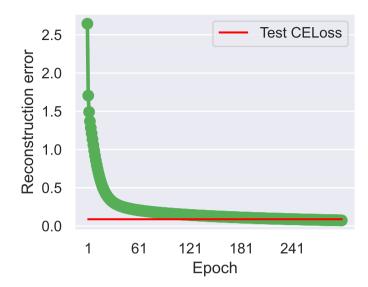
Reconstruction error during training



Aminoacid changes (5 most common)

90

20

15

0

TS

Aminoacid change

DG

QR

IV

DS

Average reconstruction error on test set: CELoss: 0.08828

From 7057 sequences with right seq len:7019

precision		recall	f1-score	support	
ACDEFGHIKLMNPQRSTVWY	0.98 1.00 0.95 0.97 0.99 0.99 0.93 0.92 0.89 0.97 0.96 0.96 0.97 0.95 0.99 0.98 0.92 0.88	0.98 1.00 0.95 0.97 0.99 0.99 0.92 0.88 0.85 0.98 0.96 0.95 0.98 0.95 0.99 0.98 0.92 0.83 0.97	0.98 1.00 0.95 0.97 0.99 0.99 0.92 0.90 0.87 0.97 0.84 0.96 0.95 0.95 0.99 0.98 0.92 0.85 0.97	10474 7056 2862 5943 10783 10144 1145 1307 624 4432 356 2977 2967 6524 3131 15975 6468 1789 688 5918	
accura macro weighted	avg 0.9		.94 0.9	101563 95 101563 98 10156	

