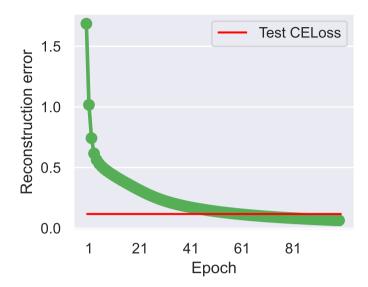
## Reconstruction error during training



Aminoacid changes (5 most common)

90
40
20
WE MI LR DG TS
Aminoacid change

Average reconstruction error on test set: CELoss: 0.11699

From 7057 sequences with right seq len:7021

	precision	recall	f1-score	support
ACDEFGHIKLMNPQRSTVWY	0.98 1.00 0.95 0.96 0.98 0.89 0.85 0.78 0.97 0.86 0.94 0.92 0.97 0.92 0.98 0.98 0.98	0.98 0.99 0.95 0.97 0.98 0.99 0.81 0.96 0.58 0.94 0.94 0.98 0.95 0.99 0.98 0.89 0.72	0.98 1.00 0.95 0.96 0.98 0.99 0.85 0.75 0.96 0.94 0.93 0.98 0.99 0.98 0.99	10461 7061 2972 5948 10809 10150 1156 1233 685 4350 398 2898 3032 6504 3193 15758 6539 1914 642 5972
accura macro weighted	avg 0.9		.91 0.9	101675 92 101675 97 101675

