Supporting Information

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SI Methods

Production of Polyhedra. We produced AcMNPV polyhedra in Sf21 cells by infection with a baculovirus encoding the G25D mutated polyhedrin protein. This mutation resulted in the formation of fewer and larger crystals in cells, as described previously (1). Polyhedra were produced and purified according to established protocols. G25D AcMNPV polyhedra incorporating selenomethionine were produced for phase determination (2). These crystals diffracted more consistently and to a higher resolution than the corresponding native polyhedra.

Polyhedra were also purified from infected larvae of porina moths (*Wiseana* spp.) collected from pastures in the Otago region (New Zealand). Infected larvae, as determined by light microscope observation of larval fat body, were homogenized in 20 mM phosphate buffer, pH 6.2, using a Polytron MR-PT 1600E homogenizer (Kinetmatica AG). The homogenate was filtered through three layers of muslin, larger debris was removed by centrifugation at $1,000 \times g$ for 5 min, and polyhedra were concentrated by centrifugation at $12,000 \times g$ for 10 min. Polyhedra were purified on a five-step 45-65% (wt/wt) sucrose gradient at $28,000 \times g$ for 1 h, and the polyhedral band was collected. The polyhedra were processed by two successive cycles of wash, followed by centrifugation at $12,000 \times g$ for 15 min. The concentration and quality of polyhedra were estimated by optical microscopy on a hemocytometer (3).

The density of G25D AcMNV polyhedra was experimentally determined, and polyhedra were analyzed by scanning electron microscopy, as previously described (4).

Scanning Electron Microscopy. Scanning electron microscopy was performed on Pt-sputter-coated samples (Polaron SC 7640 Sputter Coater, 5 mA, 1.1 kV for 5 min) and examined using an XL30S Field Emission Gun SEM unit (Philips). Electrospray ionization mass spectrometry was carried out using a QStar XL Quadrupole TOF mass spectrometer (Applied Biosystems) with acetic acid/formic acid-dissolved polyhedra. Mass spectrometry analyses identified removal of the initiating methionine in the nucleopolyhedrovirus polyhedrin proteins analyzed but no posttranslational modification.

Density Measurement. The density of recombinant AcMNPV G25D polyhedra was investigated following established protocols (4). Briefly, Nycodenz solutions at 50-80% (wt/vol) were prepared in H₂O. The density of each solution was measured in triplicate at 25 °C using a DMA 5000 density meter (Anton Paar GmbH) with an estimated accuracy to within 5×10^{-6} g·cm⁻³. The relative density of Nycodenz at 25 °C against its concentration was used to generate a standard curve. The density of AcMNPV G25D polyhedra was measured using sedimentation centrifugation. Glass Pasteur pipettes were siliconized in 2% (vol/vol) siliconizing solution. The narrow tips (1-mm diameter) were cut to 3 cm in length using a diamond-point pencil, and one end was sealed by gentle heating. Nine microliters of Nycodenz (Axis-Shield PoC AS) solution was pipetted into the sealed Pasteur pipette, which was then placed in a 1.5-mL Eppendorf tube for centrifugation (16,000 \times g, 30 s at 25 °C) to remove air bubbles. One microliter of polyhedra was carefully laid over the Nycodenz solution using a 0.18-mm diameter extra-long gelloading tip (CLP Molecular Biology). The filled pipettes were placed in a 1.5-mL Eppendorf tube and subjected to further sedimentation centrifugation (15,000 \times g, 3 h at 25 °C). The position of centrifuged polyhedra in each Nycodenz solution was determined using a microscope, and the relative density of polyhedra was assessed using the standard curve.

Heavy-Atom Soaks. Heavy-atom solutions were prepared as saturated stock solutions in 50 mM Hepes, pH 7.0, from Hampton Research kits, and a series of systematic dilutions was set up as soaking solutions for each heavy-atom compound. The only exception were soaks with triiodide ions, in which the stock solution was prepared by dissolving 1 g of KI in 4 mL of water and then adding 0.54 g of I_2 (5). For all soaks, 1 μ L of diluted AcMNPV-G25D polyhedra (~100 polyhedra/µL) was transferred to a drop of heavy-atom soaking solution on a single cavity (concave) microscope slide. The cavity was sealed with vacuum grease and a plastic cover slide to prevent evaporation. Heavyatom soaks were performed at various heavy-atom concentrations for different soaking periods (1 h to overnight) and were kept in the dark before data collection. Soaks used for structure determination were all carried out on selenomethionine crystals because they diffracted more reproducibly than the native ones. The following compounds were used AgNO₃ (10 mM, 4 h), K₂PtCl₄ (1/100 of saturation, 8 h), KI/I₂ (1/20 of stock solution, 1 h), and methylmercury phosphate (1/100, 16 h and 1/20 of saturation, 4 h).

Data Collection and Processing. Crystal samples for data collection were prepared as described previously (4). Briefly, samples were pipetted onto a MicroMesh Mount (MiTeGen) (6) with a 400- μ m diameter mesh and a 25- μ m grid size and were allowed to sediment onto the mount surface by gravitational force. Cryoprotectant containing a final concentration of 50% (vol/vol) ethylene glycol was added onto the mount, and excess residual liquid was removed with a paper liquid wick without disturbing the settled crystals. In the case of heavy-atom-soaked polyhedra, back-soaking was carried out by washing the settled polyhedra with cryoprotectant five times to remove any nonspecifically bound heavy atoms to give less background and reduce radiation damage. Mounted polyhedra were flash-frozen in liquid nitrogen before data collection at 100 K. Diffraction experiments were carried out at the Swiss Light Source X06SA microbeamline using the MD2 microfocus diffractometer with a beam of $15 \times 5 \ \mu m$ focused on the detector. A typical crystal could be exposed for about 10 s (i.e., 10 images of 1 s with an oscillation of 1°) with unattenuated beam before a drastic decay in the diffracting power. Thus, datasets were assembled from data collected on multiple crystals. In the case of WNPV polyhedra, 19 crystals were included, which resulted in a high redundancy of 15.0. To ensure that radiation damage did not deteriorate the quality of the dataset, criteria for inclusion of more images were that they had scale factor parameters to the reference image (initial image of the best crystal: K = 1 and B = 0) of K > 0.5and B <12 and a R_{svm} <50% as listed by Scalepack (7). The resolution cutoff for the whole dataset was determined as the resolution at which the mean $(I/\sigma I) \approx 2$ and $R_{pim} \approx 40\%$ (Tables S2 and S3), where R_{pim} is defined as:

$$R_{p,i.m.} = \frac{\sum_{hkl} \sqrt{\frac{1}{n-1}} \sum_{j=1}^{n} |I_{hkl,j} - \langle I_{hkl} \rangle|}{\sum_{hkl} \sum_{j} I_{hkl,j}}$$

Structure Determination. Phases were obtained from selenomethionine-substituted crystals and heavy-atom derivatives

(Table S2) at a resolution of 2.8 Å. Sites were identified using SHELXc/d (8) and refined with SHARP (9). The selenomethionine derivatives had the strongest phasing power. Additional sites observed in the KI/I2 and methyl mercury chloride soaks were treated as selenium sites in SHARP. Despite variable diffracting powers and the absence of heavy-atom sites beyond the four selenomethionines for SeMetAg and SeMetPt, all datasets mentioned in Table S2 were chosen among data collected from over 200 crystals because they contributed significantly to phasing. This was assessed by the figures of merit, phasing power, and improvement of the quality of the final map when data from these crystals were included. The model was built with the software Coot (10) in the solvent-flattened maps, starting from a scaffold of 159 residues over 245 built by RESOLVE as implemented in PHENIX (11). We initially refined the structure in Refmac5 (12) using data up to a resolution of 2.3 Å, but overfitting was evident from a rapid divergence between R and R_{free}. This may be attributable to the low data-to-parameter ratio resulting from the high protein density of the crystal and a medium resolution. The structure of AcMNPV polyhedra was then refined in PHENIX with one temperature factor per residue and a global group describing the translation, libration, and screw-rotation displacements (TLS) group for the whole protein chain. Finally, we used BUSTER 2.8.0 (13) for the last rounds of refinement. The structure could then be refined with individual B factors for each atom in the structure without signs of overfitting (target of 0.008 Å of rmsd from ideal values). Refinement statistics are summarized in Table S3. Restraints on the disulfide bonds could not be implemented, because the disulfide bonds are formed over a symmetry axis among alternate conformations. However, the geometry of the disulfide bond was close to standard values (distance between the sulfur atoms of 2.15 Å and a torsion angle of 95°).

