NRCD Human Full-Length cDNA Clone

Gene Engineering Division
RIKEN BioResource Research Center

RIKEN_Clone_ID : ARh05B02
Vector : pGCAP1

Lot# : 7674_B3Bd

Gene	WDR36	
RefSeq_mRNA	NM_139281.3	6416 bp

● Plasmid DNA purification

Date : 23.03.22 Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C O/N

Date : 23.03.23 Purification : QIAGEN Miniprep kit -> dH_2O 100 ul

● Digestion by restriction enzyme/Concentrarion calibration

Date : 23.03.23

DNA concentration (O.D.): 315 ng/ul

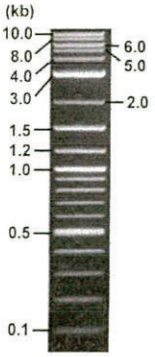
DNA	0.3 ul
Enzyme (BamHI)	1 ul
Buffer H	1 ul
dH_2O	7.7 ul
Total	10 ul

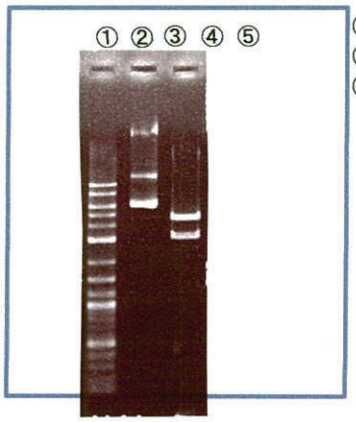
< Size of fragment expected from this clone >

BamHI 3.1kb (vector), 4.6 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 : 2026/06/18

