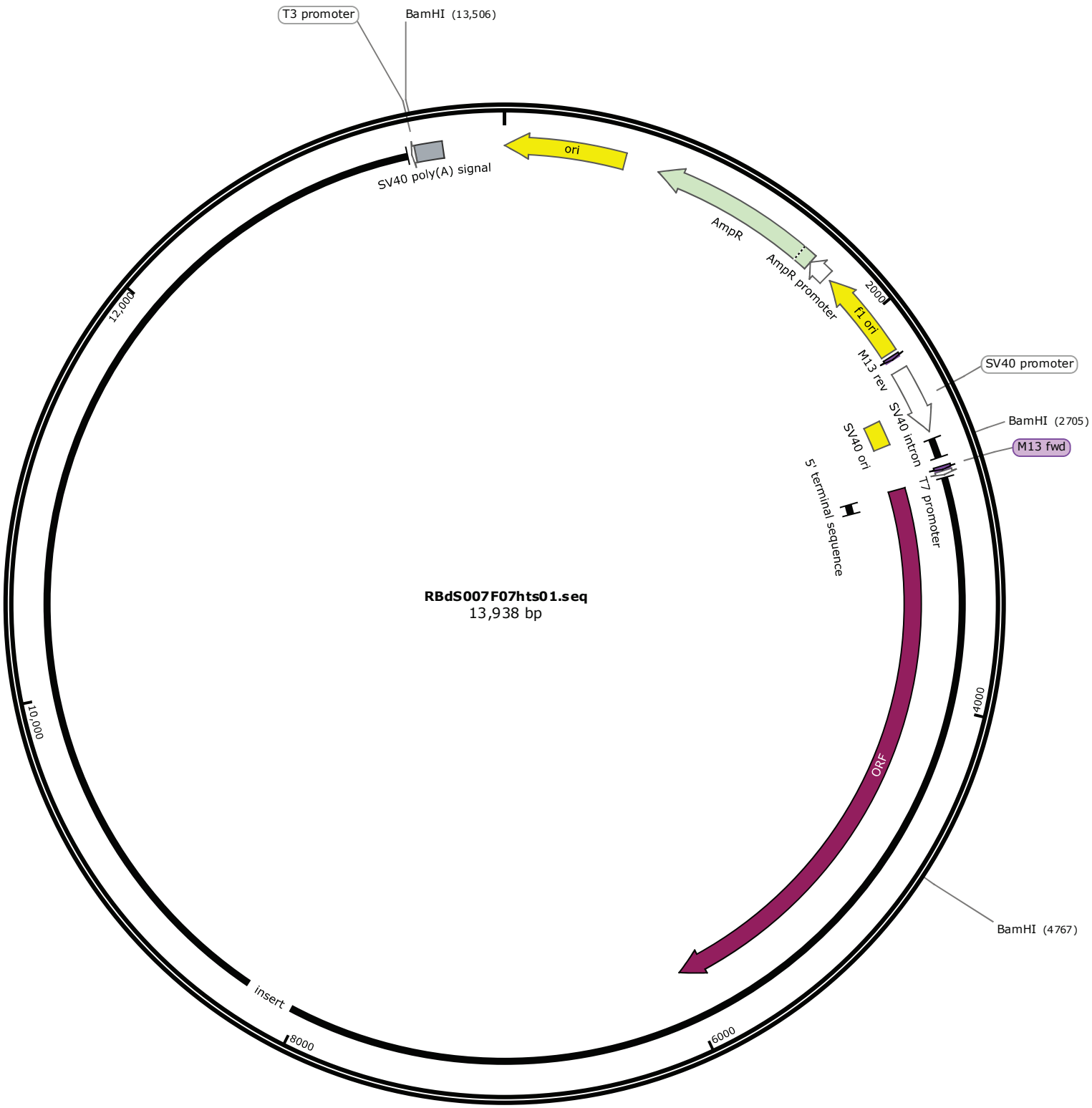
☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '26.11.17 笹沼

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

1 つのフィーチャーが非表示です



BLAST Results

Questions/comments

Blast 2 sequences

Job title: BC057801:Homo sapiens achaete-scute complex...

