

OUTILS :

PARTIE PRATIQUE

Exercice BLAST

- Quel est la localisation génomique de *BBS1*?
 - Séquence protéique:
 - Recherche de la séquence protéique BBS1 dans les archives du génome humain août 2010.
 - <http://www-bio3d-igbmc.u-strasbg.fr/~jmmuller/enseignement.html>
 - <http://www.ensembl.org/info/website/archives/index.html>
 - TBLASTN sur le génome humain

We would like to hear your impressions of blastview, especially regarding functionality that you would like to see provided in the future. Many thanks for your time. [\[Feedback\]](#)

Content-type: text/plain

TBLASTN 2.OMP-WashU [04-May-2006] [linux26-x64-I32LPF64 2006-05-10T17:22:28]

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Reference: Gish, W. (1996-2006) <http://blast.wustl.edu>

Query= unnamed
(737 letters)

WARNING: Precomputed values for Lambda, K and H are unavailable for the BLOSUM80 scoring matrix, when used with gap penalties +9 and +2. Unless overridden on the command line, the values computed for ungapped alignments will be used instead, but the reported E-values and P-values may be much too low.

Database: Homo_sapiens.GRCh37.dna.toplevel.fa
297 sequences; 32,036,512,383 total letters.

WARNING: Use of the hspsepSmax parameter should be considered with long database sequences, to improve the biological relevance of the HSP groups that are assembled and to improve the statistical discrimination of these groups from random background.

Searching...10...20...30...40...50...60...70...80...90...100% done

WARNING: hspmax=1000 was exceeded by 37 of the database sequences, causing the associated cutoff score, S2, to be transiently set as high as 73.

Sequences producing High-scoring Segment Pairs:	Reading Frame	High Score	Probability P(N)	Smallest Sum N
9 dna:chromosome chromosome:GRCh37:9:1:141213431:1 REF	-3	1765	0.	6
11 dna:chromosome chromosome:GRCh37:11:1:133888201:1 REF	-3	703	0.72	22
4 dna:chromosome chromosome:GRCh37:4:1:191154276:1 REF	+3	1542	5.5e-250	4
20 dna:chromosome chromosome:GRCh37:20:1:63025520:1 REF	-1	131	0.0035	9
16 dna:chromosome chromosome:GRCh37:16:1:90354753:1 REF	+1	120	0.014	10
12 dna:chromosome chromosome:GRCh37:12:1:133851895:1 REF	-2	126	0.060	11
19 dna:chromosome chromosome:GRCh37:19:1:59128983:1 REF	-1	128	0.069	9
22 dna:chromosome chromosome:GRCh37:22:1:51304566:1 REF	+1	130	0.10	10
GL000199.1 dna:supercontig supercontig:GRCh37:GL000199.1:...	+3	149	0.11	2
14 dna:chromosome chromosome:GRCh37:14:1:107349540:1 REF	+2	167	0.21	8
1 dna:chromosome chromosome:GRCh37:1:1:249250621:1 REF	-1	134	0.25	8
GL000220.1 dna:supercontig supercontig:GRCh37:GL000220.1:...	-3	124	0.26	4
5 dna:chromosome chromosome:GRCh37:5:1:180915260:1 REF	+1	127	0.33	9
GL000224.1 dna:supercontig supercontig:GRCh37:GL000224.1:...	-2	126	0.49	2
7 dna:chromosome chromosome:GRCh37:7:1:159138663:1 REF	-3	129	0.88	9
21 dna:chromosome chromosome:GRCh37:21:1:48129895:1 REF	-2	131	0.98	9
GL000237.1 dna:supercontig supercontig:GRCh37:GL000237.1:...	-2	89	0.98	5
GL000202.1 dna:supercontig supercontig:GRCh37:GL000202.1:...	+1	111	0.995	3
GL000218.1 dna:supercontig supercontig:GRCh37:GL000218.1:...	-1	145	0.996	5
15 dna:chromosome chromosome:GRCh37:15:1:102531392:1 REF	+2	134	0.999	12
6 dna:chromosome chromosome:GRCh37:6:1:171115067:1 REF	-2	118	0.9991	13
3 dna:chromosome chromosome:GRCh37:3:1:198022430:1 REF	-3	118	0.9998	11
GL000206.1 dna:supercontig supercontig:GRCh37:GL000206.1:...	-3	92	0.99992	6

>9 dna:chromosome chromosome:GRCh37:9:1:141213431:1 REF
Length = 141,213,431

Score = 1765 (578.9 bits), Expect = 0., Sum P(6) = 0.
Identities = 220/261 (84%), Positives = 230/261 (88%), Frame = -3

Query: 477 INPETGEQIQSWYRSGETWDSKFSSTIASSYEECRAESVGLYLCLHPQVLEIFGFEGADAE 536
INPE EQIQSWYRS+TWDSKFSSTI SSYEECRAESVGLYLCLHPQVLE FGFEGADAE
Sbjct: 76090065 INPEMREQIQSWYRSMTKWTWDSKFSSTI SSYEECRAESVGLYLCLHPQVLETFGFEGADAE 76089886