full sequence : ARh05B02hts01.seq

● Adjust plasmid DNA solution to 25 ng/ul

Date : 2026/07/23

DNA (315 ng/ul)	78 ul
10x TE	98 ul
dH_2O	807 ul
Total	983 ul

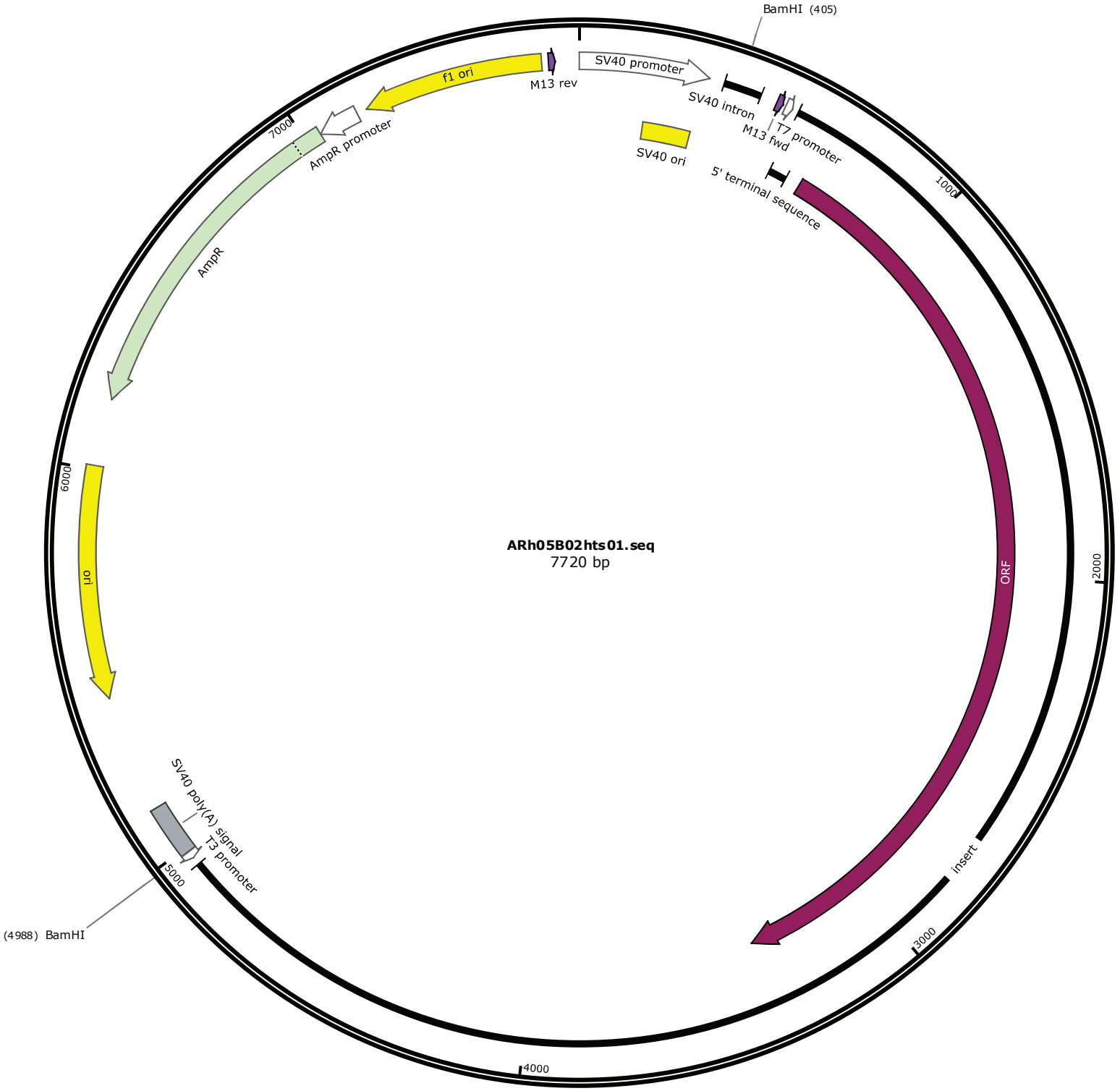
● Shipping

☑ Conc. : 25 ng/μl, Volume : 40 μl

☐ Conc. : __ ng/μl, Volume : __ μl

APPROVED BY : 検 '26.07.23 笹沼

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


BamHI (405)
SV40 promoter
f1 ori
M13 rev
SV40 intron
M13 fwd
T7 promoter
SV40 ori
5' terminal sequence
AmpR promoter
AmpR
ORF
ori
SV40 poly(A) signal
T3 promoter
(4988) BamHI
insert
1000
2000
3000
4000
5000
6000
7000
ARh05B02hts01.seq
7720 bp

BLAST Results

Questions/comments

Blast 2 sequences

Job title: NM_015431:Homo sapiens tripartite motif containing...

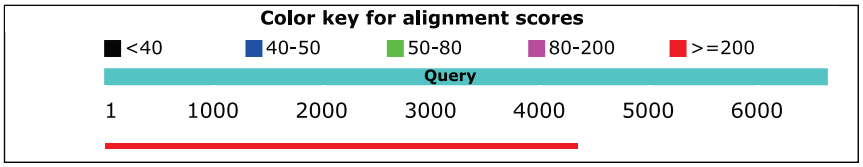
RID 36XD561C114 (Expires on 06-19 12:35 pm)

Query ID	NM_139281.3	**Subject ID**	lcl|Query_4088927
Description	Homo sapiens WD repeat domain 36 (WDR36), mRNA	**Description**	None
Molecule type	nucleic acid		See details
Query Length	6416	**Molecule type**	dna
		Subject Length	7720
		Program	BLASTN 2.17.0+

ARh05B02hts01.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	7853	7853	66%	0.0	99.93%	Query_4088927

Alignments

Sequence ID: Query_4088927 Length: 7720 Number of Matches: 1
Range 1: 571 to 4831

Score	Expect	Identities	Gaps	Strand	Frame
7853 bits(4252)	0.0()	4258/4261(99%)	0/4261(0%)	Plus/Plus	

Features:

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Query                18   GGCAGAGGACTGTTCCACTAGACACGCTGAAGGGACTGGGTACGTGTTTTCCTTCAGGAC  77
Sbjct                571  ............................................................  630

