

RIKEN Clone ID : IRAK032A07

Lot#: 7566_B4Hs

Vector : pBluescriptR

Gene	EDIL3	
Accession No.	BC030828.1	2728 bp
	<i>CDS</i>	1443 bp

● **Plasmid DNA purification**

Date : 2024/08/29

Culture : LB (100 ug/ml Ampicillin) 5 ml -> at 37 deg C over night

Date : 2024/08/30

Purification : QIAGEN Miniprep kit -> dH₂O 100 ul

● **Digestion by restriction enzyme/Concentration calibration**

Date : 2024/08/30

DNA concentration (O.D.): 222 ng/ul

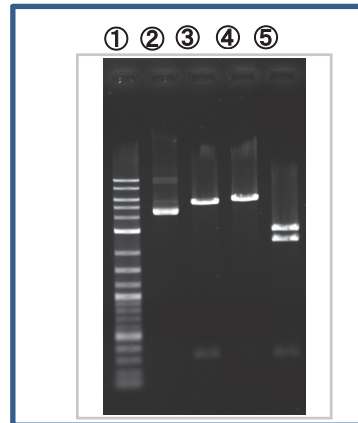
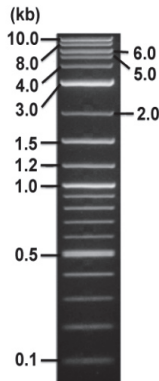
< Size of fragment expected from this clone >

DNA	0.45	ul
Enzyme (EcoRI + BamHI)	0.5 + 0.5	ul
Buffer H	1	ul
dH ₂ O	7.55	ul
Total	10	ul

EcoRI	5.2 , 0.3	kb	
BamHI	5.5	kb	
EcoRI + BamHI	2.8kb (Vector)	2.4, 0.3	kb

Electrophoresis : 1% agarose gel, 1x TAE Buffer

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



- ①:Marker
- ②:uncut
- ③:EcoRI
- ④:BamHI
- ⑤:EcoRI + BamHI

● **Adjust plasmid DNA solution to 25 ng/ul**

Date : 2024/09/17

DNA (<u>222</u> ng/ul)	84	ul
10x TE	75	ul
dH ₂ O	587	ul
Total	746	ul

● **Confirmation of the sequence**

Date : 2024/09/11

Primer A	-
Primer B	-
Primer C	IRAK032A07hts01.seq
List of Sequencing Primers	-

● **Shipping**

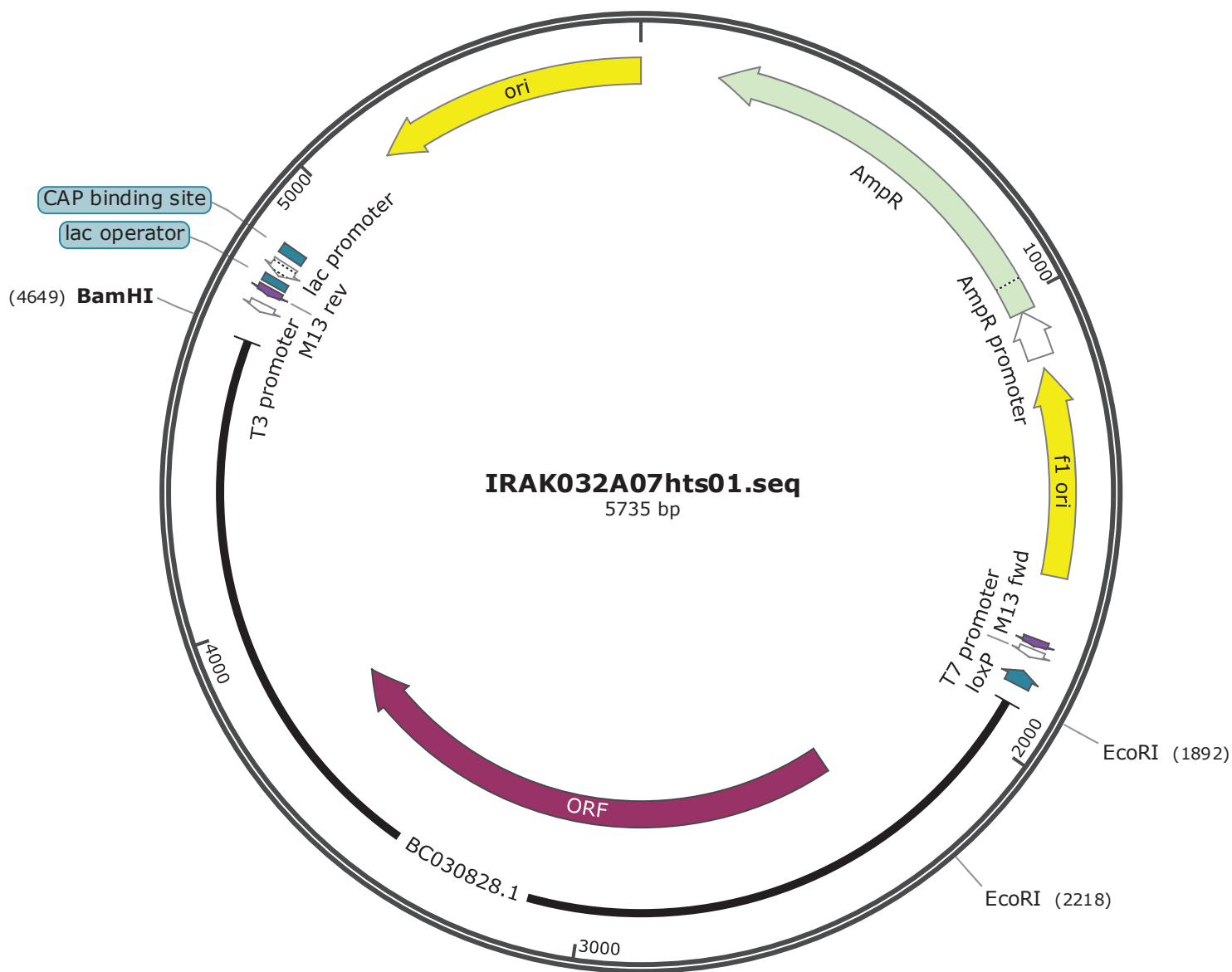
Conc. : 25 ng/ul, Volume : 40 ul

Conc. : ng/ul, Volume : ul

APPROVED BY :

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





BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: BC030828:Homo sapiens EGF-like repeats and...

