Bioinformática: QBQ-5722 Anotação Artemis: Passo-a-passo

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Na área de trabalho, dentro da pasta **QBQ2507**, dê um duplo clique no ícone **Artemis**;

O Artemis será carregado. Clique no menu superior esquerdo File e selecione a opção Open;



No diálogo que aparecerá, altere a caixa de seleção Arquivos do tipo de Sequence files para Todos os arquivos

Navegue até a pasta **QBQ2507** que está no **Desktop** e selecione o arquivo **seqs*.contig** presente. Clique em Abrir.

Select a file						
P <u>e</u> squisar em: Contigs						
🗋 seqsl.contig.aa 📄 seqsl0.contig.gff 📄 seqsl2.contig						
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🗋 seqs10.contig.codingseq 🗋 seqs12.contig 👘 🗋 seqs13.contig						
Nome do Arquivo: seqsl2.contig						
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Abrir Cancelar						

Uma nova janela se abrirá com somente os cabeçalhos dos contigs identificados

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Na nova janela, navegue até o menu superior esquerdo File e selecione a opção Read an entry...

No diálogo que aparecerá, navegue até a pasta **QBQ2507** e selecione o **GFF** correspondente ao contig aberta visualizado. Clique em Abrir

r	Artemis Entry Edit: seqs12.contig
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	Nome do Arquivo: seqsl2.contig.gff Arquivos do <u>T</u> ipo: Artemis files ▼ Abrir Cancelar

Os genes e CDS's preditos no arquivo GFF aparecerão na lista inferior

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O Artemis é dividido em 3 frames principais. Em cada frame, as barras de rolagem **horizontais** são utilizadas para navegar ao longo das sequências, ao passo de que as barras verticais são utilizadas para controlar o zoom de visualização das regiões.

Frame com zoom mínimo (visualização de todas as sequências carregadas - barra vertical de rolagem posicionada no rodapé.)

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Frame com zoom máximo (visualização dos nucleotídeos e aminoácidos das sequências)



Para exibir a porcentagem de conteúdo GC, clique em Graph no menu superior e depois selecione a opção GC Content (%). Um gráfico com a quantidade de GC's por região aparecerá na parte superior da janela.



Para ocultar o gráfico, repita os passos anteriores, ou clique no menu Graph e selecione a opção Hide all graphs



No frame inferior, dê um duplo clique no conjunto desejado (**gene** ou **CDS**) para que o visualizador seja posicionado nas sequências correspondentes ao conjunto.



Diversos parâmetros podem ser modificados:

- 1. base de dados utilizada;
- 2. filtros (baixas complexidades, repetições, etc.);
- 3. limiar do e-value;
- 4. gap open;
- 5. ...

É possível visualizar as estatísticas de uma feature selecionando-a, clicando no menu View e selecionando a opção Feature Statistics

		Feature info	mation: g6			×
Ala (A): 41 Met (M): 28		Т	C	A	G	Ν
Arg (R): 59 Phe (F): 88 Asn (N): 79 Pro (P): 42 Asp (D): 40 Ser (S): 126 T Cys (C): 61 Thr (T): 85 Glu (2): 70 Trp (W): 18 Glu (E): 40 Tyr (Y): 52 Gly (G): 48 Val (V): 78 His (H): 40 Opl (*): 37 Ile (I): 138 Ocr (#): 40 Leu (L): 179 Amb (+): 17 C Lys (K): 87 (.): 0	ALL: 1487 33% 1st: 468 31% 2nd: 511 34% 3rd: 508 34%	Phe 72 81% Phe 16 18% Leu 39 21% Leu 44 24%	Ser19 15% Ser13 10% Ser37 29% Ser3 2%	Tyr 40 76% Tyr 12 23% Ocr 40 ALL Amb 17 ALL	Cys 41 67% Cys 20 32% Opl 37 ALL Trp 18 ALL	t c g
	ALL: 721 16% 1st: 262 17% 2nd: 240 16% 3rd: 219 14%	Leu 31 17% Leu 16 8% Leu 13 7% Leu 36 20%	Pro 11 26% Pro 9 21% Pro 19 45% Pro 3 7%	His 25 62% His 15 37% Gln 43 61% Gln 27 38%	Arg 6 10% Arg 4 6% Arg 1 1% Arg 3 5%	t c g
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	ALL: 779 17% 1st: 247 16% 2nd: 277 18% 3rd: 255 17%	Val 23 29% Val 10 12% Val 25 32% Val 20 25%	Ala 16 39% Ala 5 12% Ala 16 39% Ala 4 9%	Asp 29 72% Asp 11 27% Glu 32 80% Glu 8 20%	Gly 21 43% Gly 4 8% Gly 20 41% Gly 3 6%	t c g
Mol weight: 159585.53 Start: 194184 End: 198662 Bases: 4479 AA length: 1493 position 1/2 score = 51.0 C3/G1/G3 (o-e)/e = -8.8 -4.8 -1.7 33.48% GC Close						