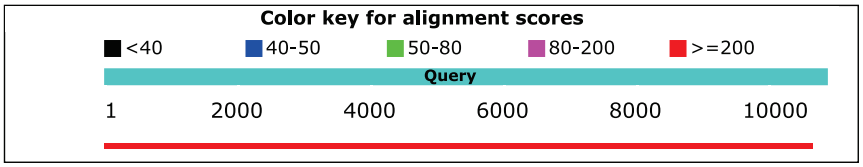
RID FAWKXD3D114 (Expires on 11-13 15:02 pm)

Query ID	NM_133263.4	**Subject ID**	lcl|Query_2016731
Description	Homo sapiens PPARG coactivator 1 beta (PPARGC1B), transcript variant 1, mRNA	**Description**	None See details
Molecule type	nucleic acid	**Molecule type**	dna
Query Length	10569	**Subject Length**	13938
		Program	BLASTN 2.17.0+

RBdS007F07hts01.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	19481	19481	100%	0.0	99.97%	Query_2016731

Alignments

Sequence ID: Query_2016731 Length: 13938 Number of Matches: 1
Range 1: 2884 to 13441

Score	Expect	Identities	Gaps	Strand	Frame
19481 bits(10549)	0.0()	10555/10558(99%)	0/10558(0%)	Plus/Plus	

Features:

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CDS:peroxisome proli  1                                    M  A  G  N  D  C  G  A  L
Query                 1     GACTCCGCCGCACGCTGCAGCCGCGGCTGGAAGATGGCGGGGAACGACTGCGGCGCGCTG  60
Sbjct                 2884  ............................................................  2943

CDS:peroxisome proli  10     L  D  E  E  L  S  S  F  F  L  N  Y  L  A  D  T  Q  G  G  G
Query                 61    CTGGACGAAGAGCTCTCCTCCTTCTTCCTCAACTATCTCGCTGACACGCAGGGTGGAGGG  120
Sbjct                 2944  ............................................................  3003

CDS:peroxisome proli  30     S  G  E  E  Q  L  Y  A  D  F  P  E  L  D  L  S  Q  L  D  A
Query                 121   TCCGGGGAGGAGCAACTCTATGCTGACTTTCCAGAACTTGACCTCTCCCAGCTGGATGCC  180
Sbjct                 3004  ............................................................  3063

CDS:peroxisome proli  50     S  D  F  D  S  A  T  C  F  G  E  L  Q  W  C  P  E  N  S  E
Query                 181   AGCGACTTTGACTCGGCCACCTGCTTTGGGGAGCTGCAGTGGTGCCCAGAGAACTCAGAG  240
Sbjct                 3064  ............................................................  3123

CDS:peroxisome proli  70     T  E  P  N  Q  Y  S  P  D  D  S  E  L  F  Q  I  D  S  E  N
Query                 241   ACTGAACCCAACCAGTACAGCCCCGATGACTCCGAGCTCTTCCAGATTGACAGTGAGAAT  300
Sbjct                 3124  ............................................................  3183

CDS:peroxisome proli  90     E  A  L  L  A  E  L  T  K  T  L  D  D  I  P  E  D  D  V  G
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Query                301    GAGGCCCTCCTGGCAGAGCTCACCAAGACCCTGGATGACATCCCTGAAGATGACGTGGGT  360
Sbjct                3184   ..............................................................  3243

CDS:peroxisome proli 110     L  A  A  F  P  A  L  D  G  G  D  A  L  S  C  T  S  A  S  P
Query                361    CTGGCTGCCTTCCCAGCCCTGGATGGTGGAGACGCTCTATCATGCACCTCAGCTTCgcct  420
Sbjct                3244   ..............................................................  3303

CDS:peroxisome proli 130     A  P  S  S  A  P  P  S  P  A  P  E  K  P  S  A  P  A  P  E
Query                421    gccccctcatctgcaccccccagccctgccccggagaagccctcggccccagcccctgAG  480
Sbjct                3304   ..............................................................  3363