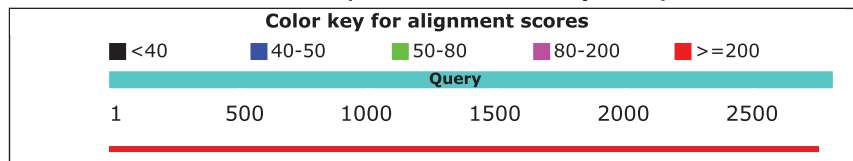
RID [E2C5VBPV114](#) (Expires on 09-12 13:55 pm)
Query ID [BC030828.1](#)
Description Homo sapiens EGF-like repeats and discoidin I-like domains 3, mRNA (cDNA clone MGC:26287 IMAGE:4791845), complete cds
Molecule type nucleic acid
Query Length 2728

Subject ID Icl|Query_1468879
Description None
[See details](#)
Molecule type dna
Subject Length 5735
Program BLASTN 2.16.0+

IRAK032A07hts01.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	5038	5038	100%	0.0	100.00%	Query_1468879

[Alignments](#)

Sequence ID: Query_1468879 Length: 5735 Number of Matches: 1
 Range 1: 1909 to 4636

Score	Expect	Identities	Gaps	Strand	Frame
5038 bits(2728)	0.0()	2728/2728(100%)	0/2728(0%)	Plus/Plus	

Features:

Query	1	AGAAGCCCGCAGCCGCGCGGAGAACAGCGACAGCCGAGCGCCGGTCCGCCTGTCT	60
Sbjct	1909	AGAAGCCCGCAGCCGCGCGGAGAACAGCGACAGCCGAGCGCCGGTCCGCCTGTCT	1968
Query	61	GCCGGTGGGTCTGCCTgcccgcgcagcagaccggggcggcgggagcccgccgcccgc	120
Sbjct	1969	GCCGGTGGGTCTGCCTGCCGCGCAGCAGACCCGGGGCGCCGCGGGAGCCCGGCCCG	2028
Query	121	ccgcccgcgcccctgcccgggaccaccgcAGCGGAGGGCTGAGCCCGCCGGCGGCTCCC	180
Sbjct	2029	CCCGCCGCGCCTTGCCGGGACCCACCCGAGCGGAGGGCTGAGCCCGCCGGCGGCTCCC	2088
Query	181	CGGAGCTACCCACCTCCGCGCGCCGGAGCGCAGGCAAAAGGGGAGGAAAGGCTCCTCTC	240
Sbjct	2089	CGGAGCTACCCACCTCCGCGCGCCGGAGCGCAGGCAAAAGGGGAGGAAAGGCTCCTCTC	2148
Query	241	TTTAGTCACCACTCTCGCCCTCCAAGAATTTGTTTAAACAAGCGCTGAGGAAAGAGAA	300
Sbjct	2149	TTTAGTCACCACTCTCGCCCTCCAAGAATTTGTTTAAACAAGCGCTGAGGAAAGAGAA	2208
Query	301	CGTCTTCTTGAATTTAGTAGGGGCGGAGTGTGTGCTGCCCTGCCACCTCGG	360
Sbjct	2209	CGTCTTCTTGAATTTAGTAGGGGCGGAGTGTGTGCTGCCCTGCCACCTCGG	2268