Query: 537 DVIIYVNWLNVMVRAGLLALEFYTPFAFNWRQAHMQARFVILRVLLEAGEGLVITITPTTGS 596
+VI VNWLNMV AGLLALEFYTPFA NW+QAH++AR VILRVL EAGEGL TITPT GSD
Sbjct: 76089885 EVISVNWLNVMVGAGLLALEFYTPFA SNWQAHIRARIVILRVLPEAGEGLTITPTAGSD 76089706

Query: 597 GRPDARVRLDRSKIRSVGKPALEFRRLRQLVKSTGDVAGGRALYEGYATVTDAPPECFL 656
GRP+A+VRLDRSKI+SVG PALERFLRR STGDVAGG LYE YA V DAPPE FL
Sbjct: 76089705 GRPEAQVRLDRSKIQSVGNPALERFLRRCC---STGDVAGGWTLTYERYAAVADAPPEGFL 76089535

Query: 657 TLRDVTLLRKESRKLIVQPNTRLEGS DVQLLEYEASAAGLIRSFSEFPEDGPELEEILT 716
TLRD VLLRKES KLIVQPN RLEGS DVQLLEYE SAAGLIRSFSE FPEG ELE+ILT
Sbjct: 76089534 TLRDRVLLRKESWKLVQPNTRLEGS DVQLLEYEVSAAAGLIRSFSEHFPEDELEEDILT 76089355

Query: 717 QLATADARFWKGPSEAPSGQA 737
QLATADA+F KGPSEAPSGQA
Sbjct: 76089354 QLATADAQF*KGPSEAPSGQA 76089292

Score = 1700 (557.6 bits), Expect = 0., Sum P(6) = 0.
Identities = 212/252 (84%), Positives = 221/252 (87%), Frame = -2

Query: 224 PSLDSEVTSKLKSYEFRGSPFQVTRGDYAPILQKVVEQLEKAKAYAANSHQGMQLAQYIE 283
P L + SKLKS EFRGSPFQVT G+Y PILQKVVEQLEKAK YAANSHQ QMLAQYIE
Sbjct: 76090816 PGLRGD--SKLKS*EFRGSPFQVTWGNYPILQKVVEQLEKAKTYAANSHQGMQLAQYIE 76090643

Query: 284 SFTQGSIEAHRKGRSFRWIQDKGPIVESYIFGIESYRDPFGSRGFEFVAVVNKAMSAKF 343
SFTQGS EAHK+GSRFWI DKGPIVESYI FI+SYRD FGSRG EGFVAVVNKAMSAKF
Sbjct: 76090642 SFTQGSIEAHRKGRSFRWI*DKGPIVESYIEFIQSYRDSFGSRGCEGFVAVVNKAMSAKF 76090463

Query: 344 ERLVASAEQLLKEPWPPTFEKDKFLTPDFTSLDVLTFAGSGIPAGINIPNYDDLRTQTEG 403
E LV SAEQLLKEPWP P FEKDKFLTPDFTS+DVLTFAGSGI AGINI NY+DL+QTEG
Sbjct: 76090462 EWLVSVAEQLLKEPWPAPFEKDKFLTPDFTSVDVLTFAGSGIAAGINISNYNDLRTQTEG 76090283

Query: 404 FKNVSLGNVLAVAYATQREKLTFLFEEDDKDLYILWKGPSFDVQVGLHELLGHGSGKFLVQ 463
FKNVSLGNVLAV ATQ EKLT LEE DKDLYI+ GPSFDVQVGLHELLG+GSGKL Q
Sbjct: 76090282 FKNVSLGNVLAVV*ATQWEKLTVLEESDKDLYIIVLWKGPSFDVQVGLHELLGHGSGKFLVQ 76090103

Query: 464 DEKGAFNFDQET 475
DEKGAFNFDQET
Sbjct: 76090102 DEKGAFNFDQET 76090067

Est-ce que le chromosome 9 est la bonne localisation?

Exercice BLAST

new SETUP CONFIG RESULTS DISPLAY

Displaying unnamed sequence alignments vs Homo_sapiens LATESTGP database

Showing top 100 alignments of 1961, sorted by Raw Score

refresh

Alignment Locations vs. Karyotype (click arrow to hide)

Alignment Locations vs. Query (click arrow to hide)

coverage

HSPs

HSPs

refresh Online Help

Summary

setup

- Homo_sapiens
- Genomic sequence
- TBLASTN
- Low sensitivity

configure

- E: 10
- B: 100
- filter: seg
- W: 4
- hitdist: 40
- matrix: BLOSUM80
- T: 16

results

Alignment Summary (click arrow to hide)

Select rows to include in table, and type of sort (Use the 'ctrl' key to select multiples)

