Criteria	Ratings							
Section 1:	Excellent	Good	Acceptable	Needs	Not Done			
Explain the				Improvement				
use of the	Describes what	Declares that this is	Declares that this is	Declares that this is	At least 2 questions			
global	they would expect	what they expect	what they expect	what they expect	not answered.			
alignment	the scoring matrix	with no	with no	with no				
programs	ms (a) to look like and explanations for the ex		explanations for the	-				
provided	why. Can identify	scoring matrix (a).	scoring matrix (a).	scoring matrix (a).				
	the traceback	Can identify the	Can identify the	Cannot identify the				
	matrix (d) and	traceback matrix	traceback matrix traceback matrix					
	explain how it is	(d). Discusses why	(d). Identifies that	(d). Does not				
	used. Discusses	this is a good	this is a good	identify this is a				
	why this is a good	alignment. Includes	alignment. Includes	good alignment.				
	alignment and	the potential	the potential	Includes an				
	provides reasoning	number of	number of	incorrect potential				
	for this. Includes	alignments	alignments as a	number of				
	the potential	(1,352,078).	calculation but not	alignments. Does				
	number of	Identified that	the final number.	not identify that				
	alignments	changing the	Identified that	changing the				
	(1,352,078).	weights of the	changing the	weights of the				
	Discussed the way	mismatch and gap	weights of the	mismatch and gap				
	that changing the	penalty change the	mismatch and gap	penalty change the				
	weights of the	alignment score	penalty change the	alignment score				
	mismatch and gap	and alignment.	alignment score	and alignment.				
	penalty change the		and alignment.					
	alignment score							
	and alignment.		. , , ,	., ,				
Section 2:	Excellent	Good	Acceptable	Needs	Not Done			
Perform	Y 11	x 11 .	x 11 .	Improvement	4.1			
alignment on	Is able to	Is able to	Is able to successfully run R	Is not able to	At least 2 questions			
mRNA	successfully run R	·		successfully run R	not answered.			
sequences.	program and edit to	program and edit to	program and edit to	program and edit to				

determine the Reason from determine the determine the determine the alignment differences differences differences differences scores about between the between the between the between the similarity. various RNAs. various RNAs. various RNAs. various RNAs. Incorrectly Identifies the size of Identifies the size of Identifies the size of matrix a (number of matrix a (number of matrix a (number of identifies the size of bases seq1x bases seq1x bases seq1x matrix a (number of number of bases number of bases number of bases bases seq1x seq2), 627x631. seq2), 627x631. seq2), 627x631. number of bases seg2), 627x631. Explains why. Alignment score Provides an Alignment score should be 175 M=1, alignment score but Provides an should be 175 if alignment score but X=-2, g=-5. (With doesn't specify the built in scores. If penalties used to doesn't specify the using M=1, X=-2, they have changed penalties used to g=-5. Potential achieve it. Just says alignments are this might be they can't calculate achieve it. Just says HUGE (too large for different.) Potential it. Identifies that they can't calculate Excel to calculate). alignments are mouse is closer, but it. Incorrectly Explain why so HUGE (too large for doesn't provide an identifies that HBA is closer. Depending Excel to calculate). large. If using accurate reason for If using default why. Depending on on the values they default scores, scores, human HBB the values they use, use, they may get human HBB is different answers. closer to mouse is closer to mouse they may get HBB than human HBB than human different answers. They should HBA. Discuses that They should HBA. Discusses that identify one pair. Does not describe the alignment score the alignment score identify one pair. is lower for human is lower for human Does not describe why this pair is the HBB to HBA than best. Does not HBB to HBA than why this pair is the human HBB to best. Provides an provide an image of human HBB to mouse HBA. image of the the alignment of at mouse HBA. Depending on the Depending on the alignment of at least one of the values they use. values they use. least one of the RNAs with another. they may get they may get RNAs with another. different answers. different answers.

	They should	They should			
	identify one pair	identify one pair			
	and discuss why	and identify that			
	they think they are	this pair has the			
	the most similar	highest edit			
	(highest edit	distance. Provides			
	` ` `				
	distance score).	an image of the			
	Provides an image	alignment of at least one of the			
	of the alignment of				
	at least one of the	RNAs with another.			
Coation 2.	RNAs with another. Excellent	Cood	Aggortoble	Needs	Not Done
Section 3: Understand	Excellent	Good	Acceptable		Not Done
	To able to	To alala da	To alala da	Improvement	D
and explain	Is able to	Is able to	Is able to	Is unable to	Does not attempt to
use of local	successfully run R	successfully run R	successfully run R	successfully run R	edit R program.
alignment and	program and edit to	program and edit to	program and edit to	program and edit to	
difference	determine the	determine the	determine the	determine the	
between local	differences	differences	differences	differences	
and global	between the RNA	between the RNA	between the RNA	between the RNA	
alignments	and genome.	and genome.	and genome.	and genome.	
	Discusses how the	Discusses that the	Discusses that the	Doesn't think the	
	alignment doesn't	alignment doesn't	alignment doesn't	alignment is bad.	
	align the exons well,	align well. Doesn't	align well. Doesn't	Can not identify	
	as one would like	identify that it's	identify that it's	that exons should	
	for an RNA→	because it's not	because it's not	be identified.	
	genome alignment.	aligning exons	aligning exons	Identifies that a	
	Describes a method	properly. Describes	properly. Describes	local alignment	
	to make the	a method to make	a method to make	would be better.	
	alignment better,	the alignment	the alignment	They do not edit the	
	either local	better, either local	better, either local	R program to make	
	alignment, or using	alignment, or using	alignment, or using	a 4 th option, 0. The	
	an additional type	an additional type	an additional type	program doesn't	
	of penalty, gap	of penalty, gap	of penalty, gap	run.	