Query	361	CTACACTGCCCTCCGCGACGACCCCTGACCAGCCGGGGTACGTCGGGAGACGGGATCA	420
Sbjct	2269	CTACACTGCCCTCCGCGACGACCCCTGACCAGCCGGGGTACGTCGGGAGACGGGATCA	2328
CDS:EGF-like repeats	1	M K R S V A V W L L V G L S L S V P Q F	
Query	421	TGAAGCGCTCGGTAGCCGCTGGCTCTGGTCGGGCTCAGCCTCAGTGTCCCCAGTTCC	480
Sbjct	2329	TGAAGCGCTCGGTAGCCGCTGGCTCTGGTCGGGCTCAGCCTCAGTGTCCCCAGTTCC	2388
CDS:EGF-like repeats	21	G K G D I C D P N P C E N G G I C L P G	
Query	481	GCAAAGGTGATATTTGTATCCCAATCCATGTGAAAATGGAGGTATCTGTTGCCAGGAT	540
Sbjct	2389	GCAAAGGTGATATTTGTATCCCAATCCATGTGAAAATGGAGGTATCTGTTGCCAGGAT	2448
CDS:EGF-like repeats	41	L A D G S F S C E C P D G F T D P N C S	
Query	541	TGGCTGATGGTTCCCTTTCTGTGAGTGTCCAGATGGCTTACAGACCCCAACTGTTCTA	600
Sbjct	2449	TGGCTGATGGTTCCCTTTCTGTGAGTGTCCAGATGGCTTACAGACCCCAACTGTTCTA	2508
CDS:EGF-like repeats	61	S V V E V A S D E E E P T S A G P C T P	
Query	601	GTGTTGTGGAGGTTGCATCAGATGAAGAAGAACCACTTACAGAGTCCCTGCACTCCTA	660
Sbjct	2509	GTGTTGTGGAGGTTGCATCAGATGAAGAAGAACCACTTACAGAGTCCCTGCACTCCTA	2568
CDS:EGF-like repeats	81	N P C H N G G T C E I S E A Y R G D T F	
Query	661	ATCCATGCCATAATGGAGGAACCTGTGAAAATAGTGAAGCATAACCGAGGGGATACATTCA	720
Sbjct	2569	ATCCATGCCATAATGGAGGAACCTGTGAAAATAGTGAAGCATAACCGAGGGGATACATTCA	2628
CDS:EGF-like repeats	101	I G Y V C K C P R G F N G I H C Q H N I	
Query	721	TAGGCTATGTTTGTAAATGTCCCGAGGATTTAATGGGATTCAGTGTACGACACAACATAA	780
Sbjct	2629	TAGGCTATGTTTGTAAATGTCCCGAGGATTTAATGGGATTCAGTGTACGACACAACATAA	2688
CDS:EGF-like repeats	121	N E C E V E P C K N G G I C T D L V A N	
Query	781	ATGAATGCGAAGTTGAGCCTTGCAAAAATGGTGAATATGTACAGATCTTGTGCTAACT	840
Sbjct	2689	ATGAATGCGAAGTTGAGCCTTGCAAAAATGGTGAATATGTACAGATCTTGTGCTAACT	2748
CDS:EGF-like repeats	141	Y S C E C P G E F M G R N C Q Y K C S G	
Query	841	ATTCCTGTGAGTGGCCAGGCCGAAATTTATGGGAAGAAATGTCAATACAAATGCTCAGGCC	900
Sbjct	2749	ATTCCTGTGAGTGGCCAGGCCGAAATTTATGGGAAGAAATGTCAATACAAATGCTCAGGCC	2808
CDS:EGF-like repeats	161	P L G I E G G I I S N Q Q I T A S S T H	
Query	901	CACTGGGAATTAAGGTGGAATATATCAAACAGCAAAATCACAGCTTCTCTACTCACC	960
Sbjct	2809	CACTGGGAATTAAGGTGGAATATATCAAACAGCAAAATCACAGCTTCTCTACTCACC	2868
CDS:EGF-like repeats	181	R A L F G L Q K W Y P Y Y A R L N K K G	
Query	961	GAGCTCTTTTGGACTCCAAAAATGGTATCCCTACTATGCAGCTTAAATAAGAAGGGGC	1020
Sbjct	2869	GAGCTCTTTTGGACTCCAAAAATGGTATCCCTACTATGCAGCTTAAATAAGAAGGGGC	2928
CDS:EGF-like repeats	201	L I N A W T A A E N D R W P W I Q I N L	
Query	1021	TTATAAATGCGTGGACAGCTGCAGAAAATGACAGATGGCCGTGGATTCAGATAAATTTGC	1080
Sbjct	2929	TTATAAATGCGTGGACAGCTGCAGAAAATGACAGATGGCCGTGGATTCAGATAAATTTGC	2988
CDS:EGF-like repeats	221	Q R K M R V T G V I T Q G A K R I G S P	
Query	1081	AAAGGAAAAATGAGAGTTACTGGTGTGATACCCAAGGAGCCAAGAGGATTTGGAAGCCAG	1140
Sbjct	2989	AAAGGAAAAATGAGAGTTACTGGTGTGATACCCAAGGAGCCAAGAGGATTTGGAAGCCAG	3048
CDS:EGF-like repeats	241	E Y I K S Y K I A Y S N D G K T W A M Y	
Query	1141	AGTATATAAAAATCCTACAAAAATGCCTACAGTAATGATGAAAGACTTTGGGCAATGTACA	1200
Sbjct	3049	AGTATATAAAAATCCTACAAAAATGCCTACAGTAATGATGAAAGACTTTGGGCAATGTACA	3108
CDS:EGF-like repeats	261	K V K G T N E D M V F R G N I D N N T P	
Query	1201	AAGTGAAAGGCACCAATGAAGACATGGTGTTCGTGGAAACATTGATAACACACTCCAT	1260
Sbjct	3109	AAGTGAAAGGCACCAATGAAGACATGGTGTTCGTGGAAACATTGATAACACACTCCAT	3168
CDS:EGF-like repeats	281	Y A N S F T P P I K A Q Y V R L Y P Q V	
Query	1261	ATGCTAACTCTTTACACCCCCCAATAAAGCTCAGTATGTAAGACTCTATCCCAAGTTT	1320
Sbjct	3169	ATGCTAACTCTTTACACCCCCCAATAAAGCTCAGTATGTAAGACTCTATCCCAAGTTT	3228
CDS:EGF-like repeats	301	C R R H C T L R M E L L G C E L S G C S	
Query	1321	GTCGAAGACATGCACTTTGCGAATGGAACCTTCTGGCTGTGAACTGTGGGTTGTTCTG	1380
Sbjct	3229	GTCGAAGACATGCACTTTGCGAATGGAACCTTCTGGCTGTGAACTGTGGGTTGTTCTG	3288
CDS:EGF-like repeats	321	E P L G M K S G H I Q D Y Q I T A S S I	
Query	1381	AGCCTCTGGGTATGAAATCAGGACATATACAAGACTATCAGATCACTGCCTCCAGCATCT	1440
Sbjct	3289	AGCCTCTGGGTATGAAATCAGGACATATACAAGACTATCAGATCACTGCCTCCAGCATCT	3348
CDS:EGF-like repeats	341	F R T L N M D M F T W E P R K A R L D K	
Query	1441	TCAGAACGCTCAACATGGACATGTTCACTTGGGAACCAAGGAAAGCTCGGCTGGACAAGC	1500
Sbjct	3349	TCAGAACGCTCAACATGGACATGTTCACTTGGGAACCAAGGAAAGCTCGGCTGGACAAGC	3408
CDS:EGF-like repeats	361	Q G K V N A W T S G H N D Q S Q W L Q V	
Query	1501	AAGGCAAGTGAATGCCTGGACCTCTGGCCACAATGACCAGTCAATGGTTACAGGTGG	1560
Sbjct	3409	AAGGCAAGTGAATGCCTGGACCTCTGGCCACAATGACCAGTCAATGGTTACAGGTGG	3468
CDS:EGF-like repeats	381	D L L V P T K V T G I I T Q G A K D F G	
Query	1561	ATCTTCTTGTTCCAACCAAGTGACTGGCATATTACACAAGGAGCTAAAGATTTTGGTC	1620
Sbjct	3469	ATCTTCTTGTTCCAACCAAGTGACTGGCATATTACACAAGGAGCTAAAGATTTTGGTC	3528
CDS:EGF-like repeats	401	H V Q F V G S Y K L A Y S N D G E H W T	
Query	1621	ATGTACAGTTTGTGGCTCCTACAAACTGGCTTACAGCAATGATGGAGAACACTGGACTG	1680
Sbjct	3529	ATGTACAGTTTGTGGCTCCTACAAACTGGCTTACAGCAATGATGGAGAACACTGGACTG	3588
CDS:EGF-like repeats	421	V Y Q D E K Q R K D K V F Q G N F D N D	
Query	1681	TATACCAGGATGAAAAGCAAGAAAAGATAAGGTTTCCAGGGAAATTTGACAATGACA	1740
Sbjct	3589	TATACCAGGATGAAAAGCAAGAAAAGATAAGGTTTCCAGGGAAATTTGACAATGACA	3648
CDS:EGF-like repeats	441	T H R K N V I D P P I Y A R H I R I L P	
Query	1741	CTCACAGAAAAATGTCATCGACCTCCCACTATGCAGCAGACATAAAGATCCTTCCTT	1800

