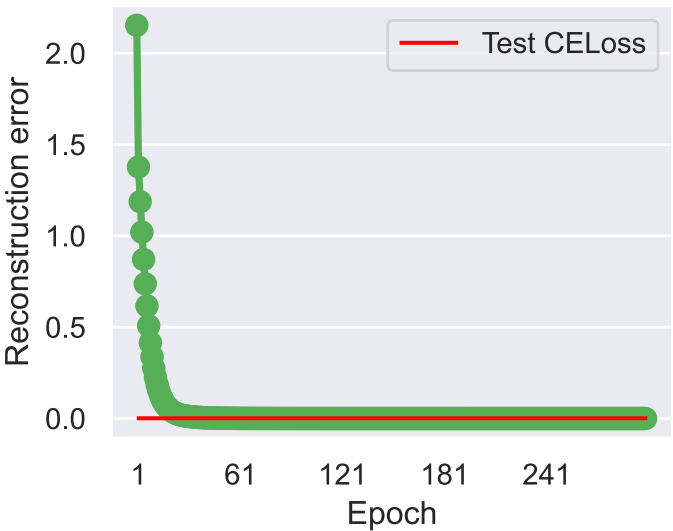


One-hot encoder with arch 399->128 on test set

Reconstruction error during training

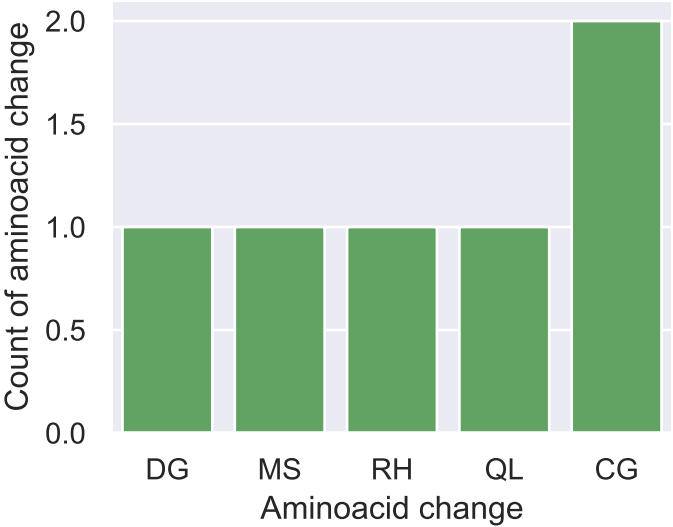


Average reconstruction error on test set:
CELoss: 0.00137

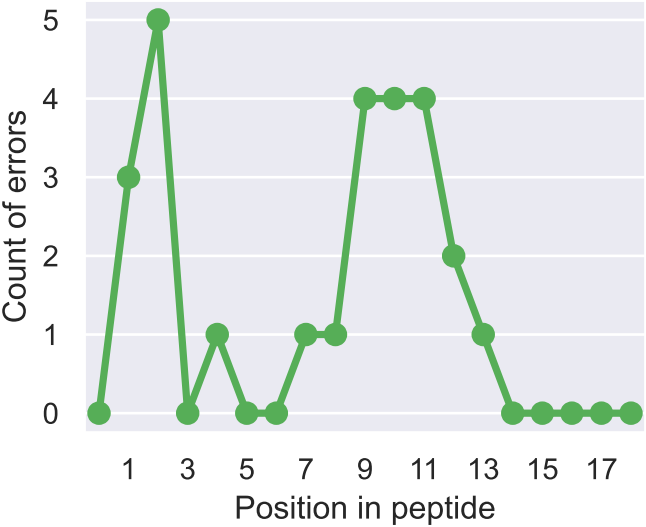
From 7057 sequences with right seq len:7057

	precision	recall	f1-score	support
A	1.00	1.00	1.00	10544
C	1.00	1.00	1.00	7093
D	1.00	1.00	1.00	2937
E	1.00	1.00	1.00	5900
F	1.00	1.00	1.00	10811
G	1.00	1.00	1.00	10157
H	1.00	1.00	1.00	1155
I	1.00	1.00	1.00	1284
K	1.00	1.00	1.00	670
L	1.00	1.00	1.00	4347
M	0.99	1.00	1.00	383
N	1.00	1.00	1.00	3043
P	1.00	1.00	1.00	2984
Q	1.00	1.00	1.00	6561
R	1.00	1.00	1.00	3175
S	1.00	1.00	1.00	15959
T	1.00	1.00	1.00	6548
V	1.00	1.00	1.00	1913
W	1.00	1.00	1.00	641
Y	1.00	1.00	1.00	6034
accuracy			1.00	102139
macro avg	1.00	1.00	1.00	102139
weighted avg	1.00	1.00	1.00	102139

Aminoacid changes (5 most common)



Count of errors by position



Count of errors by position (in %)

