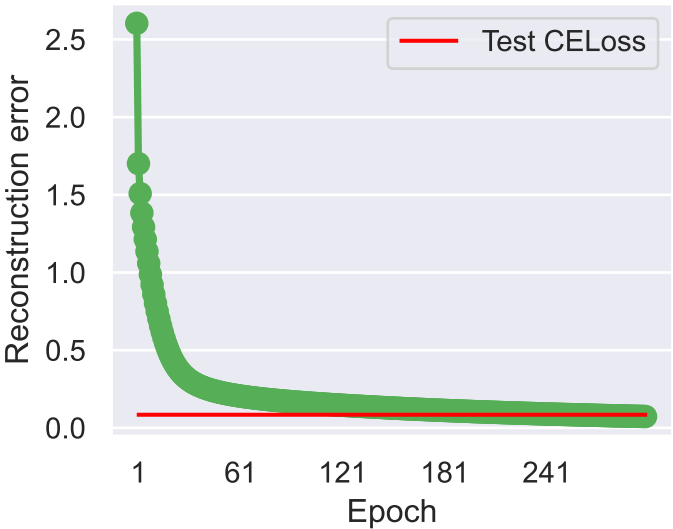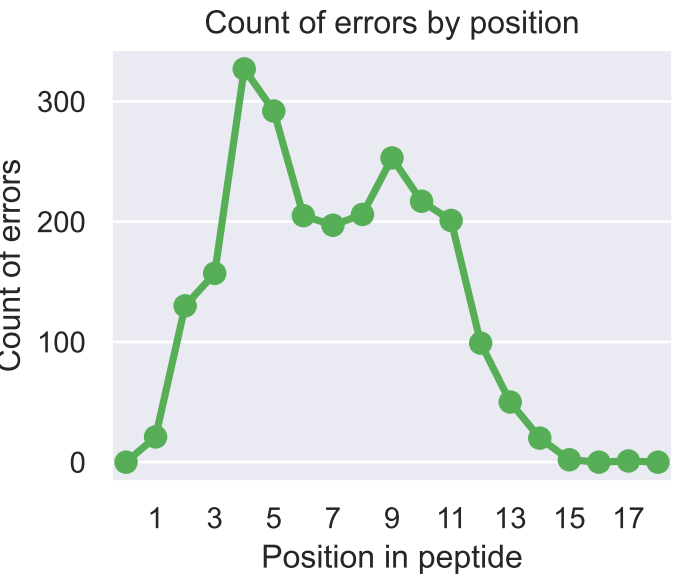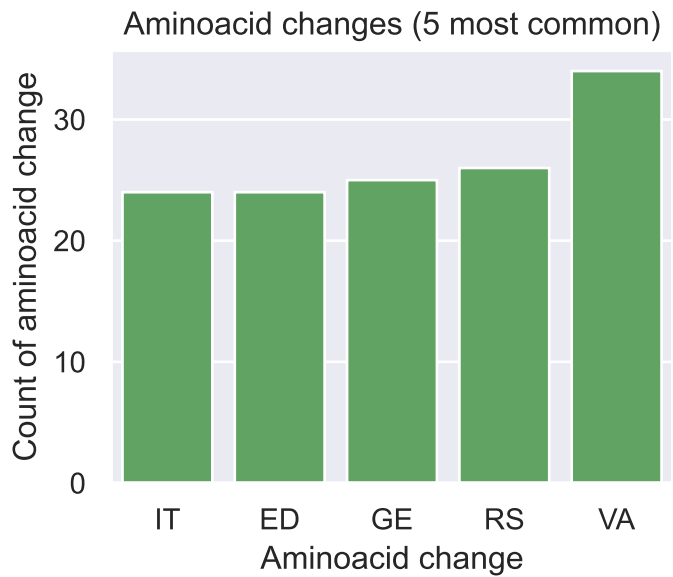# One-hot encoder with arch 399->32 on test set

Reconstruction error during training

Average reconstruction error on test set:
CELoss: 0.08454

From 7057 sequences with right seq len:7019

	precision	recall	f1-score	support
A	0.98	0.99	0.99	10466
C	1.00	1.00	1.00	7052
D	0.96	0.96	0.96	2813
E	0.97	0.98	0.98	5957
F	0.99	0.99	0.99	10850
G	0.99	0.99	0.99	10250
H	0.94	0.91	0.92	1130
I	0.90	0.90	0.90	1264
K	0.88	0.83	0.85	659
L	0.97	0.97	0.97	4199
M	0.86	0.85	0.85	352
N	0.95	0.95	0.95	2977
P	0.95	0.95	0.95	2904
Q	0.98	0.98	0.98	6527
R	0.96	0.96	0.96	3176
S	0.99	0.99	0.99	15773
T	0.97	0.98	0.97	6534
V	0.94	0.92	0.93	1929
W	0.92	0.83	0.87	717
Y	0.98	0.98	0.98	5929
accuracy			0.98	101458
macro avg	0.95	0.94	0.95	101458
weighted avg	0.98	0.98	0.98	101458

Aminoacid changes (5 most common)

Count of errors by position

Count of errors by position (in %)