

Summary

Name	Jack Rutherford	
	Assigned	Possible
Adequate	11	13
Good	5	7
Excellent	2	2
Superior	0	8
Total	18	30
Score	76	

Adequate

Item	Assigned	Possible	Comment
Error message given if no command line arguments are given	1	1	Make sure you know how to exit with a particular status for the kmeans project. Including a -1 in the error message doesn't do it; call the exit function passing it a specific value as the exit code instead.
Error message given if more than 1 command line arguments is given	0	1	The first command line argument is treated as a file, and the 2nd one is ignored, rather than signalling an error condition.
Error message given if the file being opened does not exist	1	1	
Lines of the specified file are read correctly	1	1	
Each line is chomp'ed to eliminate the newline character	1	1	
Line correctly split into individual amino acids	1	1	
Error message given if file contains an invalid character	1	1	
Hash containing counts by letter is maintained correctly	2	2	
Output contains key and correct value for each amino acid that is present	2	2	
Amino acids are displayed in sorted order by key	1	1	
Nothing is printed for those amino acids that don't appear in the input file	0	1	Instead, a value of 0 is printed. You could check for this value in your loop on lines 19-22
Total	11	13	

Other comments

Good

Item	Assigned	Possible	Comment
			The way version 2 is structured, this doesn't work.
Number of distinct amino acids is printed correctly	1	2	It is fixed in version 3.
Acids that don't appear are output	1	2	
			These 2 aspects appear as if
Missing acids are displayed in alphabetical order	1	1	they would work.
Formatting of non-appearing acids matches the assignment specification	2	2	
Total	5	7	

Other comments

Excellent

Item	Assigned	Possible	Comment
Display of occurrences sorted by number of occurrences appears	2	2	
Total	2	2	

Other comments

Superior

Item	Assigned	Possible	Comment
2nd command line argument is allowed	0	1	Nothing is implemented for this part of the assignment
Error message is given if a non-amino acid is present in 2nd command line argument	0	1	
Error message is given if an amino acid is present in the 2nd command line argument more than once	0	1	
When 2nd command line argument is present, it restricts which acids are shown in the output of counts	0	2	
When 2nd command line argument is present, it restricts which acids are shown as missing	0	2	
Number of distinct amino acid count is not impacted by presence of argument	0	1	
Total	0	8	

Other comments