

A)

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1                               50
PPIA .....MVKRPV FTDAVGGP
PPIE .....MDKIKGSP
PPIH .....MAY ANSSEKPVV FFDVIGGG
PPIG .....MGEKIQRFAC FFDKLNNG
PPI1 .....M AALPPDSRQ .PNNVLETS
PPW1 MTKRKPNDT KSAISRDVF NKKPKKGMV AAYQAKSPAR VSDSAIHTS
PPI2 .....MVPETT HAAAIDGV TRYQVAKK .LCYRIITN
PPI3 .....LKSVELLITD
CWC27 .....KSNVIOGEPD TNGKVLKITT
Consensus .....td.....L

51                               100
PPIA IGVSPNLPK DNVPKVAVK RALSGS...KQKGY KGSCHRIIP
PPIE ACFQNLGSR DVENMADNF RCLDTIE...KQKGF KGSCHRIIE
PPIH VGRKRIELFA DVVKTAEIN RQCTGEE...KQKGVPIGY KGSCHRIIK
PPIG AGRVVFELFS DVCPKTCENF RCLCTSEGT GKSTQKFLRY KSLPFRVVK
PPI1 MGLIVLELYM KHAPKTCENF AELARR...YY NGCHPHRIIK
PPW1 MGDHVKLFP VECPRVSENF CVHSRNG...YY NGCHPHRIIK
PPI2 KGMNLKSLIC DLKPKTCENF DRICKKI...YY DGLDHRSLR
PPI3 VDCDKIEVEFC ERCPKTCENF LALCASN...YY NGCHPHRIIK
CWC27 AGDDCELEMS KEAPKACRFN IQLCLEA...YY DNTIHRVVP
Consensus .G.L..eif. d..PRTceNF .Lc.....y .g..PFR.lk

101                              150
PPIA GFWQGGSDPT RINCGGKSI YCKPDEE.N FIKKICTPGI LSKANSGPT
PPIE GFWQGGSDPT RINCGGKSI YCKPDEE.N FIKKICTPGI LSKANSGPT
PPIH DFMVGGSDPV NGDGGVAVI YRGPFAE.N FIKRHGAPGL LSKANSGPT
PPIG DFMVGGSDFS EGMGGGSEI YGPFDEE.S FAVKHNEFL LSKANSGKT
PPI1 DFMVGGSD.P TGGGGGSAI YGKPFDEE.H FDLKFTAGI LSKANSGPT
PPW1 GFMVGGSD.P TGGGGGSAI YGKPFDEE.H FDLKFTAGI LSKANSGPT
PPI2 MFMVGGSD.P TGGGGGSAI YGKPFDEE.H FDLKFTAGI LSKANSGPT
PPI3 GFMVGGSD.P TGGGGGSAI YGKPFDEE.H FDLKFTAGI LSKANSGPT
CWC27 GFMVGGSD.P TGGGGGSAI YGKPFDEE.H FDLKFTAGI LSKANSGPT
Consensus .FMVGGSD.p tggG.GgeS1 yg..FeDE...Lkh...g. LSKAN.Sp.e

151                              200
PPIA NGSQFFITCA KIPSLGKIV VCKVKG.M NIVFAMRNG S.RN.GKPK
PPIE NGSQFFITCD KIDSLGKIV VCKVTEG.L DVLKQIEAGG S.KD.GKPK
PPIH NGSQFFITCS KCDLGGKIV VCKVIDG.L LVKRIENVP TGEN.NKPKL
PPIG NGSQFFITTK DTDLGGKIV VFGVIGG.Q EVVREIENQ TDA.....
PPI1 NGSQFFITLA PTDLGGKIV IFGRVQG.I GAVNRVAVVE TNSQ.DRPVD
PPW1 NGSQFFITVV PTDLGGKIV VGRVYKG.M EVVQKISAVK VNPKDRPK
PPI2 NGSQFFITFR SCAYLGGKIV IGRVYKG.L DVLAMAVC SDPKDRPK
PPI3 NGSQFFITYG KQHLGGKIV VCKVIDG.L ETLDELEKLP VNEKTYRPLN
CWC27 NGSQFFITG RADELGGKIV IFGRVTEIV YNKLLESEVD IDDD.ERPLN
Consensus NgsQFFIT...L..Lgkai IFG...g...v....nav.....p..

201                              234
PPIA KIVAKGGK...
PPIE KVIADGGK...
PPIH FVVISGCEM...
PPIG .....
PPI1 DVKIRAVDS...
PPW1 DVSTNITVK...
PPI2 EIRDAFVE VDPYK...
PPI3 DVHKKDITIE ANFFAQ...
CWC27 FHKRSCEVL ENFFDIIER EIKRLKSKP EEEV
Consensus .V.L.....

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B)

	% 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

C)

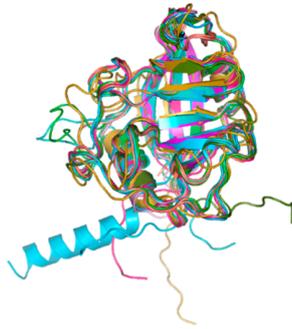


Figure S1. Alignment of the spliceophilins against the canonical cyclophilin PPIA. (A) Sequence alignment as performed by the MULTALIN server. (B) Quantification of % identity and % similarity across the primary sequence of the cyclophilin domains as calculated in pairwise alignment within BLASTp. Also, 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.