

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:

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

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TTPR

| Search Parameters | | |
|----------------------------|----------------------|---------|
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| Word size | 6 | |
| Expect value | 50 | |
| Hitlist size | 1000 | |
| Gapcosts | 15,2 | |
| Matrix | BLOSUM45 | |
| Low Complexity Filter | Yes | |
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| Genetic Code | 1 | |
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| Threshold | 21 | |
| Composition-based stats | 2 | |
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| Database | | |
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| Number of letters | 43,196,422,130 | |
| Number of sequences | 77,551,161 | |
| Entrez query | None | |
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| Lambda | 0.224821 | 0.203 |
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| H | 0.239842 | 0.12 |
| Alpha | 0.9113 | 1.7 |
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| Sigma | | 45.0604 |

Blast Output:

| Alignments | | Download Graphics | | | | | | | | | |
|--------------------------|------------------------|--|-----------|-------------|-------------|---------|-----------|-------------|--|--|--|
| | | Description | Max Score | Total Score | Query Cover | E value | Per Ident | Accession | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0241 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 917 | 917 | 82% | 0.0 | 87.32% | J2534339.1 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0271 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 889 | 889 | 80% | 0.0 | 86.71% | J2534342.1 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0580 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 760 | 760 | 69% | 0.0 | 85.04% | J2719078.1 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0221 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 750 | 750 | 69% | 0.0 | 84.89% | J2534337.1 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0211 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 707 | 707 | 65% | 0.0 | 84.17% | J2534336.1 | | | |
| <input type="checkbox"/> | ILUMIGEN_MCO_37794 | Katze_MMBR Macaca mulatta cDNA clone JBUW-15671 5' similar to Bases 1 to 978 highly similar to human CBFA2T1 (Hs 90858)_mRNA sequence | 633 | 633 | 53% | 0.0 | 90.80% | C8802185.1 | | | |
| <input type="checkbox"/> | ILUMIGEN_MCO_8705 | Katze_MMBR Macaca mulatta cDNA clone JBUW-3993 5' similar to Bases 1 to 1027 highly similar to human CBFA2T1 (Hs 90858)_mRNA sequence | 631 | 631 | 54% | 0.0 | 89.09% | C8643811.1 | | | |
| <input type="checkbox"/> | ILUMIGEN_MCO_26195 | Katze_MMBR Macaca mulatta cDNA clone JBUW-8574 5' similar to Bases 1 to 1016 highly similar to human CBFA2T1 (Hs 90858)_mRNA sequence | 617 | 617 | 52% | 0.0 | 91.77% | C8646434.1 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0571 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 614 | 614 | 57% | 0.0 | 83.77% | J2719077.1 | | | |
| <input type="checkbox"/> | FY489999 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-028C01 5' mRNA sequence | 580 | 580 | 49% | 0.0 | 89.63% | FY489999.1 | | | |
| <input type="checkbox"/> | JGI_CAAR13181 | rev NIH_XGC_tropLvl Xenopus tropicalis cDNA clone IMAGE:7745385 3' mRNA sequence | 575 | 575 | 50% | 0.0 | 80.11% | DN038564.1 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0511 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 556 | 556 | 52% | 0.0 | 82.76% | J2719071.1 | | | |
| <input type="checkbox"/> | ILUMIGEN_MCO_36701 | Katze_MMBR Macaca mulatta cDNA clone JBUW-12939 5' similar to Bases 1 to 969 highly similar to human CBFA2T1 (Hs 90858)_mRNA sequence | 544 | 544 | 53% | 0.0 | 80.75% | C8806491.1 | | | |