CDS:WD repeat-contai 1                                      M  E  R  A  S  E  R  R  T
Query                78   CAGAGCTGAGAGGAGCTGGGATCGCGGCGGCAATGGAACGGGCCTCAGAAAGGCGCACGG  137
Sbjct                631  ............................................................  690

CDS:WD repeat-contai 10   A  S  A  L  F  A  G  F  R  A  L  G  L  F  S  N  D  I  P  H
Query                138  CCAGCGCGCTTTTTGCGGGGTTCCGGGCCTTGGGACTTTTCAGCAACGACATTCCACACG  197
Sbjct                691  ............................................................  750

CDS:WD repeat-contai 30   V  V  R  F  S  A  L  K  R  R  F  Y  V  T  T  C  V  G  K  S
Query                198  TGGTGCGGTTCAGCGCGCTCAAGCGCCGGTTCTATGTAACAACCTGCGTGGGCAAGAGTT  257
Sbjct                751  ............................................................  810

CDS:WD repeat-contai 50   F  H  T  Y  D  V  Q  K  L  S  L  V  A  V  S  N  S  V  P  Q
Query                258  TCCACACCTATGACGTTCAGAAACTTAGTCTGGTTGCAGTAAGTAATTCTGTTCCACAGG  317
Sbjct                811  ............................................................  870

CDS:WD repeat-contai 70   D  I  C  C  M  A  A  D  G  R  L  V  F  A  A  Y  G  N  V  F
Query                318  ATATCTGCTGTATGGCAGCTGATGGCAGATTAGTCTTTGCTGCTTATGGAAATGTTTTCT  377
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Sbjct                 871  ..........................................................  930

CDS:WD repeat-contai   90  S  A  F  A  R  N  K  E  I  V  H  T  F  K  G  H  K  A  E  I
Query                 378  CTGCATTTGCCCGTAATAAAGAGATAGTACATACCTTTAAGGGTCATAAGGCAGAAATCC  437
Sbjct                 931  ..........................................................  990

CDS:WD repeat-contai  110  H  F  L  Q  P  F  G  D  H  I  I  S  V  D  T  D  G  I  L  I
Query                 438  ATTTCTTGCAACCCTTTGGAGACCACATTATCTCTGTTGATACTGATGGCATTCTTATTA  497
Sbjct                 991  ..........................................................  1050

CDS:WD repeat-contai  130  I  W  H  I  Y  S  E  E  E  Y  L  Q  L  T  F  D  K  S  V  F
Query                 498  TTTGGCACATATATTCAGAAGAAGAATACCTGCAGTTGACTTTTGATAAATCAGTATTTA  557
Sbjct                1051  ..........................................................  1110

CDS:WD repeat-contai  150  K  I  S  A  I  L  H  P  S  T  Y  L  N  K  I  L  L  G  S  E
Query                 558  AAATTTCTGCAATTTTGCATCCAAGTACCTACTTGAATAAAATACTTCTGGGCAGTGAAC  617
Sbjct                1111  ..........................................................  1170

CDS:WD repeat-contai  170  Q  G  S  L  Q  L  W  N  V  K  S  N  K  L  L  Y  T  F  P  G
Query                 618  AAGGAAGCCTGCAGTTGTGGAATGTAAAATCCAATAAACTTCTATATACATTTCCAGGAT  677
Sbjct                1171  ..........................................................  1230

CDS:WD repeat-contai  190  W  K  V  G  V  T  A  L  Q  Q  A  P  A  V  D  V  V  A  I  G
Query                 678  GGAAAGTTGGAGTGACAGCTCTTCAGCAGGCACCAGCCGTGGATGTTGTTGCTATTGGTC  737
Sbjct                1231  .....................................................G....  1290

CDS:WD repeat-contai  210  L  M  S  G  Q  V  I  I  H  N  I  K  F  N  E  T  L  M  K  F
Query                 738  TTATGTCAGGTCAAGTTATCATTCACAACATTAAATTTAATGAAACATTAATGAAGTTTC  797
Sbjct                1291  ..........................................................  1350

