



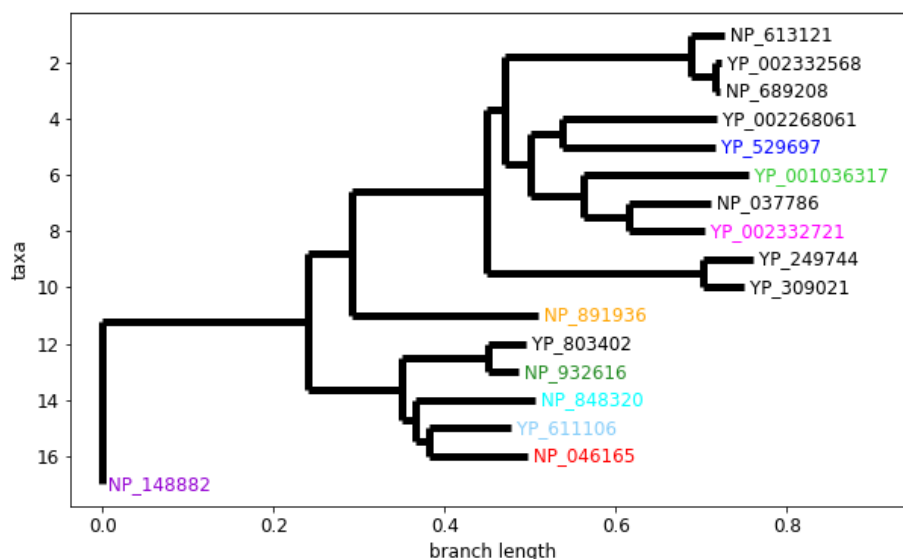
STRUCTURAL BIOLOGY
COMMUNICATIONS

Volume 75 (2019)

Supporting information for article:

Crystal structure of *Cydia pomonella* granulovirus PTP-2

**Guangmei Huang, Michael R. Oliver, Jeremy R. Keown, David C. Goldstone
and Peter Metcalf**



Index

taxon	NCBI genome code	Host species, virus name
1	NP_613121	<i>Mamestra configurata</i> nucleopolyhedrovirus A
2	YP_002332568	<i>Helicoverpa armigera</i> multiple nucleopolyhedrovirus
3	NP_689208	<i>Mamestra configurata</i> nucleopolyhedrovirus B
4	YP_002268061	<i>Agrotis ipsilon</i> multiple nucleopolyhedrovirus
5	YP_529697	<i>Agrotis segetum</i> nucleopolyhedrovirus A
6	YP_001036317	<i>Spodoptera frugiperda</i> multiple nucleopolyhedrovirus
7	NP_037786	<i>Spodoptera exigua</i> multiple nucleopolyhedrovirus
8	YP_002332721	<i>Spodoptera litura</i> nucleopolyhedrovirus II
9	YP_249744	<i>Chrysodeixis chalcites</i> nucleopolyhedrovirus
10	YP_309021	<i>Trichoplusia ni</i> single nucleopolyhedrovirus
11	NP_891936	<i>Cryptophlebia leucotreta</i> granulovirus
12	YP_803402	<i>Anticarsia gemmatalis</i> nucleopolyhedrovirus
13	NP_932616	<i>Choristoneura fumiferana</i> DEF multiple nucleopolyhedrovirus
14	NP_848320	<i>Choristoneura fumiferana</i> multiple nucleopolyhedrovirus
15	YP_611106	<i>Antheraea pernyi</i> nucleopolyhedrovirus
16	NP_046165	<i>Orgyia pseudotsugata</i> multiple nucleopolyhedrovirus
17	NP_148882	<i>Cydia pomonella</i> granulovirus

Figure S1 Rooted phylogenetic tree for the PTP-2 NCBI proteincluster 2945255. The root sequence on the left side of the figure is *Cydia pomonella* PTP-2 (NP_148882). Coloured sequences were included in the multiple sequence alignment shown in Fig. 3.