| <input type="checkbox"/> | FY475876 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-009B12 5' mRNA sequence | 539 | 539 | 43% | 0.0 | 92.54% | FY475876.1 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0201 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 537 | 607 | 52% | 0.0 | 92.22% | J2534335.1 | | | |
| <input type="checkbox"/> | AGENCOURT_15564393 | Organ of Corti Mus musculus cDNA clone IMAGE:30519742 5' mRNA sequence | 531 | 531 | 45% | 0.0 | 91.64% | CF554058.1 | | | |
| <input type="checkbox"/> | AGENCOURT_8932057 | NIH_MGC_94 Mus musculus cDNA clone IMAGE:6465835 5' mRNA sequence | 526 | 526 | 41% | 0.0 | 96.02% | B0946132.1 | | | |
| <input type="checkbox"/> | FY486469 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-023G13 3' mRNA sequence | 526 | 526 | 44% | 0.0 | 90.00% | FY486469.1 | | | |
| <input type="checkbox"/> | 603765010F1 | CSEQRBN13 Gallus gallus cDNA clone CHEST68944 5' mRNA sequence | 523 | 523 | 43% | 0.0 | 93.08% | B4445478.1 | | | |
| <input type="checkbox"/> | 60374890F1 | CSEQRBN10 Gallus gallus cDNA clone CHEST35602 5' mRNA sequence | 515 | 562 | 45% | 0.0 | 93.65% | B0356862.1 | | | |
| <input type="checkbox"/> | 603121328F1 | CSEQRBN12 Gallus gallus cDNA clone CHESTR388 5' mRNA sequence | 511 | 511 | 43% | 8e-180 | 89.85% | B0133396.1 | | | |
| <input type="checkbox"/> | G1142P33RG15.T0 | Anolis carolinensis pooled normalized Brain cDNA Library Anolis carolinensis cDNA_mRNA sequence | 512 | 512 | 42% | 9e-180 | 92.91% | F0665317.1 | | | |
| <input type="checkbox"/> | gPGC_EST05636 | Embryonic gonadal PGC cDNA Library Gallus gallus cDNA 5' mRNA sequence | 516 | 516 | 50% | 4e-179 | 81.82% | D8416794.1 | | | |
| <input type="checkbox"/> | JGI_CAAS16566 | rev CAAS Pimephales promelas brain 7-8 month adults_males and females pooled (H) Pimephales promelas cDNA clone CAAS16566 5' mRNA sequence | 508 | 508 | 43% | 2e-178 | 88.39% | D7210543.1 | | | |
| <input type="checkbox"/> | 296646 | Pigtailed macaque ovary library Macaca nemestrina cDNA 5' mRNA sequence | 502 | 502 | 42% | 5e-176 | 91.41% | E8522745.1 | | | |
| <input type="checkbox"/> | AGENCOURT_6752472 | NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5768973 5' mRNA sequence | 503 | 503 | 50% | 2e-175 | 79.41% | B09067971.1 | | | |
| <input type="checkbox"/> | 0206050FLV1011028HT | OFVY Ovis aries cDNA_mRNA sequence | 496 | 496 | 42% | 6e-174 | 91.86% | E0771493.1 | | | |
| <input type="checkbox"/> | CCUA7226.b1 | CCUA Peromyscus polionotus subgriseus P.O.Rc.Ts Peromyscus polionotus subgriseus cDNA clone CCUA7226 5' mRNA sequence | 493 | 493 | 39% | 0e-173 | 94.19% | G8468648.1 | | | |
| <input type="checkbox"/> | JGI_CAAL6363 | rev NIH_XGC_tropRmd Xenopus tropicalis cDNA clone IMAGE:7664626 3' mRNA sequence | 491 | 491 | 40% | 7e-172 | 92.68% | C8849619.2 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0111 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 490 | 490 | 47% | 9e-171 | 81.53% | J2534326.1 | | | |
| <input type="checkbox"/> | FY516285 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-063J11 3' mRNA sequence | 487 | 487 | 40% | 6e-170 | 91.50% | FY516285.1 | | | |
| <input type="checkbox"/> | FY475875 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-009B12 5' mRNA sequence | 484 | 484 | 48% | 1e-168 | 79.79% | FY475875.1 | | | |
| <input type="checkbox"/> | FY729972 | full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone METC-203H19 5' mRNA sequence | 481 | 481 | 47% | 1e-167 | 80.14% | FY729972.1 | | | |
| <input type="checkbox"/> | FY486468 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-023G13 3' mRNA sequence | 481 | 481 | 48% | 2e-167 | 80.00% | FY486468.1 | | | |
| <input type="checkbox"/> | 603119770F1 | CSEQRBN12 Gallus gallus cDNA clone CHEST73918 5' mRNA sequence | 478 | 551 | 44% | 1e-166 | 87.80% | B0132241.1 | | | |
