Daniel Johnson A53072130

BGGN213 2019 Midterm "Find a Gene Project"

[Q1] Protein Name

Protein Name: CBFA2T1 (Product of RUNX1T1 Gene)

Species: Human

Accession: NX Q06455

[Q2] Blast Search Results

Blast Input:

Sigma

>sp|Q06455|MTG8_HUMAN Protein **CBFA2T1** OS=**Homo sapiens** OX=9606 GN=**RUNX1T1** PE=1 SV=2

45.0604

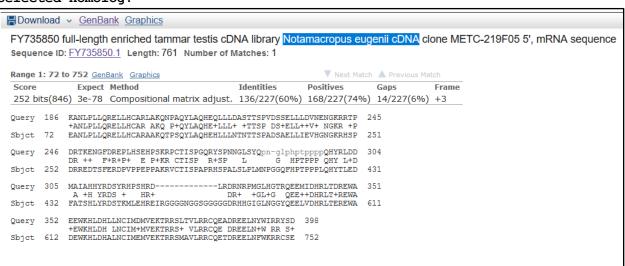
MISVKRNTWRALSLVIGDCRKKGNFEYCQDRTEKHSTMPDSPVDVKTQSRLTPPTMPPPP
TTQGAPRTSSFTPTTLTNGTSHSPTALNGAPSPPNGFSNGPSSSSSSSSLANQQLPPACGA
RQLSKLKRFLTTLQQFGNDISPEIGERVRTLVLGLVNSTLTIEEFHSKLQEATNFPLRPF
VIPFLKANLPLLQRELLHCARLAKQNPAQYLAQHEQLLLDASTTSPVDSSELLLDVNENG
KRRTPDRTKENGFDREPLHSEHPSKRPCTISPGQRYSPNNGLSYQPNGLPHPTPPPPQHY
RLDDMAIAHHYRDSYRHPSHRDLRDRNRPMGLHGTRQEEMIDHRLTDREWAEEWKHLDHL
LNCIMDMVEKTRRSLTVLRRCQEADREELNYWIRRYSDAEDLKKGGGSSSSHSRQQSPVN
PDPVALDAHREFLHRPASGYVPEEIWKKAEEAVNEVKRQAMTELQKAVSEAERKAHDMIT
TERAKMERTVAEAKRQAAEDALAVINQQEDSSESCWNCGRKASETCSGCNTARYCGSFCQ
HKDWEKHHHICGQTLQAQQQGDTPAVSSSVTPNSGAGSPMDTPPAATPRSTTPGTPSTIE
TTPR

Search Parameters								
Program		tblastn						
Word size		6						
Expect value		50						
Hitlist size		1000						
Gapcosts		15,2						
Matrix		BLOSUM45						
Low Complexity Filter		Yes						
Filter string		L;						
Genetic Code		1						
Window Size		40						
Threshold		21						
Composition-based stats		2						
Database								
Posted date		Mar 13, 2019 8:21 PM						
Number of letters		43,196,422,130						
Number of sequences		77,551,161						
Entrez query		None						
Karlin-Altschul statistics								
Lambda	0.224821		0.203					
K	0.0883194		0.041					
Н	0.239842		0.12					
Alpha	0.9113		1.7					
Alpha_v	9.61106		44.8257					

Blast Output:

11 Alianments IELDownload v Gentlank Graphics						0
Description	Max	Total	Query	Е	Per.	Accession
· · · · · · · · · · · · · · · · · · ·	Score	Score	Cover	value	Ident	
☐ RUNKY/RUNKYTT [II 0.24] RUNKY/RUNKYTT alternative mRNA Library-Homo sapiens cDNA. mRNA sequence	917		82%	0.0		JZ534339.1
☐ RUNKY/RUNKYT1 [II 027] RUNKY/RUNKYT1 alternative mRNA Library Homo sapiens cDNA. mRNA sequence	889	889	80%	0.0		JZ534342.1
☐ RUNIXI-RUNIXITI [II 058] RUNIXI/RUNIXITI alternative mRNA Library Homo sapiens cDNA. mRNA sequence	760		69%	0.0		JZ719078.1
RURXIRUNKITI [II.022] RURXIRUNKITI allemathe mRNA Library Homo sapiens cDNA. mRNA sequence	750	750	69%	0.0		JZ534337.1
☐ RUNXTRUNXTT1 [II 021] RUNXTRUNXTT1 alternative mRNA Library Homo sapiens cDNA, mRNA sequence	707		65%	0.0		JZ534336.1
LUMIGEN_MCQ_37794 Katze_MMSR Macaca mulatta cDNA clone IBRUW-15671 S similar to Bases 1 to 978 highly similar to human CBFAZTI (#s. 90858), mRNA sequence	633		53%	0.0		CN802185.1
LLUMIGEN_MCQ_8705 Katze_MMBR Macaca mulatta cDNA clone IBIUW-3093 5 similar to Bases 1 to 1027 highly similar to human CBFAZT1 (Hs 90858), mRNA sequence	631		54%	0.0		CN643811.1
LLUMIGEN_MCQ_26195 Katze_MMBR Macaca mulatta cDNA clone IBIUW:8574 5' similar to Bases 1 to 1016 highly similar to human CBFAZT1 (Hs 90858), mRNA sequence	617		52%	0.0		CN646434.1
☐ RUNX1-RUNX1T1 (II 057) RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence	614		57%	0.0		JZ719077.1
☐ FY489999 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-028C01.5. mRNA sequence	580 575		49% 50%	0.0		FY489999.1 DN039564.1
□ JGI_CAAR13181 rev NIH_XGC_tropLin1 Xenopus tropicalis cDNA clone IMAGE:7745385.3. mRNA sequence	5/5	556	50%	0.0		JZ719071.1
D RUNKYT-RUNKYT-I (II. 051) RUNKYTRUNKYTT alternative mRNA Library-Homo sagiens cDNA, mRNA sequence	544		53%	0.0		CN805491.1
LLUMMCEN, MCQ_36701 Katze, MMBR Macaca mulatta cDNA clone IBIUW-1239 5 similar to Bases 1 to 969 highly similar to human CBFAZT1 (Hs 90858), mRNA sequence FY475876 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-009812 3; mRNA sequence			43%	0.0		FY475876.1
RUNK/IRUNK/11 [II 020] RUNK/IRUNK/11 alternative mRNA Library Homo sagiens cDNA, mRNA sequence	539 537		52%	0.0		.17534335.1
☐ ROUNCH MUNICHT ILL ZUJ KUNCHIKONCHT attemative mixtua. Lordary Homo saperins curvus. mixtua. sequence	537		45%	0.0		CF554058.1
☐ AGENCOURT 832057 NIH MGC 94 Mus musculus cDNA clone IMAGE: 5455835 5. mRNA sequence	526		41%	0.0		BQ946132.1
FY486169 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-023G13.7. mRNA sequence	526		44%	0.0		FY486469.1
C1400405 Tull-length entirched talmmar grave uterlus curvix library violamacropus eugemi curvix crone NESC-VCX513.3. mixtux sequence 603765010F1 CSEQRBN13 Gallus gallus cDNA clone ChEST68964.5. mRNA sequence	528		43%	0.0		BU445478.1
503474890F1 CSEQCHV70 Gallus gallus cDNA clone ChEST356323 5, mRNA sequence	515		45%	0.0		BU356862.1
☐ 933121328F1 CSEOCHL2 Callus gallus CDNA clone ChEST8389 5". mRNA sequence	511	511		8e-180		BU133936.1
S1142P33FG15.T0 Anolis carolinensis pooled normalized Brain CDNA Library Anolis carolinensis cDNA mRNA sequence	512					FG663117.1
☐ gPSC_EST05638 Embryonic gonadal PSC_CDNA Library, Gallus gallus cDNA 5; mRNA sequence	516	516		4e-179		DR415794.1
[] JGI CAAS15565 fixd CAAS Pimephales promelas brain 7.8 month adults, males and females pooled (H) Pimephales promelas cDNA clone CAAS15565 5, mRNA sequence	508			2e-178		DT210543.1
286545 Pigtailed macaque ovary library Macaca nemestrina cDNA 7. mRNA sequence	502	502	42%	5e-176		EB522745.1
☐ AGENCOURT 6792472 NIH MGC 121 Homo saziens cDNA clone IMAGE-5768973 5: mRNA sequence	503	503	50%	2e-175	79.41%	BQ067971.1
2056050FLV1011028HT OFLV Oxis aries cDNA. mRNA sequence	496	496	42%	6e-174	91.86%	EE771493.1
☐ CCUA7236 bf CCUA Peromiscus polionotus suborisieus PO Bt Ts Peromiscus polionotus suborisieus CNA clone CCUA7236 5 mRNA sequence	493	493	39%	5e-173	94.19%	GH468648.1
USI CAAL6363 rev NIH XGC trop8m4 Xenopus tropicalis cDNA clone IMAGE-7654626 3: mRNA sequence						
SOURCE AND A SECURITY AND A SECURITY ASSOCIATION ASSOCIATION AND A SECURITY ASSOCIATION AS	491	491	40%	7e-172	92.68%	CX849519.2
	491 490			7e-172 9e-171		CX849519.2 JZ534326.1
RADA LOSA SENSIN ST. JAKE, TROPORTH XMORDAN TORGERS CUMA CORE INVASC: Toketop 3. TH KINA Sequence RADA THE RESTAURANT I BUSTI RUNKI FRUNKT I alternative mRNA Library Homo spagens cDNA. mRNA sequence PYS16286 full-ength enriched tammar grand utensu cDNA library Notamancropus eugeni cDNA clore MEGC-063/11 3. THRNA sequence	490	490	47%		81.53%	
RUNKTRURKTT [II.011] RUNKTRUNKTT alternative mRNA Library Homo sapiens cDNA, mRNA sequence	490 487	490 487	47% 40%	9e-171	81.53% 91.50%	JZ534326.1
□ RUNXIRUNXITI (II 011) RUNXIRUNXITI alternative mRNA Library Homo sagens cDNA. mRNA sequence □ FYS16286 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-063J11 3. mRNA sequence □ FY475875 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-099812 5. mRNA sequence	490 487 484	490 487 484	47% 40% 48%	9e-171 6e-170	81.53% 91.50% 79.79%	JZ534326.1 FY516286.1
RUNXIRURXITI III 0111 RUNXIRURXITI alternative mRNA Library Homo sapiens cDNA. mRNA sequence PY516286 full-length enriched tammar gravid utenus cDNA library Notamacropus eugenii cDNA clone MEGC-063J11 3. mRNA sequence	490 487 484 481	490 487 484 481	47% 40% 48% 47%	9e-171 6e-170 1e-168	81.53% 91.50% 79.79% 80.14%	J7534326.1 FY516286.1 FY475875.1
☐ RUNXIRUNXITI III 0111 RUNXIRUNXITI alternative mRNA Library Homo sagens cDNA. mRNA sequence ☐ FYS16286 full-length enriched tammar grand uterus cDNA library Notamacropus eugenii cDNA clone MEGC-063311 3. mRNA sequence ☐ FY475875 full-length enriched tammar grand uterus cDNA library Notamacropus eugenii cDNA clone MEGC-009812 5. mRNA sequence ☐ FY729972 full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone METC-203H19 5. mRNA sequence	490 487 484 481 481	490 487 484 481 481	47% 40% 48% 47% 48%	9e-171 6e-170 1e-168 1e-167	81.53% 91.50% 79.79% 80.14% 80.00%	JZ534326.1 FY516286.1 FY475875.1 FY729972.1
☐ RUNXIRUNXITI (II. 0111 RUNXIRUNXIT1 alternative mRNA Library Homo sapiens cDNA mRNA sequence ☐ FYS16286 full-length enriched tammar granid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-063311 3. mRNA sequence ☐ FY475875 full-length enriched tammar granid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-009812 5. mRNA sequence ☐ FY729972 full-length enriched tammar trastis cDNA library Notamacropus eugenii cDNA clone METC-203H19 5. mRNA sequence ☐ FY486486 full-length enriched tammar granid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-023G13 5. mRNA sequence	490 487 484 481 481 478	490 487 484 481 481 551	47% 40% 48% 47% 48%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166	81.53% 91.50% 79.79% 80.14% 80.00% 87.80%	JZ534326.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1