The structures of WNPV polyhedra were determined by isomorphous molecular replacement and refined with PHENIX at a resolution of 2.18 Å. The same set of "free" reflections was kept throughout refinements of both AcMNPV and WNPV polyhedrins because of the strong isomorphism between the crystals. In the first cycle of refinement, rigid body refinement, simulated annealing (starting temperature of 10,000 K), coordinate refinement, and refinement of one temperature factor per residue were performed in PHENIX. The model was subsequently improved by several rounds of rebuilding and refinement

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(coordinate refinement and temperature factor refinement as two groups per residue for the main chain and side chain atoms). We used BUSTER 2.8.0 for the three final rounds of refinement, with a target of 0.008 Å of rmsd and individual B factors.

The final model of the WNPV polyhedrin includes residues 10 to 243 with three disordered regions. The first region is a long helical linker (residues 28–47) for which only weak density was visible. The main chain could be traced to the exception of a short break consisting of residues 37–39. The second region is a short loop comprising residues 142–145 for which no electron density is visible. The third region comprises residues 171–202. A short helix (residues 186–194) could be built in clear electron density and resulted in a 1.1% drop in the R_{free}, but connections to the rest of the molecule are absent.

Cysteine 131 (equivalent to C132 in AcMNPV) forms a disulfide bond across a two-fold axis. The side chain of the cysteine is in two alternate conformations, and conformation A in one molecule makes a disulfide bond with the symmetry-related cysteine in conformation B. Occupancies of 0.5 yielded difference maps devoid of large peaks in this region and accept-able side chain temperature factors for Cys-131.

The model for G25D AcMNPV polyhedrin is very similar [rmsd of 0.441 Å over 167 residues (14)] and includes residues 10–245. The only notable difference with WNPV polyhedrin is the absence of well-defined electron density for residues 29–48.

Structure Analysis. Contact areas and numbers of hydrogen bonds were determined using the Protein Interfaces, Surfaces, and Assemblies Service (PISA) at the European Bioinformatics Institute (http://www.ebi.ac.uk/msd-srv/prot_int/pistart.html) for most interfaces (15). The intertrimer interface was determined with the CPP4 program Areaimol (14). The surface complementarity among relevant interfaces was determined by the program Sc with default parameters (16).

We have constructed an alignment of 62 full-length nonredundant sequences of the nucleopolyhedrosis viruses (cutoff of 98% sequence identity for nonredundancy) using ClustalW (17). These proteins share sequence identities with AcMNPV polyhedron, ranging from 34 to 57% for granuloviruses and higher than 75% for α -baculoviruses. Analysis of this multiple-sequence alignment by the Consurf server (18) was mapped onto the structure of the WNPV polyhedrin.

Illustrations were prepared with PyMOL 1.0 (http://www.pymol.org).

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Fig. S1. Conserved surfaces of the baculovirus polyhedrin. Surface representation of the polyhedrin trimer with residues colored according to their conservation in a blue-white-red gradient from the most conserved to the most variable as determined by Consurf from a nonredundant alignment of 62 sequences of polyhedrin and granulin proteins.

