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Searching for nuclear localization signals

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Nuclear localization signals (NLSs) are motifs that mediate the transport of proteins to the nucleus, but finding an NLS within your protein of interest can be tricky. In the 15 November *EMBO Reports* (*EMBO Reports* 2000, **1**:411-415), Cokol *et al.* describe an 'expert database' of NLSs, created by collecting 91 experimentally determined NLSs and extending the dataset by '*in silico* mutagenesis'. They initially increased the database by adding homologous proteins, and then analyzed sets of proteins with known nuclear localization. The *in silico* approach involved altering the sequence of known motifs and then testing whether they gave 'true' (nuclear) or 'false' (non-nuclear) matches. Strict selection criteria (exclusively nuclear matches and presence in two distinct protein families) yielded a set of 214 potential NLSs, and the authors estimate that about 17% of all eukaryotic proteins are imported. They also show that in 90% of cases NLS motifs overlap with known DNA-binding regions. The group encourages colleagues to add experimentally verified NLSs to their [database](#) to improve NLS recognition and prediction.

References

1. Nuclear localization signals (NLS).
2. *EMBO Reports*, [<http://www.embo-reports.oupjournals.org>]
3. PredictNLS server , [<http://maple.bioc.columbia.edu/predictNLS/>]