□ RUNXIRURAKITI (II.011) RUNXIRURKITI alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PYS16286 full-length enriched tammar gravid utenus cDNA library Notamacropus sugenii cDNA clone MEGC-063J11 3. mRNA sequence □ PYS15975 full-length enriched tammar gravid utenus cDNA library Notamacropus sugenii cDNA clone MEGC-005912 5. mRNA sequence □ PYS29972 full-length enriched tammar testis cDNA library Notamacropus sugenii cDNA clone METC-203H19 5. mRNA sequence □ PYS89686 full-length enriched tammar gravid utenus cDNA library Notamacropus sugenii cDNA clone METC-203H19 5. mRNA sequence □ S031H9770F1 CSEQCH 22 Gallus gallus cDNA clone ChEST7918 5. mRNA sequence	490 487 484 481 481 478	490 487 484 481 481 551 474	47% 48% 48% 44% 39%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44%	JZ534326.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1 BU132241.1
□ RUNXIRURXIT III 0111 RUNXIRURXIT1 alternative mRNA Library Homo sagens cDNA. mRNA sequence □ PY516286 full-length enriched tammar gravid utenus cDNA library Notamacropus eugenii cDNA clone MEGC-063J11 3. mRNA sequence □ PY276176 full-length enriched tammar gravid utenus cDNA library Notamacropus eugenii cDNA clone MEGC-069812 5. mRNA sequence □ PY276972 full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone METC-203H19 5. mRNA sequence □ PY286486 full-length enriched tammar gravid utenus cDNA library Notamacropus eugenii cDNA clone MEGC-023G13 5. mRNA sequence □ S931917761 CSEGOH12 Callaus gallus cDNA clone CREST7918 5. mRNA sequence □ JGL CAAL9015.rev.NH XGC_ttopRm4 Xenopus tropicalis cDNA clone IMAGE-7666775 3. mRNA sequence	490 487 484 481 481 478	490 487 484 481 481 551 474 462	47% 48% 48% 44% 49% 40%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26%	JZ534326.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1 BU132241.1 CX852794.2
□ RUNKIRUNKITI 011 RUNKIRUNKITI alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PY516286 full-length enriched tammar gravid utenus cDNA library Notamacropus suganii cDNA clone MEGC-0631/1 3, mRNA sequence □ PY37875 full-length enriched tammar gravid utenus cDNA library Notamacropus suganii cDNA clone MEGC-06981/2 5, mRNA sequence □ PY37877 full-length enriched tammar testis cDNA library Notamacropus suganii cDNA clone MEGC-03981/3 5, mRNA sequence □ PY388488 full-length enriched tammar gravid utenus cDNA library Notamacropus suganii cDNA clone MEGC-03361/3 5, mRNA sequence □ 593197707 € CSG-0CH-82 Gallus gallus cDNA clone CMS-17981/8 7, mRNA sequence □ JGI CAAL9015 rev NH JGC (uppdm/ Xenopus tropicalis cDNA clone MAGE-768775/3 2, mRNA sequence □ RUNKI/RUNKI/1 1440 RUNKI/RUNKI/1 alternative mRNA Library Homo sapiens cDNA mRNA sequence	490 487 484 481 481 478 474 462	490 487 484 481 481 551 474 462 459	47% 40% 48% 47% 44% 39% 40% 37%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56%	JZ534326.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1 BU132241.1 CX862794.2 JZ534361.1
□ RUNKURUNKUTI [II 011] RUNKURUNKUTI alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PYS16286 full-length enriched tammar gravid utenus cDNA library Notamacropus eugenii cDNA clone MEGC-063.11 3. mRNA sequence □ PY375875 full-length enriched tammar gravid utenus cDNA library Notamacropus eugenii cDNA clone MEGC-009812 5. mRNA sequence □ PY375875 full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone MEGC-009812 5. mRNA sequence □ PY386486 full-length enriched tammar gravid utenus cDNA library Notamacropus eugenii cDNA clone MEGC-023G13 5. mRNA sequence □ S03119770F1 CSEQCH 22 Gallus gallus cDNA clone ChEST7918 5. mRNA sequence □ GIL CAAL9015 rev NH H. XGC 10096mt Xenopus tropicalis cDNA clone MAGE 7686775 3. mRNA sequence □ RUNKURUNKUTI [II 040] RUNKURUNKUTI alternative mRNA Library Homo sapiens cDNA mRNA sequence	490 487 484 481 481 478 474 462 459	490 487 484 481 481 551 474 462 459	47% 40% 48% 47% 44% 39% 40% 45%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56% 79.78%	JZ534326.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1 BU132241.1 CX852794.2 JZ534361.1 BP141580.1
□ RUNKIRUNKIT III 011 RINKIRUNKIT alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PY516266 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-063J11 3. mRNA sequence □ PY4516376 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-063J11 5. mRNA sequence □ PY459372 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-2039119 5. mRNA sequence □ PY458686 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-2039119 5. mRNA sequence □ S03191770° LOSE-0CH-12 Callus gallus cDNA clone ChEST7918 5. mRNA sequence □ JGL-CAAL-9015 rev NH XGC_tropBrn4 Xenopus tropicalis cDNA clone IMAGC 7669715 7. mRNA sequence □ JGL-CAAL-9015 rev NH XGC_tropBrn4 Xenopus tropicalis cDNA clone IMAGC 7669715 7. mRNA sequence □ BP141590 full-length enriched savers cDNA library, adult coary Sus scrola cDNA clone AVR010004415 5. mRNA sequence □ PY719472 full-length enriched tammar testis cDNA library, Notamacropus supenii cDNA clone MRCC-175D16 5. mRNA sequence □ PY9947031 full-length enriched tammar testis cDNA library, Adult coary Sus scrola cDNA clone MRCC-175D16 5. mRNA sequence □ HX771542 Lonchura striata domestica juvenile P50 brain cDNA library Lonchura striata domestica cDNA clone over 50906812. mRNA sequence	490 487 484 481 481 478 474 462 459 458	490 487 484 481 481 551 474 462 459 458 457	47% 48% 47% 48% 44% 39% 40% 37% 45% 45%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56% 79.78% 80.29%	JZ534326.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1 BU132241.1 CX852794.2 JZ534361.1 BP141580.1 FY719472.1
□ RUNXIRUARXIT III.011 RUNXIRUARXIT alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PY516286 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGG-063111 3. mRNA sequence □ PY516286 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGG-069812 5. mRNA sequence □ PY728972 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGG-029813 5. mRNA sequence □ PY488688 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGG-028013 5. mRNA sequence □ S03119770F1 CSEQCH_22 Gallus gallus cDNA clone ChEST7918 5. mRNA sequence □ GLO-CAAL9015 rev NH_XGC_tropfem Xenopus tropicalis cDNA clone MAGG-769677 5. mRNA sequence □ RUNXIRUARXIT III.0491 RUNXIRUARXIT alternative mRNA Library Homo sapiens cDNA mRNA sequence □ PP141890 full-length enriched swine cDNA library, adult coary Sus scorla cDNA clone OXF010094A10 5. mRNA sequence □ PY719472 full-length enriched swine cDNA library, adult coary Sus scorla cDNA clone MEGG-175016 5. mRNA sequence □ PY719472 full-length enriched swine cDNA library, adult coary Sus scorla cDNA clone OXF010098508 5. mRNA sequence	490 487 484 481 481 478 474 462 459 458 457	490 487 484 481 481 551 474 462 459 458 457	47% 48% 48% 44% 39% 40% 37% 45% 45% 40%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56% 79.78% 80.29% 88.21%	JZ534326.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1 BU132241.1 CX852794.2 JZ534361.1 BP141580.1 FY719472.1 BW967031.1
