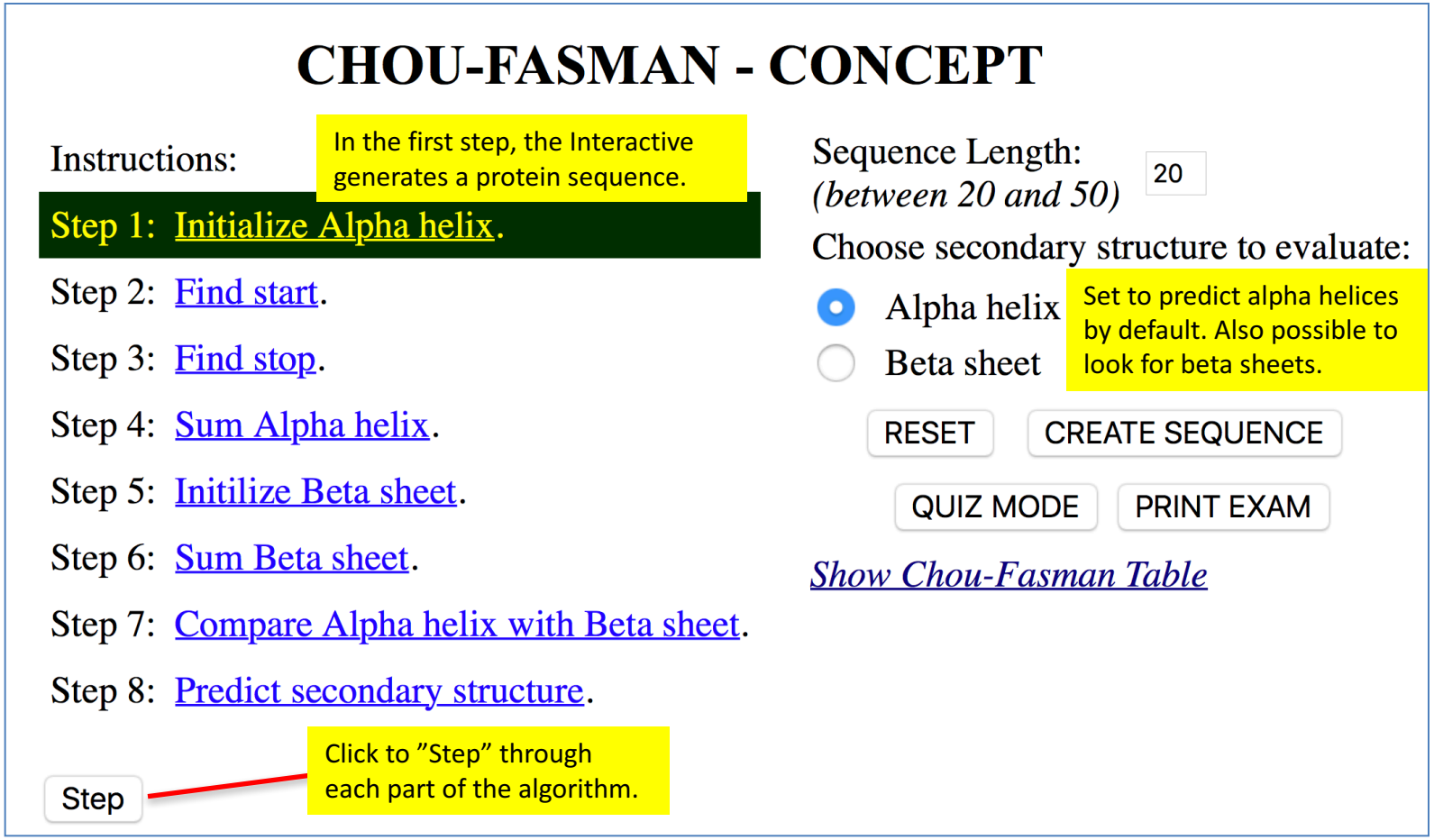
Chou-Fasman Algorithm: Concept Mode

This exercise teaches how to use the Chou-Fasman Interactive. The Chou-Fasman method predicts protein secondary structures in a given protein sequence. In the concept example, the Interactive shows how to predict if a sequence has an alpha helix.



Chou-Fasman Algorithm: Concept Mode

Choose secondary structure to evaluate:

- (•) Alpha helix
- ( ) Beta sheet

RESET CREATE SEQUENCE

QUIZ MODE PRINT EXAM

Show Chou-Fasman Table

Click link to see the propensity table.
P(a)=propensity of being in an alpha helix.
P(b)=propensity of being in a beta sheet.

