

[illegible]

	% ident	%sim	RMSD (Å)	notes	residues in alignment
PPIH	54	69	0.477	cyclophilin only	9-177
PPIE	68	82	0.406	cyclophilin only	1-156
PPIL1	51	67	1.604	NMR structure	12-139
PPIL2	50	61	0.699	cyclophilin only	35-161
PPIL3	48	61	0.731		9-144
CWC27	43	61	0.797	cyclophilin only	22-133
PPWD1	49	59	0.814	cyclophilin only	38-184
PPIG	57	66	0.46	cyclophilin only	8-155

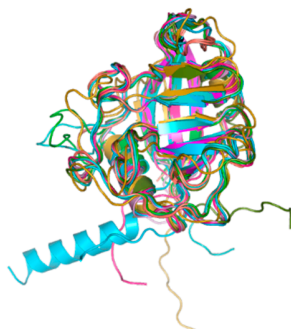


Figure S1. Alignment of the spliceophilins against the canonical cyclophilin PPIA. **(A)** Sequence alignment as performed by the MULTALIN server. **(B)** Quantification of % identity and % similarity across the primary sequence of the cyclophilin domains as calculated in pairwise alignment within BLASTp. Also, quantification of structural alignment (RMSD) between each spliceophilin structure and PPIA as reported by pyMOL. **(C)** Visual representation in cartoon format of a representative of each spliceophilin structure aligned with PPIA.