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

Reconstruction error during training
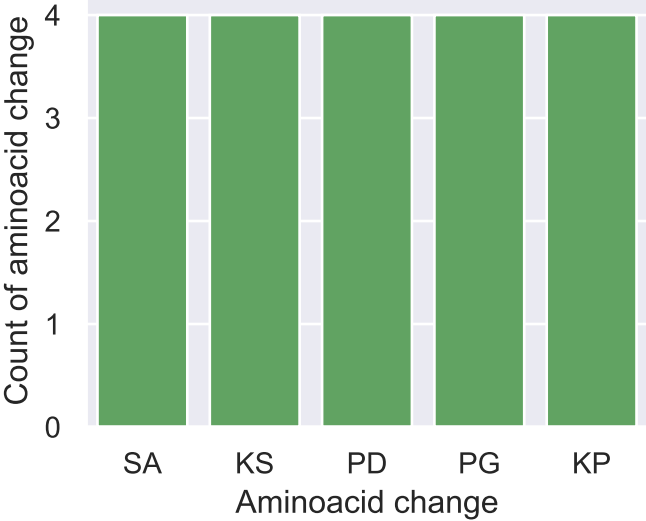
Reconstruction error
2.0
1.5
1.0
0.5
0.0

— Test CELoss
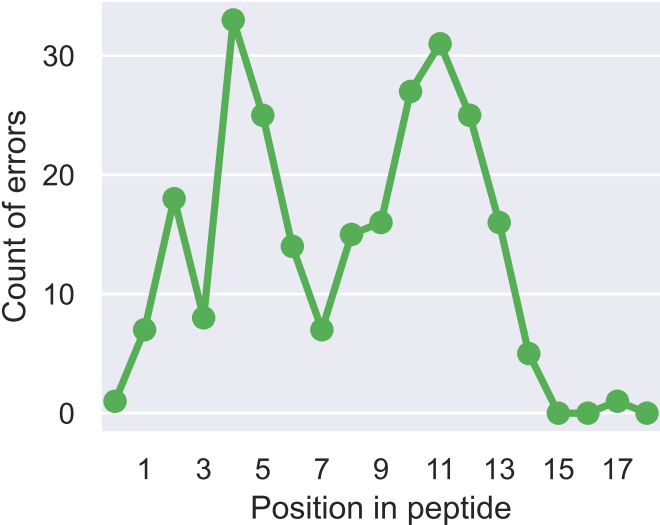
Epoch: 1 61 121 181 241
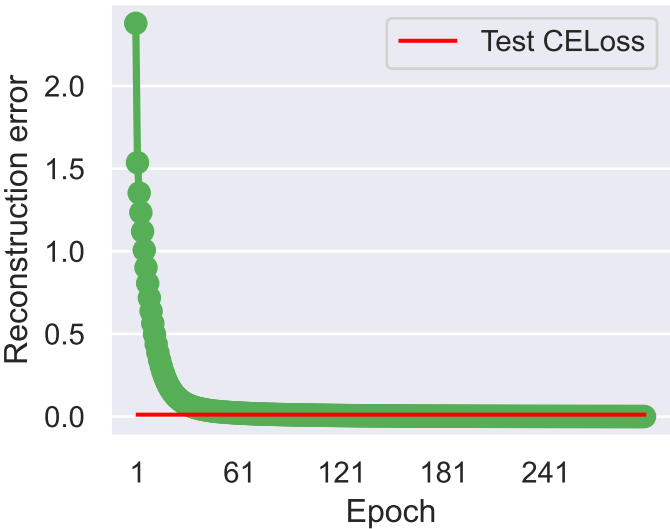
Average reconstruction error on test set:
CELoss: 0.01152

From 7057 sequences with right seq len:7053

	precision	recall	f1-score	support
A	1.00	1.00	1.00	10547
C	1.00	1.00	1.00	7082
D	0.99	1.00	1.00	2817
E	1.00	1.00	1.00	6008
F	1.00	1.00	1.00	10834
G	1.00	1.00	1.00	10358
H	0.98	0.99	0.99	1124
I	0.99	0.99	0.99	1289
K	0.98	0.98	0.98	647
L	1.00	1.00	1.00	4439
M	0.99	0.98	0.99	407
N	1.00	1.00	1.00	3017
P	1.00	0.99	0.99	3015
Q	1.00	1.00	1.00	6475
R	1.00	0.99	1.00	3181
S	1.00	1.00	1.00	15824
T	1.00	1.00	1.00	6443
V	0.99	0.99	0.99	1833
W	0.99	0.98	0.99	655
Y	1.00	1.00	1.00	6012
accuracy			1.00	102007
macro avg	1.00	0.99	0.99	102007
weighted avg	1.00	1.00	1.00	102007

Aminoacid changes (5 most common)

Count of aminoacid change
4
3
2
1
0

SA KS PD PG KP

Aminoacid change

Count of errors by position

Count of errors
30
20
10
0

Position in peptide: 1 3 5 7 9 11 13 15 17

Count of errors by position (in %)

Percent of errors
90
80
70
60
50
40
30
20
10

Position in peptide: 1 3 5 7 9 11 13 15 17