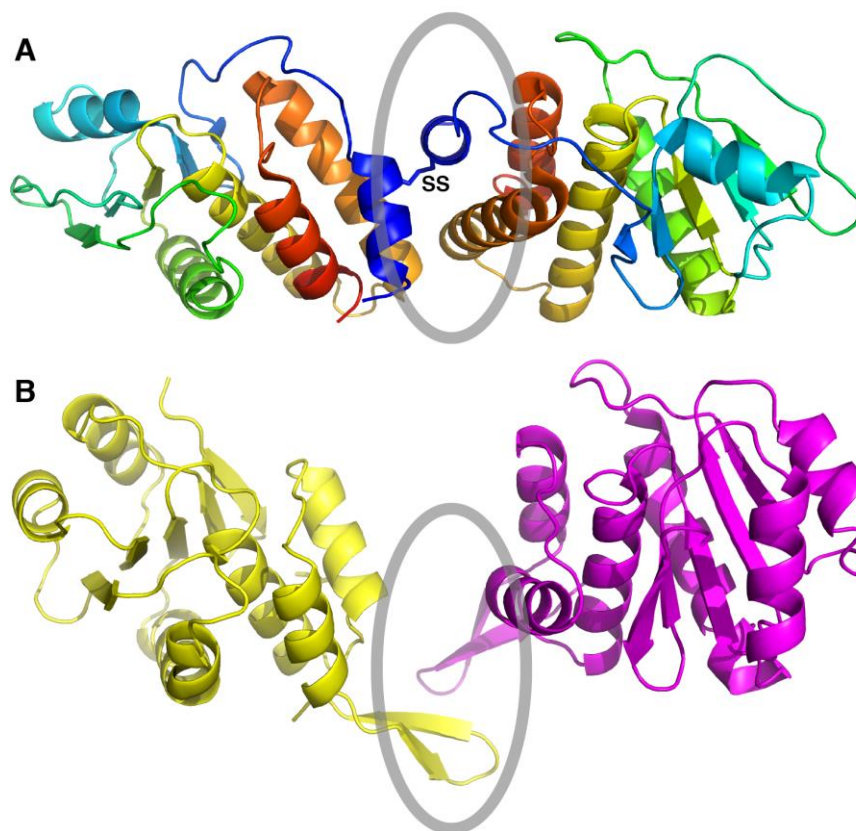


Figure S2 A. Cartoon representation of the dimeric Orf Virus OH1 phosphatase(PDB 5NCR) (Segovia *et al.*, 2017) showing monomers A and B which are linked by a disulphide bond (SS) joining the N-terminal α -helices, shown in blue. The circle indicates the dimeric interface. B. PTP-2 molecules separately aligned onto the OH1 A and B monomers. The N-terminal α -helices are absent in PTP-2. The C-terminal β -strands of PTP-2 are located in the same region as the OH1 AB interface (circled).

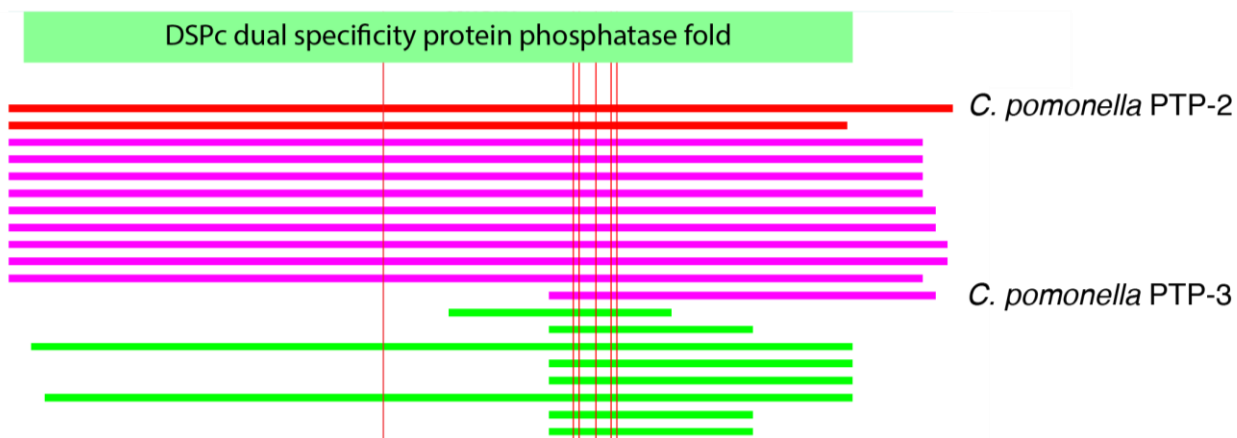


Figure S3 Results summary from a *Cydia pomonella* PTP-2 protein sequence BLAST search against the NCBI refseq_protein database. Horizontal coloured lines represent the 20 best matching pairwise sequence alignments listed in order below the target *C. pomonella* PTP-2, shown by the top red line. Except for *C. pomonella* PTP-3 the magenta lines all represent alphabaculovirus PTP-2 homologues. The shorter green lines are protein fragments from a variety of insects. The two longer green lines are full-length entomopox insect viral PTP-2 homologues. The vertical red lines represent the active site residues shown in Figures 2 and 3. The green box shows the region of PTP-2 that corresponds to the DSPc superfamily fold-type identified by the NCBI routines. All matches have E values $< 1e-6$.

