GTPB

The Gulbenkian Training Programme in Bioinformatics
(Since 1999)

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INSTITUTO GULBENKIAN DE CIÊNCIA

IB16S

Introductory Bioinformatics

12-16 December 2016

(Second 2016 run of this Course)

Basic Bioinformatics Sessions

Practical 3: Database Searching

Friday 2 December 2016

Searching for sequence similarities in databases.

The most popular way to investigate a sequence has always been to compare it with one of the sequence databases now accessible from sites all over the world. When sequences databases were more sparsely populated than now, the objective was to search hopefully, not always with success, for any convincingly similar sequence(s). When such a match was discovered, it could be supposed that known properties of the "similar" database sequence might provide insight to the properties of the query sequence. Now, the databases are full of sequences representative of most interesting conditions. Similarity searches are conducted in the expectation of finding many close "hits" for almost any sequence. Fewer database searches are conducted in complete ignorance of what the query sequence might be.

Here, take the **PAX6** genomic DNA sequence retrieved from **Ensembl** and conduct two searches analogous to those run in the **Ensembl** pipeline (or the equivalent **NCBI** pipeline for **Map Viewer**). Results should confirm that which has already been discovered using other sources.

blast is not the only sequence database searching program available, but it is the most popular by a very long way. **blast** searches are offered in many forms by many servers all over the world, but the most comprehensive and reliable service has to be that offered by the **NCBI**.

Go to the **NCBI** homepage at:

```
http://ncbi.nlm.nih.gov
```

Select the BLAST option (from the **Popular Resources** list). In the **Basic BLAST** section, select **nucleotide blast**. Use the **Enter Query Sequence Browse** (or **Choose File**) button to upload the file:

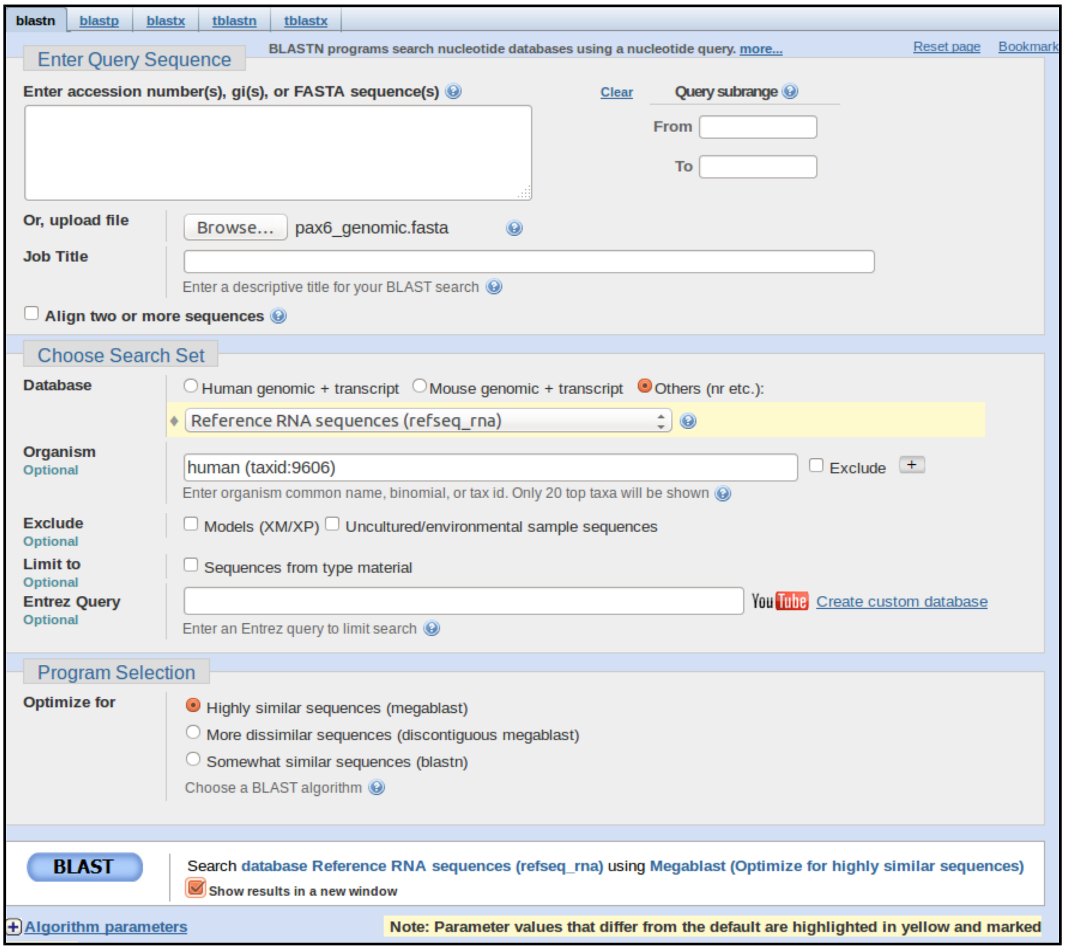
pax6_genomic.fasta.

For results like those used by **Ensembl** to predict **PAX6** transcripts, you must compare your genomic sequence to a reliable set of human mRNA/cDNA (or similar) sequences.

In the **Choose Search Set** section, set the **Database** to **Reference RNA sequences (refeseq_rna)**.

You are now able to specify an **Organism**, choose **Human**.

blast is now set to compare the **PAX6** genomic region with all **Human** mRNA sequences in **RefSeq**.



BLASTN programs search nucleotide databases using a nucleotide query. more...

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

Or, upload file: Browse... pax6_genomic.fasta

Job Title: Enter a descriptive title for your BLAST search

□ Align two or more sequences

Choose Search Set

Database: ○ Human genomic + transcript ○ Mouse genomic + transcript ● Others (nr etc.):

Reference RNA sequences (refseq_rna)

Organism Optional: human (taxid:9606) □ Exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown

Exclude Optional: □ Models (XM/XP) □ Uncultured/environmental sample sequences

Limit to Optional: □ Sequences from type material

Entrez Query Optional: Enter an Entrez query to limit search

Program Selection

Optimize for: ● Highly similar sequences (megablast) ○ More dissimilar sequences (discontiguous megablast) ○ Somewhat similar sequences (blastn)

Choose a BLAST algorithm

BLAST

Search database Reference RNA sequences (refseq_rna) using Megablast (Optimize for highly similar sequences)

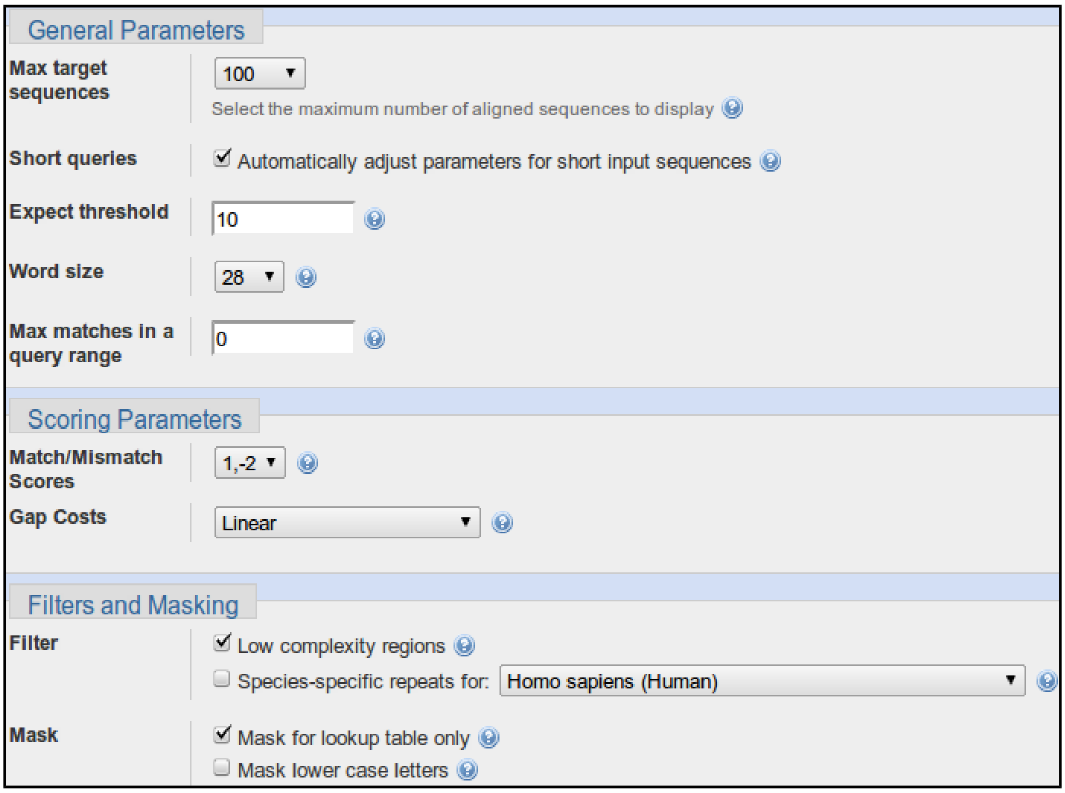
☑ Show results in a new window

Note: Parameter values that differ from the default are highlighted in yellow and marked

Note that the default **Program Selection** is **Highly similar sequences (megablast[1])**, which seems appropriate here as all the mRNA that correctly match should surely do so almost perfectly.

[1] **megablast** is a less sensitive but even faster version of **blast** only suitable when, as now, almost identical matches are sought.

Click on the **Algorithm Parameters** button. The defaults are fine here, but before starting your search, try changing the **Program Selection** and observing the different **Algorithm Parameters**.



