**Table S2. Linker domain sequences for the p27-KID variants designed to be more and less helical.**

|  |  |
| --- | --- |
| **Variant** | **Sequence of linker domain** |
| *p27-KIDwt* | *H****EE****LT****R****DLE****K****HC****RD****ME****EA****SQ****RK****a* |
| p27-KIDA10 | HAALTADLEAHCAAMEAASQAAb |
| p27-KIDA22 | AAAAAAAAAAAAAAAAAAAAAAb |
| p27-KIDSL1 | HLELTLDLELHCLLMELLSQRKb |
| p27-KIDSL2 | HEELTLDLELHCLLMELLSQRKb |
| *p27-KIDSL3 (p27-KID+H)* | *HEELTKDLELHCLLMELLSQRKb* |
| p27-KIDSL4 | HEELTKDLELHCKLMEELSQKKb |
| p27-KIDSL5 | HLELTLDLEEHCLKMELESQLKb |
| p27-KIDSL6 | HLLLTLDLELHCLLMELASQLLb |
| *p27-KID-H* | *HEELTEDLEEHCEEMEEESQEEb* |
| *p27-KIDloop* | *TNPGNGGHGGTGVGGNGGNGHGb* |

Sequences used in the present study are italicized.

a The residues determined to be suitable for mutagenesis are underlined and are in bold font in the linker domain sequence of the wild-type p27-KID (p27-KIDwt).

b The mutated residues are underlined.