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	WNPV polyhedrin	1		10	A1	TT A2	• 2222	α1 000000000 30	40	α2 <u>00000000</u> 5	TTT 0 60
	Wisconn signata NPV	MV m A S	D	VDVC	VTVTVT		NTCOV	TUNAUPPU		VUEPEEDCI	DVVI VARDDECCD
	Spodontera litura NPV-2	MVSRV	SAVN	VSPHLC	KTVVVI	NKVVK	NLCHV	TKNAKRKAN	ALERE.	ADERELDHL	DKYLVAEDPFCGP
	Spodoptera litura NPV-3	MYSRY	SAYN.	YSPHLG	ONYVYI	NKYYF	NLGHV	TONAKRKHD	ALERE .	ADERELDHL	DKYLVAEDPFMGP
	Leucania separata NPV-2	MYTRY	s	LSPSLG	RTYVYI	NKYYF	NLGHV	IKNAKRKHD	LIERE.	ADERELDHL	DKYLVAEDPFMGP
	Mamestra brassicae NPV-1	MYTRY	s	YNPSLG	RTYVYI	NKYYF	NLGAV	IKNANRKKH	FIEHE.	LEEKTLDPL	DRFLVAEDPFLGP
	Panolis_flammea_NPV	MYTRY	s	YNPSL <mark>G</mark>	RTYVYI	N K Y <mark>Y F</mark>	NLGAV	IKNANRKKH	FIEHE.	LEEKTLDPL	DRYLVAEDPFLGP
	Mamestra_brassicae_NPV-2	MYTRY	8 <mark></mark>	YNPSLG	R T Y V Y I	N K Y <mark>Y F</mark>	NLGSV	IKNANRKRH	YIEHE.	LEEKTLDPL	DRYLVAEDPFLGP
	Leucania_separata_NPV-1	MYTRY	(<mark>S</mark>	YNPSL <mark>G</mark>	RTYVYI	N K Y Y F	NLGSV	IKNANRKKH	FIEHE.	LEEKTLDPL	DRYLVAEDPFLGP
	Ecotropis_obliquaobliqua_NPV	MYTRY	S	YNPSLG	RTYVYI	N K Y F F	NLGAV	I KNAKRKK	QLEHE.	VEEHALDPL	DRYLVAEDPFMGP
	Orgyia_pseudotsugata_NPV-1	MYTRY	S	YNPSLG	RTYVYI		NLGAV	IKNAKRKKH	QIEHE.	AEEHTLDPL	DKYLVAEDPFLGP
	Buzura_suppressaria_NPV	MYTRI	8	YEDSLG	RTYVYI			IKNAKRKKH	ELEHE.	VEERTLDPL.	DKILVAEDPFLGP
	Trichoplusia_ni_NPV-1	MYTRI	b	VNDCIC				TENAKEKKH	YAEHE.	LEEATLDPL IFFKTIDDI	DNYLVAEDPFLGP
	Adoxophyes hopmai NPV	MYTR	s	FNPHLG	KTVVVI		NLGSV	TKNAKRRRH	OLEHE.	LEERNLDPL	DKVLVAEDPFLGP
	Malacosoma neustria NPV-1	MYTRY	s	YNPTI.G	RTYVYI	NKYYK	NLGHV	TKNAKRKKN	AAEHE	LEERNLDPL	DKYLVAEDPELGP
	Malacosoma neustria NPV-3	MYTRY	s	YNPTLG	RTYVYI	NKYYF	NLGHV	IKNAKRKKN	AAEHE.	LEERNLDPL	DKYLVAEDPFLGP
	Malacosoma neustria NPV-2	MYTRY	s	YNPTLG	RTYVYI	NKYYF	NLGHV	IKNAKRKKN	AAEHE.	LEERNLDPL	DKYLVAEDPFLGP
	Helicoverpa armigera NPV-1	MYTRY	s	YSPTLG	K T Y V Y I	NKYFF	NLGAV	IKNAKRKKH	LEEHE.	HEERNLDSL	D K Y L V A E D P F L G P
	Helicoverpa_armigera_NPV-2	MYTRY	S	YSPTLG	K T Y <mark>V Y I</mark>	NKYFF	NLGAV	IKMP.TQEH	LEEHE.	HEERNLDSL	D K Y L V A E D P F L G P (
	Clanis_bilineata_NPV	MYTRY	S	YSPALG	RTYVYI	NKYYF	NLGHV	IKAAKRTKH	HEENE.	VAERAYDSL	DKYLVAEDPFLGP
α	Spodoptera_exigua_NPV	MYTRY	(<mark>S</mark>	YNPALG	R T Y V Y I	NKF YF	NLGSV	IKNAKRKE H	LLQHE.	IEERTLDPL	E R Y V V A E D P F L G P
	Spodoptera_frugiperda_NPV	MYTRY	2 <mark>8</mark>	YNPSL <mark>G</mark>	RTYVYI	NKF YF	NLGSV	IKNAKRKE H	LALHE.	IEERTLDPL	ERYVVAEDPFLGP
	Spodoptera_litura_NPV-1	MYTPY	S	YNPSLG	RTYVYI	NKFYF	NLGSV	I KNAKRKE H	LVHHE.	IEERTLDPL	ERYVVAEDPFLGP
	Agrotis_segetum_NPV-1	MYTRY	<mark>s</mark>	YNPHVG	RTYVYI	ONKF YF	NLGSV	IKNAKRKEH	LIQHE.	IEEKSLDPL	DKFLVAEDPFLGP
	Lymantria_dispar_NPV	MHNFY	N	YSPALG	KTYVYI			IKQAKROKH	LEQHE.	IEERSLDHL.	DRYLVAEDPFYGP
	Autographa_californica_NPV	. MPDI	b	VRPTIG				TKNAKKKKH	TTEHE.	I E E ATLDPL	DHYMUNEDPFLGP
	Hyphantria_cunea_NPV-1	. MPDF	B	VPDTC		NKIII		TVNAVBVV		APEKELDPL	DHYMUAEDPFLGP
	Amsacta albistriga NPV	MPDY	SVA	VRPTTG	RTVVVI		NLGSV	TKNAKRKKS	LLEHE.	FAFKYLDPL	DHYMVAEDPFLGP
	Choristoneura fumiferana NPV-2	MPDY	S	VRPTTG	RTYVYI	NKYYK	NLGSV	TK. RKRKKH	LLEHE	EDEKHLDPL	DHYMVAEDPELGP
	Orgvia pseudotsugata NPV-2	MPDY	s	YRPTIG	RTYVYI	NKYYF	NLGSV	IKNAKRKKH	LLEHE.	EDEKHLDPL	DHYMVAEDPFLGP