| <input type="checkbox"/> | JGI_CAAL9015 | rev NIH_XGC_tropRmd Xenopus tropicalis cDNA clone IMAGE:7666775 3' mRNA sequence | 474 | 474 | 39% | 3e-165 | 92.44% | C8852794.2 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0401 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 462 | 462 | 40% | 4e-160 | 89.26% | J2534361.1 | | | |
| <input type="checkbox"/> | BP141580 | full-length enriched swine cDNA library adult ovary Sus scrofa cDNA clone OVR010004A10 5' mRNA sequence | 459 | 459 | 37% | 4e-159 | 95.56% | BP141580.1 | | | |
| <input type="checkbox"/> | FY719472 | full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone METC-175D16 5' mRNA sequence | 458 | 458 | 45% | 9e-159 | 79.78% | FY719472.1 | | | |
| <input type="checkbox"/> | BW967031 | full-length enriched swine cDNA library adult ovary Sus scrofa cDNA clone OVR010085G08 5' mRNA sequence | 457 | 457 | 45% | 1e-158 | 80.29% | BW967031.1 | | | |
| <input type="checkbox"/> | HX771542 | Lonchura striata domestica juvenile P60 brain cDNA library Lonchura striata domestica cDNA clone 60P06B12 mRNA sequence | 456 | 456 | 40% | 2e-157 | 88.21% | HX771542.1 | | | |
| <input type="checkbox"/> | FY545165 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-102M15 5' mRNA sequence | 446 | 446 | 42% | 7e-154 | 83.20% | FY545165.1 | | | |
| <input type="checkbox"/> | FY516285 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-063J11 3' mRNA sequence | 446 | 446 | 45% | 8e-154 | 79.78% | FY516285.1 | | | |
| <input type="checkbox"/> | FY474447 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-007C15 3' mRNA sequence | 440 | 440 | 36% | 9e-152 | 91.52% | FY474447.1 | | | |
| <input type="checkbox"/> | 1472073 | MARC_7BOV Bos taurus cDNA 3' mRNA sequence | 434 | 434 | 43% | 2e-149 | 80.08% | D7090969.1 | | | |
| <input type="checkbox"/> | F8709366 | full-length enriched swine cDNA library adult pituitary gland Sus scrofa cDNA clone PTG010056G11 5' mRNA sequence | 432 | 432 | 35% | 3e-149 | 93.58% | F8709366.1 | | | |
| <input type="checkbox"/> | 171385 | Pigtailed macaque ovary library Macaca nemestrina cDNA 5' mRNA sequence | 431 | 490 | 38% | 7e-149 | 94.31% | DY760558.1 | | | |
| <input type="checkbox"/> | RUNX1/RUNX1T1 [J] 0521 | RUNX1/RUNX1T1 alternative mRNA Library Homo sapiens cDNA_mRNA sequence | 433 | 433 | 41% | 1e-148 | 83.20% | J2719072.1 | | | |
| <input type="checkbox"/> | 11034662 | ZF260L Danio rerio cDNA clone 3522197 mRNA sequence | 428 | 428 | 36% | 7e-148 | 87.50% | E8896866.1 | | | |
| <input type="checkbox"/> | G1142P33RG15.T0 | Anolis carolinensis pooled normalized Brain cDNA Library Anolis carolinensis cDNA_mRNA sequence | 424 | 424 | 35% | 1e-145 | 91.63% | F0665316.1 | | | |
| <input type="checkbox"/> | 960177 | MARC_1BOV Bos taurus cDNA 3' mRNA sequence | 423 | 423 | 42% | 6e-145 | 74.90% | Ck771788.1 | | | |
| <input type="checkbox"/> | JGI_CAAV2085 | rev CAAV Pimephales promelas testis 7-8 month adults_males and females pooled (H) Pimephales promelas cDNA clone CAAV2085 5' mRNA sequence | 419 | 419 | 43% | 1e-143 | 76.43% | D7268011.1 | | | |
| <input type="checkbox"/> | AGENCOURT_30545169 | NIH_ZGC_19 Danio rerio cDNA clone IMAGE:7433658 5' mRNA sequence | 419 | 419 | 43% | 3e-143 | 72.53% | C0935493.1 | | | |
| <input type="checkbox"/> | AGENCOURT_10809605 | MAPcL Homo sapiens cDNA clone IMAGE:6720124 5' mRNA sequence | 412 | 412 | 45% | 1e-140 | 70.96% | C4488368.1 | | | |
| <input type="checkbox"/> | FY474446 | full-length enriched tammar grauid uterus cDNA library Notamacropus eugenii cDNA clone MEGC-007C15 3' mRNA sequence | 411 | 502 | 43% | 8e-140 | 92.23% | FY474446.1 | | | |
| <input type="checkbox"/> | JGI_CAAL12111 | rev NIH_XGC_tropRmd Xenopus tropicalis cDNA clone IMAGE:7669806 5' mRNA sequence | 372 | 524 | 43% | 1e-139 | 90.58% | C8876387.1 | | | |
| <input type="checkbox"/> | FY727998 | full-length enriched tammar testis cDNA library Notamacropus eugenii cDNA clone METC-198C23 5' mRNA sequence | 407 | 407 | 44% | 1e-138 | 71.54% | FY727998.1 | | | |