CDS:WD repeat-contai  230  R  Q  D  W  G  P  I  T  S  I  S  F  R  T  D  G  H  P  V  M
Query                 798  GTCAAGACTGGGGACCCATTACTTCAATTTCATTTCGCACAGATGGTCATCCAGTAATGG  857
Sbjct                1351  ..........................................................  1410

CDS:WD repeat-contai  250  A  A  G  S  P  C  G  H  I  G  L  W  D  L  E  D  K  K  L  I
Query                 858  CAGCTGGAAGCCCATGTGGCCATATTGGACTCTGGGATCTAGAAGACAAAAAATTAATCA  917
Sbjct                1411  ..........................................................  1470

CDS:WD repeat-contai  270  N  Q  M  R  N  A  H  S  T  A  I  A  G  L  T  F  L  H  R  E
Query                 918  ACCAAATGAGAAATGCACACTCTACAGCAATTGCCGGACTGACATTTCTCCATAGAGAGC  977
Sbjct                1471  ..........................................................  1530

CDS:WD repeat-contai  290  P  L  L  V  T  N  G  A  D  N  A  L  R  I  W  I  F  D  G  P
Query                 978  CACTTCTTGTCACAAATGGCGCTGACAATGCTCTTAGGATATGGATATTTGATGGTCCTA  1037
Sbjct                1531  ..........................................................  1590

CDS:WD repeat-contai  310  T  G  E  G  R  L  L  R  F  R  M  G  H  S  A  P  L  T  N  I
Query                1038  CAGGTGAAGGCCGACTTTTGAGATTCAGAATGGGTCATAGTGCTCCTCTTACCAATATCA  1097
Sbjct                1591  ..........................................................  1650

CDS:WD repeat-contai  330  R  Y  Y  G  Q  N  G  Q  Q  I  L  S  A  S  Q  D  G  T  L  Q
Query                1098  GATATTATGGACAGAATGGACAGCAGATTCTAAGTGCAAGTCAAGATGGAACTCTTCAGT  1157
Sbjct                1651  ..........................................................  1710

CDS:WD repeat-contai  350  S  F  S  T  V  H  E  K  F  N  K  S  L  G  H  G  L  I  N  K
Query                1158  CATTTTCCACGGTACATGAAAAATTCAATAAGAGCTTGGGACATGGATTAATAAATAAAA  1217
Sbjct                1711  ..........................................................  1770

CDS:WD repeat-contai  370  K  R  V  K  R  K  G  L  Q  N  T  M  S  V  R  L  P  P  I  T


Query                1218  AGAGAGTTAAACGTAAAGGACTTCAGAATACCATGTCAGTGAGACTTCCACCCATCACAA  1277
Sbjct                1771  ..........................................................  1830

CDS:WD repeat-contai  390  K  F  A  A  E  E  A  R  E  S  D  W  D  G  I  I  A  C  H  Q
Query                1278  AGTTTGCAGCAGAGGAAGCTCGTGAAAGTGACTGGGATGGTATCATTGCTTGCCATCAAG  1337
Sbjct                1831  ..........................................................  1890

CDS:WD repeat-contai  410  G  K  L  S  C  S  T  W  N  Y  Q  K  S  T  I  G  A  Y  F  L
Query                1338  GTAAGCTATCTTGCTCAACCTGGAATTATCAGAAATCTACAATAGGCGCTTACTTTCTCA  1397
Sbjct                1891  ..........................................................  1950

CDS:WD repeat-contai  430  K  P  K  E  L  K  K  D  D  I  T  A  T  A  V  D  I  T  S  C
Query                1398  AGCCAAAAGAGTTGAAGAAAGATGACATAACTGCAACAGCAGTGGATATAACTTCTTGTG  1457
Sbjct                1951  ..........................................................  2010

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Query                1458  GAAACTTTGCTGTAATTGGCCTCTCATCAGGAACTGTAGATGTATATAACATGCAGTCTG  1517
Sbjct                2011  ..........................................................  2070

