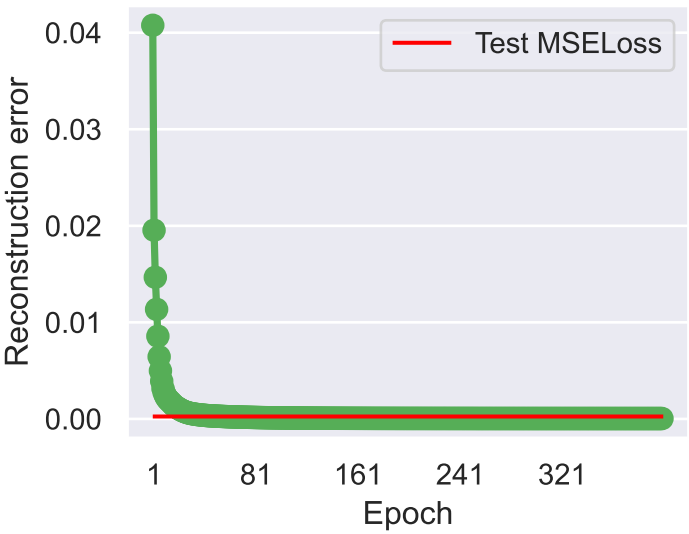


One-hot encoder with arch 399->64 on test set

Reconstruction error during training



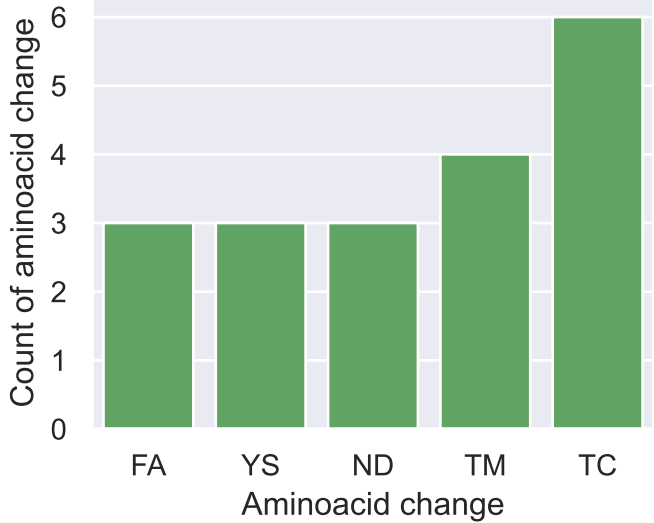
Average reconstruction error on test set:
MSELoss: 0.00025

From 7057 sequences with right seq len:7042

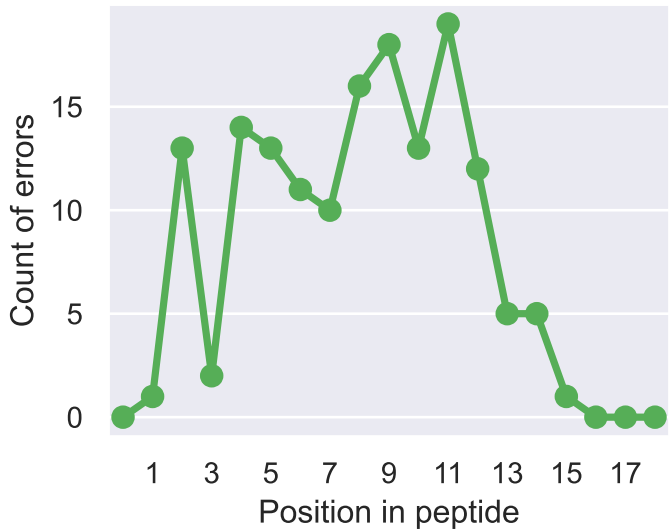
	precision	recall	f1-score	support
A	1.00	1.00	1.00	10521
C	1.00	1.00	1.00	7072
D	1.00	1.00	1.00	2885
E	1.00	1.00	1.00	5909
F	1.00	1.00	1.00	10850
G	1.00	1.00	1.00	10347
H	1.00	0.99	1.00	1111
I	0.99	1.00	1.00	1295
K	0.99	0.99	0.99	664
L	1.00	1.00	1.00	4323
M	0.98	0.98	0.98	375
N	1.00	1.00	1.00	2983
P	1.00	1.00	1.00	3017
Q	1.00	1.00	1.00	6526
R	1.00	1.00	1.00	3126
S	1.00	1.00	1.00	15928
T	1.00	1.00	1.00	6530
V	1.00	1.00	1.00	1892
W	0.99	0.99	0.99	673
Y	1.00	1.00	1.00	6083

accuracy			1.00	102110
macro avg	1.00	1.00	1.00	102110
weighted avg	1.00	1.00	1.00	102110

Aminoacid changes (5 most common)



Count of errors by position



Count of errors by position (in %)