□ RUNKIRUNKIT III 011 RINKIRUNKIT alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PY516266 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-063J11 3. mRNA sequence □ PY4516376 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-063J11 5. mRNA sequence □ PY459372 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-2039119 5. mRNA sequence □ PY458686 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-2039119 5. mRNA sequence □ S03191770° LOSE-0CH-12 Callus gallus cDNA clone ChEST7918 5. mRNA sequence □ JGL-CAAL-9015 rev NH XGC_tropBrn4 Xenopus tropicalis cDNA clone IMAGC 7669715 7. mRNA sequence □ JGL-CAAL-9015 rev NH XGC_tropBrn4 Xenopus tropicalis cDNA clone IMAGC 7669715 7. mRNA sequence □ BP141590 full-length enriched savers cDNA library, adult coary Sus scrola cDNA clone AVR010004415 5. mRNA sequence □ PY719472 full-length enriched tammar testis cDNA library, Notamacropus supenii cDNA clone MRCC-175D16 5. mRNA sequence □ PY9947031 full-length enriched tammar testis cDNA library, Adult coary Sus scrola cDNA clone MRCC-175D16 5. mRNA sequence □ HX771542 Lonchura striata domestica juvenile P50 brain cDNA library Lonchura striata domestica cDNA clone over 50906812. mRNA sequence	490 487 484 481 481 478 474 462 459 458 457 456	490 487 484 481 481 551 474 462 459 458 457 456	47% 48% 47% 48% 44% 39% 40% 45% 45% 40% 42%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 2e-157	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56% 79.78% 80.29% 88.21% 83.20%	JZ534326.1 FY516286.1 FY475875.1 FY72972.1 FY486468.1 BU132241.1 CX852794.2 JZ534361.1 BP141580.1 FY719472.1 BW967031.1 HX771542.1
□ RUNKURUNKUT III 0111 RINKURUNKUT1 alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PY515286 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-053111 3. mRNA sequence □ PY25157875 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-059812 5. mRNA sequence □ PY299272 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-029813 5. mRNA sequence □ PY285468 full-length enriched tammar gravid uterus cDNA library Notamacropus supenii cDNA clone MEGC-027813 5. mRNA sequence □ S93191770F1 CSEGCH2 22 Gallus gallus cDNA clone CREST7918 5. mRNA sequence □ GS1191770F1 CSEGCH2 22 Gallus gallus cDNA clone CREST7918 5. mRNA sequence □ GLAAL9015.rev.NH XGC_tropRed Xenopus tropicalis cDNA clone IMAGE 7666775 3. mRNA sequence □ RUNKURUNKUT1 [IL400] RUNKURUNKUT1 alternative mRNA Library Homo sapiens cDNA mRNA sequence □ PY1941580 full-length enriched savine cDNA library, Joidt creary Sizu screla cDNA clone MRNA clone MEGC-0296815. mRNA sequence □ PY19412 full-length enriched tammar testis cDNA library Notamacropus supenii cDNA clone MEGC-0278115 5. mRNA sequence □ PY19412 full-length enriched tammar testis cDNA library Lotamacropus supenii cDNA clone MEGC-0278115 5. mRNA sequence □ HXT71542 Lonchura striata domestica µovenile P50 brain cDNA library Lonchura striata domestica CDNA clone MEGC-0278115 5. mRNA sequence	490 487 484 481 481 478 474 462 459 458 457 456	490 487 484 481 481 551 474 462 459 458 457 456 446	47% 40% 48% 47% 48% 44% 39% 40% 45% 45% 42% 45% 45%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 2e-157 7e-154	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56% 79.78% 80.29% 88.21% 83.20% 79.78%	JZ534326.1 FY516286.1 FY475875.1 FY72972.1 FY486468.1 BU132241.1 CX852794.2 JZ534361.1 BP141580.1 FY719472.1 BW967031.1 HX771542.1 FY545165.1
□ RUNKIRURKITI III 0111 RINKIRURKITI alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PY516286 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-063111 3. mRNA sequence □ PY75972 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-063011 5. mRNA sequence □ PY729972 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-020911 5. mRNA sequence □ PY489858 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-023013 5. mRNA sequence □ S0211977091 CSEQCHL22 Gallus gallus cDNA clone CnEST7918 5. mRNA sequence □ GU, CAAL9015 rev NH XGC_tropfem4 Xenopus tropicalis cDNA clone IMAGE 766775 5. mRNA sequence □ GU, CAAL9015 rev NH XGC_tropfem4 Xenopus tropicalis cDNA clone IMAGE 766775 5. mRNA sequence □ PY418982 full-length enriched swine cDNA library, adult conys Sus scorda cDNA clone CVR010094A10 5. mRNA sequence □ PY418912 full-length enriched tammar testis cDNA library, adult conys Sus scorda cDNA clone CVR01009508 5. mRNA sequence □ PY418912 full-length enriched swine cDNA library, adult conys Sus scorda cDNA clone MECC-175016 5. mRNA sequence □ PY418912 full-length enriched swine cDNA library, scorda cDNA clone CVR01009508 5. mRNA sequence □ PY418912 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-007015 3. mRNA sequence □ PY418912 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-007015 3. mRNA sequence □ PY418915 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-007015 3. mRNA sequence	490 487 484 481 481 478 474 462 459 459 457 456 446	490 487 484 481 481 551 474 462 459 458 457 456 446 446 440	47% 40% 48% 47% 48% 47% 48% 44% 39% 40% 45% 45% 45% 45% 43% 45%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 2e-157 7e-154 8e-154 9e-152 2e-149	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56% 79.78% 80.29% 88.21% 83.20% 79.78% 91.52% 80.08%	UZ534326.1 FY515286.1 FY475875.1 FY475875.1 FY485458.1 BU132241.1 CX862794.2 UZ534361.1 BP141580.1 FY719472.1 BW967031.1 HX771542.1 FY545165.1 FY516285.1 FY474447.1 DT890969.1
□ RUNKIRUNKIT III 0111 RINKIRUNKIT1 alternative mRNA Library Homo sapiens cDNA. mRNA sequence □ PY515295 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-063111 3. mRNA sequence □ PY515275 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-069112 5. mRNA sequence □ PY29972 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-039113 5. mRNA sequence □ PY29972 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-029113 5. mRNA sequence □ PY29972 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-023613 5. mRNA sequence □ GUI CAAL9015 rev NIH XGC tropRmd Xenopus tropicalis cDNA clone IMAGE 7669775 7. mRNA sequence □ GUI CAAL9015 rev NIH XGC tropRmd Xenopus tropicalis cDNA clone IMAGE 7669775 7. mRNA sequence □ PY19472 full-length enriched xenopus customa companii cDNA clone CVRS10000A10 5. mRNA sequence □ PY19472 full-length enriched xenopus customa companii cDNA clone MEGC-075016 5. mRNA sequence □ PY49472 full-length enriched xenopus customa companii cDNA clone MEGC-075018 5. mRNA sequence □ PY49474 full-length enriched xenopus desus cDNA library Notamacropus supenii cDNA clone MEGC-070115 5. mRNA sequence □ PY416474 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-070115 5. mRNA sequence □ PY416474 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-070115 5. mRNA sequence □ PY416474 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-070115 5. mRNA sequence □ PY416497 full-length enriched tammar gunid uterus cDNA library Notamacropus supenii cDNA clone MEGC-070115 7. mRNA sequence	490 487 484 481 481 478 474 462 459 459 457 456 446 446 440	490 487 484 481 481 551 474 462 459 458 457 456 446 446 440 434	47% 48% 47% 48% 44% 39% 40% 45% 45% 45% 45% 45% 35%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 8e-154 9e-152 2e-149	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56% 79.78% 80.29% 88.21% 83.20% 79.78% 80.08% 91.52% 80.08% 93.58%	UZ534326.1 FY515286.1 FY475875.1 FY475875.1 FY485458.1 BU132241.1 CX862794.2 UZ534361.1 BP141580.1 FY719472.1 BW967031.1 HX771542.1 FY545165.1 FY515285.1 FY474447.1 DT890969.1