	Archips cerasivoranus NPV	. MPDY	s	YRPTIG	RTYVYI	NKYYF	NLGSV	IK. SKRKKH	LLEHE.	DDEKHLDPL	DHYMVAEDPFLGP
	Choristoneura fumiferana NPV-1	. MPN3	s	YRPTIG	RTYVYI	N K Y Y F	NLGSV	IKNAKRKKH	LLEHE.	EDEKHLDPL	D H Y M V A E D P F L G P
	Anticarsia_gemmatalis_NPV	. MPDY	T	YRPTI <mark>G</mark>	RTYVYI	N K Y <mark>Y F</mark>	NLGSV	IKNAKRKK	LLEHQ.	EEEKSLDGL	DHYIVAEDPFLGP
	Antheraea_pernyi_NPV	. MPD3	S	YRPTIG	RTYVYI	NKYYF	NLGSV	IKNAKRKK	LVEHE.	EEEKHWDPL	DNYMVAEDPFLGP
	Attacus_ricini_NPV	. MPD3	2 <mark>8</mark>	YRPTI <mark>G</mark>	RTYVYI	N K Y Y F	NLGSV	IKN <mark>AKAKK</mark> H	LVEHE.	EEEKHWDPL	DNYMVAEDPFLGP
	Maruca_vitrata_NPV	. MPD3	S	YRPTV <mark>G</mark>	RTYVYI	N K Y Y F	NLGSV	IKNAKRKKH	LVEHE.	EEEKHWDPL	DNYMVAEDPFLGP
	Rachiplusia_ou_NPV	. MPDS	(<mark>S</mark>	YRPTIG	RTYVYI	N K Y Y F	(NLGSV	I KNAKRKKH	LIEHE.	EEEKHLDPL	DNYMVAEDPFLGP
	Thysanoplusia_orichalcea_NPV	. MPDI	S	YRPTIG	RTYVYI		NLGSV	IKNAKRKKH	LIEHE.	EDEKHLDPL	DNYMVAEDPFLGP
	Bombyy_mori_NPV-2	. MPNI	P	YTPTIG VECETC	RTYVYI DUVVV		NLGCL	IKNAKRKKH	LVEHE.	QEEKQWDLL	DNYMVAEDPFLGP
	Bombyy mori NPV-1	MDNN	B	VNPTTC	RTTVUVI			TKNAKRKKH	LTEHE	VEEKOWDLL.	
	Lonomia obligua NPV	MPDS	TPDVT.	VRSTHG	RTYVCI	NKVVK	NLGAV	TKNAKRKK	LLEHE	EEEKOWDSI.	DNYMYAEDPEVAP
	Agrotis segetum NPV-2	MRNFY	S	YNPTIG	RTYVYI	NKFY	NLGSV	IKNAKRKOH	LIEHL.	KEEKOLDPL	DTFMVAEDPFLGP
	Cryptophlebia leucotreta GV	MG3	NKSLR	YSRHDG	TTCVII	NHHLF	SLGAV	LHDVRRKKD	RIREA.	EYEPIIDIA	DOYMVTEDPFRGP
	Cydia pomonella GV	MG3	NKSLR	YSRHDG	TSCVII	NHHLF	SLGAV	LNDVRRKKD	RIREA.	EYEPIIDIA	DQYMVTEDPFRGP
	Andraca bipunctata GV	<mark>M</mark> G3	NKSLR	YSRHDG	TTCVII	NHHLF	SLGSV	LNDVRHKKD	RIREA.	EYEPIVDVA	NQYMVTEDPFRGP
	Choristoneura_occidentalis_GV	<mark>M</mark> G3	NKSLR	Y S R H D G	TSCVII	NHHLF	SLGSV	L N D V R H K K D	RIREA.	EYEPILDIA	NQYMVTEDPFRGP
	Adoxophyes_orana_GV	<mark>M</mark> G 3	NK <mark>SLR</mark>	YSRHE <mark>G</mark>	TTC VII	NHHLF	SLGSV	L N D V R R K K D	RIREA.	EYEPILDIA	DQYMVTEDPFRGP
	Harrisina_brillians_GV	<mark>M</mark> G Y	NK <mark>SLR</mark>	YSRHE <mark>G</mark>	TTCVII	NHHLF	SLGSV	L H D V R R K K D	RIREA.	EYEPIIDLA	DQYMVTEDPFRGP
R	Phthorimaea_operculella_GV	<mark>M</mark> G S	NKTLR	Y S R H D G	TTCVII	NHHLF	SLGSV	LNDVRRKKD	RIRDA.	EYEPIIDIA	DQYMVTEDPFRGP
D	Epinotia_aporema_GV	MG3	NKSLR	YSRHEG	TTCVII	NHHLF	SLGSV	LNDVRRKKD	HIRDE.	EFGPIKDIA	NOYMVTEDPFRGP
	frichopiusia_ni_Gv	· · MG1	NRSLR	VCDUNG	TTCVII	KHLI	LGSV	LOUVREKEE	LIKEA.	PEDPIKDIA	NOVMUTEDPFRGP
	Agrotis segetum GV_1	MGS	NKSIP	VSPHAC	TTCVII	NKHT	SLCSV	LODTHKKD	RISEA	KVAPI.KDIA	NOVMUTEDPFRGP
	Agrotis segetum GV-2		NKSLP	VSRHAG	TSCLT	NOHVE	OTASN	GKDVRRKDR	RTSEA.	KVAPLKDLA	NOVMUTEDPERCE
	Plutella xvlostella GV	MG	NKSLR	VSRHDG	STCVT	NKHL	SLGSV	LGDVRRKKE	TRES	EFDPIKDIA	NOVMUTEDPERCE
	Pieris rapae GV	MG	NRALR	YSKHEG	TTCVT	NOHVE	SLGAV	LKDVKHKKD	RLREA	EIEPVLDTA	DOYMVTEDPFRGP
	Pieris brassicae GV	MGS	NRALR	YSKHEG	TTCVII	NOHYP	SLGAV	LKDVKHKKD	RLREA.	EIEPVLDIA	DOYMVTEDPFRGP
	Neodiprion abietis NPV	ME	N. LAA	GYQTSA	KSYIYI	NKYYF	GLGDI	INSAKKRKH	DODWE.	KHAEERRAL	NGFILPLDPRTGP
Y	Neodiprion_lecontei_NPV	M B	NNLAA	GYQTSA	KSYIYI	NKYYF	GLGDI	INSAKKRKH	DQDWE.	KHAEERRAL	NGFILPLDPRTGP
•	_ Neodiprion_sertifer_NPV	M B	N. LAQ	GYQTSA	KSYIYI	NKYYF	GLGDI	INSAKKRKH	DQDWE.	KHADERRAL	NGFILPLDPRTGP