Amino Acid		P(a)	P(b)
Alanine	A	142	83
Arginine	R	98	93
Asparagine	N	67	89
Aspartic acid	D	101	54
Cysteine	C	70	119
Glutamic Acid	E	151	37
Glutamine	Q	111	110
Glycine	G	57	75
Histidine	H	100	87
Isoleucine	I	108	160
Leucine	L	121	130
Lysine	K	114	74
Methionine	M	145	105
Phenylalanine	F	113	138
Proline	P	57	55
Serine	S	77	75
Threonine	T	83	119
Tryptophan	W	108	137
Tyrosine	Y	69	147
Valine	V	106	170

Chou-Fasman Algorithm: Concept Mode

Step 1: Initialize Alpha helix.

Step 2: Find start.

Step 3: Find stop.

Step 4: Sum Alpha helix.

Step 5: Initilize Beta sheet.

Step 6: Sum Beta sheet.

Step 7: Compare Alpha helix with Beta sheet.

Step 8: Predict secondary structure.

FIND START. Select the first ***6 in a row with at least 4 values >= 100***. Notice that the green squares indicate amino acids equal to or greater than 100 alpha helix propensity. Notice that 5 out of 6 of the amino acids are >=100.

(between 20 and 30)

Choose secondary structure to evaluate:

RESET CREATE SEQUENCE

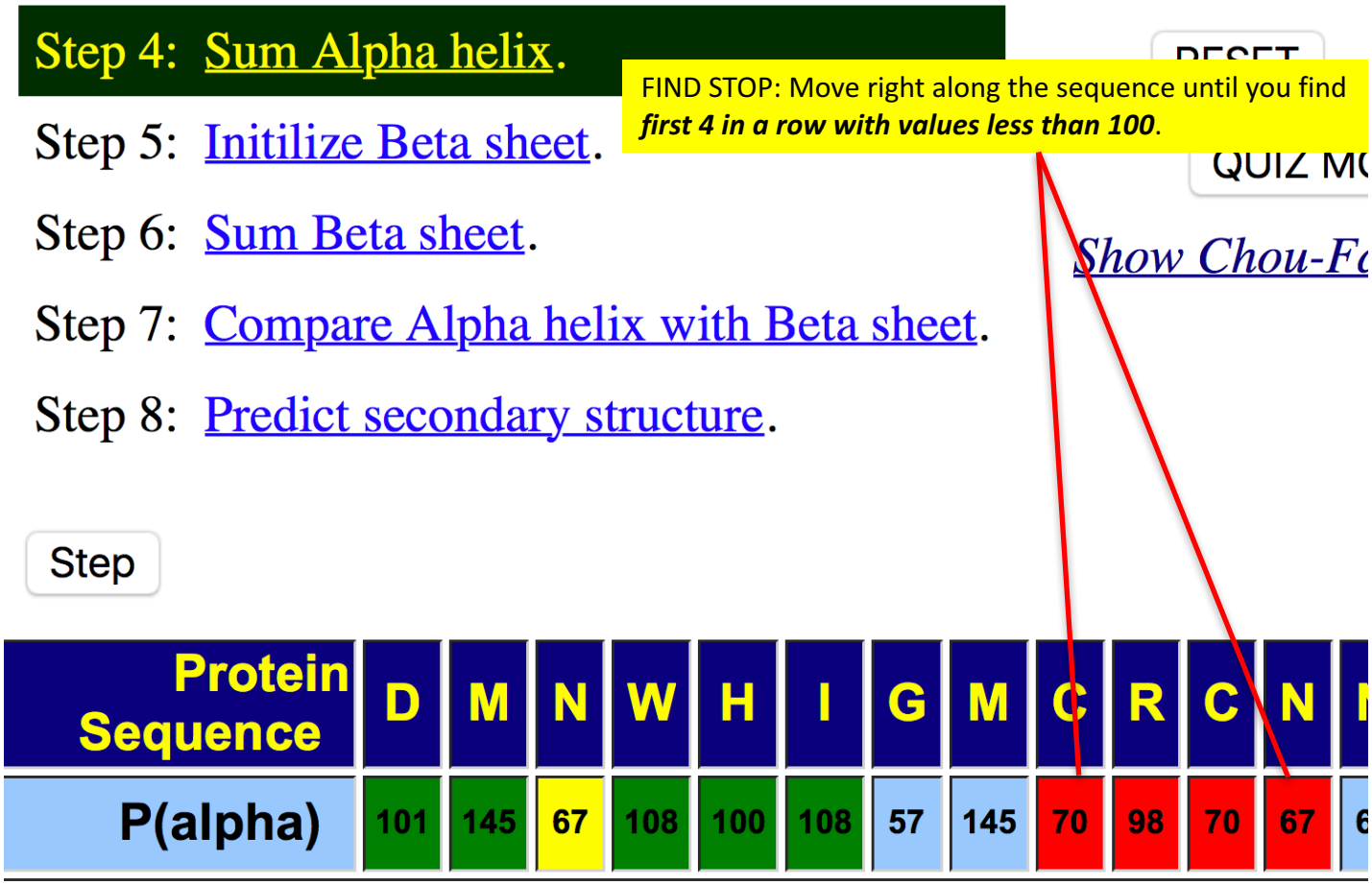
QUIZ MODE PRINT EXAM

Show Chou-Fasman Table

Step

Protein Sequence	D	M	N	W	H	I	G	M	C	R	C	N	N	T	K	W	C	Q	A	T
P(alpha)	101	145	67	108	100	108	57	145	70	98	70	67	67	83	114	108	70	111	142	83

Chou-Fasman Algorithm: Concept Mode



Chou-Fasman Algorithm: Concept Mode

Step 5: Initilize Beta sheet.