General Parameters

Max target sequences: 100 — Select the maximum number of aligned sequences to display

Short queries: ☑ Automatically adjust parameters for short input sequences

Expect threshold: 10

Word size: 28

Max matches in a query range: 0

Scoring Parameters

Match/Mismatch Scores: 1,-2

Gap Costs: Linear

Filters and Masking

Filter: ☑ Low complexity regions
☐ Species-specific repeats for: Homo sapiens (Human)

Mask: ☑ Mask for lookup table only
☐ Mask lower case letters

The default settings of all shared parameters are identical for the two slower more sensitive **Program Selections**.

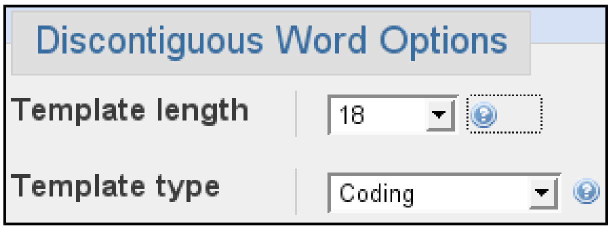
There are differences for **megablast**, where speed is of the essence and sensitivity can be sacrificed.

Smaller **Word sizes** slow searches but increase sensitivity. For **megablast** the default **Word size** is **28** otherwise it is **11**.

Gapped alignment is time consuming and, by default, considered more crudely by **megablast** than the other two algorithms[2].

Filtering and Masking matches with organism specific repeats and/or low complexity regions takes time, and so only avoiding **Low complexity regions**[3] is on by default for all **Program Selections**.

When **discontinuous megablast** is selected, an extra options section appears. Discussing how this flavour of **blast** works is a little beyond the scope of these note, but briefly. Unlike the other **Program Selections**, **discontinuous megablast** does not just look for exactly matching "words" of given size as a first step towards identifying matching regions between sequences. It looks for a pattern of matching bases within a word. For example, the default choice assumes your query is **coding** and looks for **11** matching bases within a word of **18**. Approximately, every third base is allowed not to match. Biologically, this can be justified as allowing for third codon position wobble. For more detail, use the appropriate ? button. Notice there are ? buttons by every parameter selection. Try one or two. In the process, discover:



Discontiguous Word Options

Template length: 18

Template type: Coding

When would **Mask lower case letters** be a useful thing to do? ________________________________

____

Automatically adjust parameters for short input sequences is independent of **Program selection**, and so remains unaltered.

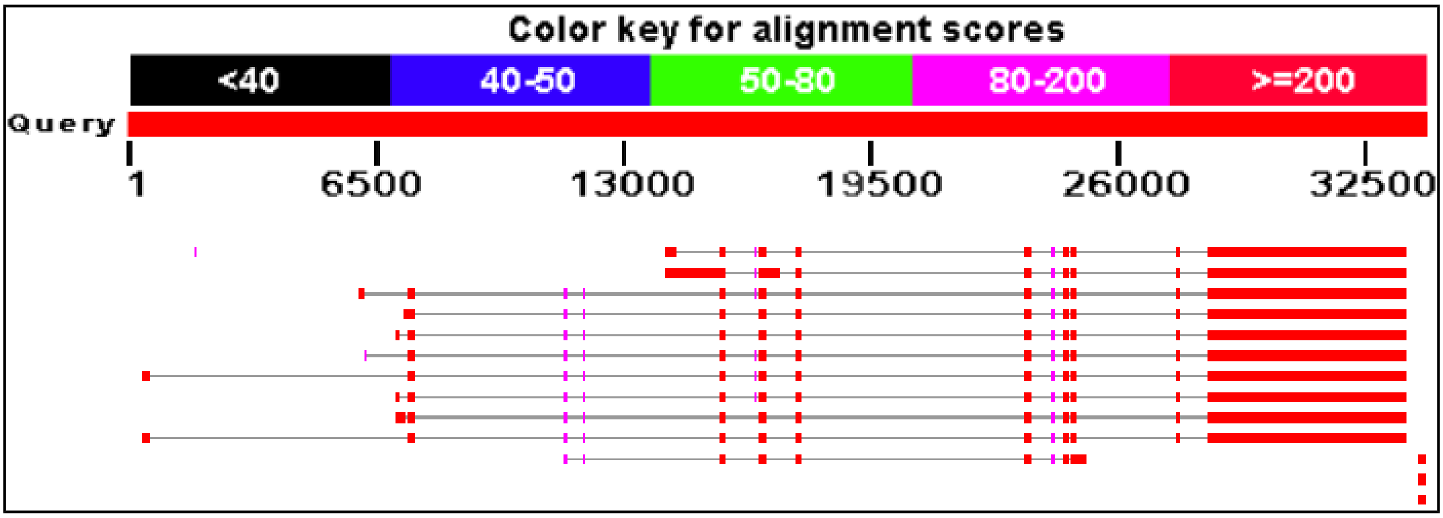
Which parameters would **blast** need to **automatically adjust** to cater for short input sequences (such as primers being tested for uniqueness), and why? ________________________________

____

[2] By default, **megablast** uses **Linear Gap Costs**. That is, it just multiplies the size of the gap with the **Mismatch** penalty. The other two algorithms employ the more common **Affine** strategy, using **Existence** and **Extension** penalties. For more about **Gap Penalties**, go here.

[3] This filter avoids finding "hits" supported only by matches in regions not specific to the query. For example, a polyA tail cannot help to identify a specific mRNA as it is present is all mRNAs. The use of this filter will be evident when we look at the **blast** output.

Finally, ensure all the defaults are back in place[4] and that **megablast** is the **Program Selection**, ask **blast** to **Show results in a new window** and then click on the BLAST button. Impressively swiftly, you will have results. At the top of which will be a graphical overview.



This graphic implies that there are **11** full length matches between the genomic sequence and mRNAs in **RefSeq**. The **RefSeq** entries had to be "gapped" in order to compensate for the introns that are represented in the genomic sequence but not in the mRNA sequences. The red blocks therefore represent very closely matching (>=200 brownie points) exons, the lines joining the red blocks represent introns that have been spliced out. All **11** full length hits match reasonably uniformly except for the first few exons, implying significant variation in the **5´ UTR**.

Why do you suppose that a few of the exons of the first **11** matches do not achieve the maximum score? ___________

____

Explain why one exon in the reasonably consistent region, does not appear in all of the transcript matches? _________

____

In a previous Practical, you discovered directly that there were **11** high quality "**NM_**" **PAX6** transcripts in **RefSeq**.

Until recently, there was a further **9** "**XM_**" **PREDICTED** transcripts. However, in the last release of **RefSeq**, the **9** less reliable **XM_** transcripts were removed. Nevertheless, you saw that the **9 PREDICTED** transcripts are still evidenced in **MapViewer**. That is because the current version of **MapViewer** is built on a previous version of **RefSeq**. As soon as **MapViewer** is updated, the dubious **9** will disappear. Then, I will have to discover another way to introduce the way that **RefSeq** divides its transcript entries by quality.

Ensembl claimed to have used **10** of the **11** high quality **NM_ RefSeq** sequences to aid its transcript predictions. **Ensembl** would have ignored the **XM_ PREDICTED RefSeq** sequences even if they still existed.

blast just sees sequences and cannot be influenced by the quality of the support for their existence, so **blast** will always report all **RefSeq PAX6** mRNAs matching the **PAX6** genomic region convincingly, however questionably they are evidenced.

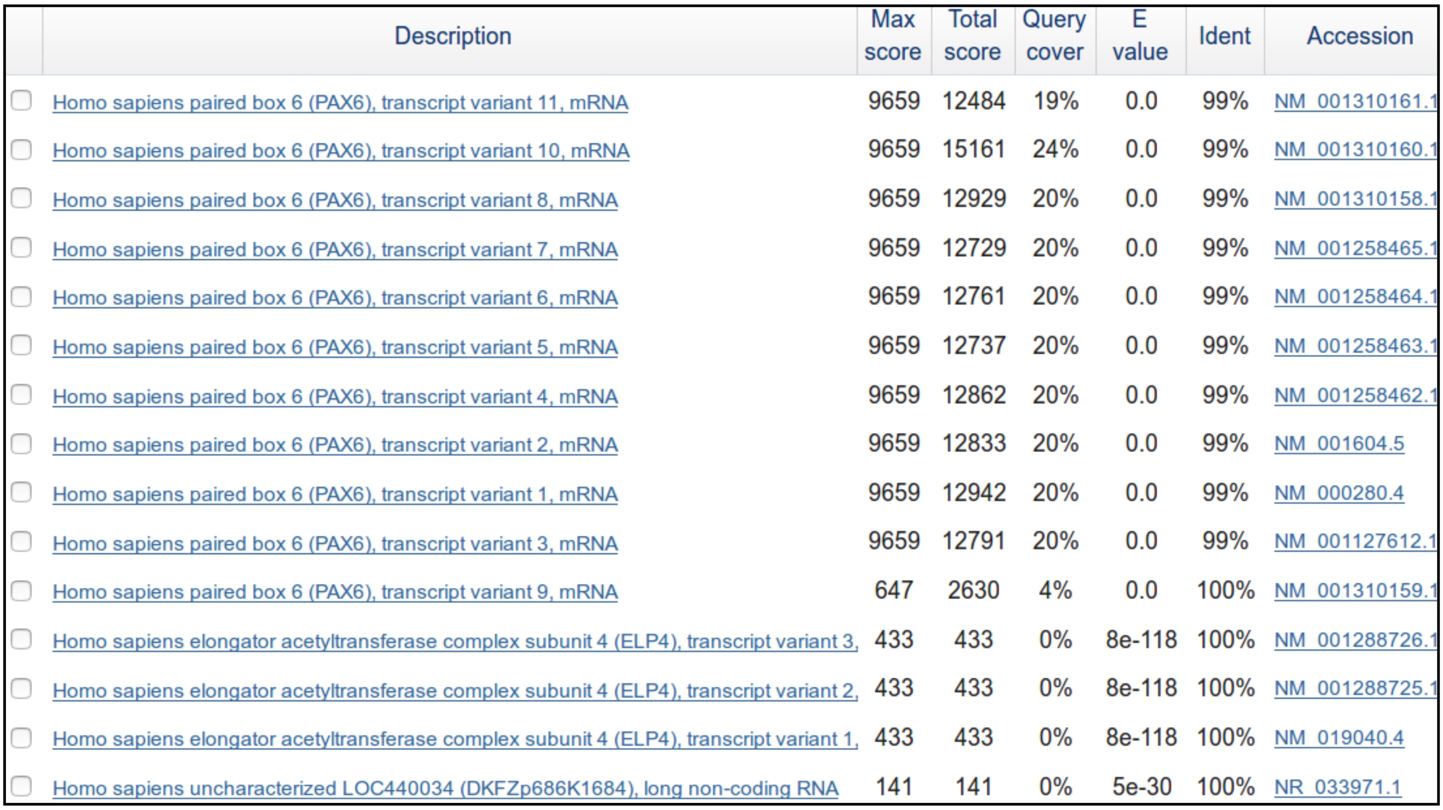
There is a point to pursuing all this detail. You reference a collection of interdependent databases, all of which are updated regularly. More often than not you will notice inconsistencies due to asynchronous updates and differences in database management policy. A small price to pay for such a rich source of information, but one of which I suggest it is wise to be aware.

