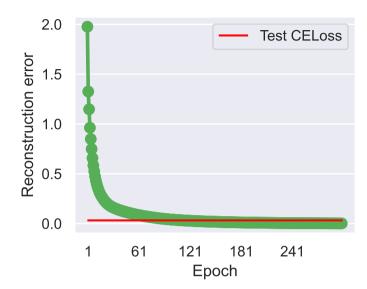
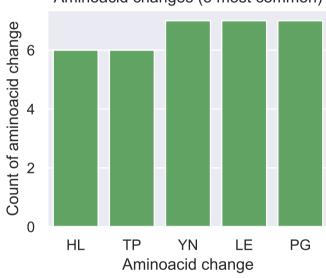
Reconstruction error during training



Aminoacid changes (5 most common)



Average reconstruction error on test set: CELoss: 0.03209

From 7057 sequences with right seq len:7045

p	recision	recall	f1-score	support	
ACDEFGHIKLMNPQR%TVWY	1.00 1.00 0.99 0.99 1.00 1.00 0.98 0.97 0.96 0.99 1.00 0.99 1.00 0.99 0.99 0.99	1.00 1.00 0.99 1.00 1.00 1.00 0.97 0.96 0.99 0.99 1.00 0.99 1.00 0.99 0.99 0.99	1.00 1.00 0.99 0.99 1.00 1.00 0.97 0.96 0.99 0.99 1.00 0.99 1.00 0.99 0.99 0.99	10575 7080 2822 5983 10891 10294 1122 1262 671 4467 375 2984 3007 6486 3131 15894 6508 1934 623 5955	
accurad macro a weighted	vg 0.9		.99 0.9	102064 99 10206 99 10206	