Sbjct	3649	CTCACAGAAAAATGTCATCGACCCCTCCCATCTATGCACGACACATAAGAATCCTTCCTT	3708
CDS:EGF-like repeats	461	W S W Y G R I T L R S E L L G C T E E E	
Query	1801	GGTCTGGTACGGGAGGATCACATTGCGGTGAGAGCTGCTGGGCTGCACAGAGGAGGAAT	1860
Sbjct	3709	GGTCTGGTACGGGAGGATCACATTGCGGTGAGAGCTGCTGGGCTGCACAGAGGAGGAAT	3768
Query	1861	GAGGGGAGGCTACATTTTACAACCCCTTCCCTATTTCCCTAAAAGTATCTCCATGGAAT	1920
Sbjct	3769	GAGGGGAGGCTACATTTTACAACCCCTTCCCTATTTCCCTAAAAGTATCTCCATGGAAT	3828
Query	1921	GAACGTGCAAAATCTGTAGGAACTGAATGGTTTTTTTTTTTTTTCATGAAAAAGTGCT	1980
Sbjct	3829	GAACGTGCAAAATCTGTAGGAACTGAATGGTTTTTTTTTTTTTTCATGAAAAAGTGCT	3888
Query	1981	CAAAATATGGTAGGCAACTAACGGTGTAAAAAGGGGCTAAGCCTGCCTTTTCAATGA	2040
Sbjct	3889	CAAAATATGGTAGGCAACTAACGGTGTAAAAAGGGGCTAAGCCTGCCTTTTCAATGA	3948
Query	2041	TTTAATTTGATTTTATTTTATCCGTCAAACTCTTAAGTAACAACACATTAAGTGTGAAT	2100
Sbjct	3949	TTTAATTTGATTTTATTTTATCCGTCAAACTCTTAAGTAACAACACATTAAGTGTGAAT	4008
Query	2101	TACTTTTCTCTCATTGTTTCTCGAATTATTCGCATTGGTAGAAATATATTAGGGAAAGAA	2160
Sbjct	4009	TACTTTTCTCTCATTGTTTCTCGAATTATTCGCATTGGTAGAAATATATTAGGGAAAGAA	4068
Query	2161	AGTAGCCTTCTTTTTATAGCAAGAGTAAAAAGTCTCAAAGTCATCAAATAAGAGCAAGA	2220
Sbjct	4069	AGTAGCCTTCTTTTTATAGCAAGAGTAAAAAGTCTCAAAGTCATCAAATAAGAGCAAGA	4128
Query	2221	GTTGATAGAGCTTTTACAATCAATACTCACCTAATCTGATAAAAAGGAATACTGCAATGT	2280
Sbjct	4129	GTTGATAGAGCTTTTACAATCAATACTCACCTAATCTGATAAAAAGGAATACTGCAATGT	4188
Query	2281	TAGCAATAAGTTTTTTTCTTCTGTAATGACTCTACGTTATCCTGTTCCCTGTGCCTACC	2340
Sbjct	4189	TAGCAATAAGTTTTTTTCTTCTGTAATGACTCTACGTTATCCTGTTCCCTGTGCCTACC	4248
Query	2341	AAACACTGTCAATGTTTATTACAAAAATTTAAAGAAGAAATGTAACTGCAGTACTGAT	2400
Sbjct	4249	AAACACTGTCAATGTTTATTACAAAAATTTAAAGAAGAAATGTAACTGCAGTACTGAT	4308
Query	2401	ATTATAATTCTCATTTTACTTTTCTAATTAAGAGATTATGTACTTCTTTTTCT	2460
Sbjct	4309	ATTATAATTCTCATTTTACTTTTCTAATTAAGAGATTATGTACTTCTTTTTCT	4368
Query	2461	TTTAGTTCTATTCTACATTCTAATATTGTATATTACCTGAATAATCAAATTTTTCTA	2520
Sbjct	4369	TTTAGTTCTATTCTACATTCTAATATTGTATATTACCTGAATAATCAAATTTTTCTA	4428
Query	2521	ATTGAATTCCTATTAGTTGACTAAAAGAAGTGCATGTTTACTCATATATGTAGAACAT	2580
Sbjct	4429	ATTGAATTCCTATTAGTTGACTAAAAGAAGTGCATGTTTACTCATATATGTAGAACAT	4488
Query	2581	GACTGCCTATCAGTAGATTGATCTGTATTTAATATTCGTTAATAAATCTGCAGTTTTAT	2640
Sbjct	4489	GACTGCCTATCAGTAGATTGATCTGTATTTAATATTCGTTAATAAATCTGCAGTTTTAT	4548
Query	2641	TTTTGAAGGAAGCCATAACTATTTAATTTCCAAATAATTGCTTCATAAAGAATCCCATAC	2700
Sbjct	4549	TTTTGAAGGAAGCCATAACTATTTAATTTCCAAATAATTGCTTCATAAAGAATCCCATAC	4608
Query	2701	TCTCAGTTTGCAaaaaaaaaaaaaaaaa	2728
Sbjct	4609	TCTCAGTTTGCAAAAAAAAAAAAAAAAA	4636

