

Supplementary material 3. Interacting residues involved in P12 and P41 binding. The interacting positions, identity and similarity are shown in the sequences **A. Pf12 vs Pv12.** Primary sequence from *Pv12*, the *Pf12*-PDB (2YMO) crystal structure and *Pf12* (C6KSX0) reference sequence. **B. Pf41 vs Pv41.**

A. Pf12 vs. Pv12

Pv12	M-RIAKAACLGQ-LLIWNL-SAPAEGFTHTCDFNDELSLEFDERQMTNGE	57
Pf12-PDB	-----LTCDNFNDVYKLEFHFPNQQTSVTKLCNLTPNVL	32
Pf12-C6KSX0	MIKLSKKYCLGISFVLYILLSVCEGH	60
	KNLTCDFNDVYKLEFHFPNQQTSVTKLCNLTPNVL	
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Pv12	DKVVIKCGAERKNYELLPPNNCFEQVFTSKSIEDAKNAHNAHNHVNVQNAQQ	117
Pf12-PDB	EKVTIKGSDKLNYNLYPPTCFE-----	55
Pf12-C6KSX0	EKVTIKGSDKLNYNLYPPTCFEEVYASRNMMHLK-----	105
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Pv12	AIVKRKQKETNADEKKSYDDVSFRVPNPNEKEQKALYCVCQNKAKIRVRKRSGEE-YDKE	176
Pf12-PDB	-----INEVSFRIPPNMMP-EKPIYCFCENK-----KD	82
Pf12-C6KSX0	MFMRRSL-----TPNKINEVSFRIPPNMMP-EKPIYCFCENKKTITINGSNGNPSSKKD	158
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Pv12	I FNLLGIIEVLIPSLPKIIDGCDFTKNTSPLFTKGYDANFY--KTIENKDDVICKVKATEG	234
Pf12-PDB	I INRGIVEIIIPSLNEVKVGCDFTTSESTIFSKGYSINEIS-----NQQDIVCTVKAHAN	137
Pf12-C6KSX0	I INRGIVEIIIPSLNEVKVGCDFTTSESTIFSKGYSINEISNKSSNNQQDIVCTVKAHAN	218
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Pv12	KLIGFKCPADYIAIEPEECFLQGFNLSGKKEQLRTKIELTDILMDHYNKIFYARVPQRIYQ	294
Pf12-PDB	DLIGFKCPSNSVEPHDCFVSAFNLSGKNENL---LKLTNIIMDHYNNTFYSRLPSLISD	194
Pf12-C6KSX0	DLIGFKCPSNSVEPHDCFVSAFNLSGKNELENKLKLTNIIMDHYNNTFYSRLPSLISD	278
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Pv12	NMHFFCACVLEEKRLVAH-FEFATTDDQNSVSEPRAANVLQGRSAGSAAF--GPGPFL	350
Pf12-PDB	NWKFFCVCSKDNNEKKLVFTVEASISSA-----	221
Pf12-C6KSX0	NWKFFCVCSKDNNEKKLVFTVEASISSLTKLAS--R-DNTYQDYISNSSFLTLSSYCAFI	335
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Pv12	LLLLSGVLFFIM 362	
Pf12-PDB	----- 221	
Pf12-C6KSX0	TFIITSFLSFIL 347	

Identity: 37%
Similarity (BLOSUM62): 56%

Interaction positions are highlighted in blue

B. Pf41 vs. Pv41

Pf41	MKGVI-FCLVVLLWRQAWSSKSHKCDFT KEKYLLSGEKEVSCEIDANPSDDITFICPNK	59
Pv41	MKRLLLALLHLVRQQLPAHAEHHICDFT KEKYLLGKNEKEYCVVNAKPFDSVTFICPKK	60
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Pf41	IDSLCFHTVNISKNINQN---KSTMSIQDLYGSVYGNLFIISPYVRTNTPFYCFCNL	116
Pv41	IGAQCFQNVNTLDISADKMESSKLSIDVLLYGSTLYGDTLLISPTVKQSTTFYCFCNLQ	120
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Pf41	TVTIQKFL KINRFLKDDDELSEADVMK --HLK-----GGNVSEAQADEYLNKALNRFKK	168
Pv41	MEDLKKY LKKRRLTKEKENAKKSTVN VNDL KNADEDMEVVVPEKQIDEHLVRALYRVKK	180
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Pf41	MKDLS EFFNDQADNTTKLNL --PKSLNI PNDI LNYDVYNSSNNRN DIVVKDEVTNKQIIS	226
Pv41	IRNII E REKNKGEGDKSTNQE D EELVIEEE-----QEEEDGE G DE E DESKVEIIT	232
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Pf41	KRGIMSVFVRSSNNNVIKGCFGNNNK NYFSHPISVAGKVNNKVCKI QGKPGEVGFKCAF	286
Pv41	KYGIMKVVVSTNNITKGCFGNNV VNYFSKPY PVERYYGGSKVCRIEA KPGEFVGFKCIY	292
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Pf41	EENGKVEPPNCFDQVLH KN KNVTDLKTLIPGYASYTNKHSSKYPYLYKIPHVFVNEQYTIQC	346
Pv41	DNQGTVEPHNCFDKV FYEG KETDLQTLMPGYISYGNKQKGKYAFYLKLPHFVQHSYTVQC	352
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Pf41	KCKSNNS-QNEYTFELDIQPGESEVVLNSFK T S	378
Pv41	KCRSTVHQYDDYVFELAVEGGESDIVAKSF Q E-	384
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Identity: 43%

Similarity (BLOSUM62): 60%

Interaction positions are highlighted in blue