Fig. S2. Sequence alignment of 62 nonredundant polyhedrin and granulin sequences. Sequences were aligned with ClustalW and processed with ESPript [Gouet P, Robert X, Courcelle E (2003) ESPript/ENDscript: Extracting and rendering sequence and 3D information from atomic structures of proteins. *Nucleic Acids Res* 31(13):3320–3323] as three groups representing α -, β -, and γ -baculoviruses. Numbering and secondary structures correspond to the WNPV polyhedrin. Residues in white characters with red box are strictly conserved, residues in black bold characters are similar within a group, residues in blue frames filled in with yellow are similar across groups, and residues in orange box are dissimilar among conserved groups. Secondary structure elements calculated by the DSSP program are represented above the alignments.

SANG SAL

	WNPV polyhedrin	В	с тт — С	• 00000	α3		D	•
		70	80	9 <u>9</u>	100	110	120	130*
1	-Wiseana_signata_NPV	KNQKLTLFKEI	RNIKPDTMKLIV	NWSGKEFLI	RETWIRFMEDSF	PIVNDQEVI	MDVFLVINMR	STKPNRCFR
	Spodoptera_litura_NPV-2	KNQKLTLFKEI	R N V K P D T M K L I V	NWNGKEFLI	RGTWTRFMEDSF	PIVNDQEVI	MDVFLVVNMR	PTRPNRCFR
	Spodoptera_litura_NPV-3	KNOKLTLFKEI	KNVKPDTMKLIV	NWNGKEFLI	RETWIRFMEDSF	PIVNDOEV	MDVFLVVNMR	PTRPNRCFR
	Mamestra brassicae NPV-1	KNOKLTLFKET	NVKPDTMKLVV	NWSGKEFL	RETWIRFMEDSF	PTVNDOEVI	MDVFLVTNMR	PTRPNRCYK
	Panolis flammea NPV	KNQKLTLFKEI	NVKPDTMKLVV	NWSGKEFLI	RETWTRFMEDSF	PIVNDOEVI	MDVFLVINMR	PTRPNRCYK
	Mamestra_brassicae_NPV-2	K N Q K L T L F K E I I	R N V K P D T M K L V V	NW <mark>SGKE</mark> FLI	RETWT <mark>RF</mark> MEDS <mark>F</mark>	P I V N D Q E V I	MDVF <mark>LVIN</mark> MR	P T R P N R C F K
	Leucania_separata_NPV-1	KNQKLTLFKEI	R Y V K P D T M K L V V	NWSGKEFLI	RETWIRFMEDSF	PIVNDQEVI	MDVFLVINMR	PTRPNRCFK
	Ecotropis_obliquaobliqua_NPV Organia_pseudotsugata_NPV_1	KNOKLTLFKEI	KNVKPDTMKLIV	NWSGKEFLI	RETWTRFMEDSF	PIVNDOEV	MDVFLVINMR.	PTRPNRCYK
	Buzura suppressaria NPV	KNOKLTLFKEI	NVKPDTMKLV V	NWSGKEFLI	RETWIRFMEDSF	PIVNDOEI	MDVFLVINMR	PTRPNRCYR
	Trichoplusia ni NPV-1	KNQKLTLFKEI	RNVKPDTMKLVV	NWSGKEFLI	RETWIRFMEDSF	PIVNDOEI	MDVFLVVNMR	PTRPNRCFK
	Trichoplusia_ni_NPV-2	K N Q K L T L F K E I I	R N V K P <mark>D T M K L V</mark> V	N <mark>wsgke</mark> fli	RETWT <mark>RF</mark> MEDSF	PIVNDQEI	M D V F L V V N M R I	P T R P N R C F K
	Adoxophyes_honmai_NPV	KNQKLTLFKEI	RNVKPDTMKLVV	NWSGKEFLI	RETWIRFMEDSF	PIVNDQEI	MDVFLVINMR	PTRPNRCYK
	Malacosoma_neustria_NPV-1 Malacosoma_neustria_NPV-3	KNOKLTLFKET	KNVKPDTMKLIV	NWSGKEFLI	RETWIRFMEDSF	PIVNDOET	MDVFLVVNMR	PTKPNRCFR
	Malacosoma neustria NPV-2	KNOKLTLFKEI	RNVKPDTMKLIV	NWSGKEFL	RETWIRFMEDSF	PIVNDOEV	MDVLLVLOIR	PTKPNRCFR
	Helicoverpa_armigera_NPV-1	TNQKLTLFKEI	R S V K P D T M K L V V	NWSGREFLI	RETWT <mark>R</mark> FMEDS <mark>F</mark>	PIVNDOEI	MDVFLSVÑMR:	P T K P N R C Y R
	Helicoverpa_armigera_NPV-2	K N Q K L T L F K E I I	R S V K P D T M K L V V	NWSGREFLI	RETWT <mark>RF</mark> MEDSF	P I V N D Q E I I	MDVFLSVNMR	P T K P N R C Y R
~	Clanis_bilineata_NPV	KNQKLTLFKEI	RNVKPDTMKLVV	NWSGKEFLI	RETWIRFMEDSF	PIVNDQEI	MDVFLVINLR	PTKPNRCYR
α	Spodoptera_exigua_NPV Spodoptera_frugiperda_NPV	KNOKLTLFKET		NWSGKEFLI	RETWIRFMEDSF	PIVNDOET	MDVFLVINMR	PTRPNRCFR
	Spodoptera litura NPV-1	KNOKLTLFKEI	LVKPDTMKLVV	NWSGKEFLI	RETWIRFMEDSF	PSVNDOEI	MDVFLVINMR	PTRPNRCYR
	Agrotis_segetum_NPV-1	KN<mark>QKLCL</mark>FKEI	RNVKPDTMKLVV	NWSGKEFLI	RETWT <mark>R</mark> FMEDSF	PIVNDQEI	MDVF <mark>LVVN</mark> M <mark>R</mark>	P V <mark>K P N R C Y R</mark>
	Lymantria_dispar_NPV	K N Q K L T L F K E I I	R N V K P <mark>D T M K L V</mark> V	NWSGKEFLI	RETWTRFMEDSF	P I V N D Q E V I	MDIYLTINVR	P T R P N R C Y K
