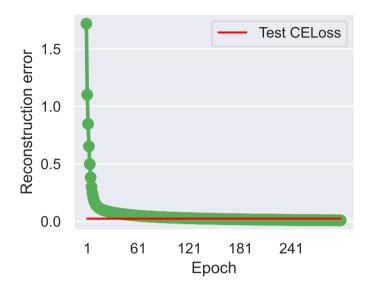
## Reconstruction error during training



Aminoacid changes (10 most common)

But to be a second of the common of

Average reconstruction error on test set: CELoss: 0.02361

From 22806 sequences with right seq len:22786

	precision		recall	f1-score	suppo	rt
ACDEFGHIKLNNPGRSTVVY		0.99 0.93 0.98 0.99 0.99 0.97 .99 0.98 0.98 0.99 0.99 0.99 0.99	0.99 0.92 0.98 0.99 0.99 0.99 0.99 0.98 0.99 0.99	0.99 0.93 0.98 0.99 0.99 0.99 0.99 1.00 0.98 0.99 0.99 0.99 0.99 0.99 0.99	20512 977 7908 11067 10970 18188 3932 10843 16620 30888 4688 6533 11136 10815 9196 11852 12399 16902 2314 8849	
accur macro weighted	acy avg	0.9	0 8	0.99 .98 0.9	226589 98 226	6589 6589

