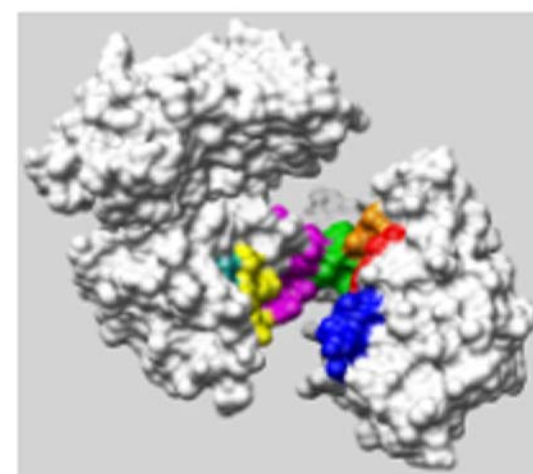
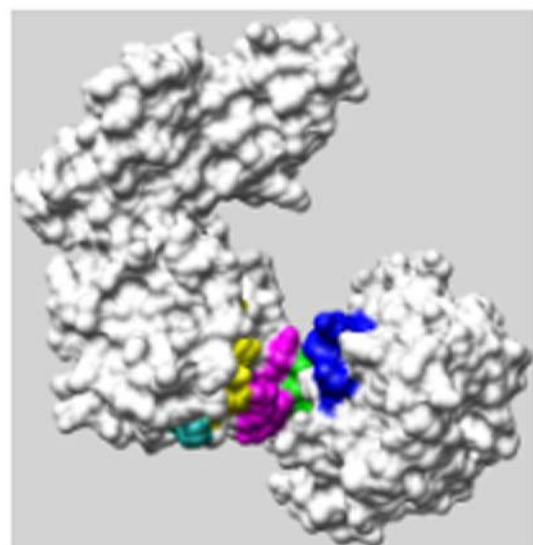


Supplementary Fig. 1. **An alignment of the primary sequence of LGP2 and the helicase domain of Hef.** A. The alignment is designed to emphasize the six motifs found in helicases, each in a different color. The Sequence alignment of LGP2 (Swissprot accession number Q96C10) and Hef (pdb accession number 1WP9) was carried out using NCBI's BLASTP version 2.2.17. B. The location of the six motifs within Hef is shown in two orientations of Hef, and the colors correspond to the motifs shown in the sequence alignments.

A

LGP2	1	-----MELRSYQWEVIMPALGKNI I IWLPTGAGKTRAAAYVAKRHLETVDGAKVTVL	I
Hef	1	MVLRRLDIQPRIYQ-EVIYAKCKETNCLIVLPTGLGKTLIAQKIAEYRLTKY-GGKVLML	
		la	
LGP2	54	VNRVHLVYQHGEEFRSMLD-GRNTVTTLSDMGSPRAGFGHLARCHDLLICTAELLQMALI	
Hef	59	APTKEPLVLQMAESFRALFNLPPEKIVALTGKSPERSKAMARAK-VIVATPQTIEHDLI	
		II	III
LGP2	110	SPREEEHVELTVFSLIVVDECHHTKDTVYVWVINSQYLELKLQRAQPLPQVLGLTASPGI	
Hef	119	A----GRISLELVSLIVFDEAMRAVGNVAYVFIAREY-----KRQAKNPLVIGLTASPGS	
LGP2	170	GGASHLDGAINHVLQLCANLDTWCIMSPQCCPQLQEHSSQPCRQYNLCHRRSQDPFGDL	
Hef	169	-----TPEKINEVINLGIETIEYRSSENSPDVRFYVVG--IRFEMVVRVDLPEIYKEV	
LGP2	200	LKKINDQIHDHLE-----MPELSRKFGTQMYEQVVKLSEAAALAGLQEQRVYA	
Hef	219	RKLLREMLRDALKPLAETGLLESSSPDIPFK--EVLRAQGIINEENAKGNHDLRGLLLYH	
LGP2	292	LHLRRYNDALLINDTVRAVDALAALQDFYREHVTKTQILCAERALLALFDDRQNE----	
Hef	277	AMALKLNHAIKLELLETQGLSALRAYIKKLYEAKAGST-----KASKEIFSDKRNKKAIS	
		IV	V
LGP2	309	-LAKLATHGPNPKLEMLEKILQRQFSSNSPRGII FTTRQSAHSLLLWLQQQQQLQTV	
Hef	301	LLVQAKIEIGLDNPFQDKLKEI IREQLQRKQMSKIIVFTNYRETAKKIV-----NELVKD	
LGP2	397	DIRAQLLIGAGNSSQSTHNTQRDQQEVIQKFGDGLNLLVATSVAAEGLDIPHCNVVRY	
Hef	395	GIKAKRFVVGQASK-----QREQLLILDEFARGEFNVLVATSVGEEGLDVPEVDLVVYF	
		VI	
LGP2	457	GLLTNEISMVQARGRA-RADQSVYAFVATEGSRELKRELINAELETINEQAVAAVQKMDQ	
Hef	445	EPVPSAIRSIQRGRTRGRNMPGRVILMAKGTREAYYWSR-----	
LGP2	516	AEYQAKIRDLOQAALTKRAAQAAQRENQSQQFFVEHVQLLCINCMVAVGSGDLRQVEGT	
RigIRD	901	-----PDKENK-----LLCRKCKALACYTADVRIIEC	
LGP2	576	EHVNVNENFSNYNVSRRDPVINKVFKDVKFGGVISC--RNCGEVWGLQMIYKSVKLPVL	
RigIRD	900	HYTVLGDADFKECFVSRPHPK--PKQFSSFEKRAKIFCARQNCSDHWGIHVKYKTFEIPVI	
LGP2	604	KVRSMLELTPQGRIGA--KKNRVVYFVDFDFLQMCARENLSDLSLD	
RigIRD	999	KIESFVVEDIATGVQTLYSKKNKDFHFEKIPFDPAEKSK	

B



Score = 125 bits (315)
 Identities = 26%,
 Similarity = 44%,
 Gaps = 9%

Supplemental Fig. 2. **LGP2-poly(I:C) complex** A) Electron micrograph of LGP2-PolyI:C complex. LGP2 oligomers are marked by ovals, while monomers and dimers are marked by diamonds and rectangles, respectively. The scale bar corresponds to 318 Å. The inset shows the dimensions of one of the oligomeric structures. B) Selected LGP2 oligomers observed in the micrographs.