The message of the particular **blast** search here is that it is so easy to predict the same **PAX6** transcripts as you discovered in **MapViewer**, just with a simple **blast** search. That is, you can look things up, or work most of it out for yourself.

[4] If you have any non-default settings, they should be highlighted in yellow.

If you hover over the graphical hits, their origin will be displayed above the graphic[5].

Below the **Graphic Summary** are the **Descriptions**, a simple list of the **15** matches represented in the graphic.



	Description	Max score	Total score	Query cover	E value	Ident	Accession
□	Homo sapiens paired box 6 (PAX6), transcript variant 11, mRNA	9659	12484	19%	0.0	99%	NM_001310161.1
□	Homo sapiens paired box 6 (PAX6), transcript variant 10, mRNA	9659	15161	24%	0.0	99%	NM_001310160.1
□	Homo sapiens paired box 6 (PAX6), transcript variant 8, mRNA	9659	12929	20%	0.0	99%	NM_001310158.1
□	Homo sapiens paired box 6 (PAX6), transcript variant 7, mRNA	9659	12729	20%	0.0	99%	NM_001258465.1
□	Homo sapiens paired box 6 (PAX6), transcript variant 6, mRNA	9659	12761	20%	0.0	99%	NM_001258464.1
□	Homo sapiens paired box 6 (PAX6), transcript variant 5, mRNA	9659	12737	20%	0.0	99%	NM_001258463.1
□	Homo sapiens paired box 6 (PAX6), transcript variant 4, mRNA	9659	12862	20%	0.0	99%	NM_001258462.1
□	Homo sapiens paired box 6 (PAX6), transcript variant 2, mRNA	9659	12833	20%	0.0	99%	NM_001604.5
□	Homo sapiens paired box 6 (PAX6), transcript variant 1, mRNA	9659	12942	20%	0.0	99%	NM_000280.4
□	Homo sapiens paired box 6 (PAX6), transcript variant 3, mRNA	9659	12791	20%	0.0	99%	NM_001127612.1
□	Homo sapiens paired box 6 (PAX6), transcript variant 9, mRNA	647	2630	4%	0.0	100%	NM_001310159.1
□	Homo sapiens elongator acetyltransferase complex subunit 4 (ELP4), transcript variant 3,	433	433	0%	8e-118	100%	NM_001288726.1
□	Homo sapiens elongator acetyltransferase complex subunit 4 (ELP4), transcript variant 2,	433	433	0%	8e-118	100%	NM_001288725.1
□	Homo sapiens elongator acetyltransferase complex subunit 4 (ELP4), transcript variant 1,	433	433	0%	8e-118	100%	NM_019040.4
□	Homo sapiens uncharacterized LOC440034 (DKFZp686K1684), long non-coding RNA	141	141	0%	5e-30	100%	NR_033971.1

These are such that:

- The top **11** hits, corresponding to the **11** full length hits of the **Graphic Summary,** are the quality (i.e. **NM_** entries with good supporting evidence) **RefSeq** transcripts.

- There follows, corresponding to the **3** small red blobs in the extreme bottom right of the **Graphic Summary**, **3** hits that are the ends of **mRNA**s for the **ELP4** gene. They are exactly where you should expect them to be, assuming you paid full attention to the **ELP4** transcript predictions shown in both the **Ensembl** and **Map Viewer** displays of the **Genomic** region around **PAX6**. Reject these contemptuously, they do not pertain to our investigation of **PAX6**.

- The **15th** match, corresponding to the barely visible tiny smudge match to the left of the top **Graphic Summary** hit, is recorded as "**uncharacterized**" and fails to fit in with my story, so I ignore it!

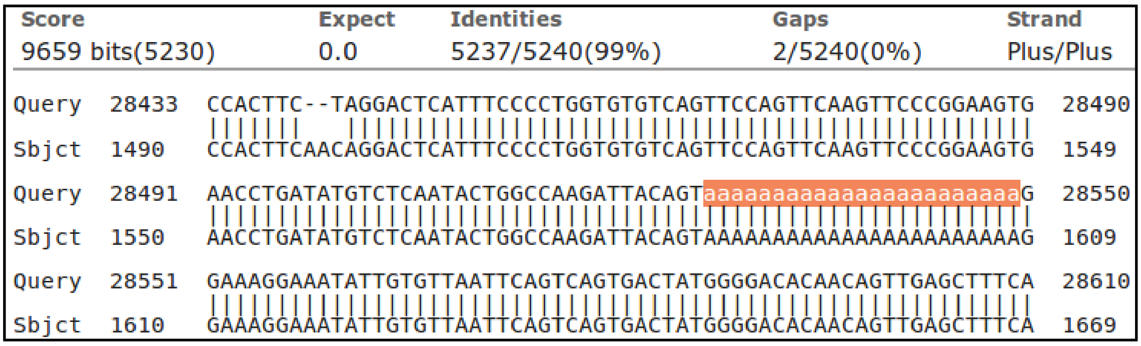
So, this **blast** search suggests the existence of **11 PAX6** transcripts supported by **RefSeq** data, as will be reported by **Map Viewer** as soon as the **NCBI** get around to bringing it up to date! Also, the results are consistent with the information discovered in **Ensembl**.

Which of the **Refseq PAX6** transcripts corresponds to **isoform 5a**? ____

[5] Or you could just read the textual list that follows the graphic if you wish to insist on the simplistic.

Moving further down the results you will come to the alignments between the **PAX6** genomic sequence and the matching database entries. All similarity searches use local alignment strategies[6], so you should not be surprised to see a number of alignments for each "hit" in the list. Here we have a genomic query sequence aligned exclusively with mRNA sequences from **RefSeq**. The expectation is therefore to find an alignments corresponding to exons. The alignments are ordered by quality, though you are provided with a **Sort by:** menu to alter the order to taste[7].

Look at the first alignment for the best matching **PAX6** transcript. It is the alignment of the very last exon of a **RefSeq** transcript with the end of the gene you exported from **Ensembl**.



```
Score              Expect   Identities          Gaps           Strand
9659 bits(5230)    0.0      5237/5240(99%)      2/5240(0%)     Plus/Plus

Query  28433  CCACTTC--TAGGACTCATTTCCCCTGGTGTGTCAGTTCCAGTTCAAGTTCCCGGAAGTG  28490
              |||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1490   CCACTTCAACAGGACTCATTTCCCCTGGTGTGTCAGTTCCAGTTCAAGTTCCCGGAAGTG  1549

Query  28491  AACCTGATATGTCTCAATACTGGCCAAGATTACAGTaaaaaaaaaaaaaaaaaaaaaaaG  28550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1550   AACCTGATATGTCTCAATACTGGCCAAGATTACAGTAAAAAAAAAAAAAAAAAAAAAAAG  1609

Query  28551  GAAAGGAAATATTGTGTTAATTCAGTCAGTGACTATGGGGACACAACAGTTGAGCTTTCA  28610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1610   GAAAGGAAATATTGTGTTAATTCAGTCAGTGACTATGGGGACACAACAGTTGAGCTTTCA  1669
```

Notice the lower case string of '**a**'s. The case indicates that they were ignored (**filtered**) as a **Low complexity region** whilst **megablast** was looking for identically matching words that might suggest matching regions. By themselves, the '**a**'s are not sufficient evidence that a biological match exists. Only because the surrounding sequence is compellingly similar, can it be assumed that such a match does exist. The '**a**'s are replaced (lower case to indicate they were filtered) when the final alignment is computed. If you look a little further down the same alignment, you will see several other runs of '**a**'s and '**t**'s for which the same explanation applies.

[6] To use a global approach would be to imply that you were only interested in database entries that matched your query sequence from end to end. Generally, this is not true. You would usually be interested in a database sequence that was similar over any significant region.

[7] Why not try them? End up with the alignments for the top hit in **E value** order.

Now use a version of **blast** (called **blastx**) to compare your genomic sequence with a protein database. **blastx** will translate a DNA query sequence in all six reading frames and compare each translation with a protein sequence database. Thus, in a similar fashion to that employed by the **Ensembl** pipeline, protein coding regions of the genomic DNA can be identified. For clarity, we will use only the well annotated human proteins of the **SwissProt** section of **Uniprot**. First go to the home of **blast** at:

`http://blast.ncbi.nlm.nih.gov/Blast.cgi`

Select **blastx** translated nucleotide ▶ protein . Use the **Enter Query Sequence Browse** (or **Choose File**) button to **upload file** pax6_genomic.fasta.

In the **Choose Search Set** section, set the **Database** to **UniProtKB/Swiss-prot prot(swissprot)**. Specify the **Organism** as **Human**.