	extension. They correctly edit the R program to make a 4 th option, 0. The program runs.	extension. They correctly edit the R program to make a 4 th option, 0. The program runs.	extension. They edit the R program to make a 4 th option, 0. The program doesn't run.		
Section 4: Multiple	Excellent	Good	Acceptable	Needs Improvement	Not Done
Sequence Alignment with Bioconductor	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than mine and identifies that the clear exon/intron boundaries without random matches between the RNA in intronic regions is why it's better. Identifies that the local alignment only provides an alignment of the last exon with the DNA as it's the exon with the highest score. They provide images of the multiple sequence alignment of both	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than mine and identifies that the clear exon/intron boundaries without random matches between the RNA in intronic regions is why it's better. Identifies that the local alignment only provides an alignment of ONE of the exons with the DNA. They provide images of the multiple sequence alignment of both the HBBs and the HBX data. They also	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than mine and identifies that the clear exon/intron boundaries without random matches between the RNA in intronic regions is why it's better. Identifies that the local alignment only provides an alignment of part of the RNA with the DNA. They provide a dendrogram and identify that most hemoglobins are more similar to the same type than	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than without explanation of why it's better. Identifies that the local alignment only provides an alignment of part of the RNA with the DNA. They do not provide a dendrogram. They identify that most hemoglobins are more similar to the same type than those from the same organism. Indicate an incorrect	Using Biostrings to perform alignment of RNA to DNA. Identifies this as a better alignment than without explanation of why it's better. No description or explanation of the local alignment. They do not provide a dendrogram. They identify that most hemoglobins are more similar to the same type than those from the same organism. Indicate an incorrect evolutionary explanation. No next step given

	the HBBs and the HBX data. They also provide a dendrogram and identify that most hemoglobins are more similar to the same type than those from the same organism. Indicates that this means these genes diverged, evolutionarily before these species diverged, so these gene duplication and evolution vents happened before speciation. They provide a reasonable next step.	provide a dendrogram and identify that most hemoglobins are more similar to the same type than those from the same organism. Indicates that this means these genes diverged, evolutionarily before these species diverged. They provide a reasonable next step.	those from the same organism. Indicates that this means these genes diverged, evolutionarily before these species diverged. They provide a reasonable next step.	evolutionary explanation. No next step given	
Section 5: Use BLAST.	Excellent	Good	Acceptable	Needs Improvement	Not Done
Reason from BLAST results about similarity and evolution.	Identifies 4 closely related sequences that are not the same sequence. They have some discussion about how similar they are. They identify at	Identifies 4 closely related sequences that are not the same sequence. They have some discussion about how similar they are. They identify at	Identifies 4 closely related sequences that are not the same sequence. They have NO discussion about how similar they are. They identify at	Identifies less than 4 closely related sequences that are not the same sequence. They have NO discussion about how similar they are. They	Does not complete one of the elements of this section.

	least beta, delta, epsilon (1&2), gamma (1&2), beta pseudogene, alpha (1&2), theta, mu, and zeta. There should be an alignment of these and an image of either the alignment or the dendrogram, or both.	least 6 of the hemoglobins. should be an alignment of t and an image either the alignment or t dendrogram, both.	hese of the	least 6 of the hemoglobins. There should be an alignment of these, but no image of the dendrogram or alignment is given.	the he	fy at least 4 of moglobins. gnment is ted	
Well written	Excellent	Excellent		Acceptable		Needs Improvement	
and clear	Answers to each section written in paragraph form. Clearly written		Answers to each section written mainly in paragraph form. Mostly		Answers to each section written in bullet form. Difficult to		
	and easy to understand.		clearly written and easy to understand.		understand.		
Extra Credit	Excellent		Part Way		Doesn't work		
	R program runs and generates local alignment(s) for regions that align		R program doesn't run, but in reading through it, looks like it would work, but has bugs.		Doesn't make sense or isn't attempted.		