	Autographa_californica_NPV	KNOKLTLFKEI	RNVKPDTMKLVV	GWKGKEFYI	RETWTRFMEDSF	PIVNDQEVI	MDVFLVVNMR	PTRPNRCYK
	Hyphantria_cunea_NPV-1 Hyphantria_cunea_NPV-2	KNOKLTLEKET	NVKPDTMKLTA	NWSGKEFLI	RETWIRFVEDSF	PIVNDOEVI	MEVFLVINLR	PTRPNRCIK
	Amsacta albistriga NPV	KNOKLTLFKEI	NVKPDTMKLIV	NWSGKEFLI	RETWIRFVEDSF	PIGNDOEV	MDVFLVVNLR	PTRPNRCYK
	Choristoneura_fumiferana_NPV-2	K <mark>n<mark>qkltl</mark>fkeii</mark>	RNVKPDTMKLIV	N <mark>wsgke</mark> fli	RETWT <mark>RF</mark> VEDS <mark>F</mark>	PIVNDQEVI	MDVF <mark>LVVN</mark> M <mark>R</mark>	P T R P N R C Y K
	Orgyia_pseudotsugata_NPV-2	KNQKLTLFKEII	R N V K P D T M K L I V	NWSGKEFLI	RETWTRF VEDSF	P I V N D Q E V I	MDVFLVVNMR	PTRPNRCYK
	Archips_cerasivoranus_NPV	KNOKLTLFKEI	NVKPDTMKLIV	NWSGKEFLO	GQTWTRFVEDSF	PIVNDOEV	MDVFLVINLR	PTRPNRCYK
	Anticarsia gemmatalis NPV	KNOKLTLFKEI	RNVKPDTMKLIV	NWSGKEFLI	RETWIRFVEDSF	PIVNDOEV	MDVFLVINLR	PTRPNRCYK
	Antheraea pernyi NPV	KNQKLTLFKEI	NVKPDTMKLIV	NWSGKEFLI	RETWIRFVEDSF	PIVNDQEVI	MDVFLVINLR	PTRPNRCYK
	Attacus_ricini_NPV	KNQKLTLFKEI	RNVKPDTMKLIV	NW <mark>SGKE</mark> FLI	RETWTRFVEDSF	P I V N D Q E V I	MDVF <mark>LVINL</mark> R	P T R P N R C Y K
	Maruca_vitrata_NPV	KNQKLTLFKEI	RIVKPDTMKLIV	NWSGKEFLI	RETWIRFVEDSF	PIVNDQEVI	MDVFLVVNLR	PTRPNRCYK
	Thusanonlusia orighalcoa NPV	KNOKLTLFKEL	NVKPDTMKLIV	NWSGKEFMI	RETWIRFVEDSF		MDVFLVVNLK.	PTRPNRCYK
	Bombyx mori NPV-2	KNOKLTLFKEI	SVKPDTMKLIV	NWSGKEFLI	RETWIRFVEDSF	PIVNDOEV	MDVYLVANLK	PTRPNRCYK
	Bombyx_mandarina_NPV	KNQKLTLFKEI	R S V K P D T M K L I V	NWSGKEFLI	RETWTRFVEDSF	PIVNDQEVI	MDVYLVANLK	PTRPNRCYK
	Bombyx_mori_NPV-1	K N Q K L T L F K E V I	R N V K P <mark>D T M K L I</mark> V	NWSGKEFLI	RET <mark>WT</mark> RFVEDSF	P I V N D Q E V I	MDVYLVANLK	P T R P N R C Y K
	Lonomia_obliqua_NPV	KNOKLTLFKEI	RNVKPDTMKLIV	NWSGKEFLI	RETWTRFVEDSF	PIVNDQEI	IDIFLVINLR	PTRPNRCYR
- 1	Cryptophlebia leucotreta GV	KNVRITLFKET	RVHPDTMKLVC	NWSGKEFLI	RETWIRFISEEF	PITTDOEL	IDLWFELOLR	PMHPNRCYK
	Cydia pomonella GV	KNVRITLFKE I	RVHPDTMKLVC	NWSGKEFLI	RETWIRFISEEF	PITTDQEI	MDLWFELQLR	PMHPNRCYK
	Andraca_bipunctata_GV	K <mark>nvritl</mark> fkeii	R R V Q P D T M K L V C	NWSGKEFLI	RETWT <mark>RF</mark> ISEE <mark>F</mark>	PITTDQEI	MDLWFEIQL <mark>R</mark>	<mark>P</mark> M <mark>Q</mark> P <mark>N R C Y K</mark>
	Choristoneura_occidentalis_GV	KNVRITLFKEI	R R V Q P D T M K L V C	NWSGKEFLI	RETWIRFISEEF	PITTDQEI	MDLWFEIQLR	PMQPNRCYK
	Adoxophyes_orana_GV	KNVRITLFKEI	R V H P D T M K L V C	NWSGKEFL	RETWTRFISEEF	PITTDOEI	MDLWFEIQLR	PMHPNRCYK
0	Phthorimaea operculella GV	KNVRITLFKEI	RVHPDTMKLVC	NWSGKEFLI	RETWIRFISEEF	PITTDOEI	MDLWFELOVR	PMHPNRCYK
В	Epinotia aporema GV	KNVRITLFKE I	RVHPDTMKLVC	NWSGKEFLI	RETWIRFICEEF	PITTDOEI	MDLWFELQLR	PMQPNRCYK
ľ	Trichoplusia_ni_GV	K N VKITL F K E I I	R R I Q P D T M K L V C	NWSGKEFLI	RETWT <mark>RFISEE</mark> F	PITTDQEI	MDLWFELQL <mark>R</mark>	<mark>P</mark> M <mark>Q</mark> P <mark>N R C Y K</mark>
	Spodoptera_litura_GV	KNVKITLFKEI	RRIHPDTMKLVC	SWSGKEFLI	RETWIRFISEEF	PIATDQEI	MDLWFELTLR	PMQPNRCYR
	Agrotis_segetum_GV-1	KNVRITLFKEI	RVQPDIMKLIC	NWSGKEFLI	RETWIRFISEEF	PITTDOEI	MNLIFELOLR	
	Plutella xvlostella GV	KNVRITLFKET	RVOPDTLKLVC	NWSGKEFLI	RETWIRFISEEF	PITTDOEI	MDLWFELOLR	PMOPNRCYK
	Pieris rapae GV	KNVRITLFKECI	RVEPDTLKLVC	NWSGKEFLI	REMWTRFISEEF	PITTDOOI	MDLWFEIQCR	PMQPNRCYK
	Pieris_brassicae_GV	KNVRITLFKECI	R V E P D T L K L V C	NWSGKEFLI	REMWT <mark>RF</mark> ISEE <mark>F</mark>	PITTDQQI	MNMWFEIQVR	PMQPNRCYK
V	Neodiprion_abietis_NPV	KHVKMVMFQEVI	RNIKANTMKLAI	NWSGREYLI	REVWTTFIEDTF	PINNYQEF	TDVFLEIRCT	PNKSNRHYR
Ĭ	Neodiprion_sertifer NPV	KHVKMVMFQEV	NIKANIMELAI	NWSGREYL	REVWITTFIEDTF	PINNYOFF	TDVFLEIRCT	
		and the state of the	A A A A A A A A A A A A A A A A A A A			Canal Supr.		OILELIN

Fig. S2. Continued.

