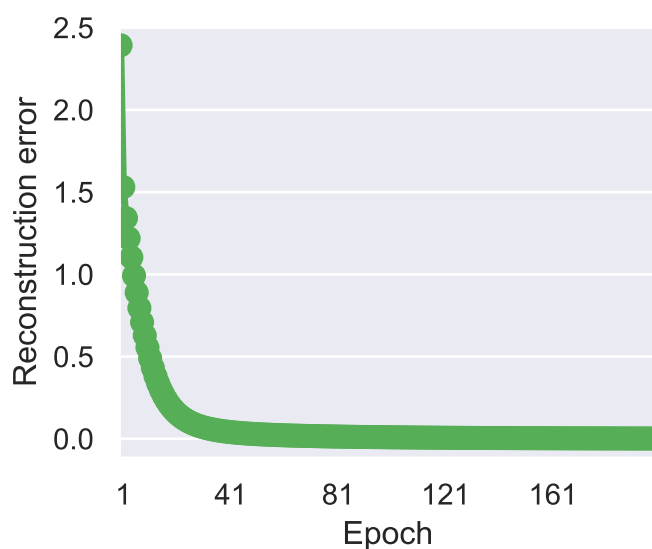


# One-hot encoder with arch 399-64 on test set

## Reconstruction error during training



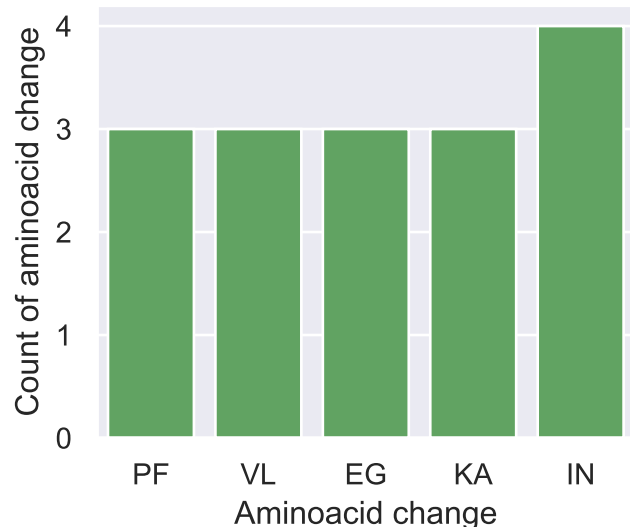
Average reconstruction error on test set:  
CELoss: 0.0111

From 7057 sequences with right seq len:7056

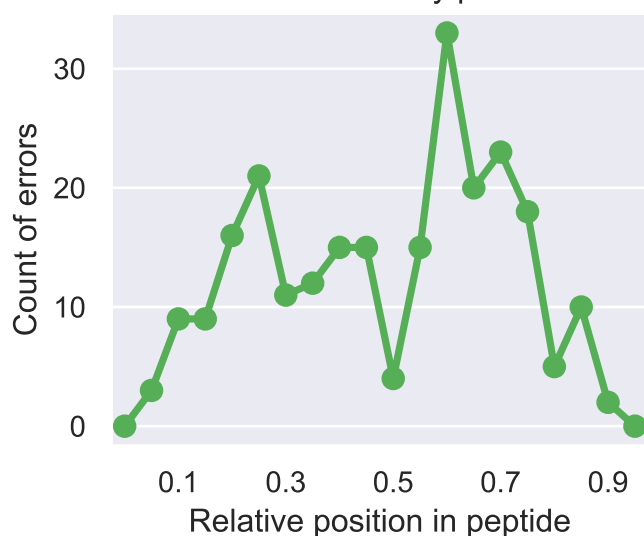
	precision	recall	f1-score	support
A	1.00	1.00	1.00	10584
C	1.00	1.00	1.00	7086
D	1.00	1.00	1.00	2883
E	1.00	1.00	1.00	5977
F	1.00	1.00	1.00	10831
G	1.00	1.00	1.00	10230
H	0.99	0.99	0.99	1107
I	0.99	0.98	0.99	1311
K	0.98	0.98	0.98	668
L	1.00	1.00	1.00	4308
M	0.99	0.97	0.98	383
N	1.00	1.00	1.00	2962
P	0.99	1.00	0.99	2899
Q	1.00	1.00	1.00	6645
R	1.00	1.00	1.00	3197
S	1.00	1.00	1.00	15918
T	1.00	1.00	1.00	6553
V	1.00	0.99	0.99	1825
W	0.99	0.99	0.99	685
Y	1.00	1.00	1.00	6029

	accuracy		1.00	102081
macro avg	1.00	0.99	0.99	102081
weighted avg	1.00	1.00	1.00	102081

## Aminoacid changes (5 most common)



## Count of errors by position



## Count of errors by position (in %)

