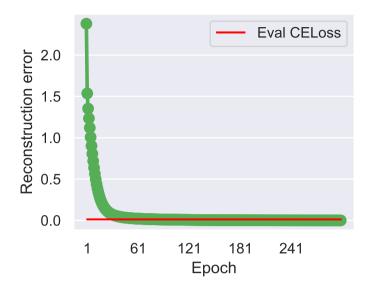
Reconstruction error during training



Aminoacid changes (5 most common)

5

Conut of aminoacid changes (5 most common)

NS DG AT YL IA

Aminoacid change

Average reconstruction error on evaluation set: CELoss: 0.01256

From 7058 sequences with right seq len:7053

	precision	recall	f1-score	support	
ACDEFGHIKLMNPQRSTVWY	1.00 1.00 1.00 1.00 1.00 0.99 0.99 0.99	1.00 1.00 0.99 1.00 1.00 0.98 0.99 0.98 1.00 0.97 0.99 1.00 1.00 1.00 0.99 0.98	1.00 1.00 1.00 1.00 1.00 0.99 0.99 0.98 1.00 0.99 1.00 1.00 1.00 1.00 0.99 0.98	10594 7089 2916 5951 10830 10189 1127 1275 646 4350 357 2996 2935 6437 3160 15901 6616 1885 646 6067	
accura macro weighted	avg 0.9		.99 0.9	101967 99 10196 00 1019	