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	WNPV polyhedrin		F a	TT G		α4 22222	
		140	150 160	o 17 o	180	190	200
1	Wiseana_signata_NPV Gradaut_signata_NPV	FLACHALRCDPD	YVPHEIIRIVEPSY	VG.NNEYRISLAKI	GGGCPIMNLHLEYTN.	SFEHFINKVI	LWENF
	Spodoptera_litura_NPV-2	FLACHALRCDPE	YUPHDVIRIVEPSY VUPHDVIRIVEPSY	V G T N N E Y R I SLAKI	CCCCPVMNLHAEYTT.	SFESFIDKV	
	Spodoptera_litura_NPV-3	FLACHALRCDPE		VGINNEY BISLAKI	CCCC DUMNLHAEITT.	SFESFIDKV.	
	Mamostra brassicao NPV-1	FLACHALRCDPD	VUDHEVIDIVEDSVI	UCSNNEVPUSTAKI	CCCC PVMNLHSEVTN	SFEETIDRV.	
	Panolic flammon NBV	FLACHALPCDPF	VUDWEVTRTVERSY	UCSNNEVPUSTAKI	CCCCPVMNLHSEVTN	SFEETINRV	
	Mamostra brassicao NPV-2	FLACHALRCDPD	VVPHEVIRIVEPSV	VGSNNEVRVSTAKI	CCCCPVMNLHSEVTN	SFEEFINRV	WENE
	Leucania separata NPV-1	FLACHALRCDPD	VVPHEVIRIVERSC	VGTNNEYRVSTAK	GGGCPVMNLHSEYTN	SFEEFINRVI	WENE
	Ecotropis obliguaobligua NPV	FLACHALRCDPD	YVPHEVIRIVEPS Y	VGSNNEYRISLAK	GGGCPVMNLHAEYTN.	SFEEFINRV	IWENF
	Orgyia pseudotsugata NPV-1	FLACHALRCDPE	YVPHEVIRIVEPSY	VGSNNEY <mark>RISL</mark> AKI	GGGC PVMNLHAEYTN.	SFEEFINRVI	HWENF
	Buzura suppressaria NPV	FLACHALRCDPD	YVPHEVIRIVEPSY	VGSNNEY <mark>RISL</mark> AKI	GGGC PVMNLHSEYTN.	SFEEFINRVI	I W E N F
	Trichoplusia_ni_NPV-1	FLAQHALRCDPD	YVPHEVIRIVEPSWV	V G S N N E Y R I S L A K H	GG <mark>GCPIMNL</mark> HSEYTN.	SFEEFINRVI	<mark>I W E N</mark> F
	Trichoplusia_ni_NPV-2	FLAQHALRCDPD	Y V P H E V I R I V E P S W '	VGNNNEY <mark>RISL</mark> AKI	GG <mark>GCPIMNL</mark> HSEYTN.	SFEEFIARVI	I W E N F
	Adoxophyes_honmai_NPV	FLAQHALRCDPD	Y V P H E V I R I V E P S W Y	VGSNNEY <mark>RISL</mark> AKI	GGGCPVMNLHAEYTN.	SFEEFISRVI	f w e n f
	Malacosoma_neustria_NPV-1	FLAOHALRCDSD	YVPHEVIRIVEPSY	VGSNNEYRISLGK I	RYNGCPVMNLHSEYTN.	SFEDFINRVI	(WENF
	Malacosoma_neustria_NPV-3	VLAQHALRCDSD	YVPHEVIRIVKPSY	VGSNNEYRISLGK	RYNGCPVMNLHSEYTN.	SFEDFINRV	IWENF
	Malacosoma_neustria_NPV-2	FLACHALRCDSD	YVPHEVIRIVEPS Y	VGSNNEYRISLGKI	GYACPVMNLHSEYTN.	SFEDFINRV	LWENF
	Helicoverpa_armigera_NPV-1	FLACHALRCDPD	Y I PHEVIRIVEPSY	V G S N N E Y R I S L AK I	YGGCPVMNLHAEYTN.	SFEDFITNV	WENF
	Clanic bilinoata NPV-2	FLACHALRCDPD	VUDUEVIRIVEPSY VUDUEVIRIVEPSY	UCCHNEVETCI AKI	CCCCPVMNLHAEYTN	SFEDFITNV.	
~	Spodoptera evigua NPV	FLACHALRCDPD	VVPHEVIRIVEPSI VVPHEVIPIVEPVV	VG5HNEIRISLAKI	CCCC PVMNLHSEIIN	SFEEFINRV.	
α	Spodoptera frugiperda NPV	FLACHALRCDPD	VVPHEVTRTVEPVV	VGNNNE VRTSTAKI	CCCC PVMNLHSEVTH	SFEEFINRV	WENE
	Spodoptera litura NPV-1	FLACHALRCDPD	VVPHEVIRIVEPSY	VGSNNEYRISLAK	GGGCPVMNLHSEYTH	SFEEFINRVI	WENF
	Agrotis segetum NPV-1	FLACHALRCDPD	YVPHEVIRIVEPV Y	VGNHNEYRISLAK	GGGCPVMNLHSEYTN	SFEEFINRV	IWENF
	Lymantria dispar NPV	FVAOHALRCDEG	YVPHEVIRIVEPST'	VE.NNEYRISLAKI	GGGCPIRNLHSAYTT.	SFEHFLNSVI	IWDNF
	Autographa_californica_NPV	FLACHALRCDPD	YVPHDVIRIVEPSWV	VGSNNEYRISLAK	GGGCPIMNLHSEYTN.	SFEQFIDRVI	I W E N F
	Hyphantria_cunea_NPV-1	FLAOHALRWDDN	YVPHEVIRIVEPSY	V G M <mark>N N E</mark> Y <mark>R I S L</mark> A K I	GG <mark>GCPIMNIHSEYT</mark> N.	SFEQFVNRV	l w e n f
	Hyphantria_cunea_NPV-2	FLAQHALRWDDN	YVPHEVIRIVEPSY	V G M N N E Y R I S L A K I	GG <mark>GCPIMNIHSEYT</mark> N.	SFEQFVNRV]	<mark>I W E N</mark> F
	Amsacta_albistriga_NPV	FLAQHALRWDDN	Y V P H E V I R I V E P S Y Y	VGM <mark>NNEYRISLA</mark> KI	GGGCPIMNIHREYTN.	SFESFVNRV I	I WENF
	Choristoneura_fumiferana_NPV-2	FLROHALRWDCD	YVPHEVIRIVEPSY	VGMNNEYRISLAKI	GGGCPIMNIHAEYTN.	SFESFVNRV:	f we n f
	Orgyia_pseudotsugata_NPV-2	FLAOHALRWDCD	YVPHEVIRIVEPS Y	VGMNNEYRISLAKI	GGGCPIMNIHAEYTN.	SFESFVNRV	IWENF
	Archips_cerasivoranus_NPV	FL.OHALRWDCD	YVPHEVIRIVEPS Y	VGMNNEYRISLAKI	GGGCPIMNIHAEYTN.	SFESFVNRV	LWENF
	Choristoneura fumiferana NPV-1	FLACHALRWDCD	Y V PHEVIRIVEPSY VUDHEVIDIVEDSY	V G M N N E Y KI SLAKI	GGGCPIMNIHSEYTN.	SFESEVNRV.	IWENF
	Anticarsia_genmatalis_NPV	FLACHALRWDCD	VUDHEVIRIVEPSI VUDHEVIDIVEDSVI	V G M N N E Y R I SLAKI	CCCCPIMNIHSEITN .	SFESFVNRV.	
	Attacus ricini NPV	FLACHAVRWDCD	VVPHEVIRIVEPSH	VCMNNE VPTST PK	CCCCPIMNIHSEVIN	SFESEVNRV	WENE
	Maruca vitrata NPV	FLACHALRWDCD	VVPHEVTRIVEPSV	VGMNNE VRTSTAK	GGGCPIMNTHSEVIN	SFETEVNRV	WENE
	Rachiplusia ou NPV	FLACHALRWDED	YVPHEVIRIVEPS Y	VGMNNEYRISLAK	GGGCPIMNIHSEYTN	SFESFVSRV	WENF
	Thysanoplusia orichalcea NPV	FLACHALRWDCD	YVPHEVIRIVEPS Y	VGMNNEYRISLAK	GGGCPIMNIHSEYTN.	SFESFVNRV	IWENF
	Bombyx mori NPV-2	FLACHALRWEED	YVPHEVIRIVEPSY	VGMNNEYRISLAKI	GGGCPIMNIHSEYTN.	SFESFVNRVI	IWENF
	Bombyx_mandarina_NPV	FLAOHALRWEED	YVPHEVIRIVEPSY	VGM <mark>NNEYRISL</mark> AKI	GG <mark>GCPIMNIHSEYT</mark> N.	SFESFVNRVI	I W E N F
	Bombyx_mori_NPV-1	FLAQHALRWDED	YVPHEVIRIMEPSY'	VGM <mark>NNEYRISLA</mark> KI	GG <mark>GCPIMNI</mark> HSEYTN.	SFESFVNRV I	<mark>I W E N</mark> F
	Lonomia_obliqua_NPV	FLAQHALRWDCN	Y V P H E V I R I V E P S Y Y	VGTNNEY <mark>RISL</mark> AKI	GGGCPIMNIHSEYTN.	SFESFVNRV	(WENF
	Agrotis_segetum_NPV-2	FLAQHALRCDPD	YVPHEVIRIVEPDY	V G V G N E Y R I S L A K H	GGGCPIMNLNSEYNN.	SFESFIERVI	(WENF
	Cryptophlebia_leucotreta_GV	FTMOYALCAHPD	YVAHDVIRQODPYY	VGPNNIERINISKI	GFAFPLTCLOSVYND.	NFENFFDDVI	JWPYF
	Cydia_pomonella_GV	FTMOYALGAHPD	Y VAHDVIRQODPYY	VGPNNIERINLSKI	GFAFPLTCLOSVIND.	NFERFFDDVI	
	Choristonoura oggidentalis CV	FTMOYALGAHPD	YVAHDVI ROODPYY	V G P N N I E R I N L R K I	GFAFPLTCLOSVIND.	NFERFFDDVI	
	Adoxophyes orana GV	FTMOVALCAHPD		UC PNNTEPTNISKI	GFAFPLICLOSVIND.	NEEREEDDUI	
	Harrisina brillians GV	FTMOVALCTHPD	Y TAHDY TROODPYFY	VGPNNTERINISKI	GFAFPLTCLOSVYND	NFEGFEDVI	WPVF
~	Phthorimaea operculella GV	FTMOYALGAHPD	YVAHDVIROODPYY:	IGPNNVERICISKO	GVAFPLTCLOSVYND	NFETFFDDVI	WPYF
R	Epinotia aporema GV	FTMOYALCAHSD	YVAHDVIROODPYY	VGPNNIERINLTKI	GFAFPLTCLOSVYNE.	NFEEFFDDVI	LWPYF
P	Trichoplusia ni GV	FTMOYALAANPD	YVAHDVIROHDPYY'	VGPDNRERINLSKI	GLAFPLTCLÕSIYNE.	NFEEFFDOVI	LWPYF
-	Spodoptera_litura_GV	FTMQYAL AANPD	YCAHDVIRQQDPYY	VGPDNRERINL SKI	GEAF <mark>PLTCL</mark> QSIYNE.	NFEEFFDSVI	LWPYF
	Agrotis_segetum_GV-1	FTMQYALGAHPD	Y V A H D V I R Q Q D P Y Y Y	VGPNNIERINL SKI	GYAYPLTCLQSVYND.	NFENFFDEHI	LWPYF
	Agrotis_segetum_GV-2	FTMQYALGAHPD	Y V A H D V I R Q G D P Y Y Y	VGPNQIERINL S <mark>KI</mark>	GYAYPLTCLQSVYNE.	NFDF <mark>F</mark> FDEHI	JWPYF
	Plutella_xylostella_GV	FLMQYALGADAD	Y V P H D V I R A Q D P Y Y	VGPHNVERISISR(QGVAF <mark>PLTCLQAVYN</mark> E.	SFETFFEDN1	WPYF
	Pieris_rapae_GV	FTMOYALGAHPD	YVPHDVIRAQDPYY:	IGPNNIERINI. KI	GFAFPLMCLQSVYND.	NFETFFEDVI	JWPYF
	Pieris_brassicae_GV	FTMOYALDAHPD	Y V P H D V I R A Q D P Y Y	IGPNNIE <mark>RINL</mark> . KI	GFAFPLMCLQSVYND.	NFETFFEDVI	WPYF
11	Neodiprion_abietis_NPV	FLACHGLRMDED	FVPCDTIRVIEPEYI	LOGNTVS.LSLLKI	DGGC PMMKI RQQFNEI	DLEOFVDRII	WCHF
Y	Neodiprion_lecontel_NPV	FLACHGLRMDED	FVPCDTIRVIEPEYI	LUGNTVS.LSLLKI	D G G C PMMKI ROOFNEI	CLDEFVDRI	WCHF
•	_ weourprion_sertifer_wev	FLAURGL KMDND	FVFCDTERLY	LEGNIVS.VSLLKI	CDGGCEVMKVKQEFNEI	STDEFIDKI	- MCHF

