

Table 1. Previously identified C-Term motifs but excluded in our analysis

| Alias | E-Value | Consensus Sequences |
|-------|----------|--------------------------------------|
| 3 | 1.4e-002 | WFKHLESELGLEEdDNQQQ |
| 5 | 4.5e-008 | DEEWLRChT |
| 11 | 1.2e-006 | RLDLLD[IL]SS[IL]L |
| 22.1 | 6.0e-006 | Vx[TA]GLYM |
| | | |
| 1.1 | 2.1e-041 | YASSTENI[SA][RK]LLQ[GN]W |
| 4 | 4.2e-048 | cPDLNL[ED]LrISPP |
| 6 | 3.9e-038 | [QL]K[IN][NG]VxKPRPRSF[ST]VNNxC[NS]H |
| 7 | 4.2e-047 | KRRGGRTx[GR]xssK |
| 12 | 8.5e-026 | SSS[ST][AS]RLLN[KR]VA |
| 20 | 2.8e-044 | LWMPRLVERI |
| 25 | 1.6e-030 | L[EQ][ND]YI[KR]S[IL]xIN |

Note: Alias indicates the corresponding motifs identified by Stracke et al. (2001). E-Value was calculated by MEME. The first four motifs have a big e-value ($>1e-10$) so that they were excluded in our analysis. The rest of motifs did not pass nonsynonymous (dN) test, i.e., dN value in motif region is >0.7 , or one of the flanking region has low dN value (≤ 0.5).