CDS:WD repeat-contai  470  G  I  H  R  G  S  F  G  K  D  Q  A  H  K  G  S  V  R  G  V
Query                1518  GCATACATCGAGGAAGTTTTGGCAAGGATCAAGCTCACAAGGGATCTGTTAGAGGTGTCG  1577
Sbjct                2071  ..........................................................  2130

CDS:WD repeat-contai  490  A  V  D  G  L  N  Q  L  T  V  T  T  G  S  E  G  L  L  K  F
Query                1578  CAGTGGATGGATTAAACCAGTTGACAGTTACAACTGGTAGTGAAGGATTACTCAAATTCT  1637
Sbjct                2131  ..........................................................  2190

CDS:WD repeat-contai  510  W  N  F  K  N  K  I  L  I  H  S  V  S  L  S  S  S  P  N  I
Query                1638  GGAACTTTAAAAACAAAATTTTAATCCATTCTGTGAGCCTCAGTTCATCTCCAAATATCA  1697
Sbjct                2191  ..........................................................  2250

CDS:WD repeat-contai  530  M  L  L  H  R  D  S  G  I  L  G  L  A  L  D  D  F  S  I  S
Query                1698  TGTTGCTACATAGGGACAGTGGCATTCTGGGACTCGCCTTGGATGACTTCTCCATTAGTG  1757
Sbjct                2251  ..........................................................  2310

CDS:WD repeat-contai  550  V  L  D  I  E  T  R  K  I  V  R  E  F  S  G  H  Q  G  Q  I
Query                1758  TTCTGGACATAGAAACTAGGAAGATTGTCAGAGAGTTTTCTGGACACCAAGGCCAAATAA  1817
Sbjct                2311  ..........................................................  2370

CDS:WD repeat-contai  570  N  D  M  A  F  S  P  D  G  R  W  L  I  S  A  A  M  D  C  S
Query                1818  ATGACATGGCTTTTAGTCCTGATGGTCGTTGGTTAATAAGTGCTGCGATGGATTGCTCTA  1877
Sbjct                2371  ..........................................................  2430

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Query                1878  TTAGGACTTGGGACCTTCCTTCTGGGTGCCTTATAGACTGCTTTTTGTTGGACTCGGCTC  1937
Sbjct                2431  ..........................................................  2490

CDS:WD repeat-contai  610  P  L  N  V  S  M  S  P  T  G  D  F  L  A  T  S  H  V  D  H
Query                1938  CTCTCAATGTTTCTATGTCTCCTACTGGAGACTTTCTGGCAACTTCCCATGTGGACCACC  1997
Sbjct                2491  ..........................................................  2550

CDS:WD repeat-contai  630  L  G  I  Y  L  W  S  N  I  S  L  Y  S  V  V  S  L  R  P  L
Query                1998  TTGGAATTTATCTATGGTCCAATATTTCCCTGTATTCAGTTGTTTCATTACGGCCACTTC  2057
Sbjct                2551  ..........................................................  2610

CDS:WD repeat-contai  650  P  A  D  Y  V  P  S  I  V  M  L  P  G  T  C  Q  T  Q  D  V
Query                2058  CTGCAGATTATGTCCCTTCAATAGTCATGCTTCCTGGTACTTGTCAAACCCAAGATGTAG  2117
Sbjct                2611  ..........................................................  2670
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731 A>G (I208V)

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CDS:WD repeat-contai  670  E  V  S  E  E  T  V  E  P  S  D  E  L  I  E  Y  D  S  P  E
Query                2118 AAGTATCAGAAGAAACAGTAGAACCAAGTGATGAATTGATAGAATATGATTCGCCAGAAC 2177
Sbjct                2671 ....T.......................................................... 2730

CDS:WD repeat-contai  690  Q  L  N  E  Q  L  V  T  L  S  L  L  P  E  S  R  W  K  N  L
Query                2178 AGTTGAATGAGCAATTGGTGACTCTTTCACTTCTTCCTGAATCACGATGGAAAAACCTTC 2237
Sbjct                2731 .......................................................... 2790