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BLAST Results

[Questions/comments](#)

Blast 2 sequences

Job title: NM_005711:Homo sapiens EGF like repeats and...

RID [CUN9C70W114](#) (Expires on 08-28 12:25 pm)Query ID [NM_005711.5](#)

Description Homo sapiens EGF like repeats and discoidin domains 3 (EDIL3), transcript variant 1, mRNA

Molecule type nucleic acid

Query Length 4814

Subject ID [BC030828.1](#)

Description Homo sapiens EGF-like repeats and discoidin I-like domains 3, mRNA (cDNA clone MGC:26287 IMAGE:4791845), complete cds

[See details](#)

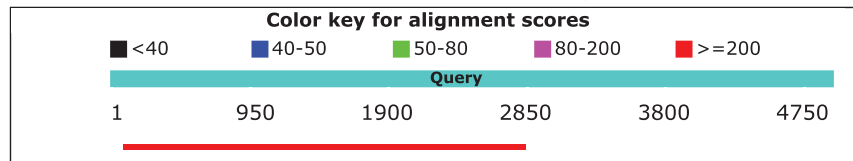
Molecule type nucleic acid

Subject Length 2728

Program BLASTN 2.16.0+

[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 EGF-like repeats and discoidin I-like domains 3, mRNA (cDNA clone MGC:26287 IMAGE:4791845), complete cds	5014	5014	56%	0.0	99.85%	BC030828.1

[Alignments](#)

Homo sapiens EGF-like repeats and discoidin I-like domains 3, mRNA (cDNA clone MGC:26287 IMAGE:4791845), complete cds

Sequence ID: **BC030828.1** Length: 2728 Number of Matches: 1

Range 1: 1 to 2727

Score	Expect	Identities	Gaps	Strand	Frame
5014 bits(2715)	0.0()	2724/2728(99%)	1/2728(0%)	Plus/Plus	
Features:					
Query	88	AGAAGCCCCGAGCCGCGCGGAGAACAGCGACAGCCGAGCGCCGGTCCGCCTGTCT			147
Sbjct	1	AGAAGCCCCGAGCCGCGCGGAGAACAGCGACAGCCGAGCGCCGGTCCGCCTGTCT			60
Query	148	GCCGGTGGGTCTGCCTgcccgcgcagcagacccggggcggcgggagccgcgcccgc			207
Sbjct	61	GCCGGTGGGTCTGCCTGCCGCGCAGCAGACCCGGGCGGGCCGCGGAGCCCGCCCG			120
Query	208	cccgcgcgcctctgcccgggaccaccgcAGCGGAGGGCTGAGCCCGCGCGGCTCCC			267
Sbjct	121	CCGCGCGGCTCTGCCGGGACCCACCGCAGCGGAGGGCTGAGCCCGCGCGGCTCCC			180
Query	268	CGGAGCTACCCACCTCCGCGCGCGGAGCGCAGGCAAAAGGGGAGGAAAGGCTCCTCTC			327
Sbjct	181	CGGAGCTACCCACCTCCGCGCGCGGAGCGCAGGCAAAAGGGGAGGAAAGGCTCCTCTC			240
Query	328	TTTAGTCACTCTCGCCCTCTCAAGAATTTGTTTAAACAAGCGCTGAGGAAAGAGAA			387

