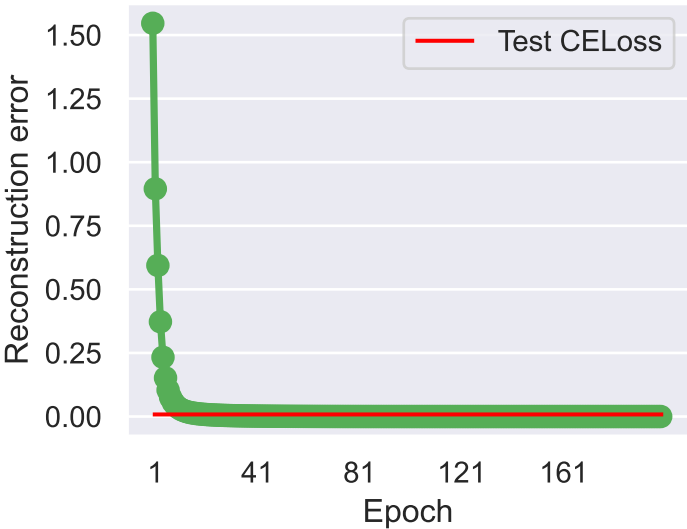


One-hot encoder with arch 420->128 on test set

Reconstruction error during training



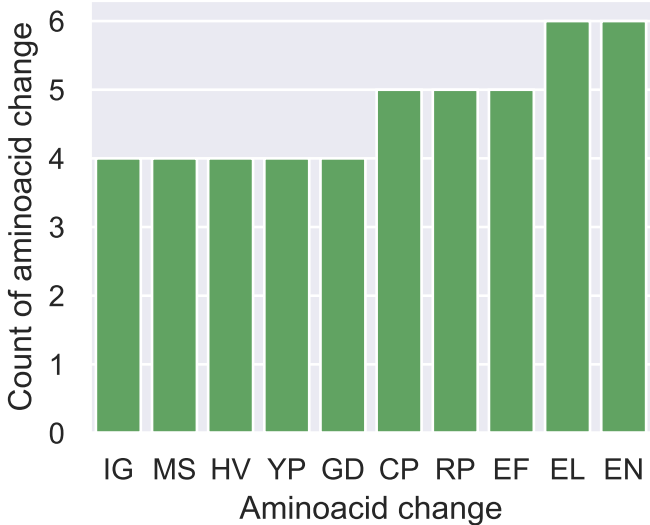
Average reconstruction error on test set:  
CELoss: 0.00816

From 22806 sequences with right seq len:22803

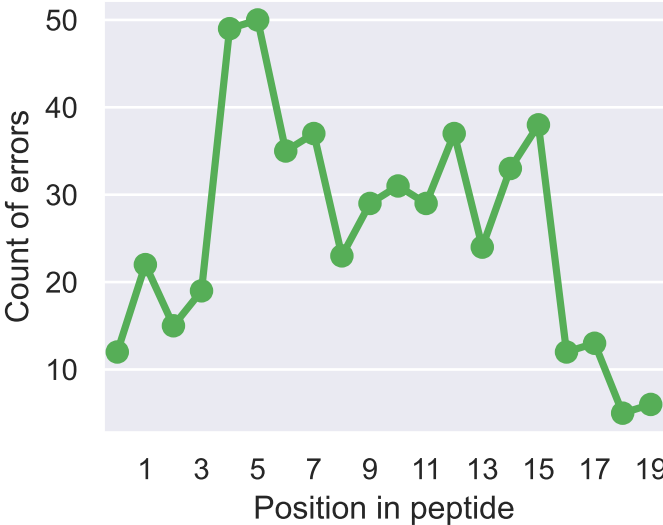
	precision	recall	f1-score	support
A	1.00	1.00	1.00	20757
C	0.98	0.97	0.98	1012
D	1.00	1.00	1.00	7861
E	1.00	1.00	1.00	11031
F	1.00	1.00	1.00	10994
G	1.00	1.00	1.00	18107
H	0.99	0.99	0.99	3965
I	1.00	1.00	1.00	10936
K	1.00	1.00	1.00	16865
L	1.00	1.00	1.00	30853
M	1.00	0.99	0.99	4737
N	1.00	1.00	1.00	6556
P	1.00	1.00	1.00	11207
Q	1.00	1.00	1.00	10747
R	1.00	1.00	1.00	9272
S	1.00	1.00	1.00	11809
T	1.00	1.00	1.00	12681
V	1.00	1.00	1.00	16664
W	0.99	0.99	0.99	2239
Y	1.00	1.00	1.00	8849

accuracy			1.00	227142
macro avg	1.00	1.00	1.00	227142
weighted avg	1.00	1.00	1.00	227142

Aminoacid changes (10 most common)



Count of errors by position



Count of errors by position (in %)