Step 6: Sum Beta sheet.

Step 7: Compare Alpha helix with Beta sheet.

Step 8: Predict secondary structure.

QUIZ MC

Show Chou-Fa

Step

Protein Sequence	D	M	N	W	H	I	G	M	C	R	C	N	
P(alpha)	101	145	67	108	100	108	57	145	70	98	70	67	6
Running total for P(alpha)	101	246	313	421	521	629	686	831					

SUM up all values from beginning of first window to the one prior to the 4 stop amino acids. **The total is 831.**

Note: Include all 6 starting amino acids the 'good' numbers. *Do not include* the 4 at the end. They are 'bad' numbers.

Chou-Fasman Algorithm: Concept Mode

Step 8: Predict secondary structure.

Step

The last step: You need to compare the scores for a Beta Sheet for the SAME SEQUENCE. If the alpha helix total is > that beta sheet total, then you can predict an alpha helix.

Protein Sequence	D	M	N	W	H	I	G	M	C	R	C	N	N
P(alpha)	101	145	67	108	100	108	57	145	70	98	70	67	67
Running total for P(alpha)	101	246	313	421	521	629	686	831					
P(beta)	54	105	89	137	87	160	75	105					
Running total for P(beta)	54	159	248	385	472	632	707	812					
Evaluation:	Structure is an ALPHA HELIX												

831 is greater than 812, so conclusion: The sequence is an alpha helix!

Chou-Fasman Algorithm: QUIZ Mode

The quiz mode begins the same way as the Concept mode. Use the step button to start the problem.

CHOU-FASMAN QUIZ

Instructions:

Step 1: Initialize Alpha helix.

Step 2: Find start.

Step 3: Find stop.

Step 4: Sum Alpha helix.

Step 5: Initilize Beta sheet.

Step 6: Sum Beta sheet.

Step 7: Compare Alpha helix with Beta sheet.

Step 8: Predict secondary structure.

Step

Sequence Length:
(between 20 and 50) 20

Choose secondary structure to evaluate:

- (•) Alpha helix
- ( ) Beta sheet

RESET CREATE SEQUENCE

CONCEPT MODE

Show Chou-Fasman Table

Chou-Fasman Algorithm: QUIZ Mode

Click/touch the first and last amino acids of the 6 starting amino acids given the rule in the Concept mode.

Then click/touch the first and last amino acids of the 4 'stop' amino acids.

Protein Sequence	D	M	K	C	E	Y	N	A	Y	Y	A	K	C	T	T	P	G
P(alpha)	101	145	114	70	151	69	67	142	69	69	142	114	70	83	83	57	57
Running total for P(alpha)												0 Evaluate					

Enter the SUM TOTAL for an alpha helix and click/touch the evaluate button.

Protein Sequence	D	M	K	C	E	Y	N	A	Y	Y	A	K	C	T	T	P	
P(alpha)	101	145	114	70	151	69	67	142	69	69	142	114	70	83	83	57	
Running total for P(alpha)	101	246	360	430	581	650	717	859	928	997	1139	1253					

YOU ARE NOT DONE YET! YOU STILL NEED TO SUM THE SCORES FOR A BETA SHEET! Click the Step button again.

Step

Chou-Fasman Algorithm: QUIZ Mode

If the score for and alpha helix is greater than a score for a beta sheet, then you can call it an alpha helix. If not, then it is NOT and alpha helix. In the answer below, the score IS greater, so the algorithm predicts it is an alpha helix.

NOTE: If the beta sheet score is greater, it *does not mean it is a beta sheet*. You would have to run the algorithm again on the same sequence with the beta sheet scores to test that hypothesis.

Protein Sequence	D	M	K	C	E	Y	N	A	Y	Y	A	K	C	T	T	P	G
P(alpha)	101	145	114	70	151	69	67	142	69	69	142	114	70	83	83	57	57
Running total for P(alpha)	101	246	360	430	581	650	717	859	928	997	1139	1253					
P(beta)	54	105	74	119	37	147	89	83	147	147	83	74	119	119	119	55	75
Running total for P(beta)	54	159	233	352	389	536	625	708	855	1002	1085	1159					
Evaluation:	● Alpha helix	○ NOT alpha helix															