Sbjct 241 TTTAGTACCACCTCTCGCCCTCTCCAAGAATTGTTTAAACAAGCGCTGAGGAAAGAGAA 300

Query 388 CGTCTTCTTGAATCTTTAGTAGGGGGCGGAGTCTGCTGCTGCCCTGCCCTGCCACCTCGG 447

Sbjct 301 CGTCTTCTTGAATCTTTAGTAGGGGGCGGAGTCTGCTGCTGCCCTGCCCTGCCACCTCGG 360

Query 448 CTACACTGCCCTCCGGCAGCAGCCCTGACCAGCCGGGGTACGCTCCGGGAGACGGGATCA 507

Sbjct 361 CTACACTGCCCTCCGGCAGCAGCCCTGACCAGCCGGGGTACGCTCCGGGAGACGGGATCA 420

CDS:EGF-like repeat 1 M K R S V A V W L L V G L S L G V P Q F

Query 508 TGAAGCGCTCGTAGCGCTGGCTCTGGTCGGGCTCAGCCTCGGTGTCCTCCAGTTCCG 567

Sbjct 421 TGAAGCGCTCGTAGCGCTGGCTCTGGTCGGGCTCAGCCTCAGTGTCCCTCCAGTTCCG 480

CDS:EGF-like repeats 1 M K R S V A V W L L V G L S L S V P Q F

CDS:EGF-like repeat 21 G K G D I C D P N P C E N G G I C L P G

Query 516 GCAAAGGTGATATTTGTGATCCCAATCCATGTGAAAATGGAGTATCTGTTGCCAGGAT 627

Sbjct 481 GCAAAGGTGATATTTGTGATCCCAATCCATGTGAAAATGGAGTATCTGTTGCCAGGAT 540

CDS:EGF-like repeats 21 G K G D I C D P N P C E N G G I C L P G

CDS:EGF-like repeat 41 L A D G S F S C E C P D G F T D P N C S

Query 612 TGGCTGATGGTTCTTTTCTGTGAGTTCACAGATGGCTTACAGACCCCAACTGTTCTA 687

Sbjct 541 TGGCTGATGGTTCTTTTCTGTGAGTTCACAGATGGCTTACAGACCCCAACTGTTCTA 600

CDS:EGF-like repeats 41 L A D G S F S C E C P D G F T D P N C S

CDS:EGF-like repeat 61 S V V E V A S D E E E P T S A G P C T P

Query 688 GTGTTGGAGGTGCATCAGATGAAGAAGAACCACTTACAGAGTCCCTCCACTCCTA 747

Sbjct 601 GTGTTGGAGGTGCATCAGATGAAGAAGAACCACTTACAGAGTCCCTCCACTCCTA 660

CDS:EGF-like repeats 61 S V V E V A S D E E E P T S A G P C T P

CDS:EGF-like repeat 81 N P C H N G G T C E I S E A Y R G D T F

Query 748 ATCCATGCCATAATGGAGAACCTGTGAAATAGTGAAGCATAACGAGGGGATACATTCA 807

Sbjct 661 ATCCATGCCATAATGGAGAACCTGTGAAATAGTGAAGCATAACGAGGGGATACATTCA 720

CDS:EGF-like repeats 81 N P C H N G G T C E I S E A Y R G D T F

CDS:EGF-like repeat 101 I G Y V C K C P R G F N G I H C Q H N I

Query 808 TAGGCTATGTTTGTAAATGTCCCGAGGATTTAATGGATTCACTGTACGACACAATAA 867

Sbjct 721 TAGGCTATGTTTGTAAATGTCCCGAGGATTTAATGGATTCACTGTACGACACAATAA 780

CDS:EGF-like repeats 101 I G Y V C K C P R G F N G I H C Q H N I

CDS:EGF-like repeat 121 N E C E V E P C K N G G I C T D L V A N

Query 868 ATGAATGCCAAGTGGACCTTGCAAAAATGGTGAATATGTACAGATCTGTTGCTAACT 927

Sbjct 781 ATGAATGCCAAGTGGACCTTGCAAAAATGGTGAATATGTACAGATCTGTTGCTAACT 840

CDS:EGF-like repeats 121 N E C E V E P C K N G G I C T D L V A N

CDS:EGF-like repeat 141 Y S C E C P G E F M G R N C Q Y K C S G

Query 928 ATTCCTGTGAGTGGCCAGGCGAATTTATGGGAAGAAATGTCAATACAAATGCTCAGGCC 987

Sbjct 841 ATTCCTGTGAGTGGCCAGGCGAATTTATGGGAAGAAATGTCAATACAAATGCTCAGGCC 900

CDS:EGF-like repeats 141 Y S C E C P G E F M G R N C Q Y K C S G

CDS:EGF-like repeat 161 P L G I E G G I I S N Q Q I T A S S T H

Query 988 CACTGGGAATGAAGTGGAAATATATCAAACAGCAAAATCACAGCTTCTCTACTCACC 1047

Sbjct 901 CACTGGGAATGAAGTGGAAATATATCAAACAGCAAAATCACAGCTTCTCTACTCACC 960

CDS:EGF-like repeats 161 P L G I E G G I I S N Q Q I T A S S T H

CDS:EGF-like repeat 181 R A L F G L Q K W Y P Y Y A R L N K K G

Query 1048 GAGCTTTTTGGACTCCAAAAATGGTATCCCTACTATGCACGCTTAATAAGAAGGGGC 1107

Sbjct 961 GAGCTTTTTGGACTCCAAAAATGGTATCCCTACTATGCACGCTTAATAAGAAGGGGC 1020

CDS:EGF-like repeats 181 R A L F G L Q K W Y P Y Y A R L N K K G

CDS:EGF-like repeat 201 L I N A W T A A E N D R W P W I Q I N L

Query 1108 TTATAAATGCGTGGACAGCTGCAGAAAATGACAGATGGCCGTGGATTGAGATAAATTTGC 1167