CDS:peroxisome proli 150     V  D  E  L  S  L  L  Q  K  L  L  L  A  T  S  Y  P  T  S  S
Query                481    GTGGACGAGCTCTCACTGCTGCAGAAGCTCCTCCTGGCCACATCCTACCCAACATCAAGC  540
Sbjct                3364   ..............................................................  3423

CDS:peroxisome proli 170     S  D  T  Q  K  E  G  T  A  W  R  Q  A  G  L  R  S  K  S  Q
Query                541    TCTGACACCCAGAAGGAAGGGACCGCCTGGCGCCAGGCAGGCCTCAGATCTAAAAGTCAA  600
Sbjct                3424   ..............................................................  3483

CDS:peroxisome proli 190     R  P  C  V  K  A  D  S  T  Q  D  K  K  A  P  M  M  Q  S  Q
Query                601    CGGCCTTGTGTTAAGGCGGACAGCACCCAAGACAAGAAGGCTCCCATGATGCAGTCTCAG  660
Sbjct                3484   ..............................................................  3543

CDS:peroxisome proli 210     S  R  S  C  T  E  L  H  K  H  L  T  S  A  Q  C  C  L  Q  D
Query                661    AGCCGAAGTTGTACAGAACTACATAAGCACCTCACCTCGGCACAGTGCTGCCTGCAGGAT  720
Sbjct                3544   ..............................................................  3603

CDS:peroxisome proli 230     R  G  L  Q  P  P  C  L  Q  S  P  R  L  P  A  K  E  D  K  E
Query                721    CGGGGTCTGCAGCCACCATGCCTCCAGAGTCCCCGGCTCCCTGCCAAGGAGGACAAGGAG  780
Sbjct                3604   ..............................................................  3663

CDS:peroxisome proli 250     P  G  E  D  C  P  S  P  Q  P  A  P  A  S  P  R  D  S  L  A
Query                781    CCGGGTGAGGACTGCCCGAGCCCCCAGCCAGCTCCAGCCTCTCCCCGGGACTCCCTAGCT  840
Sbjct                3664   ..............................................................  3723

CDS:peroxisome proli 270     L  G  R  A  D  P  G  A  P  V  S  Q  E  D  M  Q  A  M  V  Q
Query                841    CTGGGCAGGGCAGACCCCGGTGCCCCGGTTTCCCAGGAAGACATGCAGGCGATGGTGCAA  900
Sbjct                3724   ..............................................................  3783

CDS:peroxisome proli 290     L  I  R  Y  M  H  T  Y  C  L  P  Q  R  K  L  P  P  Q  T  P
Query                901    CTCATACGCTACATGCACACCTACTGCCTCCCCCAGAGGAAGCTGCCCCCACAGACCCCT  960
Sbjct                3784   ..............................................................  3843

CDS:peroxisome proli 310     E  P  L  P  K  A  C  S  N  P  S  Q  Q  V  R  S  R  P  W  S
Query                961    GAGCCACTCCCCAAGGCCTGCAGCAACCCCTCCCAGCAGGTCAGATCCCGGCCCTGGTCC  1020
Sbjct                3844   ..............................................................  3903

CDS:peroxisome proli 330     R  H  H  S  K  A  S  W  A  E  F  S  I  L  R  E  L  L  A  Q
Query                1021   CGGCACCACTCCAAAGCCTCCTGGGCTGAGTTCTCCATTCTGAGGGAACTTCTGGCTCAA  1080
Sbjct                3904   ..............................................................  3963

CDS:peroxisome proli 350     D  V  L  C  D  V  S  K  P  Y  R  L  A  T  P  V  Y  A  S  L
Query                1081   GACGTGCTCTGTGATGTCAGCAAACCCTACCGTCTGGCCACGCCTGTTTATGCCTCCCTC  1140
Sbjct                3964   ..............................................................  4023

CDS:peroxisome proli 370     T  P  R  S  R  P  R  P  P  K  D  S  Q  A  S  P  G  R  P  S
Query                1141   ACACCTCGGTCAAGGCCCAGGCCCCCCAAAGACAGTCAGGCCTCCCCTGGTCGCCCGTCC  1200
Sbjct                4024   ..............................................................  4083
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CDS:peroxisome proli 390     S  V  E  E  V  R  I  A  A  S  P  K  S  T  G  P  R  P  S  L
Query                1201   TCGGTGGAGGAGGTAAGGATCGCAGCTTCACCCAAGAGCACCGGGCCCAGACCAAGCCTG  1260
Sbjct                4084   ..............................................................  4143