Selected homolog:

Download

GenBank

Graphics

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

Sequence ID: [FY735850.1](#) Length: 761 Number of Matches: 1

Range 1: 72 to 752 [GenBank](#) [Graphics](#)

Next Match

Previous Match

| Score | Expect | Method | Identities | Positives | Gaps | Frame |
|---------------|---|------------------------------|--------------|--------------|------------|-------|
| 252 bits(846) | 3e-78 | Compositional matrix adjust. | 136/227(60%) | 168/227(74%) | 14/227(6%) | +3 |
| Query 186 | KANLPELLQRELLHCARLAKQNPAQYLAQHEQLLLDASTTSPVDSSELLLDVNENGRRTF | 245 | | | | |
| | +ANLPELLQRELLHCAR AKQ P+QYLAQHE+LLL+ +TTSP DS+ELL++V+ NGKR +P | | | | | |
| Sbjct 72 | EANLPELLQRELLHCARAAKQTPSQYLAQHEHLLNTNTTSPADSAELLIEVHGNGKRHSP | 251 | | | | |
| Query 246 | DRTKENGFDREPLHSEHPSKRPECTISPGQRYSPNNGLSYQpn-glphptppppQHYRLDD | 304 | | | | |
| | DR ++ F+R+P+ E P+KR CTISP R+SP L G HPTPPP QHY L+D | | | | | |
| Sbjct 252 | DRREDTSFERDPVPPPEPPAKRVCTISFAPRHSPALSLPLMNPGGQFHPTPPPLQHYTLED | 431 | | | | |
| Query 305 | MAIAHHYRDSYRHPSHRD-----LRDRNRPMGLHGTRQEEMIDHRLTDREWA | 351 | | | | |
| | A +H YRDS + HR+ DR+ +GL+G QEE++DHRLT+REWA | | | | | |
| Sbjct 432 | FATSHLYRDSFKMLEHREIRGGGGNGSGGGGGDRHHGIGLNGGYQEELVDHRLTEREWA | 611 | | | | |
| Query 352 | EEWKHLDDLNCIMDMVEKTRRS+VLRRCQEADREELNYWIRRYSD | 398 | | | | |
| | +EWKHLDH LNCIM+MVEKTRRS+ VLRRCQE DREELN+W RR S+ | | | | | |
| Sbjct 612 | DEWKHLDH LNCIMEMVEKTRRSMAVLRRCQETDREELNFWKRCSE | 752 | | | | |

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

GenBank: FY735850.1

[FASTA](#) [Graphics](#)[Go to:](#) ☑

LOCUS FY735850 761 bp mRNA linear EST 18-JUL-2011

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

ACCESSION FY735850

VERSION FY735850.1

DBLINK BioSample: [SAMN00626946](#)

KEYWORDS EST.

