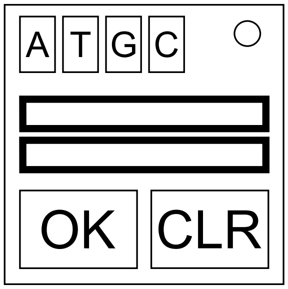
On the Subject of Genetic Sequences

Only true scientists synthesize proteins while bomb defusing.

See Appendix A for indicator identification reference.



- The module consists of four lettered buttons, a button labeled “OK”, a button labeled “CLR” and two display screens.
- To disarm the module, input the correct DNA sequence using the lettered buttons and press “OK” to submit. Submitting an incorrect sequence will cause a strike. Press “CLR” to clear all input.
- The default input sequence is the **coding strand.** If you are instructed to alternate the final input sequence, switch between the **coding strand** and the **template strand.**

Determine Starting Amino Acid

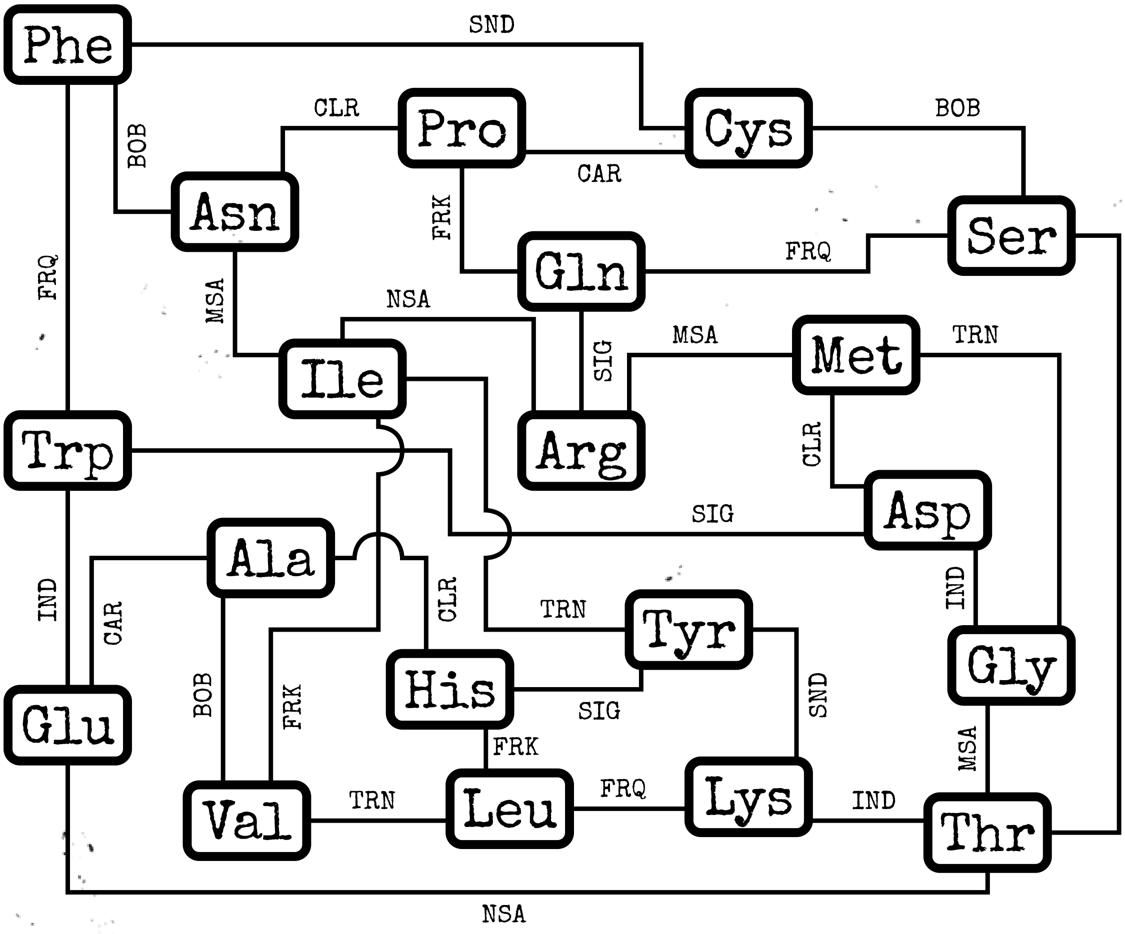
Using the table below, determine the starting amino acid by referring to the order in which the four lettered buttons appear in the module. Follow the first rule that applies.

Rule	Starting Amino Acid
The buttons appear in alphabetical order.	Trp
The subsequence “ACT” is present in the button order.	Gly
“G” is the label of the last button.	Tyr
“T” is the label of the first button.	Cys
The button labeled “C” appears before the buttons labeled “A” and “T”.	Arg
The buttons labeled “A” and “T” are next to each other.	Leu
The buttons labeled “G” and “C” are next to each other.	Ala
No other rules apply.	Asn

Determine Amino Acid Sequence

Starting with the amino acid obtained in the previous step, use the graph below to obtain a sequence of four amino acids. In order to determine the next amino acid in the sequence, locate the last amino acid determined in the graph and choose a path to the next one using the following rules:

- If the bomb has a lit indicator with a label that matches the name of a path, follow that path. If one or more paths match this rule, follow the one that comes first alphabetically.
- Otherwise, if the bomb has an unlit indicator with a label that matches the name of a path, follow that path and **alternate the final input sequence.** If one or more paths match this rule, follow the one that comes first alphabetically.
- Otherwise, follow the path that comes first alphabetically.
- No path may be followed more than once. This rule supersedes all previous rules.



Determine Input Sequence

Use the table below to decode the amino acid sequence into the corresponding **coding strand**. If that is the final input sequence, you may submit it.

Amino Acid Code	Amino Acid Name	Codon
Leu	Leucine	TTA
Ile	Isoleucine	ATC
Ser	Serine	TCG
Thr	Threonine	ACC
Tyr	Tyrosine	TAT
Gln	Glutamine	CAG
Lys	Lysine	AAA
Cys	Cysteine	TGC
Trp	Tryptophan	TGG
Gly	Glycine	GGG

Amino Acid Code	Amino Acid Name	Codon
Phe	Phenylalanine	TTT
Met	Methionine	ATG
Val	Valine	GTA
Pro	Proline	CCA
Ala	Alanine	GCT
His	Histidine	CAT
Asn	Asparagine	AAC
Asp	Aspartic acid	GAT
Glu	Glutamic acid	GAA
Arg	Arginine	CGC

If your final input sequence is the **template strand,** you need to obtain the complementary sequence of the coding strand first. Use the table below to replace every nucleobase of the sequence with its complement. Because every sequence must be input in the 5′ to 3′ direction (five prime to three prime), the template strand **must be reversed** before it is submited. The image below helps to clarify this concept.

Nucleobase	Base Complement
A	T
T	A
G	C
C	G