Table S1: Stability of the enzymatic activity of different peptidyl-prolyl *cis-trans* isomerases

Protein	k_{cat}/K_M (M^{-1}/s^{-1})[1]			
	Day 1	Day 3	Day 7	Day 10
GST-FKBP12	$2.8 \pm 0.4 \cdot 10^6$	$3.5 \pm 0.9 \cdot 10^6$	$1.8 \pm 0.6 \cdot 10^6$	$1.0 \pm 0.1 \cdot 10^7$
GST-FKBP52	$3.0 \pm 0.7 \cdot 10^6$	$3.2 \pm 0.6 \cdot 10^6$	$5.9 \pm 1.1 \cdot 10^6$	$4.5 \pm 0.9 \cdot 10^6$
His-FKBP65	$1.3 \pm 0.6 \cdot 10^6$	$3.4 \pm 0.9 \cdot 10^6$	$4.0 \pm 0.8 \cdot 10^6$	$5.3 \pm 1.3 \cdot 10^6$
CYPA	$3.1 \pm 0.7 \cdot 10^6$	$2.8 \pm 0.7 \cdot 10^6$	$4.6 \pm 1.0 \cdot 10^6$	$7.2 \pm 1.2 \cdot 10^6$
Pin1	$8.4 \pm 1.7 \cdot 10^6$	$9.0 \pm 2.2 \cdot 10^6$	$2.7 \pm 1.2 \cdot 10^6$	$3.7 \pm 1.3 \cdot 10^6$

[1]1 µM GST-FKBP12, GST-FKBP52, His-FKBP65, CYPA and Pin1 were incubated at 37°C for 10 days. Specific enzymatic activities (k_{cat}/K_M) were determined as described in *Experimental procedures* at the beginning of the experiment and after 3, 7 and 10 days of incubation. Assays were performed with purified proteins by monitoring the absorbance of released 4-nitroanilide (*p*NA) with the use of chymotrypsin as an isomer-specific protein. The substrates used are the same as in Table 1. All reactions were perfomed in 35 mM Hepes buffer, pH 7.8 at room temperature (± 22°C). SEM (n=4) are shown for each protein.

Table S2: Substrate specificity of different peptidyl-prolyl *cis-trans* isomerases

Protein	Substrate	k_{cat}/K_M (M^{-1}/s^{-1})[1]		
		Calculated values	Literature values	Ratio k_{cat}/K_m (Table 1/Table S2)
GST-FKBP12	Succ-AEPF-*p*NA	$1.2 \pm 0.6 \cdot 10^4$	$6.0 \cdot 10^2$ (60)	241.6
GST-FKBP52	Succ-AEPF-*p*NA	$4.9 \pm 0.1 \cdot 10^4$	-	62.0
His-FKBP65	Succ-AEPF-*p*NA	$6.0 \pm 0.1 \cdot 10^4$	-	22.3
CYPA	Succ-AHPF-*p*NA	$1.8 \pm 0.7 \cdot 10^4$	$6.0 \cdot 10^5$ (60)	168.0
Pin1	Succ-AAPF-*p*NA	$8.6 \pm 0.7 \cdot 10^4$	(61)	96.7

[1]Specific enzymatic activities (k_{cat}/K_M) were determined as described in *Experimental procedures.* Assays were performed with purified proteins by monitoring the absorbance of released 4-nitroanilide (*p*NA) with the use of chymotrypsin as an isomer-specific protein. All reactions were perfomed in 35 mM Hepes buffer, pH 7.8 at room temperature (± 22°C). SEM (n=3) and literature data for the same substrate, when known, are shown for each protein.

Table S3: Parameters describing the fibril formation of α-SYN followed with Thioflavin T fluorescence in the presence of different concentrations of PPIases

Protein	Concentration	x_0[1]	a[1]
Blank	control	71	83
GST-FKBP12	10 µM	39	32858
	1 µM	26	1819
	10 nM	56	205
	100 pM	47	7763
GST-FKBP52	10 µM	40	38945
	1 µM	37	3005
	10 nM	37	460
	100 pM	73	87
His-FKBP65	10 µM	35	27929
	1 µM	70	4063
	10 nM	92	1596
	100 pM	71	43
CYPA	10 µM	31	1037
	1 µM	51	144
	10 nM	51	296
	100 pM	60	133
Pin1	10 µM	56	3413
	1 µM	53	16
	10 nM	62	99
	100 pM	118	82

[1] x_0 is the half-time of fibril formation and a is the total increase in fluorescence. Both parameters were determined as described in *Experimental procedures*. Typical errors (standard deviation) were 1-10% of the calculated parameters.

Table S4: Parameters describing the aggregation of α-SYN followed with turbidity under influence of different concentrations of PPIases

Protein	Concentration	x_0 [1]	a [1]
Blank	control	87	0.002
GST-FKBP12	10 µM	32	0.583
	1 µM	20	0.132
	10 nM	82	0.003
	100 pM	63	0.057
GST-FKBP52	10 µM	38	0.412
	1 µM	16	0.073
	10 nM	22	0.013
	100 pM	82	0.003
His-FKBP65	10 µM	25	0.321
	1 µM	18	0.077
	10 nM	68	0.045
	100 pM	82	0.003
CYPA	10 µM	25	0.091
	1 µM	81	0.003
	10 nM	82	0.003
	100 pM	79	0.005
Pin1	10 µM[2]	-	-
	1 µM	71	0.003
	10 nM	75	0.010
	100 pM	94	0.003

[1] x_0 is the half-time of aggregation and a is the total increase in turbidity at 350 nm. Both parameters were determined as described in *Experimental procedures*. Typical errors (standard deviation) were 1-10% of the calculated parameters.

[2] Since the curve representing 10 µM of Pin1 did not follow an exponential course, the half-time of aggregation could not be calculated.

Supplementary figure legends

Figure S1: SDS-PAGE analysis of recombinant PPIases

Purified PPIases were separated in a 4-12% polyacrylamide gel and visualized with optimized Coomassie G-250. In each lane, 1 µg of protein was loaded. Lane 1, protein marker; lane 2, GST-FKBP12; lane 3, GST-FKBP52; lane 4, His-FKBP65; lane 5: Pin1; lane 6: CYPA; lane 7, α-SYN.

Figure S2: Co-localization of PPIases and Lewy bodies in the brain of a PD patient

Confocal microscopy for ubiquitin (A), FKBP12 (B), FKBP38 (C), FKBP52 (D), FKBP65 (E), CYPA (F) or Pin1 (G) and α-SYN positive LBs in the substantia nigra of a PD patient (Braak stage 6). Left panels (1), white light image. Left middle panels (2), immunohistochemical staining for α-SYN is shown in green. Right middle panels (3), immunohistochemical staining for ubiquitin, FKBP12, FKBP38, FKBP52, FKBP65, CYPA or Pin1 is shown in red. Right panels (4), overlap image. Scale bars, 20 µm. Red and white arrows depict the pigment of dopaminergic neurons and Lewy bodies respectively.

Figure S1

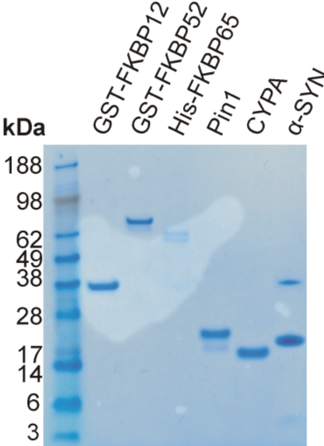

Figure S2