SOURCE Notamacropus eugenii (tammar wallaby)

ORGANISM [Notamacropus eugenii](#)Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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.

FEATURES Location/Qualifiers

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testis cDNA library"
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ORIGIN

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601 gagaatgggc tgacgagtgg aaacatcttg atcatgctct gaattgcacg atggagatgg
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721 aactcaactt ttggaagcga cgatgcagtg agaacacaga g
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[Q3] Novel Protein Information

Species: Notamacropus Eugenii (Tammar Wallaby)
Novel Protein Name: **CBFA2T1**

Novel Protein Translated.

>EMBOSS_001_Frame 1

TVSTVAPSL**WHLPGYREDQMRPTFPCCRESCCTVPGQPSRPLPSTWPSMNTSCSTQ
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CPS*ILVGSSIPPHRLSNIIPWKILPLHTSTGTTPRCWNIEKSVVVVMVA AVVVVIGI
MGLA*MEDTRRSWTTV*QRENGLTSGNILIML*IASWRW*RKPDVPWLSCGAARKLIGK
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>EMBOSS_001_Frame 2

LCPLWHLAASNNGTYPGVTVRIK*GQPSPVAERAAALCPGSQADPFVPVGPATPPAQHK
YHLPS*LCRASRSTRQWQETQS*QERRYQL*ERPSPP*ASRQESVHHQPCSPA*SSSLP
APHESWWAVPSHPTASPTLYLGRFCHFTPLQGLHQDAGTSRNPWWW*WQWRWW**AS
WDWLKWRIPGGAGGPPFDRERMGRVETS*SCSELHHGDGRENPTFHGCPAALPGN**GR
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>EMBOSS_001_Frame 3 CBFA2T1 Predicted Sequence (from EST)

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>EMBOSS_001_Frame 4

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PLLEAARCHSGHS

>EMBOSS_001_Frame 5

SVFSLHRRFQKLSSSLSVSWQRRRTAMERRVFSTISMMQFRA*SRCFHSSAHSLSVKRWS
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GVGWNCPPGFMGRERAGLCRGAGLMVHTLLAGGSGGTGSLSKLVSSLLSGLCCLLPCT
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>EMBOSS_001_Frame 6

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CHY*QLGATVDTV



[Q4]Proof of Novelty

>EMBOSS_001_Frame 3 CBFA2T1 Predicted Sequence (from EST)

GSNEANLPLLQRELLHCARAAKQTPSQYLAQHEHLLNTNTTSPADSAELLIEVHGNGKR
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LED FATSHLYR DSTKMLEHREIRGGGGNGGSGGGGGDRHHGIGLNGGYQEELVDHRLTER
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| Search Parameters | | |
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| Filter string | F | |
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| Window Size | 40 | |
| Threshold | 21 | |
| Composition-based stats | 2 | |
| | | |
| Database | | |
| Posted date | Apr 7, 2019 12:42 AM | |
| Number of letters | 75,469,528,019 | |
| Number of sequences | 209,552,778 | |
| Entrez query | None | |
| | | |
| Karlin-Altschul statistics | | |
| Lambda | 0.315062 | 0.267 |
| K | 0.133619 | 0.041 |
| H | 0.416918 | 0.14 |
| Alpha | 0.7916 | 1.9 |
| Alpha_v | 4.96466 | 42.6028 |
| Sigma | | 43.6362 |