CDS:WD repeat-contai  710  L  N  L  D  V  I  K  K  K  N  K  P  K  E  P  P  K  V  P  K
Query                2238 TTAACCTTGATGTTATTAAGAAAAAGAATAAACCAAAGGAACCACCCAAAGTACCCAAAT 2297
Sbjct                2791 .......................................................... 2850

CDS:WD repeat-contai  730  S  A  P  F  F  I  P  T  I  P  G  L  V  P  R  Y  A  A  P  E
Query                2298 CAGCACCATTTTTCATTCCAACAATTCCTGGCCTTGTACCCAGATATGCTGCACCTGAAC 2357
Sbjct                2851 .......................................................... 2910

CDS:WD repeat-contai  750  Q  N  N  D  P  Q  Q  S  K  V  V  N  L  G  V  L  A  Q  K  S
Query                2358 AAAATAATGATCCCCAGCAGTCTAAAGTGGTAAATCTTGGAGTTTTGGCTCAAAAATCAG 2417
Sbjct                2911 .......................................................... 2970

CDS:WD repeat-contai  770  D  F  C  L  K  L  E  E  G  L  V  N  N  K  Y  D  T  A  L  N
Query                2418 ATTTCTGCTTGAAACTTGAAGAAGGACTGGTAAATAATAAGTATGACACTGCTCTCAACC 2477
Sbjct                2971 .......................................................... 3030

CDS:WD repeat-contai  790  L  L  K  E  S  G  P  S  G  I  E  T  E  L  R  S  L  S  P  D
Query                2478 TTCTGAAAGAATCAGGCCCATCAGGAATTGAAACAGAGCTGCGAAGCTTGTCTCCTGATT 2537
Sbjct                3031 .......................................................... 3090

CDS:WD repeat-contai  810  C  G  G  S  I  E  V  M  Q  S  F  L  K  M  I  G  M  M  L  D
Query                2538 GTGGTGGGTCCATAGAAGTTATGCAGAGCTTCTTGAAAATGATTGGGATGATGCTGGACA 2597
Sbjct                3091 .......................................................... 3150

CDS:WD repeat-contai  830  R  K  R  D  F  E  L  A  Q  A  Y  L  A  L  F  L  K  L  H  L
Query                2598 GAAAGCGTGATTTTGAGTTAGCCCAGGCATACCTTGCATTGTTTCTAAAGTTACACCTTA 2657
Sbjct                3151 .......................................................... 3210

CDS:WD repeat-contai  850  K  M  L  P  S  E  P  V  L  L  E  E  I  T  N  L  S  S  Q  V
Query                2658 AAATGCTTCCTTCAGAGCCAGTACTCCTAGAAGAAATAACAAATTTGTCATCCCAGGTGG 2717
Sbjct                3211 .......................................................... 3270

CDS:WD repeat-contai  870  F  E  N  W  T  H  L  Q  S  L  F  N  Q  S  M  C  I  L  N  Y
Query                2718 AAGAAAACTGGACCCATTTGCAATCACTCTTCAATCAAAGCATGTGTATTTTAAATTATC 2777
Sbjct                3271 .......................................................... 3330

CDS:WD repeat-contai  890  L  K  S  A  L  L
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Sbjct                3331 .......................................................... 3390

Query                2838 GGTTCAATTGAACTCATTTCTTATTTTCCAAGTGTCAATGTGAAAAGAAAATAAATGCTA 2897
Sbjct                3391 .......................................................... 3450

Query                2898 GCACTACTGACTAGTCAGTATATCTCCACTTTAAATGCTAAATACTTTCTTGAAATAAAA 2957
Sbjct                3451 .......................................................... 3510

Query                2958 TCGCACCTCCCGGCCAGGCATGATGGATAATGCCTGTAATTCCAGCACTTTCAGAGGCCA 3017
Sbjct                3511 .......................................................... 3570

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Sbjct                3571 .......................................................... 3630
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2122 A>T