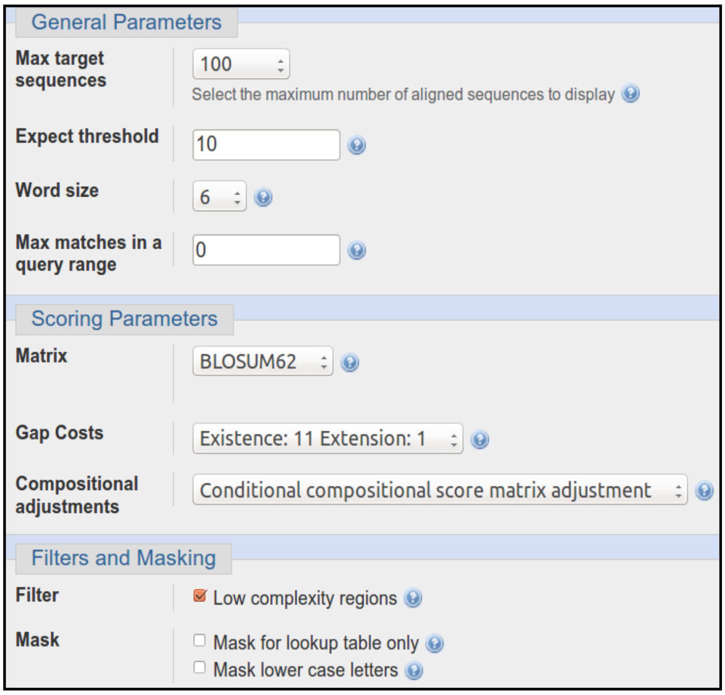
Take a look at the **Algorithm parameters**[8].

The **Word size** choice is **2, 3** or **6** . The default is **6**. We seek very close matches here, so the largest **Word size** would seem appropriate.

The default scoring matrix is **BLOSUM62**, but choices from both the **BLOSUM** and **PAM** families are offered.

The **Compositional adjustments** parameter offers the opportunity to refine the chosen scoring matrix to reflect the residue composition of the sequences being compared in one of a number of ways. Click on the relevant ? button for further enlightenment. I must admit, I was left with questions after reading the **Help**, but some attempt to customise the evaluation of an alignment to reflect sequence composition does seem like an excellent idea.

Low complexity regions will be filtered by default.



General Parameters

Max target sequences: 100 — Select the maximum number of aligned sequences to display

Expect threshold: 10

Word size: 6

Max matches in a query range: 0

Scoring Parameters

Matrix: BLOSUM62

Gap Costs: Existence: 11 Extension: 1

Compositional adjustments: Conditional compositional score matrix adjustment

Filters and Masking

Filter: ☑ Low complexity regions

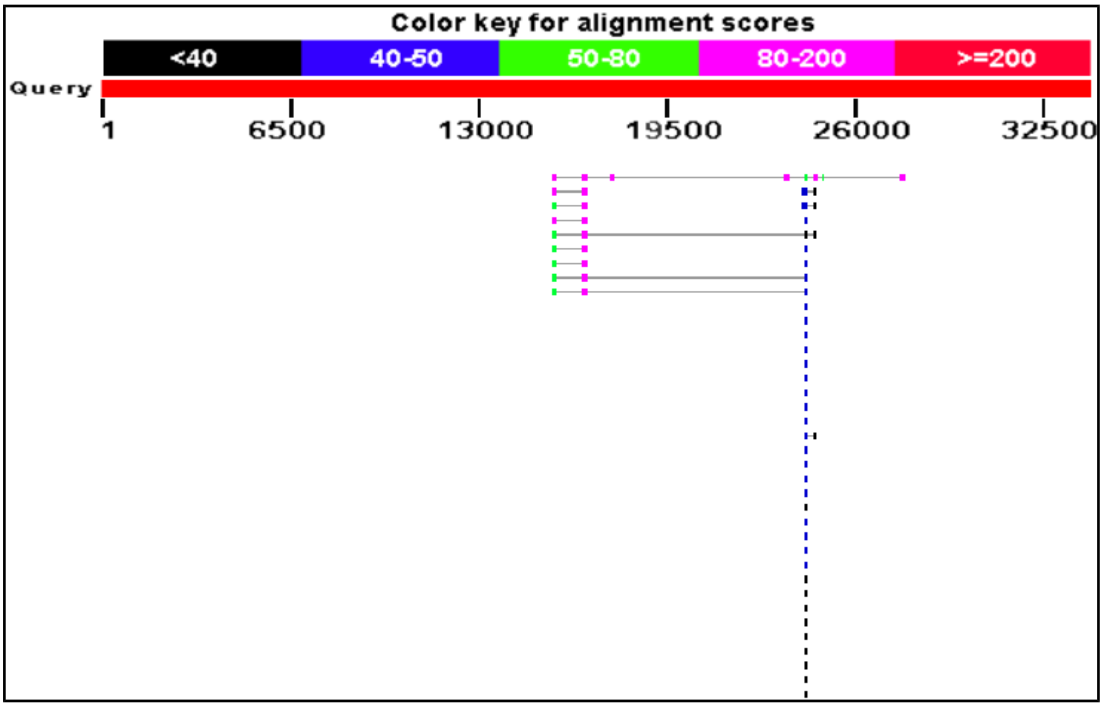
Mask: □ Mask for lookup table only

□ Mask lower case letters

Change nothing other than to ask **blast** to **Show results in a new window** and click the **BLAST** button.

After minimal thought, **blastx** will thrust its conclusions before you. Hover over the graphical hits for identification.

[8] Here I will assume we have talked about these parameter and you are reasonably well informed of the issues.

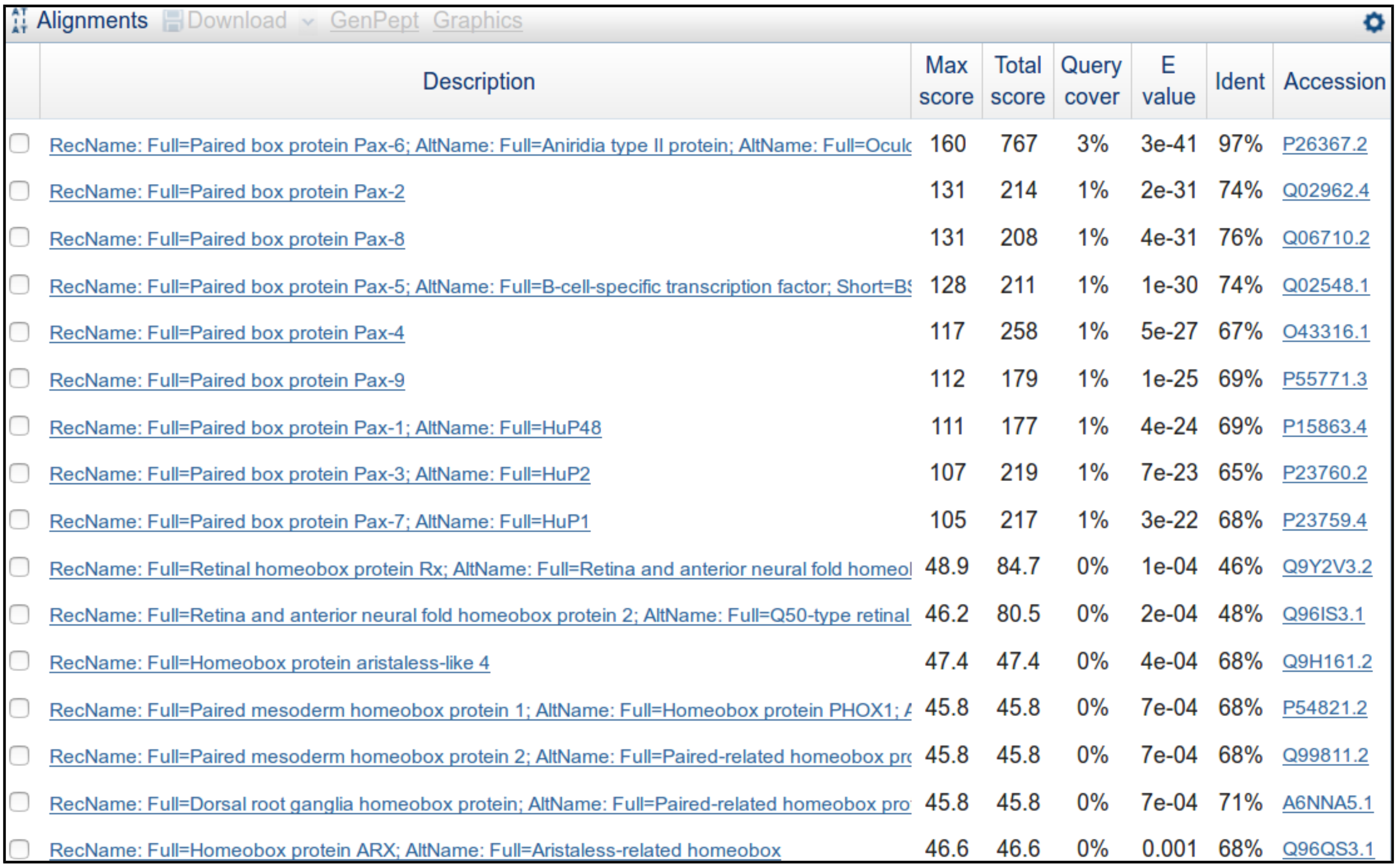


What are the **9** strongest matches around base position **16,000**? ____________________

Why would you expect exactly **9** matches around this point? ____________________

What do you make of the plethora of matches around **24,000**? ____________________

Move down to the textual list of the matches. Hopefully as you fully expected you will find the expected number of **Paired box** matches at the top of the list followed by many many **Homeobox** matches.

