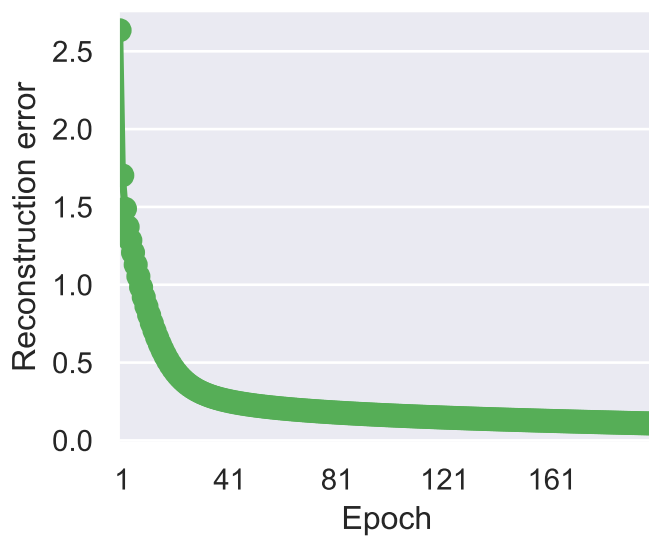


One-hot encoder with arch 399-32 on test set

Reconstruction error during training



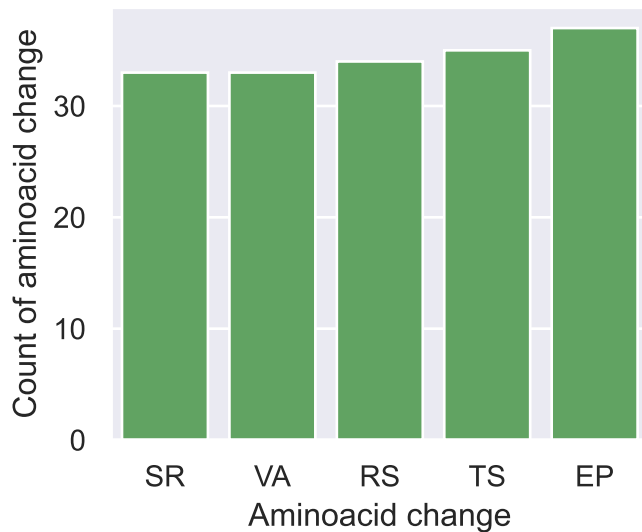
Average reconstruction error on test set:
CELoss: 0.11879

From 7057 sequences with right seq len:7010

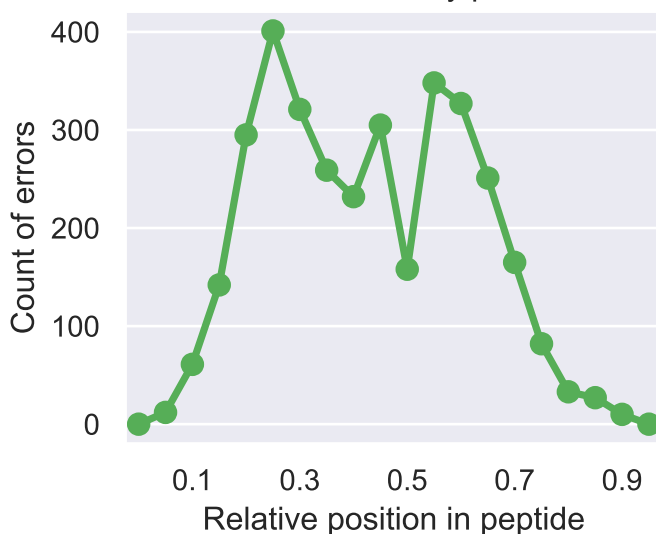
	precision	recall	f1-score	support
A	0.98	0.98	0.98	10510
C	1.00	1.00	1.00	7040
D	0.93	0.93	0.93	2859
E	0.96	0.96	0.96	5930
F	0.99	0.99	0.99	10772
G	0.98	0.98	0.98	10129
H	0.91	0.89	0.90	1100
I	0.89	0.85	0.87	1294
K	0.83	0.74	0.78	660
L	0.96	0.95	0.95	4273
M	0.85	0.74	0.79	382
N	0.94	0.94	0.94	2939
P	0.93	0.94	0.93	2876
Q	0.97	0.97	0.97	6598
R	0.92	0.93	0.93	3164
S	0.98	0.99	0.98	15817
T	0.97	0.97	0.97	6492
V	0.89	0.88	0.89	1812
W	0.86	0.78	0.82	678
Y	0.97	0.97	0.97	5982

accuracy			0.97	101307
macro avg	0.93	0.92	0.93	101307
weighted avg	0.97	0.97	0.97	101307

Aminoacid changes (5 most common)



Count of errors by position



Count of errors by position (in %)