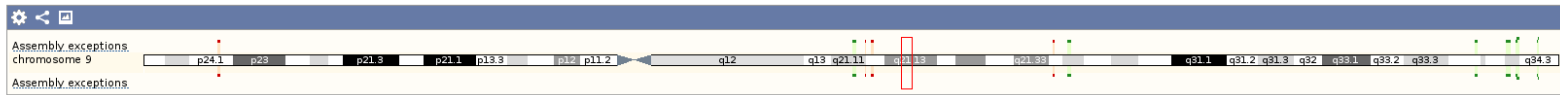
refresh

Query	Subject	Chromosome	Supercontig	Clone	Contig	Lrg	Stats	Sort By
<input type="checkbox"/> _off_	<input type="checkbox"/> off	<input type="checkbox"/> _off_	<input type="checkbox"/> off	<input type="checkbox"/> off	<input type="checkbox"/> off	<input type="checkbox"/> off	<input type="checkbox"/> _off_	>Lrg
<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Name	<input type="checkbox"/> Score	<Score
<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> Start	<input type="checkbox"/> E-val	>Score

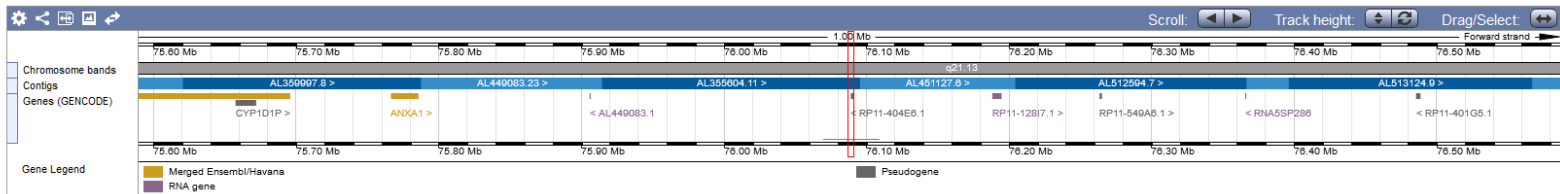
Links	Query	Subject	Chromosome	Start	End	Ori	Score	E-val	%ID	Length	
[A] [S] [G] [C]	477	737	+	Chr:9	76089292	76090065	-	1765	0.	84.29	261
[A] [S] [G] [C]	224	475	+	Chr:9	76090067	76090816	-	1700	0.	84.13	252
[A] [S] [G] [C]	119	577	+	Chr:4	65296878	65298248	+	1542	5.5e-250	49.70	497
[A] [S] [G] [C]	581	729	+	Chr:4	65298493	65298930	+	854	5.5e-250	74.83	151
[A] [S] [G] [C]	1	90	+	Chr:11	66249672	66249941	+	763	3.2e-292	100.00	90
[A] [S] [G] [C]	330	399	+	Chr:11	66260186	66260395	+	552	3.2e-292	95.71	70
[A] [S] [G] [C]	565	679	+	Chr:11	66264763	66265104	+	531	3.2e-292	63.71	124
[A] [S] [G] [C]	1	90	+	Chr:4	65296627	65296899	+	529	5.5e-250	76.09	92
[A] [S] [G] [C]	588	721	+	Chr:11	66271972	66272364	+	487	1.7e-276	55.63	142
[A] [S] [G] [C]	681	737	+	Chr:11	66276549	66276719	+	477	3.2e-292	100.00	57
[A] [S] [G] [C]	120	166	+	Chr:11	66254008	66254148	+	391	1.8e-273	97.87	47
[A] [S] [G] [C]	420	526	+	Chr:11	66262674	66262961	+	384	3.2e-292	53.57	112
[A] [S] [G] [C]	486	597	+	Chr:11	66263006	66263296	+	377	1.7e-276	51.72	116
[A] [S] [G] [C]	266	309	+	Chr:11	66258962	66259093	+	375	3.2e-292	97.73	44
[A] [S] [G] [C]	209	266	+	Chr:11	66258657	66258854	+	370	3.2e-292	75.76	66
[A] [S] [G] [C]	384	432	+	Chr:11	66260513	66260650	+	310	5.1e-263	83.67	49
[A] [S] [G] [C]	90	126	+	Chr:11	66252641	66252751	+	272	3.2e-292	89.19	37
[A] [S] [G] [C]	432	463	+	Chr:11	66261009	66261104	+	270	1.7e-276	96.88	32
[A] [S] [G] [C]	192	242	+	Chr:11	66255385	66255576	+	268	1.3e-266	64.06	64
[A] [S] [G] [C]	196	230	+	Chr:9	76090801	76090905	-	257	0.	88.57	35
[A] [S] [G] [C]	129	191	+	Chr:11	66254628	66254813	+	248	3.2e-292	56.06	66