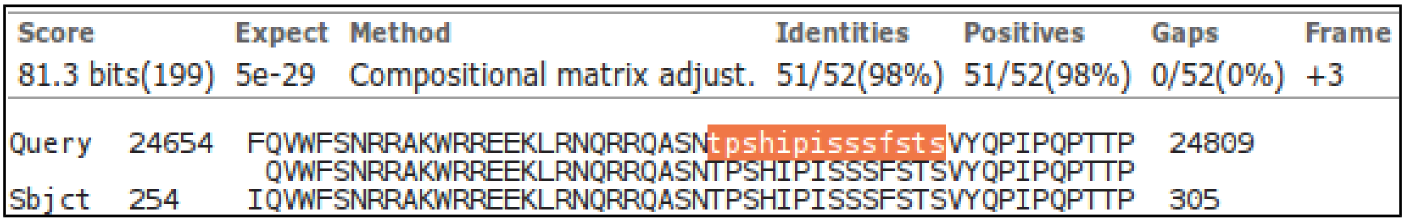


	Description	Max score	Total score	Query cover	E value	Ident	Accession
□	RecName: Full=Paired box protein Pax-6; AltName: Full=Aniridia type II protein; AltName: Full=Ocul	160	767	3%	3e-41	97%	P26367.2
□	RecName: Full=Paired box protein Pax-2	131	214	1%	2e-31	74%	Q02962.4
□	RecName: Full=Paired box protein Pax-8	131	208	1%	4e-31	76%	Q06710.2
□	RecName: Full=Paired box protein Pax-5; AltName: Full=B-cell-specific transcription factor; Short=BS	128	211	1%	1e-30	74%	Q02548.1
□	RecName: Full=Paired box protein Pax-4	117	258	1%	5e-27	67%	O43316.1
□	RecName: Full=Paired box protein Pax-9	112	179	1%	1e-25	69%	P55771.3
□	RecName: Full=Paired box protein Pax-1; AltName: Full=HuP48	111	177	1%	4e-24	69%	P15863.4
□	RecName: Full=Paired box protein Pax-3; AltName: Full=HuP2	107	219	1%	7e-23	65%	P23760.2
□	RecName: Full=Paired box protein Pax-7; AltName: Full=HuP1	105	217	1%	3e-22	68%	P23759.4
□	RecName: Full=Retinal homeobox protein Rx; AltName: Full=Retina and anterior neural fold homeol	48.9	84.7	0%	1e-04	46%	Q9Y2V3.2
□	RecName: Full=Retina and anterior neural fold homeobox protein 2; AltName: Full=Q50-type retinal	46.2	80.5	0%	2e-04	48%	Q96IS3.1
□	RecName: Full=Homeobox protein aristaless-like 4	47.4	47.4	0%	4e-04	68%	Q9H161.2
□	RecName: Full=Paired mesoderm homeobox protein 1; AltName: Full=Homeobox protein PHOX1; A	45.8	45.8	0%	7e-04	68%	P54821.2
□	RecName: Full=Paired mesoderm homeobox protein 2; AltName: Full=Paired-related homeobox prc	45.8	45.8	0%	7e-04	68%	Q99811.2
□	RecName: Full=Dorsal root ganglia homeobox protein; AltName: Full=Paired-related homeobox pro	45.8	45.8	0%	7e-04	71%	A6NNA5.1
□	RecName: Full=Homeobox protein ARX; AltName: Full=Aristaless-related homeobox	46.6	46.6	0%	0.001	68%	Q96QS3.1

Why do you suppose the **Paired box** matches precede the **Homeobox** matches? ____________________

How do you suppose the **Max matches in a query range** parameter might be of value if this order was reversed? ____________________

Take a look at the alignments. You will see many places where regions have been filtered as non-informative. I suggest the one illustrated was filtered because it would match anywhere that was sufficiently **Serine** rich.



```
 Score           Expect  Method                        Identities    Positives     Gaps       Frame
 81.3 bits(199)  5e-29   Compositional matrix adjust.  51/52(98%)    51/52(98%)    0/52(0%)   +3

Query  24654  FQVWFSNRRAKWRREEKLRNQRRQASNtpshipisssfstsVYQPIPQPTTP  24809
               QVWFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVYQPIPQPTTP
Sbjct  254    IQVWFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVYQPIPQPTTP  305
```

How does this "non-informative" region match expectations suggested by **SMART** and the **Feature table** of **UniprotKB** for **PAX6_HUMAN**? ____

THE END

DPJ – 2016.12.02

Model Answers to Questions in the Instructions Text.

Notes:

For the most part, these “**Model Answers**” just provide the reactions/solutions I hoped you would work out for yourselves. However, sometime I have tried to offer a bit more background and material for thought? Occasionally, I have rambled off into some rather self indulgent investigations that even I would not want to try and justify as pertinent to the objective of these exercises. I like to keep these meanders, as they help and entertain me, but I wish to warn you to only take regard of them if you are feeling particularly strong and have time to burn. Certainly not a good idea to indulge here during a time constrained course event!

Where things have got extreme, I am going to make two versions of the answer. One starting:

Summary:

Which has the answer with only a reasonably digestible volume of deep thought. Read this one.

The other will start:

Full Answer:

Beware of entering here! I do not hold back. Nothing complicated, but it will be long and full of pedantry.

This makes the Model answers section very big. **BUT**, it is not intended for printing or for reading serially, so I submit, being long and wordy does not matter. Feel free to disagree.

From your investigations of **Searching for sequence similarities in databases**

When would **Mask lower case letters** be a useful thing to do?

Generally, whenever one might suspect the automatic masking algorithms of **blast** might miss a non informative region in a specific query sequence, obviously.

A specific example might be when a query sequence contained a significant informative region that was known to be common amongst the sequences being searched. If this region was left unmasked, **blast** would pick up so many similar matches to this one region that other interesting similarities might be obscured. By manually masking such a region by changing it to lower case, its matches would not be seen by **blast** and matches with other regions of the query sequence should be more apparent.

Which parameters would **blast** need to **automatically adjust** to cater for short input sequences (such as primers being tested for uniqueness), and why?

The **word size**: Clearly, if you are trying to find matches for a primer (for example) of around **20** base pairs, it would be pretty silly to use a **word size** of **28** (default for **megablast**). A **word** the same size as the primer would find only exact matches. A **word** of about **7** would allow a couple of mismatches and would probably be most generally appropriate.

The **expect score**: As good chance matches between between a short query sequence and a large database will be abundant, it would not be sensible to choose a demanding (i.e. small) **expect score** to represent the limit of significance. In particular, a primer sized query sequence of around **20** base pairs might easily exactly match more than **10** times (generally the default maximum expect score for a significant match) just by chance. After all, there are only **4** bases, a string of **20** is not that long and the databases can be huge! Typically **blast** chooses very high **expect score** cut off for short query sequences, effectively removing the **expect score** filter altogether.

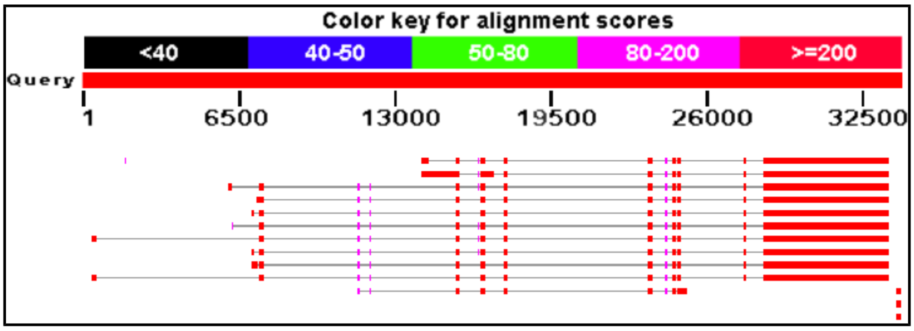
Earlier versions of **blast** did not automatically adjust these parameters. When a short query sequences were selected, suitable adjustment was left to the user. Without sensible parameter adjustment, results could be greatly confusing. For example, a **21** base pair primer could easily match perfectly more than **10** times against a large DNA sequence database. **blast** is set to ignore matches that are expected to occur more than **10** times by chance. Thus even exact matches with such a small sequences would be ignored! Now automatic parameter adjustment is undertaken by **blast**, the user does not really have to think too hard. However, it does seem to be a good idea to know what **blast** is doing and why.

Why do you suppose that a few of the exons of the first **11** matches do not achieve the maximum score?

Summary:

Each local region of significant alignment between a database entry and a query sequence is scored independently. The scoring method that governs the alignment score colour in this graphic, reflects both the quality of the match ***and*** its length. Unless a particular region is of sufficient length, it cannot achieve the **200 bit** threshold even if the alignment is perfect. Note that is is the shorter regions that fail to reach the >=200 status. All of the illustrated local alignments associated with **PAX6** transcripts are essentially perfect.

Full Answer:



In common with most database searching programs, **blast** compares query sequences with database entries using a local strategy. The overall evaluation of a particular query sequence is taken to be the highest local score.

Individual local matches are coloured according to individual quality. In this query, all true matches should be perfect, or very nearly so. Scores might therefore be expected to be maximal (>=200). However, they are not? Some only manage a score in the range 80-200.