□ RUNKURRUNKTT III 011] RUNKURRUNKTT alternative mRNA Library Homo sagiens cDNA clone MEGC-053J11 3. mRNA sequence □ YY515285 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-058J11 3. mRNA sequence □ YY25912 full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone MEGC-058J11 5. mRNA sequence □ YY25912 full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone MEGC-028G13 5. mRNA sequence □ YY35915 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-027G13 5. mRNA sequence □ YY35915 (SEGCH2 22 Gallus gallus cDNA clone CMEST918 5. mRNA sequence □ XGI CAAL-9015 rev NIH XGC tropRm4 Xenopus tropicalis cDNA clone IMAGE 7659775 3. mRNA sequence □ RUNKURRUNKTI III 040] RUNKURSUNKTI alternative mRNA Library Homo sapiens cDNA mRNA sequence □ PY119472 full-length enriched zemes cDNA library Notamacropus eugenii cDNA clone MEGC-027G13 5. mRNA sequence □ YY19472 full-length enriched zemes cDNA library Notamacropus eugenii cDNA clone MEGC-027G13 5. mRNA sequence □ HX771542 Lonchura strista domestica juvenile P50 brain cDNA library Lonchura strista domestica juvenile P50 brain cDNA library Notamacropus eugenii cDNA clone MEGC-027M15 5. mRNA sequence □ YY451555 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-027M15 5. mRNA sequence □ YY451556 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-027M15 5. mRNA sequence □ YY451556 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-027M15 5. mRNA sequence □ YY451565 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-027M15 5. mRNA sequence □ YY451565 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-027M15 5. mRNA sequence	490 487 484 481 481 476 474 462 459 458 457 456 446 446 440 434 432 431	490 487 484 481 481 551 474 462 459 458 457 456 446 446 440 434 432 490	47% 48% 47% 48% 44% 39% 40% 45% 45% 45% 45% 36% 43% 35% 38%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 2e-157 7e-154 8e-154 9e-152 2e-149 3e-149 7e-149	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.56% 79.78% 80.29% 88.21% 83.20% 79.78% 91.52% 80.08% 93.58% 94.31%	UZ534326.1 FY616286.1 FY45876.1 FY428972.1 FY428972.1 FY428972.1 BU132241.1 CX862794.2 UZ534361.1 BP141580.1 FY719472.1 BW967031.1 HX771542.1 FY545165.1 FY516285.1 FY516286.1 FY679366.1 DY760558.1
□ RUBSURDRAYTT [II 011] RUNKURUNKTT alternative mRNA Library Homo sapiens cDNA mRNA sequence □ PY515285 full-length enriched tammar graied sterus cDNA library Notamacropus eugenii cDNA clone MEGC-063111 5. mRNA sequence □ PY25975 full-length enriched tammar graied sterus cDNA library Notamacropus eugenii cDNA clone MEGC-009812 5. mRNA sequence □ PY25975 full-length enriched tammar graied sterus cDNA library Notamacropus eugenii cDNA clone MEGC-009812 5. mRNA sequence □ PY259575 full-length enriched tammar graied sterus cDNA library Notamacropus eugenii cDNA clone MEGC-009812 5. mRNA sequence □ S03119770F1 CSEQCH-22 Gallus gallus cDNA clone ChEST7918 5. mRNA sequence □ S03119770F1 CSEQCH-22 Gallus gallus cDNA clone ChEST7918 5. mRNA sequence □ GRANKINEAWXTTI (II 640) RUNKINEAWXTTI alternative mRNA Library Homo sapiens cDNA mRNA sequence □ PY18158 full-length enriched swine cDNA library, adult cranz Sus scrota cDNA clone METC-175016 5. mRNA sequence □ FY19472 full-length enriched swine cDNA library, adult cranz Sus scrota cDNA clone WTR01009508 5. mRNA sequence □ HXT1542 Conchura strata donestica juvenile PS0 brain cDNA library Notamacropus eugenii cDNA clone METC-175016 5. mRNA sequence □ FY451626 full-length enriched swine cDNA library, adult cranz Sus scrota cDNA clone METC-175016 5. mRNA sequence □ FY451626 full-length enriched tammar graied sterus cDNA library Notamacropus eugenii cDNA clone MEGC-002015 7. mRNA sequence □ FY451636 full-length enriched tammar graied sterus cDNA library Notamacropus eugenii cDNA clone MEGC-002015 7. mRNA sequence □ FY451636 full-length enriched tammar graied sterus cDNA library Notamacropus eugenii cDNA clone MEGC-007C15 7. mRNA sequence □ FY451636 full-length enriched swine cDNA library Notamacropus eugenii cDNA clone MEGC-007C15 7. mRNA sequence □ FY451636 full-length enriched swine cDNA library Notamacropus eugenii cDNA clone MEGC-007C15 7. mRNA sequence	490 487 484 481 476 474 462 459 458 457 466 446 446 440 434 432 431	490 487 484 481 481 551 474 462 459 458 457 456 446 446 444 432 490 433	47% 40% 48% 47% 48% 44% 39% 40% 45% 45% 45% 35% 38% 41%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 7e-154 8e-154 9e-152 2e-149 3e-149 7e-149 1e-148	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 89.26% 89.26% 89.25% 80.29% 88.21% 80.08% 93.58% 94.31% 83.20%	JZ534326.1 FY616286.1 FY475875.1 FY475875.1 FY475875.1 FY486468.1 BU132241.1 CX852794.2 JZ534361.1 BP141580.1 FY719472.1 BW967031.1 HX771542.1 FY545165.1 FY545685.1 FY5474447.1 DT890669.1 FS709366.1 DY760558.1
□ RUBYLIRURAYTT [II 011] RINKYIRURXYTT alternative mRNA Library Homo sapiens cDNA clone MEGC-063J11 3. mRNA sequence □ YY515285 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-063J11 3. mRNA sequence □ YY725975 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-069812 5. mRNA sequence □ YY25975 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-039813 5. mRNA sequence □ YY35975 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-032013 5. mRNA sequence □ S03119770F1 CSF-0CH-22 Gallus gallus cDNA clone ChEST7918 5. mRNA sequence □ G03119770F1 CSF-0CH-22 Gallus gallus cDNA clone ChEST7918 5. mRNA sequence □ GNA LIBRAY III III 6401 RNAX178URXXIT1 alternative mRNA Library Homo sapiens cDNA clone MA mRCG-076975 5. mRNA sequence □ PY15128 full-length enriched swine cDNA library, adult ovary. Sus scrofs cDNA clone OVR01009410 5. mRNA sequence □ PY15128 full-length enriched swine cDNA library, adult ovary. Sus scrofs cDNA clone OVR01009509 5. mRNA sequence □ PY15128 full-length enriched swine cDNA library, adult ovary. Sus scrofs cDNA clone OVR01009509 5. mRNA sequence □ PY15128 full-length enriched swine cDNA library Notamacropus eugenii cDNA clone MEGC-076115 5. mRNA sequence □ YY51528 full-length enriched swine cDNA library Notamacropus eugenii cDNA clone MEGC-076115 5. mRNA sequence □ YY51528 full-length enriched swine cDNA library Notamacropus eugenii cDNA clone MEGC-076115 7. mRNA sequence □ YY51528 full-length enriched swine cDNA library Notamacropus eugenii cDNA clone MEGC-076115 7. mRNA sequence □ YY51528 full-length enriched swine cDNA sequence cDNA library Notamacropus eugenii cDNA clone MEGC-076115 7. mRNA sequence □ YY51528 full-length enriched swine cDNA sequence cDNA library Notamacropus eugenii cDNA clone MEGC-076115 7. mRNA sequence □ YY51528 full-length enriched swine cDNA clone SDNA sequence cDNA sequence cDNA sequence cDNA sequence cDN	490 487 484 481 478 474 462 459 457 456 446 440 434 432 431 433 428	490 487 484 481 481 551 474 462 459 458 457 456 446 446 440 434 432 490 433 428	47% 48% 44% 49% 40% 45% 45% 45% 36% 41% 36%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 8e-154 9e-152 2e-149 3e-149 7e-149 1e-148 7e-148	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 69.25% 95.56% 79.78% 80.29% 88.21% 79.78% 80.06% 93.58% 94.31% 83.20% 87.50%	JZ534326.1 FY516286.1 FY475875.1 FY475875.1 FY475875.1 FY486468.1 BU132241.1 CX852794.2 JZ534361.1 BP141580.1 FY719472.1 BP141580.1 FY719472.1 FY545165.1 FY516285.1 FY474447.1 DT890969.1 FS709366.1 DYF80558.1 JZ719072.1
□ RUNKURURKUTT	490 487 484 481 481 474 462 459 456 446 446 444 434 432 431 433 428 424	480 487 484 481 481 474 462 459 458 446 446 440 434 432 490 433 428 424	47% 40% 48% 47% 48% 44% 49% 45% 45% 45% 36% 43% 35% 38% 41% 36% 35%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 8e-154 9e-152 2e-149 3e-149 7e-149 1e-148 7e-148 1e-145	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.25% 95.56% 79.76% 88.21% 83.20% 83.20% 83.20% 83.20% 83.20% 83.20% 83.20% 83.20% 83.20% 83.20% 83.20%	UZ534326.1 FY516286.1 FY475875.1 FY729972.1 FY1896468.1 BU132241.1 CX862794.2 UZ534361.1 BP141580.1 FY718472.1 BW967031.1 HX771542.1 FY545165.1 FY474447.1 DT890969.1 FS790356.1 DY760558.1 UZ719072.1 FS890666.1 FG663165.1