Exercice BLAST

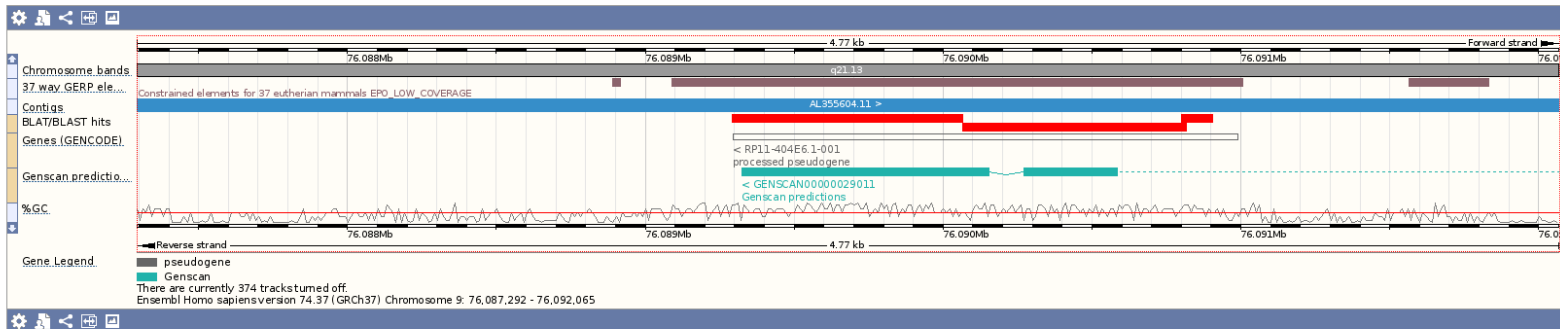
Chromosome 9: 76,087,292-76,092,065



Region in detail



Location: 9:76087292-76092065 Gene:



Exercice BLAST

>11 dna:chromosome chromosome:GRCh37:11:1:135006516:1 REF
Length = 135,006,516

Score = 763 (251.7 bits), Expect = 3.2e-292, Sum P(9) = 3.2e-292
Identities = 90/90 (100%), Positives = 90/90 (100%), Frame = +3

Query: 1 MADTQYILPNDIGVSSSLDCREAFRLSPTEERLYAYHLSRAAWYGGGLAVLLQTSPEAPYIY 60
MADTQYILPNDIGVSSSLDCREAFRLSPTEERLYAYHLSRAAWYGGGLAVLLQTSPEAPYIY
Sbjct: 66249672 MADTQYILPNDIGVSSSLDCREAFRLSPTEERLYAYHLSRAAWYGGGLAVLLQTSPEAPYIY 66249851

Query: 61 ALLSRLFRAQDPDQLRQHALLAEGLTEEEYQ 90
ALLSRLFRAQDPDQLRQHALLAEGLTEEEYQ
Sbjct: 66249852 ALLSRLFRAQDPDQLRQHALLAEGLTEEEYQ 66249941

Score = 552 (182.8 bits), Expect = 3.2e-292, Sum P(9) = 3.2e-292
Identities = 67/70 (95%), Positives = 68/70 (97%), Frame = +2

Query: 330 GFVAVVNKAMSAKFERLVAASAEQQLKELPWPPTFEKDKFLTDFDTSLDVLTFFAGSGIPAG 389
GFVAVVNKAMSAKFERLVAASAEQQLKELPWPPTFEKDKFLTDFDTSLDVLTFFAGSGIPAG
Sbjct: 66260186 GFVAVVNKAMSAKFERLVAASAEQQLKELPWPPTFEKDKFLTDFDTSLDVLTFFAGSGIPAG 66260365

Query: 390 INIPNYDDL 399
INIPN + LR
Sbjct: 66260366 INIPNCECLR 66260395

Score = 531 (175.9 bits), Expect = 3.2e-292, Sum P(9) = 3.2e-292
Identities = 79/124 (63%), Positives = 88/124 (70%), Frame = +1

Query: 565 RQAHMQARFVILRVLLEAGEGLVTIIPPTGSDGRPDARVRLDRSKIRSVGKPALEFLRR 624
RQAHMQARFVILRVLLEAGEGLVTIIPPTGSDGRPDARVRLDRSKIRSVGKPALEFLRR
Sbjct: 66264763 RQAHMQARFVILRVLLEAGEGLVTIIPPTGSDGRPDARVRLDRSKIRSVGKPALEFLRR 66264942

Query: 625 LQVLK--STGDVAGGRALYEGYATVTDAPPECFLTRDIT----VLLR--KESRKLIVQPN 676
LQV K S+G V L G T EC+ R + ++L+ K + K + P
Sbjct: 66264943 LQVSKGLSSGWVPTN--LSRG--T-----ECYQARRISCEQFLMLQ*GKVASKHVSAPG 66265092

Query: 677 -TRL 679
+RL
Sbjct: 66265093 ASRL 66265104

Score = 487 (161.6 bits), Expect = 1.7e-276, Sum P(11) = 1.7e-276
Identities = 79/142 (55%), Positives = 91/142 (64%), Frame = +1

Query: 588 TITPTGSDGRPDARVRLDRSKIRSVGK-PALERFLRLR-QVLKSTGDVAGGRALYEGYA 645
TIT G P + V R + + + G P + F QVLKSTGDVAGGRALYEGYA
Sbjct: 66271972 TIAQTIV--QG*PQSAVAYGRA-LWTPGNCPST-FTSPFSQVLKSTGDVAGGRALYEGYA 66272139