CDS:peroxisome proli 410     R  P  L  R  L  E  V  K  R  E  V  R  R  P  A  R  L  Q  Q  Q
Query                1261   CGCCCACTGCGGCTGGAGGTGAAAAGGGAGGTCCGCCGGCCTGCCAGACTGCAGCAGCag  1320
Sbjct                4144   ..............................................................  4203

CDS:peroxisome proli 430     E  E  E  D  E  E  E  E  E  E  E  E  E  E  E  K  E  E  E  E
Query                1321   gaggaggaagacgaggaagaagaggaggaggaagaggaagaagaaaaagaggaggaggag  1380
Sbjct                4204   ..............................................................  4263

CDS:peroxisome proli 450     E  W  G  R  K  R  P  G  R  G  L  P  W  T  K  L  G  R  K  L
Query                1381   gagtggggcaggaaaaggccaggccgaggcCTGCCATGGACGAAGCTGGGGAGGAAGCTG  1440
Sbjct                4264   ..............................................................  4323

CDS:peroxisome proli 470     E  S  S  V  C  P  V  R  R  S  R  R  L  N  P  E  L  G  P  W
Query                1441   GAGAGCTCTGTGTGCCCCGTGCGGCGTTCTCGGAGACTGAACCCTGAGCTGGGCCCCTGG  1500
Sbjct                4324   ..............................................................  4383

CDS:peroxisome proli 490     L  T  F  A  D  E  P  L  V  P  S  E  P  Q  G  A  L  P  S  L
Query                1501   CTGACATTTGCAGATGAGCCGCTGGTCCCCTCGGAGCCCCAAGGTGCTCTGCCCTCACTG  1560
Sbjct                4384   ..............................................................  4443

CDS:peroxisome proli 510     C  L  A  P  K  A  Y  D  V  E  R  E  L  G  S  P  T  D  E  D
Query                1561   TGCCTGGCTCCCAAGGCCTACGACGTAGAGCGGGAGCTGGGCAGCCCCACGGACGAGGAC  1620
Sbjct                4444   ..............................................................  4503

CDS:peroxisome proli 530     S  G  Q  D  Q  Q  L  L  R  G  P  Q  I  P  A  L  E  S  P  C
Query                1621   AGTGGCCAAGACCAGCAGCTCCTACGGGGACCCCAGATCCCTGCCCTGGAGAGCCCCTGT  1680
Sbjct                4504   ..............................................................  4563

CDS:peroxisome proli 550     E  S  G  C  G  D  M  D  E  D  P  S  C  P  Q  L  P  P  R  D
Query                1681   GAGAGTGGGTGTGGGGACATGGATGAGGACCCCAGCTGCCCGCAGCTCCCTCCCAGAGAC  1740
Sbjct                4564   ..............................................................  4623

CDS:peroxisome proli 570     S  P  R  C  L  M  L  A  L  S  Q  S  D  P  T  F  G  K  K  S
Query                1741   TCTCCCAGGTGCCTCATGCTGGCCTTGTCACAAAGCGACCCAACTTTTGGCAAGAAGAGC  1800
Sbjct                4624   ..............................................................  4683

CDS:peroxisome proli 590     F  E  Q  T  L  T  V  E  L  C  G  T  A  G  L  T  P  P  T  T
Query                1801   TTTGAGCAGACCTTGACAGTGGAGCTCTGTGGCACAGCAGGACTCACCCCACCCACCACA  1860
Sbjct                4684   ..............................................................  4743

CDS:peroxisome proli 610     P  P  Y  K  P  T  E  E  D  P  F  K  P  D  I  K  H  S  L  G
Query                1861   CCACCGTACAAGCCCACAGAGGAGGATCCCTTCAAACCAGACATCAAGCATAGTCTAGGC  1920
Sbjct                4744   ..............................................................  4803