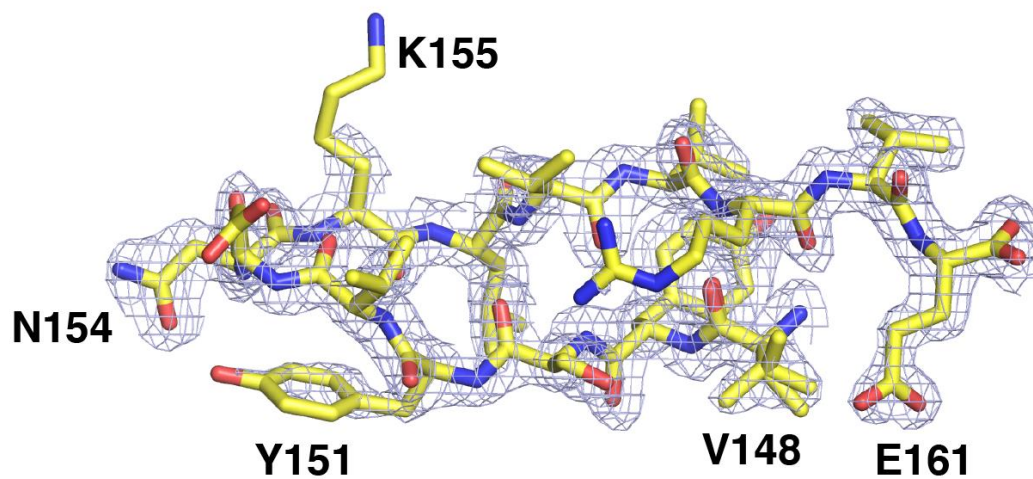


Figure S4 Electron density for the C-terminal region of *Cydia pomonella* PTP-2. The figure shows 1.5 σ contours of the 2Fo-Fc electron density map for the region from V148 to the E161 C-terminus.

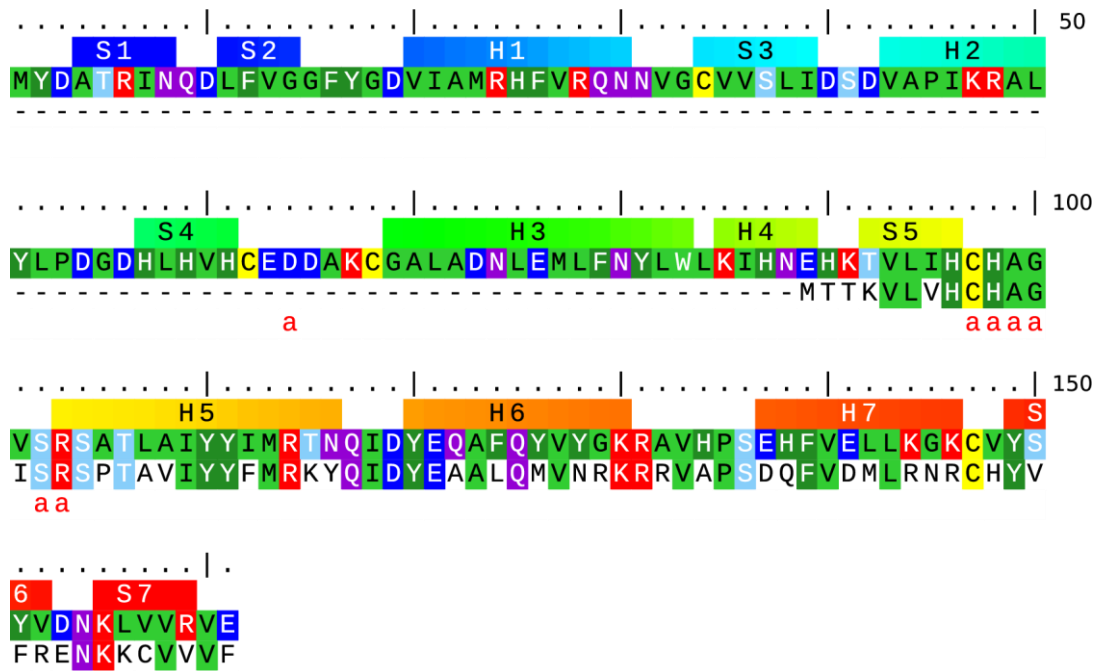


Figure S5 Sequence alignment of *C. pomonella* PTP-2 and PTP-3. The figure shows the two amino acid sequences together with an index line for PTP-2 and secondary structure elements corresponding to the Fig. 2 ribbon diagram.