□ PLYS1525 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-053113 mRNA sequence □ PLYS15275 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-053113 mRNA sequence □ PLYS1575 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-053115 mRNA sequence □ PLYS15275 full-length enriched tammar testis cDNA library Notamacropus sugenii cDNA clone MEGC-028115 mRNA sequence □ PLYS1575 full-length enriched tammar testis cDNA library Notamacropus sugenii cDNA clone MEGC-023113 mRNA sequence □ PLYS1575 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-023113 mRNA sequence □ PLYS1575 full-length enriched sevine cDNA library solamacropus sugenii cDNA clone MEGC-023113 mRNA sequence □ PLYS1575 full-length enriched sevine cDNA library Notamacropus sugenii cDNA clone MEGC-023113 mRNA sequence □ PLYS1575 full-length enriched sevine cDNA library solamacropus sugenii cDNA clone MEGC-023115 mRNA sequence □ PLYS1575 full-length enriched sevine cDNA library Notamacropus sugenii cDNA clone MEGC-023115 mRNA sequence □ PLYS1575 full-length enriched sevine cDNA library Notamacropus sugenii cDNA clone MEGC-023115 mRNA sequence □ PLYS1575 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-023115 mRNA sequence □ PLYS1575 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-033115 mRNA sequence □ PLYS1575 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-033115 mRNA sequence □ PLYS1575 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-033115 mRNA sequence □ PLYS1575 full-length enriched sevine cDNA library Notamacropus sugenii cDNA clone MEGC-033115 mRNA sequence □ PLYS1575 full-length enriched sevine cDNA library Notamacropus sugenii cDNA clone MEGC-035115 mRNA sequence □ PLYS1575 full-length enriched sevine cDNA lib	490 487 484 481 481 476 474 462 459 456 446 446 440 434 432 431 433 428 424 423	480 487 484 481 481 474 462 459 458 446 446 440 434 432 490 433 428 424 423	47% 40% 48% 47% 48% 44% 49% 45% 45% 36% 35% 38% 41% 36% 35% 42%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 9e-159 1e-158 2e-157 7e-154 8e-154 2e-149 1e-148 7e-148 1e-148 1e-145 6e-145	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 92.44% 89.26% 95.76% 80.29% 88.21% 83.20% 79.78% 80.08% 93.58% 94.32% 83.20% 83.20% 83.20% 83.20% 83.20% 83.20% 84.20% 85.20% 85.20% 85.20% 85.20% 86	UZ534326.1 FY616286.1 FY616286.1 FY7616286.1 FY7616286.1 FY7616286.1 FY7616286.1 FY761626.1
RUNXITEURINYTT	490 487 484 481 481 476 474 462 459 458 457 456 446 440 434 432 431 433 428 424 423 419	490 487 484 481 481 474 462 459 458 457 456 446 440 434 432 490 433 428 424 423 419	47% 40% 48% 47% 48% 44% 39% 40% 37% 45% 45% 45% 45% 43% 35% 45% 45% 44% 43% 44% 43%	9e-171 6e-170 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 2e-167 7e-154 8e-154 2e-149 1e-148 7e-149 1e-148 1e-145 6e-145 1e-143	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 87.80% 87.80% 80.29% 88.21% 83.20% 87.20% 80.20% 83	JZ534328.1 FY616286.1 FY475876.1 FY729972.1 FY729972.1 FY729972.1 GW62794.2 JZ534361.1 BP141580.1 FY719472.1 BW96703.1 HX771642.1 FY51628.1 FY516285.1 FY51636.1 DY760558.1 JZ719072.1 EB89686.1 FG663165.1 CK771788.1 DT268011.1
BURXYIRUPXYTT (IL 011) RURXYIRUPXYTT alternative mRNA Library Home sapiens cDNA clone MEGC-053/11 7. mRNA sequence PY515285 full-length enriched tammar gradid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-053/11 7. mRNA sequence PY72577 full-length enriched tammar gradid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-03611 5. mRNA sequence PY72577 full-length enriched tammar gradid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-03311 5. mRNA sequence PY455578 full-length enriched tammar gradid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-03311 5. mRNA sequence G03119770F1 CSECOCH.22 Gallus gallus cDNA clone CREST7918 5. mRNA sequence RURXYIRURXYIT (II 840) RURXYIRUWXIT alternative mRNA Library Home sepiens cDNA clone MACE-756575 5. mRNA sequence BY11580 full-length enriched swine cDNA library, abdit overy Sus scrote active common metric common market common market cDNA library victorascopus sugenii cDNA clone METC-175016 5. mRNA sequence BY11581 full-length enriched swine cDNA library, soluti overy Sus scrote active cDNA clone dMETC-175016 5. mRNA sequence BY151582 full-length enriched swine cDNA library, soluti overy Sus scrote active cDNA clone dMETC-175016 5. mRNA sequence BY151582 full-length enriched tammar gradid uterus cDNA silbrary Notamacropus sugenii cDNA clone MEGC-032M15 5. mRNA sequence PY5151583 full-length enriched tammar gradid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-032M15 5. mRNA sequence PY5151584 full-length enriched tammar gradid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-032M15 5. mRNA sequence BY17338 Figliallength enriched swine cDNA library solution sugenii cDNA clone MEGC-032M15 5. mRNA sequence BY17338 Figliallength enriched swine cDNA library solution sugenii cDNA clone MEGC-037C15 5. mRNA sequence BY17338 Figliallength enriched swine cDNA clone Size scrote cDN	490 487 484 481 478 474 462 459 456 446 440 434 431 433 428 424 424 421 419	490 487 484 481 481 474 462 459 456 446 440 434 432 490 433 428 424 423 419 419	47% 40% 48% 47% 48% 44% 39% 40% 37% 45% 45% 45% 45% 45% 45% 45% 45% 45% 45	9e-171 1e-168 1e-167 1e-168 1e-167 2e-167 1e-166 3e-165 4e-160 4e-159 9e-159 1e-158 8e-157 7e-154 8e-154 9e-152 2e-149 1e-148 1e-145 6e-145 1e-143 3e-143	81.53% 91.50% 79.79% 80.14% 80.00% 87.80% 87.80% 89.25% 95.56% 79.78% 80.29% 88.21% 80.29% 88.21% 80.29% 88.320% 93.58% 94.31% 83.20% 84.52% 84.52% 85.56% 85.56% 86.56% 8	\(\frac{1}{2} \) \(\frac{1} \) \(\frac{1}{2} \) \(\frac{1}{2} \) \(\frac{1}{2} \) \(\frac{1} \) \(\frac{1} \) \(\frac{1}{2} \) \(\frac{1}{2} \) \(
RURXYTRURKYTT II b11 PRINKYRWRXTT1 alternative mPRNA Library Home sagiens cDNA clone MEGC-06311 3. mRNA sequence Y515285 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-069812 5. mRNA sequence Y725975 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-069812 5. mRNA sequence Y725975 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-032013 5. mRNA sequence Y428585 full-length enriched tammar gravid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-032013 5. mRNA sequence G0319770F1 CSEGCH-22 Gallus gallus cDNA clone CREST7918 5. mRNA sequence G0319770F1 CSEGCH-22 Gallus gallus cDNA clone CREST7918 5. mRNA sequence G0319770F1 CSEGCH-22 Gallus gallus cDNA clone CREST7918 5. mRNA sequence G0319770F1 (SEGCH-22 Gallus gallus cDNA clone CREST7918 5. mRNA sequence G1415180 full-length enriched swine cDNA library Notamacropus eugenii cDNA clone MEGC-07018 5. mRNA sequence G1415180 full-length enriched swine cDNA library adult ovary. Sus scrofa cDNA clone MEGC-07018 5. mRNA sequence G1415181 clone the enriched swine cDNA library adult ovary. Sus scrofa cDNA clone MEGC-07018 5. mRNA sequence G1415182 full-length enriched swine cDNA library. Adult ovary. Sus scrofa cDNA clone