CDS:peroxisome proli 630     K  E  I  A  L  S  L  P  S  P  E  G  L  S  L  K  A  T  P  G
Query                1921   AAAGAAATAGCTCTCAGCCTCCCCTCCCCTGAGGGCCTCTCACTCAAGGCCACCCCAGGG  1980
Sbjct                4804   ..............................................................  4863

CDS:peroxisome proli 650     A  A  H  K  L  P  K  K  H  P  E  R  S  E  L  L  S  H  L  R
Query                1981   GCTGCCCACAAGCTGCCAAAGAAGCACCCAGAGCGAAGTGAGCTCCTGTCCCACCTGCGA  2040
Sbjct                4864   ..............................................................  4923

CDS:peroxisome proli 670     H  A  T  A  Q  P  A  S  Q  A  G  Q  K  R  P  F  S  C  S  F
Query                2041   CATGCCACAGCCCAGCCAGCCTCCCAGGCTGGCCAGAAGCGTCCCTTCTCCTGTTCCTTT  2100
Sbjct                4924   ..............................................................  4983
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CDS:peroxisome proli  690    G  D  H  D  Y  C  Q  V  L  R  P  E  G  V  L  Q  R  K  V  L
Query                 2101   GGAGACCATGACTACTGCCAGGTGCTCCGACCAGAAGGCGTCCTGCAAAGGAAGGTGCTG  2160
Sbjct                 4984   ............................................................  5043

CDS:peroxisome proli  710    R  S  W  E  P  S  G  V  H  L  E  D  W  P  Q  Q  G  A  P  W
Query                 2161   AGGTCCTGGGAGCCGTCTGGGGTTCACCTTGAGGACTGGCCCCAGCAGGGTGCCCCTTGG  2220
Sbjct                 5044   ............................................................  5103

CDS:peroxisome proli  730    A  E  A  Q  A  P  G  R  E  E  D  R  S  C  D  A  G  A  P  P
Query                 2221   GCTGAGGCACAGGCCCCTGGCAGGGAGGAAGACAGAAGCTGTGATGCTGGCGCCCCACCC  2280
Sbjct                 5104   ............................................................  5163

CDS:peroxisome proli  750    K  D  S  T  L  L  R  D  H  E  I  R  A  S  L  T  K  H  F  G
Query                 2281   AAGGACAGCACGCTGCTGAGAGACCATGAGATCCGTGCCAGCCTCACCAAACACTTTGGG  2340
Sbjct                 5164   ............................................................  5223

CDS:peroxisome proli  770    L  L  E  T  A  L  E  E  E  D  L  A  S  C  K  S  P  E  Y  D
Query                 2341   CTGCTGGAGACCGCCCTGGAGGAGGAAGACCTGGCCTCCTGCAAGAGCCCTGAGTATGAC  2400
Sbjct                 5224   ............................................................  5283

CDS:peroxisome proli  790    T  V  F  E  D  S  S  S  S  S  G  E  S  S  F  L  P  E  E  E
Query                 2401   ACTGTCTTTGAAGACAGCAGCAGCAGCAGCGGCGAGAGCAGCTTCCTCCCAgaggaggaa  2460
Sbjct                 5284   ............................................................  5343

CDS:peroxisome proli  810    E  E  E  G  E  E  E  E  E  D  D  E  E  E  D  S  G  V  S  P
Query                 2461   gaggaagaaggggaggaggaggaggaggacgatgaagaaagaggaCTCAGGGGTCAGCCCC  2520
Sbjct                 5344   ............................................................  5403

CDS:peroxisome proli  830    T  C  S  D  H  C  P  Y  Q  S  P  P  S  K  A  N  R  Q  L  C
Query                 2521   ACTTGCTCTGACCACTGCCCCTACCAGAGCCCACCAAGCAAGGCCAACCGGCAGCTCTGT  2580
Sbjct                 5404   ............................................................  5463

CDS:peroxisome proli  850    S  R  S  R  S  S  S  G  S  S  P  C  H  S  W  S  P  A  T  R
Query                 2581   TCCCGCAGCCGCTCAAGCTCTGGCTCTTCACCCTGCCACTCCTGGTCACCAGCCACTCGA  2640
Sbjct                 5464   ............................................................  5523