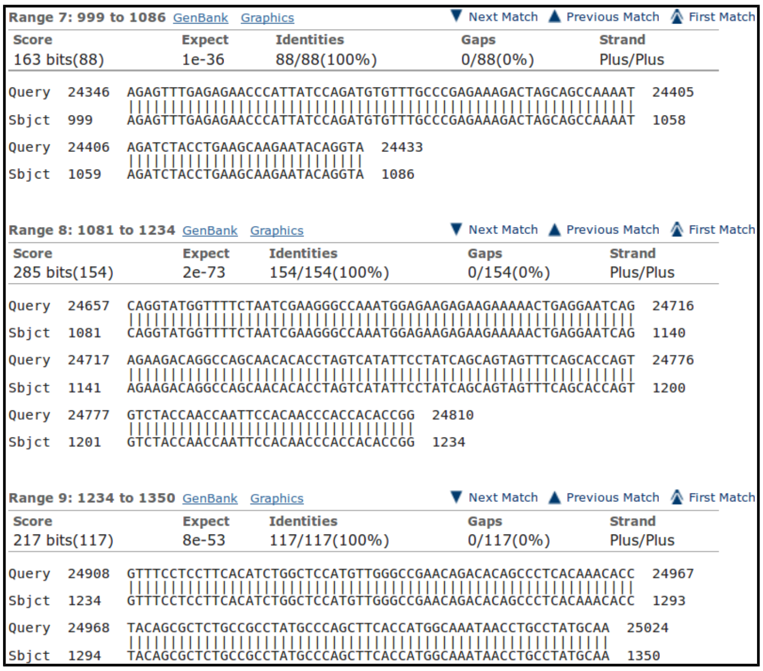
The score referenced for this purpose is the **bit score**. For a full, no holds barred definition of this score, try here. I prefer this somewhat gentler version:

> "The **bit score** gives an indication of how good the alignment is; the higher the score, the better the alignment. In general terms, this score is calculated from a formula that takes into account the alignment of similar or identical residues, as well as any gaps introduced to align the sequences. A key element in this calculation is the "substitution matrix ", which assigns a score for aligning any possible pair of residues. The **BLOSUM62** matrix is the default for most **BLAST** programs, the exceptions being **blastn** and **MegaBLAST** (programs that perform **nucleotide–nucleotide** comparisons and hence do not use protein-specific matrices). Bit scores are normalized, which means that the bit scores from different alignments can be compared, even if different scoring matrices have been used."

Still too scary? The important things to note are that:

- These scores are based on a simple DNA scoring matrix (**1** for a match, **-2** for a mismatch by default for **megablast**), plus penalties for gaps. So scores will be limited by the length of the alignment, ignoring gaps.
- The scores reflect penalties for **indel**s (**in**sertions or **del**etions).
- The scores are normalised so that they do not depend on the chosen scoring matrix. This allows bits scores from searches using different scoring matrices to be compared.

This being so, **bit scores** will reflect the length of an alignment as well as its quality. If an alignment is very short, it might be perfect but still not achieve a very high value. **bit scores** are designed to reflect significance, not just local quality. A short perfect match clearly can be less significant than a longer less perfect match. That is what you see illustrated here.

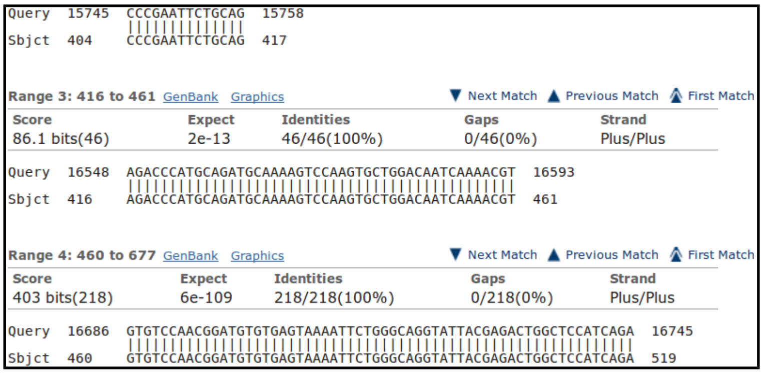


```
Range 7: 999 to 1086
Score          Expect   Identities      Gaps        Strand
163 bits(88)   1e-36    88/88(100%)     0/88(0%)    Plus/Plus

Query  24346  AGAGTTTGAGAGAACCCATTATCCAGATGTGTTTGCCCGAGAAAGACTAGCAGCCAAAAT  24405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  999    AGAGTTTGAGAGAACCCATTATCCAGATGTGTTTGCCCGAGAAAGACTAGCAGCCAAAAT  1058

Query  24406  AGATCTACCTGAAGCAAGAATACAGGTA  24433
              ||||||||||||||||||||||||||||
Sbjct  1059   AGATCTACCTGAAGCAAGAATACAGGTA  1086


Range 8: 1081 to 1234
Score          Expect   Identities      Gaps        Strand
285 bits(154)  2e-73    154/154(100%)   0/154(0%)   Plus/Plus

Query  24657  CAGGTATGGTTTTCTAATCGAAGGGCCAAATGGAGAAGAGAAGAAAAACTGAGGAATCAG  24716
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1081   CAGGTATGGTTTTCTAATCGAAGGGCCAAATGGAGAAGAGAAGAAAAACTGAGGAATCAG  1140

Query  24717  AGAAGACAGGCCAGCAACACACCTAGTCATATTCCTATCAGCAGTAGTTTCAGCACCAGT  24776
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1141   AGAAGACAGGCCAGCAACACACCTAGTCATATTCCTATCAGCAGTAGTTTCAGCACCAGT  1200

Query  24777  GTCTACCAACCAATTCCACAACCCACCACACCGG  24810
              ||||||||||||||||||||||||||||||||||
Sbjct  1201   GTCTACCAACCAATTCCACAACCCACCACACCGG  1234


Range 9: 1234 to 1350
Score          Expect   Identities      Gaps        Strand
217 bits(117)  8e-53    117/117(100%)   0/117(0%)   Plus/Plus

Query  24908  GTTTCCTCCTTCACATCTGGCTCCATGTTGGGCCGAACAGACACAGCCCTCACAAACACC  24967
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1234   GTTTCCTCCTTCACATCTGGCTCCATGTTGGGCCGAACAGACACAGCCCTCACAAACACC  1293

Query  24968  TACAGCGCTCTGCCGCCTATGCCCAGCTTCACCATGGCAAATAACCTGCCTATGCAA  25024
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1294   TACAGCGCTCTGCCGCCTATGCCCAGCTTCACCATGGCAAATAACCTGCCTATGCAA  1350
```

You can see evidence of what is occurring in the alignments further down your results. Here is illustrated one of the 80-200 exons that occur in all transcripts at position **24,346**[9]. The match is perfect, but the length of the exon is consistently just to short to get to the heady >=200 level.

[9] In order to make this illustration, I needed set **Sort by**: (top of the alignments) to **Query start position**.

Note how imperfectly **blast** finds exon/intron boundaries. If the start of an intron happens to match the start of the next exon, **blast** will included the bases in two alignments[10]. It is not looking for exons and introns as was **spline**, it just mindlessly seeks matches.



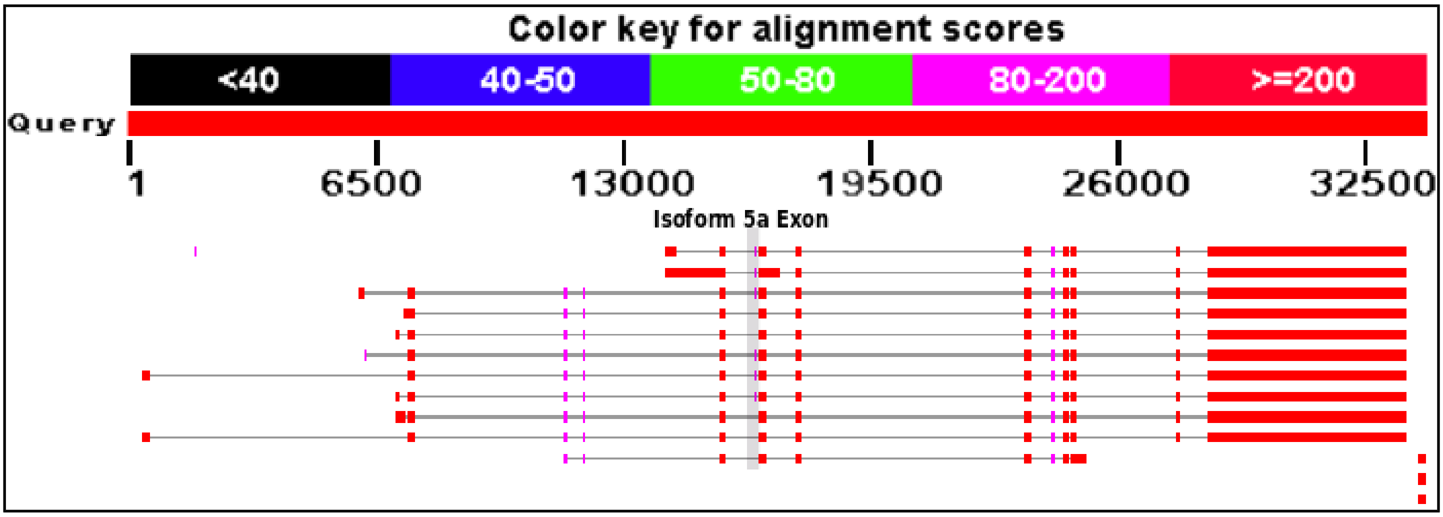
```
Query  15745  CCCGAATTCTGCAG  15758
              ||||||||||||||
Sbjct  404    CCCGAATTCTGCAG  417


Range 3: 416 to 461 GenBank  Graphics        ▼ Next Match  ▲ Previous Match  ⩓ First Match
 Score            Expect     Identities       Gaps         Strand
 86.1 bits(46)    2e-13      46/46(100%)      0/46(0%)     Plus/Plus

Query  16548  AGACCCATGCAGATGCAAAAGTCCAAGTGCTGGACAATCAAAACGT  16593
              ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  416    AGACCCATGCAGATGCAAAAGTCCAAGTGCTGGACAATCAAAACGT  461


Range 4: 460 to 677 GenBank  Graphics        ▼ Next Match  ▲ Previous Match  ⩓ First Match
 Score            Expect     Identities       Gaps         Strand
 403 bits(218)    6e-109     218/218(100%)    0/218(0%)    Plus/Plus

Query  16686  GTGTCCAACGGATGTGTGAGTAAAATTCTGGGCAGGTATTACGAGACTGGCTCCATCAGA  16745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  460    GTGTCCAACGGATGTGTGAGTAAAATTCTGGGCAGGTATTACGAGACTGGCTCCATCAGA  519
```

For a further example, look at the exon that is found only in the **isoform 5a** transcripts. It is tiny (**42** base pairs) and scores well below >=200 even thought it is a perfect match.

