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from Bio.SeqUtils import seq3
mutate_script = open("mutate_script.txt", "w")
new_mut_aa = open("mut_new_aa.csv").read().splitlines()

for line in new_mut_aa:
    line_list = line.split(",")
    if (len(line_list) > 1):
        pos = line_list[0]
        mutations = line_list[1:]
        print(mutations)
        for new_aa in mutations:
            new_aa_3 = seq3(new_aa).upper()
            mutate_script.write("mutate ste2_cystatin.pdb," + pos + "," +
                                new_aa_3 + "\n")

```