Query: 646 TVTDAPPECFLTRDITVLLRKRERKLIQVQNTRELGSDV--QLL----EYEASAAGLIRS 699
TVTDAPPECFLTRDITVLLRKRERKLIQVQNTRELG++V +LL E+ +G +
Sbjct: 66272140 TVTDAPPECFLTRDITVLLRKRERKLIQVQNTRELGNEVMRELLSSLDHHTGSPG--KQ 66272313

Query: 700 FSERFPEDGPELEEIILQLATA 721
E P G L + LQ A
Sbjct: 66272314 *-EPIP--G--LNKNLTPQGM 66272364

Score = 477 (158.3 bits), Expect = 3.2e-292, Sum P(9) = 3.2e-292
Identities = 57/57 (100%), Positives = 57/57 (100%), Frame = +3

Query: 681 GSDVQLLEYEASAAGLIRSFSEFPEDGPELEEIILQLATADARFWKGPSEAPSGQA 737
GSDVQLLEYEASAAGLIRSFSEFPEDGPELEEIILQLATADARFWKGPSEAPSGQA
Sbjct: 66276549 GSDVQLLEYEASAAGLIRSFSEFPEDGPELEEIILQLATADARFWKGPSEAPSGQA 66276719

Score = 391 (130.2 bits), Expect = 1.8e-273, Sum P(10) = 1.8e-273
Identities = 46/47 (97%), Positives = 47/47 (100%), Frame = +1

Query: 120 KEKLERVILGSEAAQQHPPEVRLWQTCGELMFSLEPRLRHLGLGKE 166
+EKLERVILGSEAAQQHPPEVRLWQTCGELMFSLEPRLRHLGLGKE
Sbjct: 66254008 QEKLERVILGSEAAQQHPPEVRLWQTCGELMFSLEPRLRHLGLGKE 66254148

Score = 384 (128.0 bits), Expect = 3.2e-292, Sum P(9) = 3.2e-292
Identities = 60/112 (53%), Positives = 68/112 (60%), Frame = +3

Query: 420 QREKLTFLLEDDKDLIYLWKGPSFDVQVGLHELLG--HGSGKLFVQDEKGFNFQDQETVI 477
Q EK F D++ I P QV E +G+G++ GA +
Sbjct: 66262674 QDEKGF--NFDQETVI---NPETGEQV--REASAEFQGTGRV---GTGGAV----ATL 66262808

Query: 478 NPETGE---QIQSWYRSGETWDSKFSSTIASSYEECRAESVGLYLCLHPQVLE 526
+P T E QIQSWYRSGETWDSKFSSTIASSYEECRAESVGLYLCLHPQVLE
Sbjct: 66262809 SP-TVELLFIQIQSWYRSGETWDSKFSSTIASSYEECRAESVGLYLCLHPQVLE 66262961

Score = 377 (125.7 bits), Expect = 1.7e-276, Sum P(11) = 1.7e-276
Identities = 60/116 (51%), Positives = 65/116 (56%), Frame = +2

Query: 486 QSWYRSGETWDSKFSSTIASSYEECRAESVGLYLCLHPQVLE---EIFGFEADAEDVIYVN 542
Q W R G W +AS G L + P IFGFEADAEDVIYVN
Sbjct: 66263006 QPWGRGG--W----VVVAGSM-----GTGQVLTILPACPSHRIFGFEADAEDVIYVN 66263149

Query: 543 WLNMMVRAGLLALEFYTPAEFNWRQAHMQARFVILRVLLEAGEGLVTIIPPTG-SDG 597
WLNMMVRAGLLALEFYTPAEFNWRQ + R L EA EG + P +G DG
Sbjct: 66263150 WLNMMVRAGLLALEFYTPAEFNWRQ--VGPWRSPL---EA-EGSLQWVFRSGCKDG 66263296

Score = 375 (125.0 bits), Expect = 3.2e-292, Sum P(9) = 3.2e-292
Identities = 43/44 (97%), Positives = 44/44 (100%), Frame = +2

Query: 266 KAYAANSHQGMQLAQYIESFTQGSIEAHKRGSRFWIQDKGPIVE 309
+AYAANSHQGMQLAQYIESFTQGSIEAHKRGSRFWIQDKGPIVE
Sbjct: 66258962 QAYAANSHQGMQLAQYIESFTQGSIEAHKRGSRFWIQDKGPIVE 66259093

Score = 370 (123.4 bits), Expect = 3.2e-292, Sum P(9) = 3.2e-292
Identities = 50/66 (75%), Positives = 53/66 (80%), Frame = +3

Query: 209 KPYYEVR-LA---SV---LGSEPSLDSEVTSKLSYEFGRSFPFQVTRGDYAPILQKVVE 260
+P+ VR L S+ L EPSLDSEVTSKLSYEFGRSFPFQVTRGDYAPILQKVVE
Sbjct: 66258657 RPFL*VRPLTPAFSL*HLLSPEPSLDSEVTSKLSYEFGRSFPFQVTRGDYAPILQKVVE 66258836