MEGC-07018 5. mRNA sequence G1415182 full-length enriched swine cDNA library. Notamacropus eugenii cDNA clone MEGC-07018 5. mRNA sequence G1415182 full-length enriched swine cDNA library. Notamacropus eugenii cDNA clone MEGC-07018 5. mRNA sequence G1415185 full-length enriched swine cDNA clone scroll shary Notamacropus eugenii cDNA clone MEGC-07018 5. mRNA sequence G142673 MARC 78017 Bost saurus cDNA 5. mRNA sequence sequence cDNA mRNA sequence cDNA clone scroll shary Notamacropus eugenii cDNA clone MEGC-07018 5. mRNA sequence G142673 MARC 78017 Bost saurus cDNA 5. mRNA sequence cDNA mRNA sequence cDNA clone scroll shary Notamacropus eugenii cDNA clone MEGC-07018 5. mRNA sequence	490 487 484 481 481 478 474 462 459 457 456 446 440 434 432 431 433 428 424 423 419 419 419	490 487 484 481 481 551 474 462 459 458 457 456 446 440 434 432 490 433 428 424 423 419 419 4112	47% 40% 48% 47% 48% 44% 39% 40% 37% 45% 40% 36% 35% 35% 41% 36% 35% 42% 43% 43% 43% 45%	9e-171 1e-168 1e-167 1e-168 1e-167 1e-166 1e-166 3e-165 4e-160 9e-159 1e-158 2e-157 7e-154 9e-152 2e-149 3e-149 1e-148 1e-145 1e-143 3e-144 1e-143 1e-143 1e-143	81.53% 91.50% 97.79% 80.14% 80.00% 87.80% 89.24% 89.25% 95.55% 79.76% 88.21% 83.20% 79.78% 83.20% 97.36% 83.20% 97.50% 97.50% 97.50% 97.50% 97.50% 97.50% 97.50% 97.50% 97.50% 97.50%	UZ534326.1 FY516286.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1 BU132241.1 GX852794.2 UZ534361.1 BP141580.1 FY719472.1 FW967031.1 HX771542.1 FY545165.1 FY416424.1 FY41647.1 DT890969.1 FX719872.1 GX8566.1 FX719872.1 GX8719872.1 GX8719872.1 GX8719872.1 GX8719872.1 GX8719872.1 GX8719872.1 GX8719872.1 GX9719872.1 GX971
BARKIRUNKTT II UTI FUNKTRURKTT i alternative mRNA Library Homo sapiens cDNA mRNA sequence CY45525 Mil-length seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-098117 5. mRNA sequence CY45525 Mil-length seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-098112 5. mRNA sequence CY45545 Mil-length seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-093119 5. mRNA sequence CY45545 Mil-length seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-093119 5. mRNA sequence CY455458 Mil-length seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-093119 5. mRNA sequence G93119778F1 CSEOCH 22 Gallus gallus cDNA close CNEST7918 5. mRNA sequence G93119778F1 CSEOCH 22 Gallus gallus cDNA close MAGE-7669775 2. mRNA sequence G941185 Mil-length seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-09316 5. mRNA sequence G97118472 Mil-length seriched tammar testis cDNA bitary Notamacropus superii cDNA close MEGC-175016 5. mRNA sequence G97118472 Mil-length seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-093111 5. mRNA sequence G97118472 Mil-length seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-093111 5. mRNA sequence G97118474 Mak seriched tammar grand uterus cDNA bitary Notamacropus superii cDNA close MEGC-093111 5. mRNA sequence G97118447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97118447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97119447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97119447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97119447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G971194467 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97119447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97119447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97119447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97119447 MAGE RDOV Bes tamurs cDNA S. mRNA sequence G97119447 MAGE R	490 487 484 481 481 474 462 459 455 446 446 444 432 431 433 428 424 423 419 419	490 487 484 481 481 551 474 462 459 458 457 456 446 440 434 432 439 433 428 424 423 419 419 412 502	47% 40% 48% 47% 48% 44% 39% 40% 37% 45% 40% 42% 45% 36% 35% 35% 42% 43% 43% 43% 43% 43% 43% 43% 43% 43%	9e-171 1e-168 1e-167 1e-168 1e-167 1e-166 1e-166 1e-166 1e-166 1e-166 1e-166 1e-169 1e-159 1e-158 1e-159 1e-158 1e-149 1e-148 1e-140 1e-143 1e-144 1e-144 1e-144 1e-144 1e-145 1e-143 1e-140	81.53% 91.50% 79.79% 80.14% 80.10% 80.20% 89.26% 99.56% 79.76% 80.29% 80.29% 83.20% 79.78% 81.52% 80.09% 93.58% 83.20% 87.50% 93.58% 87.50% 91.63% 91.63% 91	UZ534326.1 FY516286.1 FY516286.1 FY475875.1 FY729972.1 FY485458.1 BU132241.1 CX852794.2 UZ534361.1 BP141580.1 FY718472.1 BW967031.1 HX771542.1 FY545165.1 FY545165.1 FY545265.1 CX771788.1 DY769558.1 UZ719072.1 E8895656.1 FG663165.1 CKZ771788.1 DT268011.1 CQ35483363.1 CA483363.1
BURXITEURXITT (IL DIT) RUNKURUNXITT alternative mRNA Library Home sapiens cDNA clone MEGC-05311.3 mRNA sequence PYS15285 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-059812.5 mRNA sequence PYS15275 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-059812.5 mRNA sequence PYS15275 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-03211.5 mRNA sequence PYS15275 full-length enriched tammar gravid uterus cDNA library Notamacropus sugenii cDNA clone MEGC-03211.5 mRNA sequence G03119770F1 CSECCH1.22 Gallus gallus cDNA clone CREST7918.5 mRNA sequence G03119770F1 CSECCH1.22 Gallus gallus cDNA clone CREST7918.5 mRNA sequence BURXISHUNXITI (IL MG) RUNKURWIXII alternative mRNA Library Home sapiens cDNA clone MRGC-078617.5 mRNA sequence BYS15185 full-length enriched swine cDNA library. solut overy Sus scrofe cDNA clone MRTC-175016.5 mRNA sequence BYS15185 full-length enriched swine cDNA library. solut overy Sus scrofe cDNA clone MRTC-175016.5 mRNA sequence BYS15185 full-length enriched swine cDNA library. solut overy Sus scrofe cDNA clone OVR010095608.5 mRNA sequence BYS15185 full-length enriched swine cDNA library. solut overy Sus scrofe cDNA clone OVR010095608.5 mRNA sequence BYS15185 full-length enriched swine cDNA library. solut overy Sus scrofe cDNA clone oVR010095608.5 mRNA sequence BYS15185 full-length enriched swine cDNA library. solut overy Sus scrofe cDNA clone oVR010095608.5 mRNA sequence BYS15185 full-length enriched swine cDNA library. solutence suspenii cDNA clone MEGC-007C15.5 mRNA sequence BYS15185 full-length enriched swine cDNA library. solutence suspenii cDNA clone MEGC-007C15.5 mRNA sequence BYS15185 full-length enriched swine cDNA sequence suspenii cDNA clone MEGC-007C15.5 mRNA sequence BYS15185 full-length enriched swine cDNA clone solutence suspenii cDNA clone MEGC-007C15.5 mRNA sequence BYS15185 full-length enriched swine cDNA clone solutence suspenii cD	490 487 484 481 481 476 474 462 459 456 446 440 434 432 431 433 428 424 423 419 419 412 411 372	490 487 484 481 481 455 459 458 446 446 440 434 432 490 433 428 424 423 419 419 412 502 524	47% 40% 48% 47% 48% 44% 39% 40% 37% 45% 45% 45% 36% 43% 35% 38% 41% 36% 42% 43% 43% 43% 43% 43% 43%	9e-171 6e-170 1e-168 1e-167 2e-167 2e-167 2e-167 3e-165 3e-165 4e-159 9e-159 9e-159 2e-149 7e-144 8e-154 7e-144 1e-145 6e-145 1e-148 3e-143 3e-143 3e-143	81.5% 91.50% 91.50% 91.50% 91.50% 90.14% 80.14% 89.25% 99.26% 88.21% 83.20% 87.80% 93.58% 94.31% 83.20% 87.60% 76.43% 74.90% 76.43% 72.53% 70.90% 90.58% 90.58% 90.58% 90.58%	UZ534326.1 FY516286.1 FY516286.1 FY475875.1 FY729972.1 FY486468.1 BU132241.1 CX852794.2 UZ534361.1 BP141580.1 FY719472.1 FY719472.1 FY945165.1 FY4545165.1 FY474447.1 DT890969.1 FS709366.1 DY7905658.1 UZ71972.1 FG89666.1 FG663165.1 CK771788.1 CC935493.1 CQ935493.1 CA488368.1