| Sequences producing significant alignments: | | | | | | |
|---|-------------|-----------|-------------|-------------|---------|------------|
| Select All None Selected 0 | | | | | | |
| Alignments Download GenPept Graphics Distance tree of results Multiple alignment | | | | | | |
| | Description | Max Score | Total Score | Query Cover | E value | Per. Ident |
| <input type="checkbox"/> protein CBFA2T2 isoform X2 [Vombatus ursinus] | | 461 | 461 | 98% | 1e-158 | 95.65% |
| <input type="checkbox"/> protein CBFA2T2 isoform X3 [Vombatus ursinus] | | 461 | 461 | 98% | 2e-158 | 95.65% |
| <input type="checkbox"/> protein CBFA2T2 isoform X1 [Vombatus ursinus] | | 462 | 462 | 98% | 4e-158 | 95.65% |
| <input type="checkbox"/> protein CBFA2T2 isoform X3 [Phascogaster cinereus] | | 456 | 456 | 98% | 6e-157 | 94.78% |
| <input type="checkbox"/> protein CBFA2T2 isoform X1 [Phascogaster cinereus] | | 456 | 456 | 98% | 7e-157 | 94.78% |
| <input type="checkbox"/> protein CBFA2T2 isoform X2 [Phascogaster cinereus] | | 457 | 457 | 98% | 1e-156 | 94.78% |
| <input type="checkbox"/> PREDICTED: protein CBFA2T2 isoform X2 [Ornithorhynchus anatinus] | | 420 | 420 | 98% | 7e-143 | 87.39% |
| <input type="checkbox"/> PREDICTED: protein CBFA2T2 isoform X1 [Ornithorhynchus anatinus] | | 420 | 420 | 98% | 9e-143 | 87.39% |
| <input type="checkbox"/> PREDICTED: protein CBFA2T2 [Piceoides pubescens] | | 412 | 412 | 97% | 2e-140 | 85.46% |
| <input type="checkbox"/> Protein CBFA2T2 [Piceoides pubescens] | | 410 | 410 | 97% | 3e-140 | 85.46% |
| <input type="checkbox"/> PREDICTED: protein CBFA2T2 [Aquila chrysaetos canadensis] | | 413 | 413 | 98% | 6e-140 | 85.65% |
| <input type="checkbox"/> protein CBFA2T2 isoform X1 [Athene cucullata] | | 413 | 413 | 98% | 6e-140 | 85.65% |
| <input type="checkbox"/> protein CBFA2T2 isoform X2 [Athene cucullata] | | 413 | 413 | 98% | 6e-140 | 85.65% |
| <input type="checkbox"/> Protein CBFA2T2 [Lonchura striata domestica] | | 412 | 412 | 98% | 8e-140 | 85.22% |
| <input type="checkbox"/> protein CBFA2T2 isoform X2 [Lonchura striata domestica] | | 412 | 412 | 98% | 9e-140 | 85.22% |
| <input type="checkbox"/> Protein CBFA2T2 [Charadrius vociferus] | | 410 | 410 | 98% | 1e-139 | 84.78% |
| <input type="checkbox"/> protein CBFA2T2 isoform X3 [Corapipo altera] | | 412 | 412 | 98% | 1e-139 | 85.65% |
| <input type="checkbox"/> Protein CBFA2T2 [Mastomys natalensis] | | 412 | 412 | 98% | 2e-139 | 85.22% |
| <input type="checkbox"/> protein CBFA2T2 isoform X3 [Cyanistes caeruleus] | | 412 | 412 | 98% | 2e-139 | 85.22% |
| <input type="checkbox"/> PREDICTED: protein CBFA2T2 isoform X8 [Serinus canaria] | | 412 | 412 | 98% | 2e-139 | 85.22% |
| <input type="checkbox"/> PREDICTED: protein CBFA2T2 isoform X5 [Serinus canaria] | | 412 | 412 | 98% | 2e-139 | 85.22% |
| <input type="checkbox"/> PREDICTED: LOW QUALITY PROTEIN: protein CBFA2T2 [Charadrius vociferus] | | 410 | 410 | 98% | 2e-139 | 84.78% |
| <input type="checkbox"/> protein CBFA2T2 isoform X1 [Cyanistes caeruleus] | | 412 | 412 | 98% | 2e-139 | 85.22% |

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