

### A FYVE domains

Logo of motifs

Protein	Residue	Sequence	Residue
Pf_Rbsn5L	44	SELKTKEGDYCMTCKSNVKQLLYLHTKKNYCHLCEEIFCAYCVKSIDFMKDEKE	119
PF3D7_1460100	32	LWVPDEEVTNVCYSCNVVF-----NVRVRKHHCRACGNVFCSNCSDNKIKI SEYSYS-----	96
human_Protrudin	122	KRYPTNNFNGNCTGCSATF----SVLKKRRS CSNCGNSFCSRCCSFKVPKSSMGAT--	192
yeast_PEP7	206	PWRDDRSVLFNCISEPF-----GLLLRRKHHCR LCGMVVDDANRNCSEISIGYL-20aa-	297
human_EEA1	1298	KWAEDNEVQNCMACGKGF----SVTVRRHHCRQCGNIFCAECSAKNALT PSSKK-----	1411
human_Rbsn5	147	PWVNDQDVPFCPCGKNEF----SIRNRRHHCR LCGSIMCKKCMELISLPLANKLT-43aa-	260
human_FYV1	148	YWMPDSQCCKEYDCSEKF----TTFRRRHHCR LCGQIFCSRCCNQEIPGKFMGYT-----	218

Positively charged

Negatively charged

Polar Uncharged

Hydrophobic

Cysteine

\* residues critical for PI3P binding that do not follow consensus in Pf\_Rbsn5L

### B Rab-binding domains (RabBD)

Protein	Residue	Sequence	Residue
PF_Rbsn5	130	----SVDRKAI DLQNSFNDI SNCYTNLCSNVPQLNGLVLLCENNKEFLDSFKSEIKQLEE	195
yeast_PEP7	464	-----VLKE---QSYLI-ESTIQDYKKQRLEIVTLNKNLEELHSRIH-----	503
Drosophila_Rbsn5	441	ASKSSLDDPLIE---QINI I-KGYIKQARQDMNFEVVETLELNLELQREYERQRS--	494
human_Rbsn5-copy1	458	-----PLLQ---QIHNI-TSFIRQAKAAGRMDEVRTLQENLRQLQDEYDQQ-----	499
human_Rbsn5-copy2	739	-----LLQ---QIDNI-KAYIFDAKQCGRLDEVEVLTENLRLELKHITLAKQ-----	779

Positively charged

Negatively charged

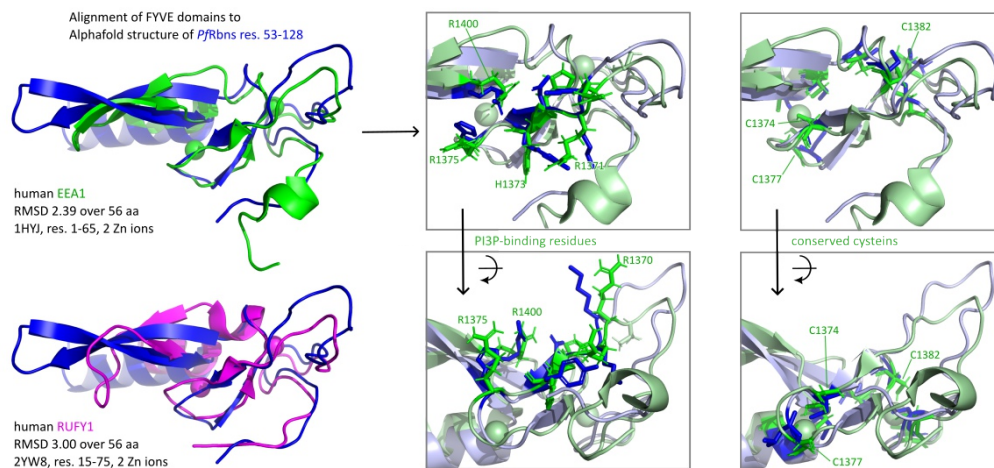
Polar Uncharged

Hydrophobic

Cysteine

+ involved in conserved hydrogen bonds in human Rbsn5

### C



### D