Selected homolog:



GenBank → Send to: →

FY735850 full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone METC-219F05 5', mRNA sequence

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GenBank: FY735850.1
FASTA Graphics
Go to: ☑
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            Notamacropus eugenii cDNA clone METC-219F05 5', mRNA sequence.
ACCESSION FY735850
VERSION
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DBT.TNK
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           Mammalia; Metatheria; Diprotodontia; Macropodidae; Notamacropus.
REFERENCE
           1 (bases 1 to 761)
 AUTHORS Fujiyama, A., Kuroki, Y., Toyoda, A. and Tatsumoto, S.
 TITLE
           Macropus eugenii testis EST
 JOURNAL
           Unpublished (2011)
COMMENT
            Contact: Fujiyama A
            Comparative Genomics Laboratory
            National Institute of Genetics
            Yata 1111, Mishima, Shizuoka 411-8540, Japan
            expressed in testis.
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      601 gagaatgggc tgacgagtgg aaacatcttg atcatgctct gaattgcatc atggagatgg
      661 tagagaaaac ccgacgttcc atggctgtcc tgcggcgctg ccaggaaact gatagggaag
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[03] Novel Protein Information

Species: Notamacropus Eugenii (Tammar Wallaby)

Novel Protein Name: CBFA2T1

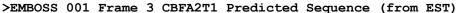
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>EMBOSS 001 Frame 1

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>EMBOSS 001 Frame 2

LCPLWHLAASNNGTYPGVTVRIK*GQPSPVAERAAALCPGSQADPFPVPGPA*TPPAQHK
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WDWLKWRIPGGAGGPPFDRERMG*RVETS*SCSELHHGDGRENPTFHGCPAALPGN**GR
TQLLEATMQ*EHRX



CVHCGT*LPLIMALTLGLP*GSNEANLPLLQRELLHCARAAKQTPSQYLAQHEHLLLNTN TTSPADSAELLIEVHGNGKRHSPDRREDTSFERDPVPPEPPAKRVCTISPAPRHSPALSL PLMNPGGQFHPTPPPLQHYTLEDFATSHLYRDSTKMLEHREIRGGGGNGGSGGGGDRHH GIGLNGGYQEELVDHRLTEREWADEWKHLDHALNCIMEMVEKTRRSMAVLRRCQETDREE LNFWKRRCSENTE

>EMBOSS 001 Frame 4

LCSHCIVASKS*VLPYQFPGSAAGQPWNVGFSLPSP*CNSEHDQDVSTRQPILSLSNGGP PAPPGILHLSQSHDAYHHHRHRCHHYHHHHGFLDVPASWWSPCRGVKWQNLPRYNVGEAV GWDGTAHQDS*GAGRELDYAGEQG*WCTLSWREAQGGLGLSQSWYLLSCQDCVSCHCRVL L*EALQSQLGRWYLC*AGGVHAGPGTGKGSAWLPGHSAAALSATGEGWPHLILTVTPG*V PLLEAARCHSGHS

>EMBOSS 001 Frame 5

SVFSLHRRFQKLSSSLSVSWQRRRTAMERRVFSTISMMQFRA*SRCFHSSAHSLSVKRWS TSSSWYPPFKPIP*CLSPPPPPLPPLPPPRISRCSSILVESL*RCEVAKSSKV*CWRGG GVGWNCPPGFMRGRERAGLCRGAGLMVHTLLAGGSGGTGSLSKLVSSLLSGLCLLPLPCT SIRSSAESAGEVVFVLSRRCSCWARYWEGVCLAARAQCSSSLCNRGRLASFDPHGNPRVS AIIRGS*VPOWTOX

>EMBOSS 001 Frame 6

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[Q4]Proof of Novelty

>EMBOSS 001 Frame 3 CBFA2T1 Predicted Sequence (from EST)

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Sigma			43.6362						

