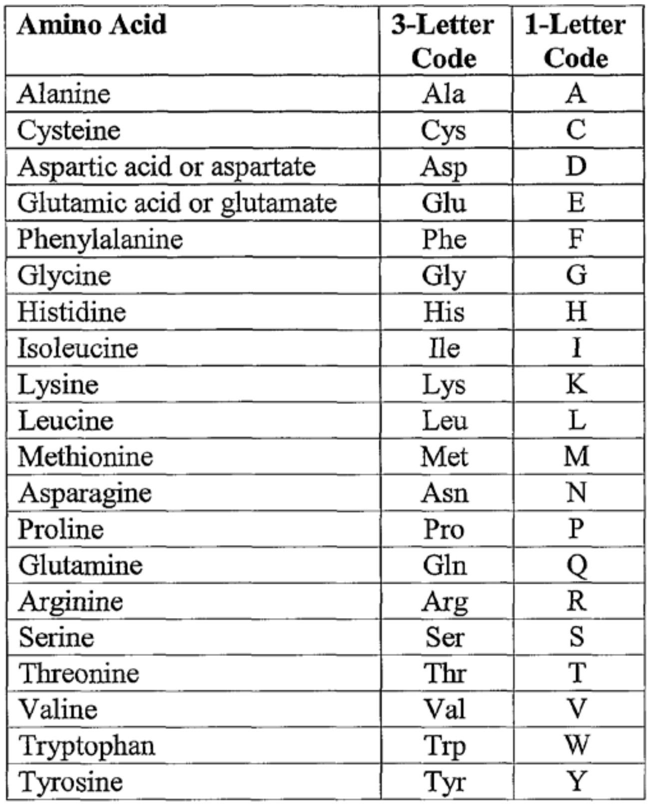
Bioinformatics Appendix for General Biology

1. Amino Acid Sequences For Species

```
>Unknown
QTAYAGDAANGMRVFNTYCSDCHSITEGKNKIGPSLWNVVGRKPASISDFNYSDAM
RKNDIIWTEDRISTYITNPQGLLPGVKMAFPGLKDPQKCADVIQFLSQQH
>Sphingomonas_echinoides
LAAYTGDAKKGETDFITCKTCHAIEAGVNKIGPSLHGVVGRKAGSIPGFTYSTANKN
SGITWTEEKLFQYLENPQRVVPGTKMTFAGWPTDPQKRADVIAYLKSNS
>Caldithrix_abyssi
ENSSFGEGMSLAELGAKLYKSKACVTCHSVDGSPLVGPTFKGVFGHTVKLNDGSSV
KADENYLRESILKPQAKVVEGFQPVMPTYQSILKPREVDALIEYIKSLGE
>Homo_sapiens
MGDVEKGKKIFIMKCSQCHTVEKGGKHKTGPNLHGLFGRKTGQAPGYSYTAANKN
KGIIWGEDTLMEYLENPKKYIPGTKMIFVGIKKKEERADLIAYLKKATNE
>Pan_troglodytes
MGDVEKGKKIFIMKCSQCHTVEKGGKHKTGPNLHGLFGRKTGQAAGYSYTVANKN
KGITWGEDTLMEYLENPKKHIPETKMIFVGIKKKEERADLIAFLKKATNE
>Apis_mellifera
MGIPAGDPEKGKKIFVQKCAQCHTIESGGKHKVGPNLYGVYGRKTGQAPGYSYTDA
NKGKGITWNKETLFEYLENPKKYIPGTKMVFAGLKKPQERADLIAYIEQASK
```

2. Amino Acid Abbreviation Codes



Amino Acid	3-Letter Code	1-Letter Code
Alanine	Ala	A
Cysteine	Cys	C
Aspartic acid or aspartate	Asp	D
Glutamic acid or glutamate	Glu	E
Phenylalanine	Phe	F
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Lysine	Lys	K
Leucine	Leu	L
Methionine	Met	M
Asparagine	Asn	N
Proline	Pro	P
Glutamine	Gln	Q
Arginine	Arg	R
Serine	Ser	S
Threonine	Thr	T
Valine	Val	V
Tryptophan	Trp	W
Tyrosine	Tyr	Y

3. Description of Species

Bacteria: (ocean dwellers)

1. ***Unknown*****:** Bacteria from sediments that live off of single carbon compounds such as methanol and methylamine
2. ***Sphingomonas***: Aerobic bacteria that is really versatile. It can "eat" almost anything!
3. ***Caldithrix abyssi***: Anaerobic isolated from a hydrothermal vent where temperature can rise up to 400ºC. Name literally means "cauldron (hot) threads of the abyss".

Eukarya:

4. ***Homo sapiens:*** Healthy human individual.
5. ***Pan troglodytes***: Chimpanzee.
6. ***Apis mellifera:*** European honey bee.

4. Description of Programs and Databases

BLAST (Basic Local Alignment Search Tool) is a program that compares DNA and amino acid sequences to a known database of sequences of organisms. It calculates the significance of matches. BLAST can be uses to test for genetic diseases. BLAST can also be used to infer functional and evolutionary relationships between sequences. BLAST is maintained by the National Center for Biotechnology Information (NCBI) which is a subdivision of the National Institutes of Health (NIH). Research groups worldwide contribute to the database.

Seaview is a graphical user interface that allows visualization of the alignment of multiple sequences. It can also organize phylogenic trees based on evolutionary relationships. It is maintained by the institution Pôle Rhône-Alpes de Bioinformatique in France. Different research groups contribute to its database.

To download Seaview4

1. go to website: http://doua.prabi.fr/software/seaview
2. Go to "Download SeaView" section and select appropriate format
3. Click "Save file"
4. Open and extract Seaview
5. Go to location Seaview file is saved. Open application "seaview.exe"