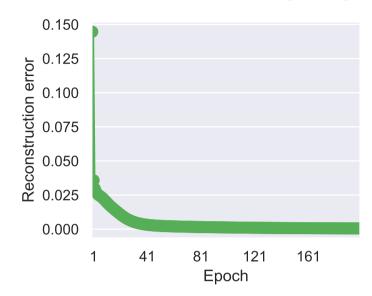
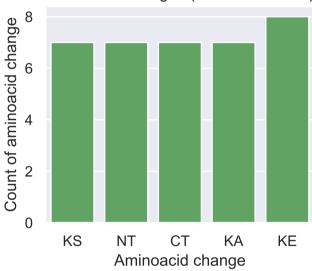
## Reconstruction error during training



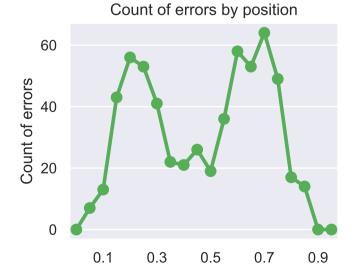




Average reconstruction error on test set: MSELoss: 0.00075

From 7057 sequences with right seq len:7045

pre	cision	recall	f1-score	support	
ACDEFGHLKLMNPQRSTVWY	1.00 1.00 0.99 0.99 1.00 0.98 0.97 0.99 0.99 1.00 0.99 1.00 0.99 0.99 0.99	1.00 0.99 0.99 1.00 1.00 1.00 0.98 0.89 1.00 0.99 1.00 0.99 1.00 0.99 0.99 0.9	1.00 1.00 0.99 0.99 1.00 1.00 0.98 0.93 0.99 0.99 1.00 0.99 1.00 0.99 0.99	10529 7084 2865 5858 10842 10174 1152 1231 663 4403 376 3024 3019 6426 3215 15915 6578 1909 645 6045	
accuracy macro avo weighted av			.98 0.9	101953 98 10195 99 1019	



Relative position in peptide