Note that the alignment is **46** base pairs long due to **blast** adding on two bases either side that are actually the highly conserved intron start and end base pairs. As you can see, these extra base pairs occur in the preceding and succeeding alignment also.

Explain why one exon in the reasonably consistent region, does not appear in all of the transcript matches?

Well I refer to the **isoform 5a** exon, of course. The tiny inconsistent one about **9** exons in from the right (when it exists). This will, clearly, only occur in **isoform 5a** transcripts.



[10] **6** base pairs (**Sbjct**: **1081-1086**, **CAGGTA**) occur in both the first two matches illustrated. Just **1** base pair is shared between the **2nd** and **3rd** match (**Sbjct**: **1234**, **G**).

Which of the **Refseq PAX6** transcripts corresponds to **isoform 5a**?

Summary:

As I am sure you are tired of noting by now, all the transcripts with the extra tiny exon around position **1,600** in the genomic sequence are **isoform 5a** transcripts. See the illustration for the previous answer.

Full Answer:

The **isoform 5a** transcripts can be spotted most easily from the graphic. They are the ones with the extra small exon slightly to the left of middle (around base position **1,600**). For example, the **first**, **second** and **third blast** matches displayed. If you hover over all the full length matches with your mouse, you will see that they are t**ranscript variants 11**, **10**, **8**, **7**, **6**, **5**, **4**, **2**, **1**, **3** and **9** (in the vertical order of the graphic).

Stated with the unequalled poetry of **RefSeq Accession Code** and lyrical **Title** Line, the list of those with the extra exon becomes:

TITLE	ACCESSION CODE
Homo sapiens paired box 6 (PAX6), transcript variant 11, mRNA	NM_001310161.1
Homo sapiens paired box 6 (PAX6), transcript variant 10, mRNA	NM_001310160.1
Homo sapiens paired box 6 (PAX6), transcript variant 8, mRNA	NM_001310158.1
Homo sapiens paired box 6 (PAX6), transcript variant 5, mRNA	NM_001258463.1
Homo sapiens paired box 6 (PAX6), transcript variant 4, mRNA	NM_001258462.1
Homo sapiens paired box 6 (PAX6), transcript variant 2, mRNA	NM_001604.5

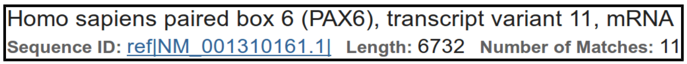
Yes well, that was fun? The message of the question was to ensure you could see how to spot the **isoform 5a** transcripts (again!), not to list them! But, never mind, doing so was in fine tune with the ennui of the moment.

Additional Meanderings:

That really should not detain anyone but me? They belong after the consideration of masking the run of As for the **megablast** you ran. I just enjoyed this detour, so I keep it somewhere low profile. The whole journey leads nowhere of any note, so, should you decide to read, expect little!

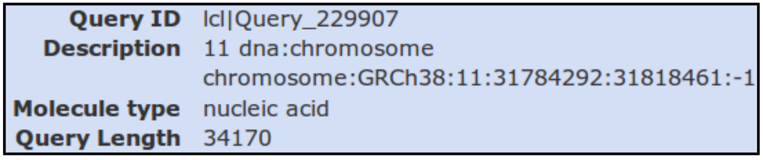
The **500** base pairs of 3' flanking sequence added on to the **Ensembl** sequence for “good measure”, is not part of the alignment (as would be expected). This can be seen easily if you look at the end of the alignment illustrated above, which is the alignment of the last exon of a transcript.

The entire length of this transcript is **6,732** base pairs.



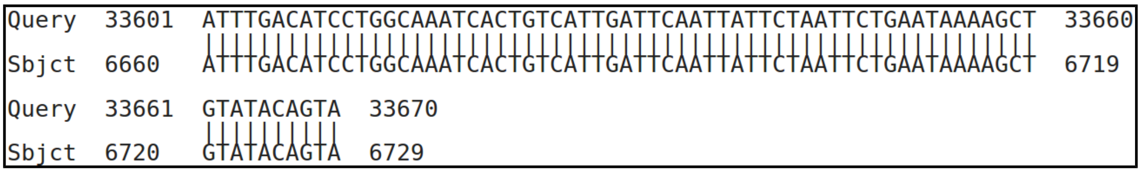
```
Homo sapiens paired box 6 (PAX6), transcript variant 11, mRNA
Sequence ID: ref|NM_001310161.1|  Length: 6732  Number of Matches: 11
```

The entire length of the genomic query sequence is **34,170** base pairs.



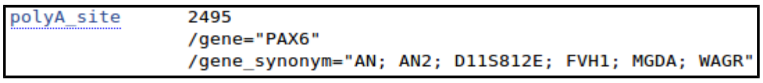
```
    Query ID  lcl|Query_229907
 Description  11 dna:chromosome
              chromosome:GRCh38:11:31784292:31818461:-1
Molecule type nucleic acid
 Query Length 34170
```

The alignment ends at position position **6,729** of the mRNA (**3** from the end) and position **33,670** of the genomic sequence (exactly **500** base pairs from the end).

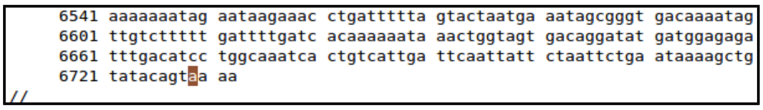


```
Query  33601  ATTTGACATCCTGGCAAATCACTGTCATTGATTCAATTATTCTAATTCTGAATAAAAGCT  33660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6660   ATTTGACATCCTGGCAAATCACTGTCATTGATTCAATTATTCTAATTCTGAATAAAAGCT  6719

Query  33661  GTATACAGTA  33670
              ||||||||||
Sbjct  6720   GTATACAGTA  6729
```

The **3** missing base pairs of the mRNA are all **A**s, due to **polyadenylation**. Position **6,729** being recorded as a **polyA** site by **RefSeq**. A very short **polyA** tail surely? But there is no telling what stage of the mRNA is recorded in **RefSeq**. **Wikipedia** says:



```
polyA_site        2495
                  /gene="PAX6"
                  /gene_synonym="AN; AN2; D11S812E; FVH1; MGDA; WAGR"
```



```
     6541 aaaaaaatag aataagaaac ctgattttta gtactaatga aatagcgggt gacaaaatag
     6601 ttgtcttttt gattttgatc acaaaaaata aactggtagt gacaggatat gatggagaga
     6661 tttgacatcc tggcaaatca ctgtcattga ttcaattatt ctaattctga ataaaagctg
     6721 tatacagtaa aa
//
```

“The tail is shortened over time, and, when it is short enough, the mRNA is enzymatically degraded.”

Of course, the neatness of this observation reflects less some profound biological truth than that this mRNA just happens to be one that extends furthest to the right in the genome, and there is no chance match between the **polyA** tail and the extra **500** bases of genomic sequence you added on when extracting it from **Ensembl**.

The journey was fun even though the destination was dubious. Much the way of a considerable portion of life in general one might reflect?

What are the **9** strongest matches around base position **16,000**?

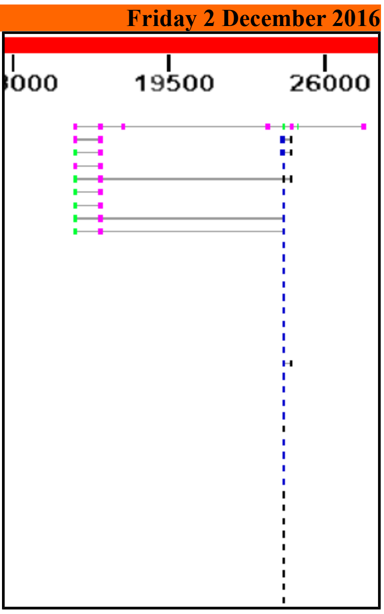
Matches between the regions of the **PAX6** genomic region encoding the **PAX6 Paired Box** domain and **SwissProt** protein sequences representing human proteins including a **Paired Box** domain.

Why would you expect exactly **9** matches around this point?

Because that is how many human proteins including a **Paired Box** domain are suggested to exist according to **Interpro** (as shown in a previous Practical). There is **PAX6** plus its **8** paralogues, imaginatively all named:

PAX1, **PAX2**, **PAX3**, **PAX4**, **PAX5**, **PAX6**, **PAX7**, **PAX8** & **PAX9**

What do you make of the plethora of matches around **24,000**?



These are matches between the regions of the **PAX6** genomic region encoding the **PAX6 Homeobox** domain and **SwissProt** protein sequences representing human proteins including a **Homeobox** domain. As you discovered earlier from **Interpro**, there are lots of such proteins.

The thin line joining features implies that those features relate to the same database entry.

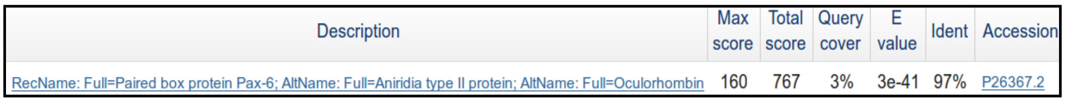
Notice that **4** of the **9** proteins including a **Paired box** domain also include a **Homeobox** domain. The remaining **5** do not. This implies that **4** of the **9** proteins corresponding to the hits detected here have a **Paired box** domain near the start of the protein and a **Homeobox** domain further along. This is exactly as was suggested by the **SMART** annotation you examined earlier.