Query: 261 QLEKAK 266
QLEKAK
Sbjct: 66258837 QLEKAK 66258854

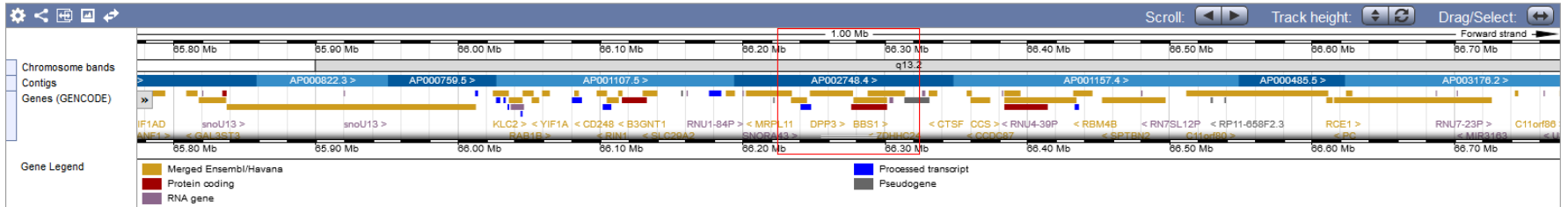
Score = 310 (103.8 bits), Expect = 5.1e-263, Sum P(12) = 5.1e-263
Identities = 41/49 (83%), Positives = 44/49 (89%), Frame = +2

Query: 384 SGIPAGINIPNYDDLRTQTEGFKNVSLGNVLA VAYATQREKLTFLLEDDK 432
SG P+ + P+ DDLRQTEGFKNVSLGNVLA VAYATQREKLTFLLEDDK
Sbjct: 66260513 SG-PSPPS-PD-DDLRQTEGFKNVSLGNVLA VAYATQREKLTFLLEDDK 66260650

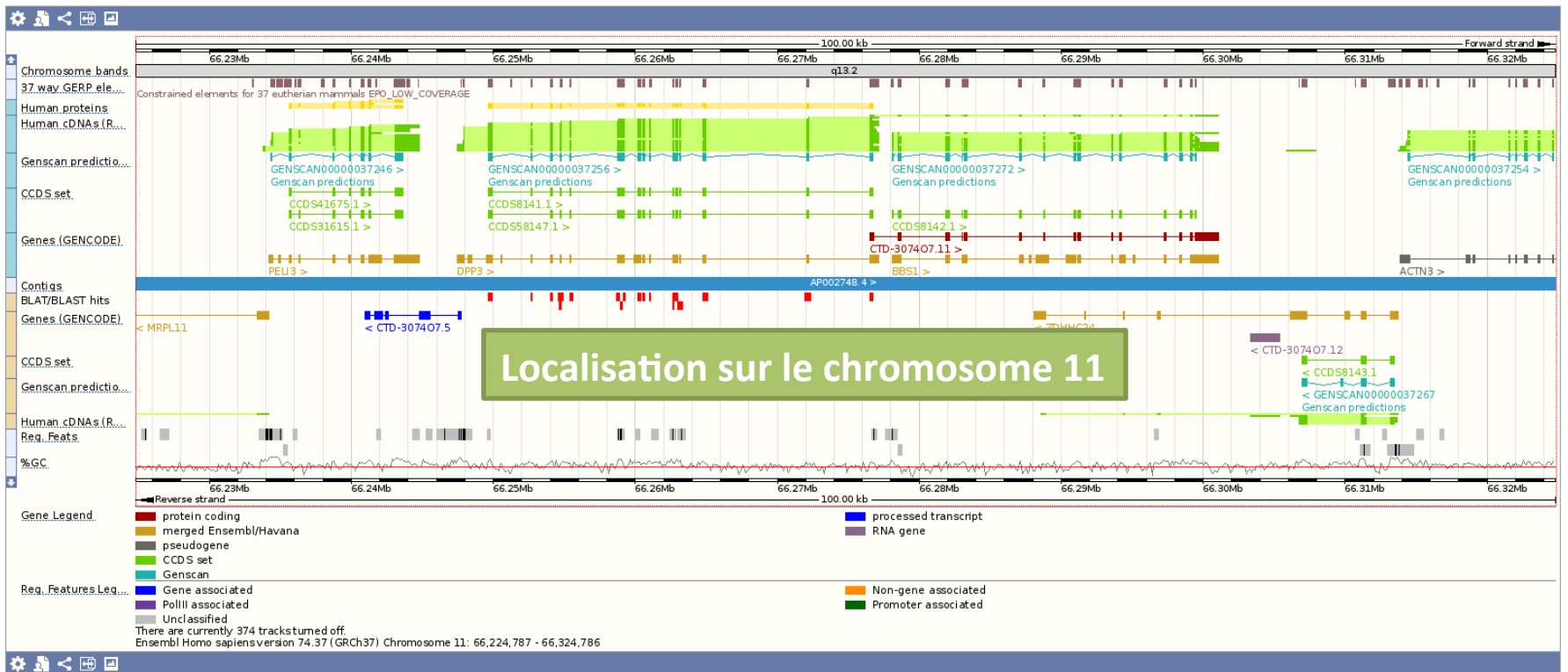
Score = 272 (91.4 bits), Expect = 3.2e-292, Sum P(9) = 3.2e-292
Identities = 33/37 (89%), Positives = 33/37 (89%), Frame = +2