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Query                3078 GATCCCATCTCTACAAAAAGTTaaaaaaaTAAATTACACCTGCCTTTTGTTTTGAAGACT 3137
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Query                3138 TAAAGAATCTGCTCAAATGATTTATTTTCTGAGTCTCTTCACATTAACTTTTATATGATT 3197
Sbjct                3691 .......................................................... 3750

Query                3198 TTTAAAAAATTATTACCTGCTTATATTTTTTGAGTATCTGTTTCATATAAAGAGATGCTG 3257
Sbjct                3751 .......................................................... 3810

Query                3258 CATGTTCACTGTGAAGTATTGCTGAATTAAATTGAAAATGTCAGATAAAACTGATACATG 3317
Sbjct                3811 .......................................................... 3870

Query                3318 ATGTAGTTATAAAAATGCTGTTATGAAGAAAAAAGGAATGCTTTTTTCCTCGGTGGCCTT 3377
Sbjct                3871 .......................................................... 3930

Query                3378 TGATAAAAATATGAATGATTGACTCTCAGAGTTGGAGGATAAACTAATCATCTTCTAGCA 3437
Sbjct                3931 .......................................................... 3990

Query                3438 CAGCCCTGTTGTGTTGCAGGAGAGGAATCAGGCTAAAGTCTGCTGGTATTTCAGTGACAG 3497
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Query                3498 ATTAAAACTTTCTAACAGTGGCCTAGTGCTTTCTCCATTGTAATGTACTGAAAGGAAGTT 3557
Sbjct                4051 .......................................................... 4110

Query                3558 GTTCATGGATCAGAAATGTGGGAGGCCCTTCCTTGCCCAAGGCAAGTCGCTGTAGATGGT 3617
Sbjct                4111 .......................................................... 4170

Query                3618 TAAACTGATACCAAGGATAGGTAAGGGAAATTCCAAATTCCATTGGAAGATGGCCTTTTA 3677
Sbjct                4171 .......................................................... 4230

Query                3678 CTGACACTGCAGACATGTAGATAACAATAGTTTAATGTCCTCTGAAAAGGTAAAAATTCC 3737
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Query                3738 ATAAATCCTTGCAAACAATTTTTAGCAATATTGTTTATTGCTACCACAGCCAAGAATGGG 3797
Sbjct                4291 .......................................................... 4350

Query                3798 TATTTCAAAGCCAGGGttttttttattttgttttgttttgttttttttttttttttttttG 3857
Sbjct                4351 ..........................................G............... 4410

Query                3858 GCTACACTTTTTTgggggggACCTTTTAATTTGGGAAGAAAATGCTGAGTATACTTTTCT 3917
Sbjct                4411 .......................................................... 4470

Query                3918 TTCACAACCATTGCAAACCCAGGTAGCCCTGGAGttttctttttttctcatcatcattgt 3977
Sbjct                4471 .......................................................... 4530

Query                3978 tttgtttttttttATGGTTCAAGACTTTTGCAATACATGAATTAAAAATAAGCAGTTCTTT 4037
Sbjct                4531 .......................................................... 4590

Query                4038 AAAGCATAGCGCTCTAAAAACTATTCTTAGTTTATACCCTCAAAAGTTGGGTCTTTCATG 4097
Sbjct                4591 .......................................................... 4650

Query                4098 AAACACAGTGGTTTGAATATGAACACCAGTAGCATTCTCGTTCGTTGTTAGGGTAAGAGA 4157
Sbjct                4651 .......................................................... 4710

Query                4158 GTTTTGTAGAATGATCTCCAAAAGAAGCAGTCCTCAAAAGGCATTTACCAGTGATATCTT 4217
Sbjct                4711 .......................................................... 4770

Query                4218 TTAATATTCATGTTTTTATTTAATGATGTAAGATAGAATTAATAAACTACTAAGGAAATA 4277
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Sbjct  4771 ..........................................................  4830

Query  4278  A  4278
Sbjct  4831  .  4831
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