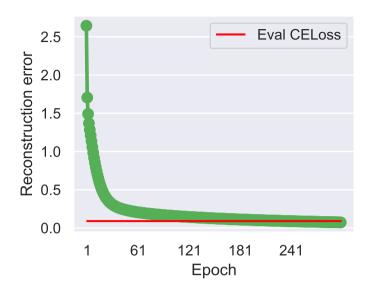
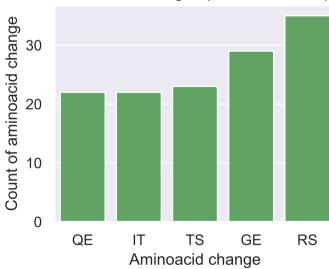
## Reconstruction error during training



Aminoacid changes (5 most common)



Average reconstruction error on evaluation set: CELoss: 0.09032

From 7058 sequences with right seq len:7020

	precision			f1-sco	ore su	pport
ACCEFGHIKLMNPGRSTVVY		0.99 1.00 0.95 0.97 0.99 0.93 0.92 0.89 0.97 0.95 0.95 0.97 0.93 0.90 0.97	0.99 1.00 0.95 0.98 0.99 0.91 0.88 0.97 0.79 0.95 0.95 0.95 0.98 0.93 0.93	0.9 0.9 0.9 0.9 0.9 0.8 0.9 0.9 0.9 0.9 0.9	0 70 5 28 7 59 9 10 9 10 2 11 6 62 7 43 6 29 5 29 7 64 5 31 9 15 8 65 3 19	158 118 122 354 372 74 94 29 27 67 182 39 165 04 757
accur macro weighted	avg		0.95 0.98	0.98 0.94 0.98	3 1016 0.95 0.98	664 101664 101664