Why do you suppose the **Paired box** matches precede the **Homeobox** matches?

Because they score more highly and so, in the opinion of **blast**, are more worthy. Primarily, they score more highly because they are longer. The list is ranked by **E Value**. Good matches with long sequence are less likely to occur by chance than equally good matches with shorter sequences.

Possibly a more interesting question[11] might have been: "Why are not all the hits which include both domains at the top of the list?". Surely they should be, as they match over a longer proportion of the query sequence and so must, in general at least, be of the greatest significance.

They do not always come at the top of the list because **blast** scores each matching region individually and uses the ranking scores associated with the single region with the highest **E Value** to evaluate the similarity of the entire database entry with the query. This has to be a dubious practice surely? But, it appears to work, so why complain.

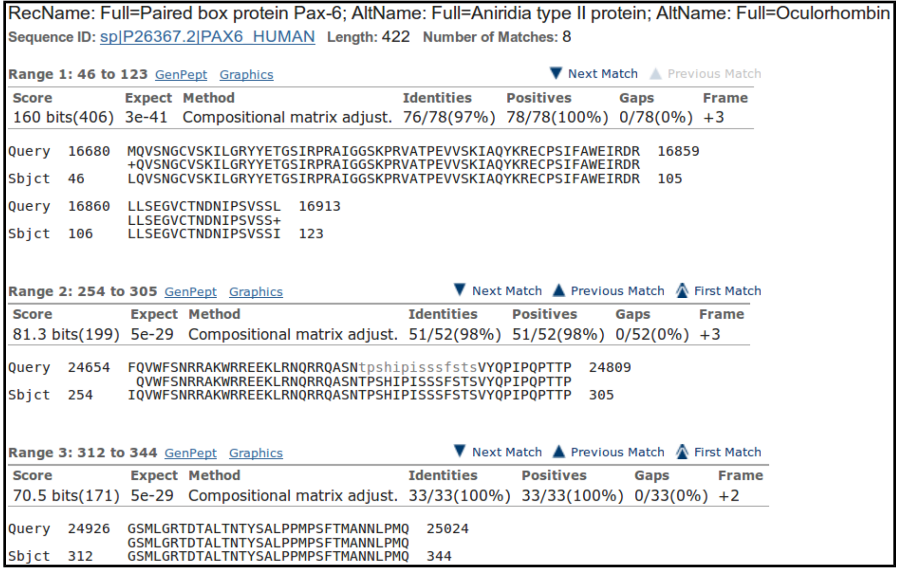


Description	Max score	Total score	Query cover	E value	Ident	Accession
RecName: Full=Paired box protein Pax-6; AltName: Full=Aniridia type II protein; AltName: Full=Oculorhombin	160	767	3%	3e-41	97%	P26367.2

To justify this last assertion, Look at your top hit.

E Val = 3e-41, **Max score = 160**, **Total score 767** associated with the whole of P26367.2

Now look at the first few individual regional alignments for this hit.



RecName: Full=Paired box protein Pax-6; AltName: Full=Aniridia type II protein; AltName: Full=Oculorhombin

Sequence ID: sp|P26367.2|PAX6_HUMAN Length: 422 Number of Matches: 8

Range 1: 46 to 123 GenPept Graphics ▼ Next Match ▲ Previous Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
160 bits(406)	3e-41	Compositional matrix adjust.	76/78(97%)	78/78(100%)	0/78(0%)	+3

```
Query  16680  MQVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATPEVVSKIAQYKRECPSIFAWEIRDR  16859
              +QVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATPEVVSKIAQYKRECPSIFAWEIRDR
Sbjct  46     LQVSNGCVSKILGRYYETGSIRPRAIGGSKPRVATPEVVSKIAQYKRECPSIFAWEIRDR  105

Query  16860  LLSEGVCTNDNIPSVSSL  16913
              LLSEGVCTNDNIPSVSS+
Sbjct  106    LLSEGVCTNDNIPSVSSI  123
```

Range 2: 254 to 305 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
81.3 bits(199)	5e-29	Compositional matrix adjust.	51/52(98%)	51/52(98%)	0/52(0%)	+3

```
Query  24654  FQVWFSNRRAKWRREEKLRNQRRQASNtpshipisssfstsVYQPIPQPTTP  24809
               QVWFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVYQPIPQPTTP
Sbjct  254    IQVWFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVYQPIPQPTTP  305
```

Range 3: 312 to 344 GenPept Graphics ▼ Next Match ▲ Previous Match ▲ First Match

Score	Expect	Method	Identities	Positives	Gaps	Frame
70.5 bits(171)	5e-29	Compositional matrix adjust.	33/33(100%)	33/33(100%)	0/33(0%)	+2

```
Query  24926  GSMLGRTDTALTNTYSALPPMPSFTMANNLPMQ  25024
              GSMLGRTDTALTNTYSALPPMPSFTMANNLPMQ
Sbjct  312    GSMLGRTDTALTNTYSALPPMPSFTMANNLPMQ  344
```

As you can see, the **E Value** and **Max score** values used to evaluate the whole protein were computed from just the best (ranked by **E Value**) local alignment! Crude, but never mind.

The **Total score** for the entire protein is the sum (rounded up to the nearest integer) of all the bit scores for all **8** local alignments computed for this protein (I suggest you just trust me on this assertion).

[11] That I did not ask, because I only just thought of it.

How do you suppose the **Max matches in a query range** parameter might be of value if this order was reversed?

If **Paired boxes** had been more prolific, then the number of **Paired box** matches might have filled the **blast** hit list before the highest scoring **Homeo box** hit was registered.

If **Homeo boxes** were longer, and so justified a better **E value**, then the number of **Homeo box** matches might have filled the **blast** hit list before the highest scoring **Paired box** hit was registered.

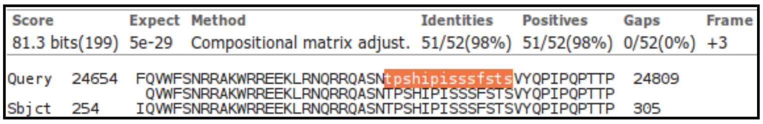
Either of these situations would be very unfortunate, but easily avoided by setting the **Max matches in a query range** parameter to something sensible (**50** say). This would ensure that only the top **50** items in the **blast** hit list would be dominated by the strongest hit.

UNFORTUNATELY … although that is the intention of this parameter, it currently simply will not work, except in very particular circumstances, because of the way it is implemented. This is a great pity, because it is a very good idea, in principle.

I will spare you the details until the energetic debate I am having with the **NCBI** people has come to a satisfactory (or more probably, otherwise) conclusion.

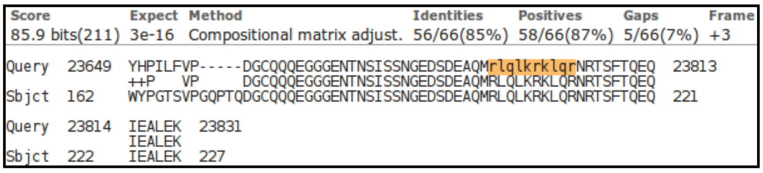
How does this "non-informative" region match expectations suggested by **SMART** and the **Feature table** of **UniprotKB** for **PAX6_HUMAN**?

blast identifies two non-informative regions. I only discussed the prettiest one above. The region discussed is comprised largely of **Serines**, **Prolines**, **Threonines** & **Isoleucines** the **15** residues between **294-308**.



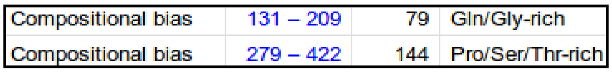
```
Score           Expect  Method                        Identities   Positives    Gaps      Frame
81.3 bits(199)  5e-29   Compositional matrix adjust.  51/52(98%)   51/52(98%)   0/52(0%)  +3

Query  24654   FQVWFSNRRAKWRREEKLRNQRRQASNtpshipisssfstsVYQPIPQPTTP  24809
                QVWFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVYQPIPQPTTP
Sbjct  254     IQVWFSNRRAKWRREEKLRNQRRQASNTPSHIPISSSFSTSVYQPIPQPTTP  305
```

The second (to be found much further down your **blast Alignments** output) is comprised entirely of **Arginines**, **Luecines** and **Lysines** and **Glutamines**, the **10** residues between **203 - 212**.



```
Score           Expect  Method                        Identities   Positives    Gaps      Frame
85.9 bits(211)  3e-16   Compositional matrix adjust.  56/66(85%)   58/66(87%)   5/66(7%)  +3

Query  23649  YHPILFVP-----DGCQQQEGGGENTNSISSNGEDSDEAQMrlqlkrklgrNRTSFTQEQ  23813
              ++P   VP     DGCQQQEGGGENTNSISSNGEDSDEAQMRLQLKRKLQRNRTSFTQEQ
Sbjct  162    WYPGTSVPGQPTQDGCQQQEGGGENTNSISSNGEDSDEAQMRLQLKRKLQRNRTSFTQEQ  221

Query  23814  IEALEK  23831
              IEALEK
Sbjct  222    IEALEK  227
```

UniprotKB also suggests there are two **compositionally biased regions**.



Compositional bias	131 – 209	79	Gln/Gly-rich
Compositional bias	279 – 422	144	Pro/Ser/Thr-rich

Well, hardly an exact match, but there is approximate agreement? One would certainly suppose that **blast** is only willing to mask fairly severe cases of **compositional bias**. It is also probable that **blast** has a rather more mechanistic (i.e. non-biological) interpretation of what **computational bias** is?

SMART also predicts the more obvious region of **computational bias**, rather more generally:

> "An octapeptide and/or a homeodomain can occur C-terminal to the paired domain, as well as a Pro-Ser-Thr-rich C-terminus"

Not important points in themselves of course, the real message of the exercise is that you can discover so much by either:

> Looking things up in databases

or:

> Using the simple analytical software tools yourself.

DPJ – 2016.12.02