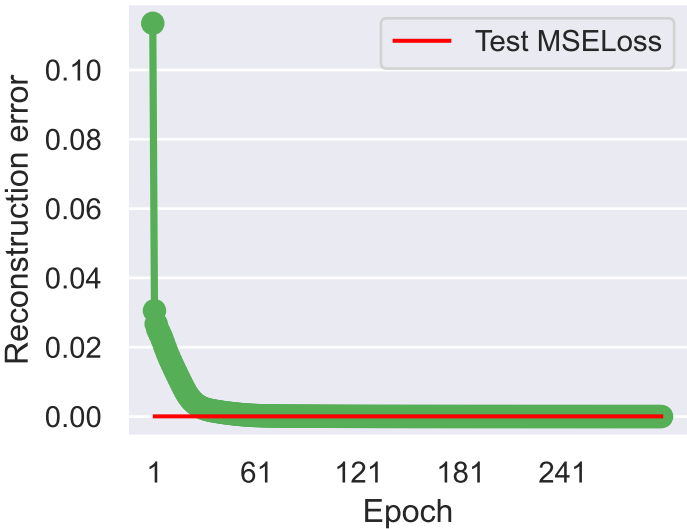


One-hot encoder with arch 399->128 on test set

Reconstruction error during training

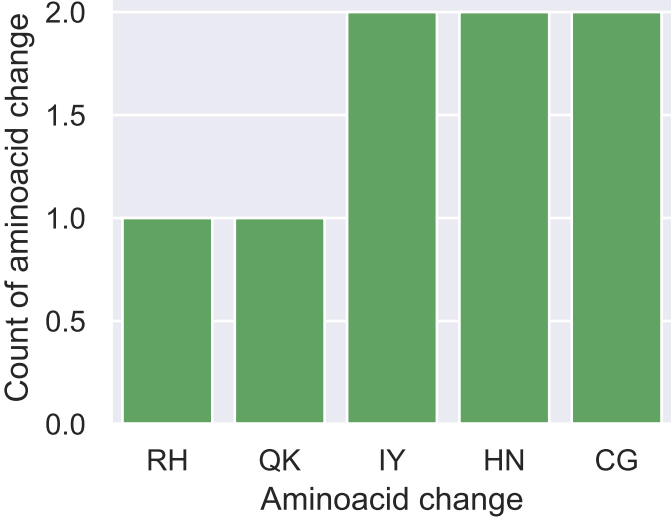


Average reconstruction error on test set:
MSELoss: 5e-05

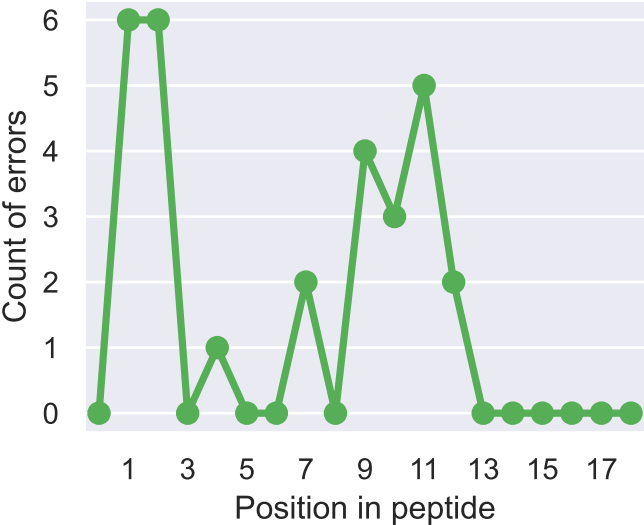
From 7057 sequences with right seq len:7056

	precision	recall	f1-score	support
A	1.00	1.00	1.00	10542
C	1.00	1.00	1.00	7092
D	1.00	1.00	1.00	2936
E	1.00	1.00	1.00	5899
F	1.00	1.00	1.00	10810
G	1.00	1.00	1.00	10156
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	4345
M	1.00	0.99	1.00	383
N	1.00	1.00	1.00	3043
P	1.00	1.00	1.00	2983
Q	1.00	1.00	1.00	6560
R	1.00	1.00	1.00	3174
S	1.00	1.00	1.00	15956
T	1.00	1.00	1.00	6547
V	1.00	1.00	1.00	1912
W	1.00	1.00	1.00	641
Y	1.00	1.00	1.00	6032
accuracy			1.00	102120
macro avg	1.00	1.00	1.00	102120
weighted avg	1.00	1.00	1.00	102120

Aminoacid changes (5 most common)



Count of errors by position



Count of errors by position (in %)