Query: 90 QAFVLVYAAAGVYSNMGNYSFGDTKFVFNLPKPEKLERV 126
QAFVLVYAAAGVYSNMGNYSFGDTKFVFNLPK RV
Sbjct: 66252641 QAFVLVYAAAGVYSNMGNYSFGDTKFVFNLPKVSQGRV 66252751

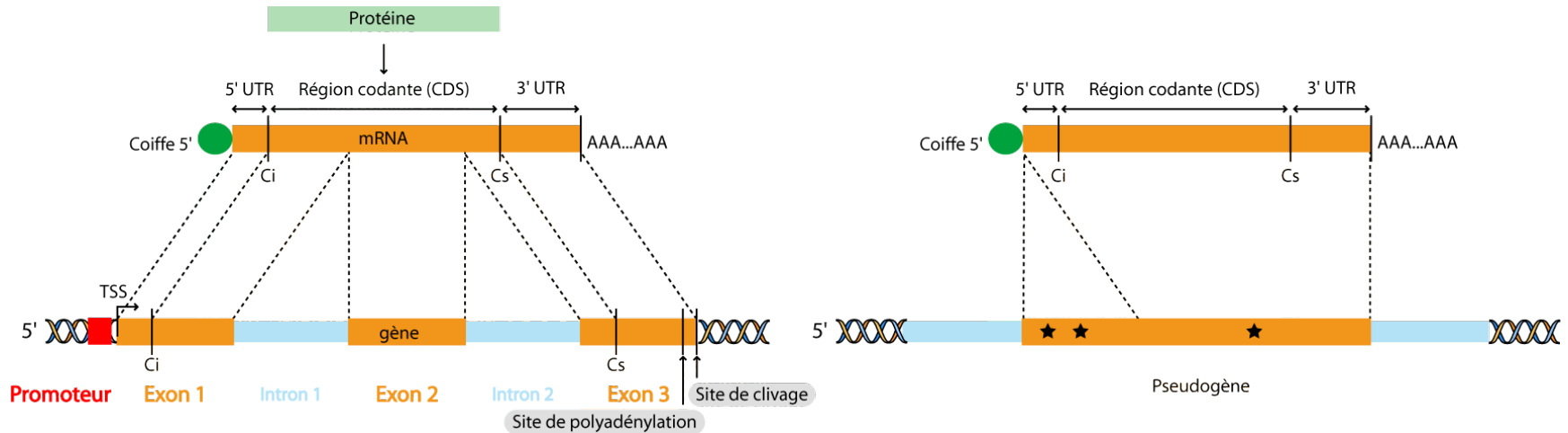
Exercice BLAST



Location: 11:66224787-66324786 Gene:



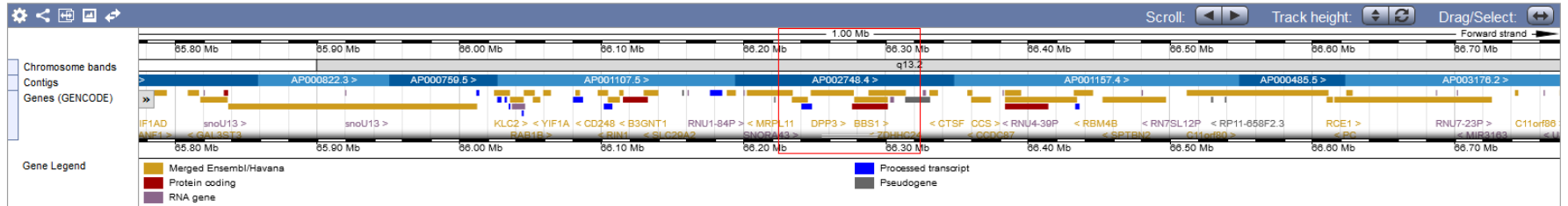
Alignement vs génome



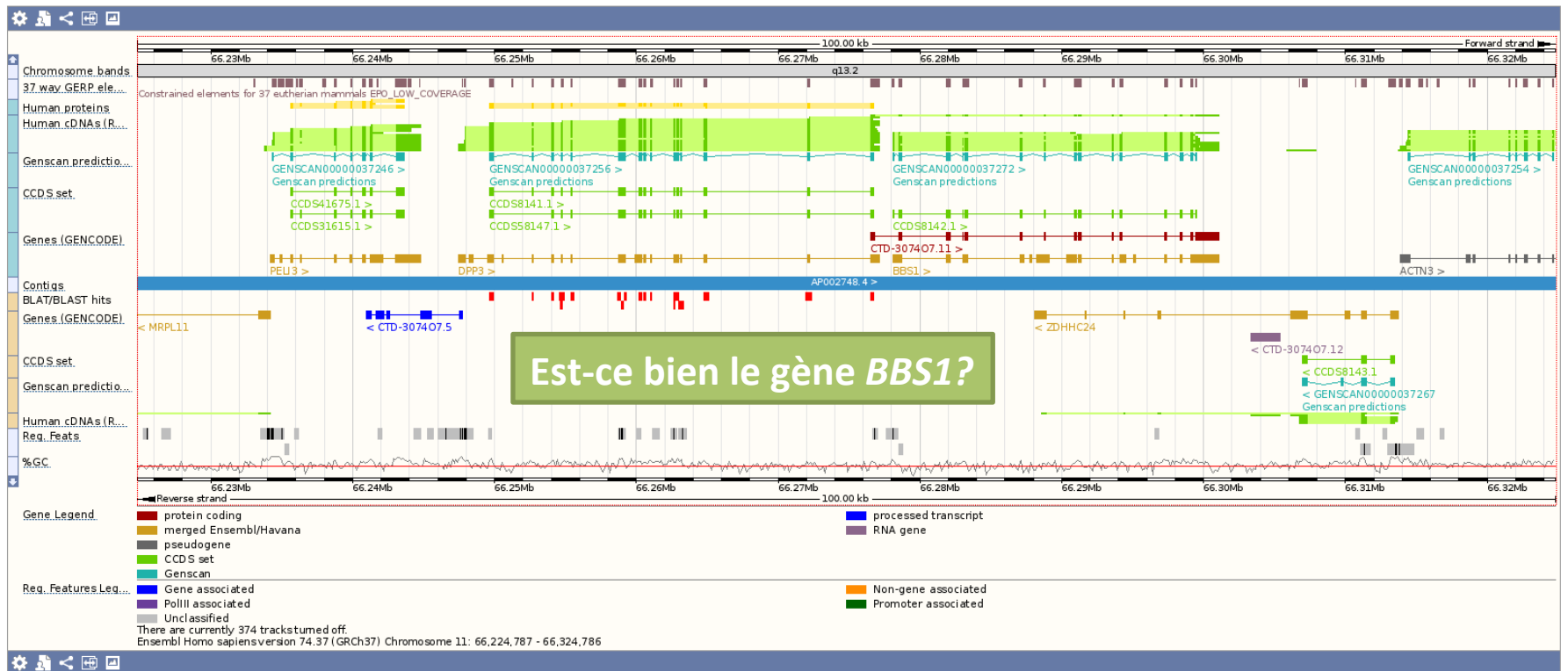
Plusieurs HSP 100% ID
 E-value plus élevée car calculée sur le
 chromosome en entier

1 ou 2 HSP >80% ID
 E-value plus faible car alignement en
 un seul bloc

Exercice BLAST



Location: Go Gene: Go



Exercice BLAST

Human (GRCh37) Location: 11:66,247,880-66,301,084 Gene: DPP3

Gene: DPP3 (ENSG00000174483)

Bardet-Biedl syndrome 1 [Source:HGNC Symbol;Acc:966]
 Location [Chromosome 11: 66,247,880-66,301,084 forward strand.](#)
 Transcripts There are 8 transcripts in this gene

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
DPP3-201	ENST00000318312	3370	ENSP00000317469	593	Protein coding	CCDS8142
DPP3-202	ENST00000335157	1722	ENSP00000335550	463	Protein coding	-
DPP3-203	ENST00000347422	1394	ENSP00000309957	317	Protein coding	-
DPP3-204	ENST00000360510	2687	ENSP00000353701	737	Protein coding	CCDS8141
DPP3-205	ENST00000393994	1382	ENSP00000377563	446	Protein coding	-
DPP3-206	ENST00000419755	2075	ENSP00000398526	630	Protein coding	-
DPP3-207	ENST00000453114	2684	ENSP00000389943	737	Protein coding	CCDS8141
DPP3-208	ENST00000455748	1678	ENSP00000405764	496	Protein coding	-

Transcript and Gene level displays

In Archive Ensembl a gene is made up of one or more transcripts. We provide displays at two levels:

- Transcript views which provide information specific to an individual transcript such as the cDNA and CDS sequences and protein domain annotation.
- Gene views which provide displays for data associated at the gene level such as orthologues, paralogues, regulatory regions and splice variants.

This view is a gene level view. To access the transcript level displays select a Transcript ID in the table above and then navigate to the information you want using the menu at the left hand side of the page. To return to viewing gene level information click on the Gene tab in the menu bar at the top of the page.

Gene summary [help](#) [Splice variants >](#)

Name [DPP3](#) (HGNC Symbol)
 CCDS This gene is a member of the Human CCDS set: [CCDS8141](#), [CCDS8142](#)
 Gene type Known protein coding
 Prediction Method Transcripts were annotated by the Ensembl [genebuild](#).

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