Sbjct 1021 TTATAAATGCGTGGACAGCTGCAGAAAATGACAGATGGCCGTGGATTGAGATAAATTTGC 1080

CDS:EGF-like repeats 201 L I N A W T A A E N D R W P W I Q I N L

CDS:EGF-like repeat 221 Q R K M R V T G V I T Q G A K R I G S P

Query 1168 AAAGGAAAAAGAGTACTGGTGTGATTACCAAGGACCAAGAGGATTGGAAGCCAG 1227

Sbjct 1081 AAAGGAAAAAGAGTACTGGTGTGATTACCAAGGACCAAGAGGATTGGAAGCCAG 1140

CDS:EGF-like repeats 221 Q R K M R V T G V I T Q G A K R I G S P

CDS:EGF-like repeat 241 E Y I K S Y K I A Y S N D G K T W A M Y

Query 1228 AGTATATAAAATCTACAAAATTCCTACAGTATGATGGAAAGACTTGGCAATGTACA 1287

Sbjct 1141 AGTATATAAAATCTACAAAATTCCTACAGTATGATGGAAAGACTTGGCAATGTACA 1200

CDS:EGF-like repeats 241 E Y I K S Y K I A Y S N D G K T W A M Y

CDS:EGF-like repeat 261 K V K G T N E D M V F R G N I D N N T P

Query 1288 AAGTGAAAGGCACCAATGAAGACATGGTGTTCGTGGAAACATTGATAACAACACTCCAT 1347

Sbjct 1201 AAGTGAAAGGCACCAATGAAGACATGGTGTTCGTGGAAACATTGATAACAACACTCCAT 1260

CDS:EGF-like repeats 261 K V K G T N E D M V F R G N I D N N T P

CDS:EGF-like repeat 281 Y A N S F T P P I K A Q Y V R L Y P Q V

Query 1348 ATGCTAACTCTTTACACCCCCATAAAAGCTCAGTATGTAAGACTCTATCCCCAAGTT 1407

Sbjct 1261 ATGCTAACTCTTTACACCCCCATAAAAGCTCAGTATGTAAGACTCTATCCCCAAGTT 1320

CDS:EGF-like repeats 281 Y A N S F T P P I K A Q Y V R L Y P Q V

CDS:EGF-like repeat 301 C R R H C T L R M E L L G C E L S G C S

Query 1408 GTCGAAGACATTGCACTTTGGCAATGGAACCTTCTGGCTGTGAACGTGGGTTGTTCTG 1467

Sbjct 1321 GTCGAAGACATTGCACTTTGGCAATGGAACCTTCTGGCTGTGAACGTGGGTTGTTCTG 1380

CDS:EGF-like repeats 301 C R R H C T L R M E L L G C E L S G C S

CDS:EGF-like repeat 321 E P L G M K S G H I Q D Y Q I T A S S I

Query 1468 AGCCTTGGGTATGAAATCAGGACATATACAAGACTATCAGATCACTGCCCTCCAGCATCT 1527

Sbjct 1381 AGCCTTGGGTATGAAATCAGGACATATACAAGACTATCAGATCACTGCCCTCCAGCATCT 1440

CDS:EGF-like repeats 321 E P L G M K S G H I Q D Y Q I T A S S I

CDS:EGF-like repeat 341 F R T L N M D M F T W E P R K A R L D K

Query 1528 TCAGAACGCTCAACATGGACATGTTCACTTGGAAACCAAGGAAAGCTCGGCTGGACAAGC 1587

Sbjct 1441 TCAGAACGCTCAACATGGACATGTTCACTTGGAAACCAAGGAAAGCTCGGCTGGACAAGC 1500

CDS:EGF-like repeats 341 F R T L N M D M F T W E P R K A R L D K

552 G>A (G16S)

CDS:EGF-like repeat 361 Q G K V N A W T S G H N D Q S Q W L Q V 1647
 Query 1588 AAGGCAAAGTGAATGCCTGGACCTCTGGCCACAATGACCAGTCACAATGGTTACAGGTGG 1647
 Sbjct 1501 AAGGCAAAGTGAATGCCTGGACCTCTGGCCACAATGACCAGTCACAATGGTTACAGGTGG 1560
 CDS:EGF-like repeats 361 Q G K V N A W T S G H N D Q S Q W L Q V 1560

CDS:EGF-like repeat 381 D L L V P T K V T G I I T Q G A K D F G 1707
 Query 1648 ATCTTCTTGTCCAACCAAAGTACTGGCATCATTACACAAGGAGCTAAAGATTTTGGTC 1707
 Sbjct 1561 ATCTTCTTGTCCAACCAAAGTACTGGCATCATTACACAAGGAGCTAAAGATTTTGGTC 1620
 CDS:EGF-like repeats 381 D L L V P T K V T G I I T Q G A K D F G 1620

CDS:EGF-like repeat 401 H V Q F V G S Y K L A Y S N D G E H W T 1767
 Query 1708 ATGTACAGTTTGTGGCTCTACAACCTGGCTTACAGCAATGATGGAGAACTGGACTG 1767
 Sbjct 1621 ATGTACAGTTTGTGGCTCTACAACCTGGCTTACAGCAATGATGGAGAACTGGACTG 1680
 CDS:EGF-like repeats 401 H V Q F V G S Y K L A Y S N D G E H W T 1680

CDS:EGF-like repeat 421 V Y Q D E K Q R K D K V F Q G N F D N D 1827
 Query 1768 TATACCAGGATGAAAAGCAAAGAAAAGATAAGGTTTTCCAGGAAATTTTGACAATGACA 1827
 Sbjct 1681 TATACCAGGATGAAAAGCAAAGAAAAGATAAGGTTTTCCAGGAAATTTTGACAATGACA 1740
 CDS:EGF-like repeats 421 V Y Q D E K Q R K D K V F Q G N F D N D 1740