CDS:peroxisome proli  870    R  N  F  R  C  E  S  R  G  P  C  S  D  R  T  P  S  I  R  H
Query                 2641   AGGAACTTCAGATGTGAGAGCAGAGGGCCGTGTTCAGACAGAACGCCAAGCATCCGGCAC  2700
Sbjct                 5524   ............................................................  5583

CDS:peroxisome proli  890    A  R  K  R  R  E  K  A  I  G  E  G  R  V  V  Y  I  Q  N  L
Query                 2701   GCCAGGAAGCGGCGGGAAAAGGCCATTGGGGAAGGCCGCGTGGTGTACATTCAAAATCTC  2760
Sbjct                 5584   ............................................................  5643

CDS:peroxisome proli  910    S  S  D  M  S  S  R  E  L  K  R  R  F  E  V  F  G  E  I  E
Query                 2761   TCCAGCGACATGAGCTCCCGAGAGCTGAAGAGGCGCTTTGAAGTGTTTGGTGAGATTGAG  2820
Sbjct                 5644   ............................................................  5703

CDS:peroxisome proli  930    E  C  E  V  L  T  R  N  R  R  G  E  K  Y  G  F  I  T  Y  R
Query                 2821   GAGTGCGAGGTGCTGACAAGAAATAGGAGAGGCGAGAAGTACGGCTTCATCACCTACCGG  2880
Sbjct                 5704   ............................................................  5763

CDS:peroxisome proli  950    C  S  E  H  A  A  L  S  L  T  K  G  A  A  L  R  K  R  N  E
Query                 2881   TGTTCTGAGCACGCGGCCCTCTCTTTGACAAAGGGCGCTGCCCTGAGGAAGCGCAACGAG  2940
Sbjct                 5764   ............................................................  5823

CDS:peroxisome proli  970    P  S  F  Q  L  S  Y  G  G  L  R  H  F  C  W  P  R  Y  T  D
Query                 2941   CCCTCCTTCCAGCTGAGCTACGGAGGGCTCCGGCACTTCTGCTGGCCCAGATACACTGAC  3000
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Sbjct                 5824   ............................................................  5883

CDS:peroxisome proli  990    Y  D  S  N  S  E  E  A  L  P  A  S  G  K  S  K  Y  E  A  M
Query                 3001   TACGATTCCAATTCAGAAGAGGCCCTTCCTGCGTCAGGGAAAAGCAAGTATGAAGCCATG  3060
Sbjct                 5884   ............................................................  5943

CDS:peroxisome proli  1010   D  F  D  S  L  L  K  E  A  Q  Q  S  L  H
Query                 3061   GATTTTGACAGCTTACTGAAAGAGGCCCAGCAGAGCCTGCATTGATAACAGCCTTAACCC  3120
Sbjct                 5944   ............................................................  6003

Query                 3121   TCGAGGAATACCTCAATACCTCAGACAAGGCCCTTCCAATATGTTTACGTTTTCAAAGAA  3180
Sbjct                 6004   ............................................................  6063

Query                 3181   ATCAAGTATATGAGGAGAGCGAGCGAGCGTGAGAGAACACCCGTGAGAGAGACTTGAAAC  3240
Sbjct                 6064   ............................................................  6123

Query                 3241   TGCTGTCCTTTaaaaaaaaaaaaaaTCAATGTTTACATTGAACAAAGCTGCTTCTGTCTG  3300
Sbjct                 6124   ............................................................  6183

Query                 3301   TGAGTTTCCATGGTGTTGACGTTCCACTGCCACATTAGTGTCCTCGCTTCCAACGGGTTG  3360
Sbjct                 6184   ............................................................  6243

Query                 3361   TCCCGGGTGCACCTCGAAGTGCCGGGTCCGTCACCCATCGCCCCTTCCTTCCCGACTGAC  3420
Sbjct                 6244   ............................................................  6303

