Open BioEdit and create a new alignment.

BioEdit Sequence Alignment Editor										
File Accesory Application RNA World Wide Web Options Window Help										
New Alignment	Ctrl+N									
Open	Ctrl+O	_								
Open motif descriptor										
New from Clipboard										
Retrieve sequences from GenBank or GenPept										
New Text										
Open As Text										
Run script										
Batch ABI to SCF Trace File Conversion										
Batch Export of Raw Sequence Trace Data										
C:\Users\Ray\IRES\Kenyan_sequences\Growth_Hormone\Intron 2\INtron2PrankALignment.phy										
C:\Users\Ray\IRES\2012\2012_IRES_Data\Sequences\Garra\Garra.phy										
Untitled1										
$\label{eq:c:Users} C: Users \ Ray \ Desktop \ Chiloglanis \ Manuscript \ Guinea \ Chiloglanis \ Molecular \ Chiloglanis \ S_{13} \ For \ Manuscript \ fas \ Not \ S_{13} \ For \ Manuscript \ fas \ Not \ S_{13} \ For \ Manuscript \ fas \ Not \ S_{13} \ For \ Manuscript \ fas \ Not \ S_{13} \ For \ Manuscript \ fas \ Not \ S_{13} \ For \ Manuscript \ fas \ For \ For \ For \ Manuscript \ fas \ For \ F$										
Exit										

Import your sequences including those downloaded from GenBank

BioEdit Sequence Alignment Editor							
File Edit Sequence Alignment View Accessory Application	RNA	World Wide Web	Options	Window	Help		
New Alignment						Ctrl+N	
Open						Ctrl+0	
New from Clipboard							
New Text							
Open As Text							1
Save						Ctrl+S	•
Save As							🖣 fast
Retrieve sequences from GenBank or GenPept							70 80
Copy file name to clipboard							
Export						•	
Import						•	Sequence alignment file
Import from Clipboard							From tab delimited file (eg Excel)
Merge into Alignment based on a Reference Sequence						-	
Merge from Clipboard							
Append Alignment							
Go to GenBank							
Close							
Batch ABI to SCF trace file conversion							
Batch Export of Raw Sequence Trace Data							
Revert to Saved						Ctrl+R	I

Once all of your sequences are imported you can then align them with Clustal W.

*	BioEc	dit S	equence A	lignment Edito	or						
Fil	e Ec	dit	Sequence	Alignment	View	Accessory Application	RNA	World Wide W	eb Options	Window	Help
	Add	d / N	lodify / Rei	move an Acces	sory Ap	oplication					
	Clus	stalV	V Multiple	alignment							
	BLA	\ST						+			
	CAP DNA	P co ADis	ntig assem t> Neig) Mask: None) Mask: None							
	DNA	ADis	t DNA dista	ance matrix					6	MI 🖬	Scro
	DNADist DNA distance matrix DNAml DNA Maximum Likelihood program DNAmlk DNA Maximum Likelihood program with molecular clock DNAPars DNA parsimony method FastDNAml DNA maximum likelihood Fitch Fitch-Margoliash and Least-Squares Distance Methods Kitsch Fitch-Margoliash and Least Squares Methods with Evolutionary Clock NEIGHBOR Neighbor-Joining and UPGMA methods ProML Protein Maximum Likelihood program Protdist> Fitch phylogenetic tree Protdist> Neighbor phylogenetic tree Protdist protein distance matrix Protpars protein parsimony method								AGCACCA CGACTAG CTAGTCG CTACCAG AACGACGA ACGACGACGA ACGACGCACT	STORACA STOCAACA STOCGACCA ACCTACCC CACCAACC CACCAACC CACCAACC CACCAACCA ACTAGTCC AGTCGAT	spee 60 ICTCAG IACCAG AGCACC CAATAT CGACCT CGACCT SATCTA CTACCA

Once selected hit Run and OK. Change mode to edit so that we can trim the ends of the alignments.



Do this at the end of the alignment as well. Go through the alignment and correct any gaps that may occur.

You also need to make sure that the names do not contain any spaces or stange symbols. If you want to have spaces use_underscores_to_complete_this.

Now you can save this file as a phylip 4 file. Go to file, Save as, and select the folder you want to save the alignment in.