CDS:EGF-like repeat 441 T H R K N V I D P P I Y A R H I R I L P 1887
 Query 1828 CTCACAGAAAAATGTCATCGACCTCCCATCTATGCACGACACATAAGAACTCTTCCTT 1887
 Sbjct 1741 CTCACAGAAAAATGTCATCGACCTCCCATCTATGCACGACACATAAGAACTCTTCCTT 1800
 CDS:EGF-like repeats 441 T H R K N V I D P P I Y A R H I R I L P 1800

CDS:EGF-like repeat 461 W S W Y G R I T L R S E L L G C T E E E 1947
 Query 1888 GGTCTGGTACGGGAGGATCACATTGCGGTGAGAGCTGCTGGCTGCACAGAGGAGGAAT 1947
 Sbjct 1801 GGTCTGGTACGGGAGGATCACATTGCGGTGAGAGCTGCTGGCTGCACAGAGGAGGAAT 1860
 CDS:EGF-like repeats 461 W S W Y G R I T L R S E L L G C T E E E 1860

Query 1948 GAGGGGAGGCTACATTTACAACCTCTCCCTATTTCCCTAAAAGTATCTCCATGGAAT 2007
 Sbjct 1861 GAGGGGAGGCTACATTTACAACCTCTCCCTATTTCCCTAAAAGTATCTCCATGGAAT 1920

Query 2008 GAACTGTCAAAAATCTGTAGGAACTGAATGGTTTTTTTTTTTTTTCATGAAAAAGTGC 2067
 Sbjct 1921 GAACTGTCAAAAATCTGTAGGAACTGAATGG-TTTTTTTTTTTTTTTCATGAAAAAGTGC 1979

Query 2068 TCAAATATGGTAGGCAACTAACGGTGTTTTTAAGGGGGTCTAAGCCTGCCTTTTCAATG 2127
 Sbjct 1980 TCAAATATGGTAGGCAACTAACGGTGTTTTTAAGGGGGTCTAAGCCTGCCTTTTCAATG 2039

Query 2128 ATTTAAATGATTTTATTTATCCGTCAAATCTTAAAGTAAACAACATTAAGTGTGAA 2187
 Sbjct 2040 ATTTAAATGATTTTATTTATCCGTCAAATCTTAAAGTAAACAACATTAAGTGTGAA 2099

Query 2188 TTACTTTTCTCTATTGTTTCTGAATATTTCGATTGGTAGAAATATATTAGGAAAGA 2247
 Sbjct 2100 TTACTTTTCTCTATTGTTTCTGAATATTTCGATTGGTAGAAATATATTAGGAAAGA 2159

Query 2248 AAGTAGCCTCTTTTTATAGCAAGAGTAAAAAGTCTCAAAGTCATCAATAAGAGCAAG 2307
 D I R K V N A W T S G H N D Q S Q W L Q V

Sbjct 2160 AAGTAGCCTCTTTTTATAGCAAGAGTAAAAAGTCTCAAAGTCATCAATAAGAGCAAG 2219
 Query 2308 AGTTGATAGAGCTTTTACAATCAACTCACCTAATTCGATAAAAAGGAATACTGCAATG 2367
 Sbjct 2220 AGTTGATAGAGCTTTTACAATCAACTCACCTAATTCGATAAAAAGGAATACTGCAATG 2279

Query 2368 TTAGCAATAAGTTTTTTCTTCTGTAATGACTCTACGTTATCCTGTTTCCCTGTGCTAC 2427
 Sbjct 2280 TTAGCAATAAGTTTTTTCTTCTGTAATGACTCTACGTTATCCTGTTTCCCTGTGCTAC 2339

Query 2428 CAACACGTCAATGTTTATTACAAAAATTTAAAGAAGAATATGTAAATGCAGTACTGA 2487
 Sbjct 2340 CAACACGTCAATGTTTATTACAAAAATTTAAAGAAGAATATGTAAATGCAGTACTGA 2399

Query 2488 TATTATAATCTCATTTTACTTTCAATTTCTAATAAGAGATTATGTACTCTTTTTTCT 2547
 Sbjct 2400 TATTATAATCTCATTTTACTTTCAATTTCTAATAAGAGATTATGTACTCTTTTTCT 2459

Query 2548 TTTTAGTTCTATTCTACATTTAATATTGTATATTACCTGAATAATTCAATTTTTTCT 2607
 Sbjct 2460 TTTTAGTTCTATTCTACATTTAATATTGTATATTACCTGAATAATTCAATTTTTTCT 2519

Query 2608 AATTGAATTTCCATTAGTTGACTAAAAGAAGTGTATGTTTACTCATATATGTAGAACA 2667
 Sbjct 2520 AATTGAATTTCCATTAGTTGACTAAAAGAAGTGTATGTTTACTCATATATGTAGAACA 2579

Query 2668 TGACTGCCTATCAGTAGATTGATCTGTATTTAATTTCTGTTAATTAATCTGCAGTTTTA 2727
 Sbjct 2580 TGACTGCCTATCAGTAGATTGATCTGTATTTAATTTCTGTTAATTAATCTGCAGTTTTA 2639

Query 2728 TTTTGAAGGAAGCCATAACTATTTAATTTCCAATAATTTGCTTCATAAAGAAATCCATA 2787
 Sbjct 2640 TTTTGAAGGAAGCCATAACTATTTAATTTCCAATAATTTGCTTCATAAAGAAATCCATA 2699

Query 2788 CTCTCAGTTTGCACAAAAGAACAAAAA 2815
 Sbjct 2700 CTCTCAGTTTGCACAAAAGAACAAAAA 2727

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