Para visualizar as bases de uma determinada feature, basta selecioná-la, clicar no menu View e selecionar a opção Bases of Selection, ou ainda, Bases of Selecion As Fasta, caso queira visualizar as bases em formato FASTA.



Da mesma maneira, é posível visualizar os aminoácidos de um CDS. Selecione o CDS, clique no menu View e selecione a opção Aminoacids of Selection, ou ainda, Aminoacids of Selecion As Fasta.

Feature base viewer for feature:g6.t1:CDS	
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>g6.1:CD5 - 194184: 198662 MW: 16799.324 ATIRTIFSTKQMIFLUVIALVSGILUGCEKTMFTKHTLINEDATCGVANGFKMFVF 10 20 30 40 50 60 KSCMNVSPLIPLNLVSLFLSYYTINTYSHVPINFLTKISYFYIVKTSANCICLNK 70 80 90 100 110 120 ISIYSLPLITSGQTTCLN/VTTSY QHFLDFNICVS 130 140 150	
Close Save	

O Artemis permite a execução de 5 tipos diferentes de BLAST utilizando a interface web do NCBI;

Selecione a Feature que deseja "blastar", clique com o botão direito e navegue pela opção Run até NCBI Searches;

000	Artemis Entry Edit: seqs12.cont	ig	
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		Run blastp on selected features against	· ·
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CDS 1070 11444 c	
internal 1070 1235 c	
internal 4552 4755 c internal 7021 7235 c	
internal 7394 7586 c	
internal 8544 8694 c	
1nternal 9734 9994 c	

O resultado do BLAST em formato HTML é automaticamente aberto pelo Browser (não confundir com Bowser).



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Home Recent Results Saved Strategies Help		[Sign In] [Register]
The information on this web site remains accessible; but, due to to	he lapse in government funding, the information may not be up to date, and the agency may not t	e able to respond to inquiries until appropriations are enacted. For
updates regarding government operating status see <u>USA.gov</u> .		
NCBI/ BLAST/ blasto suite/ Formatting Results - 53CHN9SU013		
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g1.t1:CDS g1.t1:CDS undefined product 1070:1144	4	
RID 53CHN9SU013 (Expires on 10-08 02:55	am)	
Query ID lcl 63507	Database Name nr	
Description g1.t1:CDS g1.t1:CDS undefined product 1 Molecule type amino acid	070:11444 reverse MW:56817 Description All non-redundant Ge environmental sample	nBank CDS translations+PDB+SwissProt+PIR+PRF excluding es from WGS projects
Query Length 512	Program BLASTP 2.2.28+ > C	tation
Other reports: > Search Summary [Taxonomy reports] [Dis	ance tree of results] [Multiple alignment]	
Graphic Summary		
	Distribution of 200 Blast Hits on the Query Sequence @	
	Mouse over to see the define, click to show alignments	
		7
	Color key for alignment scores	
	Query	
		D

O resultado do BLAST pode ser utilizado para caracterizar o gene através do Artemis;

