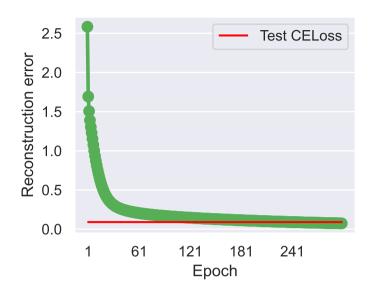
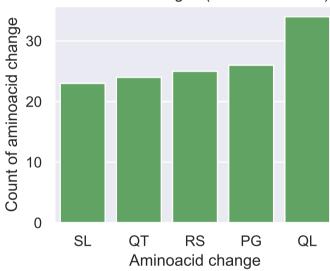
Reconstruction error during training



Aminoacid changes (5 most common)



Average reconstruction error on test set: CELoss: 0.09012

From 7057 sequences with right seq len:6999

1	precision	recall	f1-score	support
ACDEFGHIKLMNPQRSTVWY	0.99 1.00 0.96 0.97 0.99 0.98 0.94 0.93 0.88 0.96 0.94 0.98 0.95 0.99 0.97 0.93 0.89	0.99 1.00 0.95 0.98 0.99 0.91 0.90 0.83 0.97 0.81 0.95 0.95 0.95 0.99 0.98 0.94 0.85 0.98	0.99 1.00 0.95 0.97 0.99 0.99 0.92 0.91 0.86 0.96 0.94 0.98 0.95 0.99 0.97 0.93 0.87	10482 7030 2871 5888 10687 10149 1128 1290 629 4263 339 2924 2982 6457 3173 15948 6532 1844 669 6053
accura macro a weighted	avg 0.9		.94 0.9	101338 95 101338 98 101338

