

Table S4 | NLS predicted by different NLS predictors.

Proteins tested in our study	Residues showed nuclear targeting activity ¹	Predicted NLS		
		pSORT II ²	NLS-Stradamus ³	cNLS mapper ⁴
PSL28 ₁₋₃₃	1-33	pat4, 9-RKKR-12 pat4, 24-KHRK-27 bipartite, 11-KRGHVSAGHGRIGKHRK-27	2s, 6-SKNRKKRGHVSAGHGRIGKHRKHPGGRG-33 2d, 4s, 7-KNRKKRGHVSAGHGRIGKHRKHPGGRG-33	bipartite, 4-RFSKNRKKRGHVSAGHGRIGKHRKHP-29 (11.5)
PS22a ₁₋₃₄	None	None	None	None
PS22a	N/A	pat4, 117-RRKH-120	None	None
PSL3 ₁₋₃₆	None	pat4, 18-PKKR-21 pat7, 18-PKKRTKH-24	2s, 2d, 18-PKKRTKHHRGVRKFPDD - 36 2d, 14-LGFLPKKRTKHHRGVRKFP - 34 4s, 10-RHGLGFLPKKRTKHHRGVRKFP-34	None
PSH3	1-75	bipartite, 116-KRVTIMPKDIQLARRIR-132	2s, 8-ARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYRP-44 2d, 7-TARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYRP-44 4s, 9-RKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYR-43	None
PSH4	1-42 (I) 1-80 26-80 (I)	pat4, 17-KRHR-20 pat4, 18-RHRK-21	2s, 4-RGKGGKGLGKGGAKRHRKVLDRDNIQGITKPAIRRLARRGGVKR-46 2d/4s, 4-RGKGGKGLGKGGAKRHRKVLDRDNIQGITKPAIRRLARRGGVK-45	None
PHYSO_357835	338-387	370-RHKR-373	No	6-EFKRLVLKQFPATTEVETAENTYWKKFHAP-35 (5.9) 410-RLRVGLKRALGGRDEETLEPLLAFLIKYVTD-441 (6.9)
PHYSO_480605	1-32 (I) 1-60	None	None	None

Table S4, continued

Proteins tested in our study	Residues showed nuclear targeting activity	Predicted NLS		
		pSORT II	NLSstradamus	cNLS mapper
PHYSO_251824	239-419	100-RKRH-103 363-PSKRSKP-369	2s, 2d, No 4s, 335-RRAGRDPLAKR-346	bipartite, 339- RDPRLAKRPYPGEQGLAPPTGDNDPSKRSKPS- 370 (7.7) 339- RDPRLAKRPYPGEQGLAPPTGDNDPSKRSKP- 369 (5.0) 339- RDPRLAKRPYPGEQGLAPPTGDNDPSKRSKPSG -371 (6.0)
PHYSO_561151	504-520	pat4, 344-PKRK-347 pat4, 345-KRKK-348 pat7, 344-PKRKKEL-350 bipartite, 504-KRRSTSGHPGLSAKRNK-520 bipartite, 505-RRSTSGHPGLSAKRNNK-521	2s, 88-RKKSPAVKWLRKSF-101 490-GKTSKHSEKAIRAAKRRSTSGHPGLSAKRNNKVP-524 2d, 88-RKKSPAVKWLRK-99 489-KGKTSKHSEKAIRAAKRRSTSGHPGLSAKRNNKVP-524 4s, 88-RKKSPAVKWLRK-99 345-KRK-347 491-KTSKHSEKAIRAAKRRSTSGHPGLSAKRNNKVP-523	bipartite, 401- RPMPTKPVCEFTDKLRQDAVGLLSLRKHLKSK- 432 (6.6) 425- LRKHLKSKQNEVQALRERYHALTGKEYKPI- 454 (6.3) 500-IRAAKRRSTSGHPGLSAKRNNK-521 (6.9)

Table S4, continued

Proteins tested in our study	Residues showed nuclear targeting activity	Predicted NLS		
		pSORT II	NLStradamus	cNLS mapper
PHYSO_533817	172-314	pat4, 33-PRRR-36 pat4, 34-RRRR-37 pat4, 216-RKRH-219 pat4, 279-RKRK-282 pat7, 31-PDPRRR-37 pat7, 33-PRRRVL-39	2s, 2d, 278-SRKR-281 4d, 277-KSRKRK-282	monopartite, 276-RKSRKRKAESE-286 (14.0) 426-RSAKRKCATCSREF-440 (5.0) 426-RSAKRKCATC-436 (6.0) bipartite, 189- RALSAGLKLHRQVDNVSDAKFGLEYERKRHQN -221 (6.4) 275- ERKSRKRKAESLEPLEFACTQCERSFKSAQG- 305 (8.7) 275- ERKSRKRKAESLEPLEFACTQCERSFKSAQGL- 306 (5.3)

¹. I, incomplete nuclear localization (GFP signal is visible in the cytoplasm, approximately 1<LNC<3).

². *PSORTII* differentiates monopartite and bipartite cNLSs. The detection and classification of monopartite cNLSs is based on two rules: pat 4, 4 residue pattern, which composes of 4 basic amino acids (K or R), or composed of three basic amino acids (K or R) and either H or P. pat 7, 7 residue pattern, which start with P and followed within 3 residues by a basic segment containing 3 K/R residues out of 4. Ref. PSORT, (1997).

³. NLStradamus does not classify NLS types. The NLS prediction is based on three hidden markov models (HHM). 2s, 2 state HHM static; 2d, 2 state HHM dynamic; 4s, 4 state HHM static. Ref. Ba et al, (2009).

⁴. *cNLS Mapper* generates and distinguishes monopartite and bipartite cNLSs. The predictions shown are based on a cut-off score, 5.0 (a candidate protein fused reporter localizes to both the nucleus and the cytoplasm). Score for each predicted NLS is shown in a parenthesis at the end of the sequence. Ref. Kosugi et al., (2009).