Downlo	ad	GenPept Graphics						Artemis Gene Builder: g2	
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<pre># F F I Y L</pre>	L I V N S + 1 11444 c 1070 11444 c 1070 11444 c 2936 c 2936 2930 c 4552 4755 c 7021 7235 c 7024 8081 c 8544 8694 c 9734 9694 c 11396 11444 c 11442 11444 c 105872 108398 c 108384 108398 c 108384 108398 c 139363 145079 c 139663 139979 c	/ID=q1.11 /P /Parent=q1.11 /gene_id=g1' /gene_id=g1' /gene_id=g1' /gene_id=g1' /gene_id=g1' /gene_id=g1' /gene_id=g1' /gene_id=g1' /gene_id=g2' /ID=g2 /scor /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2' /gene_id=g2'	S + F + T V Parent=g1 (/codon_start=1 /transcript_id=	/ID=q1.t1: ('g1.t1' /co 'g1.t1' /co 'g2.t1' /co 'g2.t1' /co 'g2.t1' /co 'g2.t1' /co 'g2.t1' /co 'g2.t1' /co 'g2.t1' /co 'g2.t1' /co	C V S * V H S * V H DS don_start=3 don_start=3 don_start=3 don_start=2 don_start=2 don_start=1 don_s	="junction pla	* M V N V H R Q	H L T D <u>A I Y (</u>		<u><u> </u></u>	<u>QQEI</u>	
<pre># F F I Y L</pre>	L I V N S + H Q N 1 11444 c 1070 1235 c 2796 2930 c 4552 4755 c 7021 7235 c 7024 8081 c 8544 8694 c 9734 9994 c 11390 11444 c 105872 108398 c 108384 108398 c 108384 108398 c 108384 108398 c 108384 108398 c 139663 139070 c 1405070 c	<pre>/ + I L F /ID=q1.11 // /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2'</pre>	S + F + T V Parent=g1 (/ codon_start=1 / transcript_id= / tra	/ID=q1.t1:C 'q1.t1' /co 'q1.t1' /co 'q2.t1' /co	DS don_start=3 don_start=3 don_start=3 don_start=3 don_start=3 don_start=3 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1	="junction pla	* M V N <u>V H R Q</u> 	н L T D <u>A I Y (</u>		<u><u><u></u></u></u>	<u>QQEI</u>	
<pre># F F I Y I</pre>	L I V N S + 1 11444 c 1070 1235 c 2796 2938 c 4552 4755 c 7021 7235 c 7024 7586 c 7024 8081 c 8544 8694 c 9734 9994 c 11340 11444 c 105672 105874 c 105672 105875 c 105672 105876 c 105672 105876 c 105672 105877 c 105672 105876 c 105672 105877 c 105672 105976 c 139663 139677 c 139663 139677 c 139663 139677 c 139663 139677 c	() + I L F () + I L F () + I L F () + I L F () +	S + F + T V Parent=g1 / codon_start=1 /transcript_id=	/ID=q1.t1:C 'g1.t1' /co 'g1.t1' /co 'g2.t1' /co	DS don_start=3 don_start=3 don_start=3 don_start=3 don_start=2 don_start=2 don_start=2 don_start=3 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=1 don_start=3	="junction pla	* M V N <u>V H R Q</u>	"		<u><u><u></u></u></u>	<u>Q Q E I</u>	
<pre># F F I Y I</pre>	L I V N S + 1 11444 c 1070 11444 c 1070 11444 c 1070 11444 c 1070 11444 c 1070 11444 c 1070 1235 c 2796 2939 c 2792 4758 c 7021 7235 c 7024 7026 48694 c 9734 9994 c 11390 11444 c 11442 11444 c 114527 108395 c 105672 108396 c 105672 106917 c 105673 106917 c 108386 116399 c 139663 139070 c 139663 139070 c 139663 145732 c	(J= I L F /ID=q1.11 //F /Parent=g1.11 /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g1' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g2' /gene_id='g3' /gene_id='g3' /fD=q3.11 /F	S + F + T V Parent=g1 (/codon_start=1 /transcript_id=	/ID=q1.t1:/ 'ID=q1.t1:/ 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g1.t1'/cc 'g2.t1'/cc 'g2.t1'/cc 'g2.t1'/cc 'g2.t1'/cc 'g2.t1'/cc 'g2.t1'/cc 'g2.t1'/cc 'g2.t1'/cc	S * V H S * V H DS don_start=3 don_start=3 don_start=3 don_start=3 don_start=1 don_start=1 don_start=1 dom_start=1 dom_start=3 dom_start=1 dom_start=1 dom_start=1 dom_start=1 dom_start=1 dom_start=1	="junction pla	* M V N <u>V H R Q</u>	"		<u><u><u></u></u></u>	<u>Q Q E I</u>	

Também é possivel fazer uma busca por domínios conservados do Pfam diretamente pelo Artemis.



As sequências podem ser caracterizadas com diversas informações diferentes, e essas informações podem ser adicionadas diretamente pelo Artemis (assim como feito no BLAST).

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