Query                 3421   TTCCTCTCGTAGACTTGCAGCTGTGTTCACCATAACATTTCTTGTCTGTAGTGTGTGATG  3480
Sbjct                 6304   ............................................................  6363

Query                 3481   ATGAAATTGTTACTTGTGAATAGAATCAGGACTATAAACTTCATTTTTAATTGaaaaaaa  3540
Sbjct                 6364   ............................................................  6423

Query                 3541   aaGTATATCCTTAAAATAATGTATTTATGGCTCAGATGTACTGTGCCTGGGATTATTGTA  3600
Sbjct                 6424   ............................................................  6483

Query                 3601   TTGCTTCCTTGATTTTTTAACTATGCACTGTCATGAGGTGTTTGCCACTGAGCTGCCCTG  3660
Sbjct                 6484   ............................................................  6543

Query                 3661   CTCCCCTTGCCAGATTGCCCTGGAGGTGCTGGGTGGCCGCTAGGCTGGTCTGCAGGAAAG  3720
Sbjct                 6544   ............................................................  6603

Query                 3721   CGCGGCCTGCCGTTTCCGGGCCGTATCTGCCAAGCCCTGCCTTGTCTCTTACTGAGCAAG  3780
Sbjct                 6604   ............................................................  6663

Query                 3781   TTTGGCTCAAATTATAGGAGCCCCCATCTTGTGCCCAGCTCATGCTCCAAGTGTGTGTCT  3840
Sbjct                 6664   ............................................................  6723

Query                 3841   ATCCATTTGTACTCAGACTCTTGAGTACCTTGTAAGGAAGGCGGGGCAAGCTGCATCATT  3900
Sbjct                 6724   ............................................................  6783

Query                 3901   CCTGTTTTCCAGGGGAGGCTGGCAGCTCCTCAAGAGGCGAAATGACTGTGGGAGGTCCGG  3960
Sbjct                 6784   ............................................................  6843

Query                 3961   TTACCAGTGAGGAGGCAGAGCGGTGACCCAGACCAGGCCTTCTGGTTCTTGGTCCCGTGC  4020
Sbjct                 6844   ............................................................  6903

Query                 4021   TTCCGTAGTAGCTGGGGTAAAGACACCGTTTCAGGGACTGGTAGAGGTGAGTTCGGCTAA  4080
Sbjct                 6904   ............................................................  6963

Query                 4081   ATTGGGCACCGGGCTAGAAGCCTAAGGGCTCATTTTAGGGGTTACATTAGGTGTTGATTC  4140
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Sbjct  6964  ..................................................  7023

Query  4141  ACCAGCATCAGGTGAATTCAAGCCCTGGCATGTGTCTTGGATGCACCATCAGCTTTGATC  4200
Sbjct  7024  ..................................................  7083

Query  4201  CTGAGTGGTCCTGCGGTTTGTCTGTGCCTGTGGACACACTGTCAGAACTTCAGTGACACC  4260
Sbjct  7084  ..................................................  7143

Query  4261  CCTGGCAGCGGTACAGACAGGTGGTCTGGGAGCAGTCATCTTTTTTGGGCCAGCCACCAG  4320
Sbjct  7144  ..................................................  7203

Query  4321  CCCATCCTACTCCCTCAGGTAGTCCTTCGTCTTTACCTTGTCCTTGTCTGTAAAGTTGTT  4380
Sbjct  7204  ..................................................  7263

Query  4381  TTGGTGGCTGGGGCAGGGGAGCCAGGAGGAGGGAGTGAAGGTTGGGAATAGATAGGACAA  4440
Sbjct  7264  ..................................................  7323

Query  4441  TCTCCTAGCTCTCCTCCAATTGAGAAAACACTCCAATTGGGCTTTGCTTTAAACTTTGTG  4500
Sbjct  7324  ..................................................  7383

Query  4501  TTCTTAAGTGATGTCAAAGCCATTTCCAGCTTAATGTTCTGTGGGTACCTTGGGGGCCAT  4560
Sbjct  7384  ..................................................  7443

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Sbjct  7504  ..................................................  7563

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Sbjct  7564  ..................................................  7623

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Sbjct  7624  ..................................................  7683

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