Fig. S2. Continued.

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WNPV polyhedrin		<u>н</u>	I	
		210	220	230 240
	- Wiseana signata NPV	YKPIVYIGTDSA	DEEVLFEVSLVFK	IKEFAPDAPLFSGPAY
	Spodoptera_litura_NPV-2	Y <mark>K P I V Y V G T</mark> D <mark>S</mark> A I	EEEILL <mark>EVSLV</mark> FK	<mark>IKEF<mark>APDAPLYT</mark>GP<mark>A</mark>Y</mark>
	Spodoptera_litura_NPV-3	Y K P I V Y V G T D S AI	SEEEILLEVSLVFK	IKEFAPDAPLYTGPAY
	Leucania_separata_NPV-2	YKPIVYVGTDSAI	SEEEILLEVSLVFK	IKEFAPDAPLYTGPAY
	Panolis flammea NPV	VKPIVIVGTDSAL	CEFETLLEVALVER	TKEFAPDAPLINGPAI
	Mamestra brassicae NPV-2	YKPIVYVGTDSAI	EEEILLEVSLVFK	IKEFAPDAPLYNGPAY
	Leucania separata NPV-1	Y K P I V Y V G T D S AI	EEEILLEVSLVFK	IKEFAPDAPLYNGPAY
	Ecotropis_obliquaobliqua_NPV	Y <mark>K P I V Y V G T</mark> D <mark>S</mark> A I	E E E I L L E <mark>V S L V F</mark> K	<mark>IKEF</mark> APDAPLYS <mark>GP</mark> A
	Orgyia_pseudotsugata_NPV-1	Y <mark>K P I V Y V G T</mark> D <mark>S</mark> A I	EEEILLEVSLVFK	IKEF <mark>APDAPLYS</mark> GP <mark>A</mark> Y
	Buzura_suppressaria_NPV	YKPIVYVGTDSAI	EEEILLEVSLVFK	VKEFAPDAPLYTGPAY
	Trichoplusia_ni_NPV-1	YKPIVYVGTDSAI	SEEEILLEVSLVFK	IKEFAPDAPLYSGPAY
	Adoxophyes hopmai NPV	VKPTVYTGTDSA	EEETLLEVSLVFK	VKEFAPDAPL VTGPAV
	Malacosoma neustria NPV-1	YKPLVYIGTDSAI	EEEILLEVSLVFK	IKEFAPDAPLYTGPAY
	Malacosoma neustria NPV-3	Y K P L V Y I G T D S AI	EEEILLE <mark>VSLV</mark> FK	IKEF <mark>APDAPLYT</mark> GP <mark>A</mark> Y
	Malacosoma_neustria_NPV-2	Y KPLLYIGTDSAI	E <mark>EEEILL</mark> EVSLVFK	<mark>IKEF<mark>APDAPLYT</mark>GP<mark>A</mark>Y</mark>
	Helicoverpa_armigera_NPV-1	Y <mark>K P I V Y V G T</mark> D S A I	EEEILLEVSLIFK	<mark>IKEFAPDAPLYT</mark> GP <mark>A</mark> Y
	Helicoverpa_armigera_NPV-2	YKPIVYVGTDSAI	SEEEILLEVSLIFK	IKEFAPDAPLYTGPAY
	Clanis_bilineata_NPV	YKPIVYIGTDSAI	SEEEILMEVSLVFK	IKEFAPDAPLYTGPAY
α	Spodoptera_exigua_NPV Spodoptera_frugiperda_NBV	YKPIVIVGTDSG	EEEILLELSLVFK	TKEFAPDAPLINGPAI
	Spodoptera litura NPV-1	YKPTVYVGTDSGI	SEEETLLEVALVEK	TKEFAPDASLYNGPAY
	Agrotis segetum NPV-1	YKPIVYIGTDSA	EEEILLELSLVFK	IKEFAPDAPLYNGPAY
	Lymantria_dispar_NPV	Y <mark>K P I V Y V G T</mark> T <mark>S</mark> A I	EEEILL <mark>EVSLV</mark> FK	<mark>IKEFAPDAPLFQ</mark> GP <mark>A</mark> Y
	Autographa_californica_NPV	Y <mark>K P I V Y I G T</mark> D <mark>S</mark> A I	EEEILL <mark>EVSLV</mark> FK	V K E F <mark>A P D A P L F T</mark> G P <mark>A</mark> Y
	Hyphantria_cunea_NPV-1	Y K P I V Y I <mark>G T</mark> D S G I	EEEILIEVSLVF K	VKEFAPDAPLFTGPAY
	Hyphantria_cunea_NPV-2	YKPIVYIGTDSGI	EEEILIEVSLVFK	VKEFAPDAPLFTGPAY
	Amsacta_albistriga_NPV Choristonoura_fumiforana_NBW_2	YKPIVDIGTDSG	SEEEILIEVSLVFK	VKEFAPDAPLF TGPAY
	Orgyja pseudotsugata NPV-2	VKPTVYIGTDSSI	CEEETLIEVSLVFK	VKEFAPDAPLFTGPAT
	Archips cerasivoranus NPV	YKPIVYIGTDSG	EEEILIEVSLVFK	VKEFAPDAPLFTGPAY
	Choristoneura fumiferana NPV-1	Y K P I V Y I G T D S G I	EEEILIEVSLVF K	VKEFAPDAPLFT GPAY
	Anticarsia_gemmatalis_NPV	Y <mark>K P I V Y I <mark>G T</mark> D <mark>S</mark> G I</mark>	E <mark>eeilievslv</mark> fk	VKEF <mark>APDAPLFT</mark> GP <mark>A</mark> Y
	Antheraea_pernyi_NPV	Y <mark>K P I V Y I G T</mark> D S G I	EEEILIEVSLVFK	VKEFAPDAPLFTGPA Y
	Attacus_ricini_NPV	YKPIVYIGTDSGI	EEEEILIEVSLVFK	VKEFVPDAPLFTGPAY
	Maruca_vitrata_NPV	YKPIVYIGTDSG	SEEEILIEVSLVFK	VKEFAPDAPLFTGPAY
	Thysanonlusia orichalcea NPV	VKPTVVIGTDSG	EEEILIEVSLVFK	VKEFAPDAPLF TGPAI
	Bombyx mori NPV-2	YKPIVYIGTDSAI	SEEETLIEVSLVFK	TKEFAPDAPLFTGPAY
	Bombyx mandarina NPV	Y K P I V Y I G T D S AI	EEEILIEVSLVFK	IKEFASDAPLFTGPAY
	Bombyx_mori_NPV-1	Y <mark>K P I V Y I G T</mark> D S A I	E <mark>eeilievslv</mark> fk	<mark>IKEF</mark> APDAPLFT <mark>GP</mark> AY
	Lonomia_obliqua_NPV	Y <mark>K P V V Y I G T</mark> D S A I	EEEILIEVSLVFK	IKEF <mark>APDAPLFT</mark> GP <mark>A</mark> Y
	Agrotis_segetum_NPV-2	YRNNVYIGTDSAI	EEEILLELSLLFK	VKEFAPDIPLYSGPAY
	Cryptophiebia_leucotreta_GV	HRPLVYVGTTSAI	SIEEIMIEVSLLFK TEEIMIEVSLIEV	IKEFAPDVPLFTGPAY
	Andraca bipunctata GV	HRPLVVVGTTSA	STEETMIEVSLIFK STEETMIEVSLIFK	TKEFAPDVPLFTGPAT
	Choristoneura occidentalis GV	HRPLVYVGTTSA	LEEIMIEVSLLFK	IKEFAPDVPLFTGPAY
	Adoxophyes orana GV	H R P L V Y I G T T S A I	VEEIMIEVSLLF K	IKEFAPDVPLFTGPAY
	Harrisina_brillians_GV	H <mark>R P L V Y V G T</mark> T <mark>S</mark> G I	E <mark>IEEIMIEVSLL</mark> FK	<mark>IKEFAPDVPLFT</mark> GP <mark>A</mark> Y
0	Phthorimaea_operculella_GV	Y <mark>r p l v y v </mark> gt t s s i	E <mark>IEEIMIEVSLL</mark> FK	IKEF <mark>APDVPLFT</mark> GP <mark>A</mark> Y
5	Epinotia_aporema_GV	H R P L V Y V G T T S A I	STEEIMIEVSLLFK	IKEFAPDVPLFTGPAY
1-	Trichoplusia_ni_GV	HRPLVYVGTTSAI	EIEEVMIEVALLFK	IKEFAPDVPLFTGPAY
	Agrotic sogotum GV 1	HRPLVIVGTTSAI	SIEEVMIEVALLFK TEETMIEVSIIEV	TKEFAPDVPLFTGPAY
	Agrotis segetum GV-2	HRPLVYVGMNSA	TEETMIEVSVIEK	TKEFAPDVPLFTGPAV
	Plutella xylostella GV	HRPLVYVGTTSG	VEEIMIEVALIEK	IKEFAPDVPLFTGPAY
	Pieris rapae GV	HRPLVYIGTTSSI	TEEILLEVSFLFK	IKEFAPDVPLYTGPAY
	Pieris_brassicae_GV	H <mark>R P L V Y I G T T S</mark> S I	E <mark>teeillevsfl</mark> fk	IKEF <mark>APDVPLYT</mark> GP <mark>A</mark> Y
~1	Neodiprion_abietis_NPV	H <mark>R P I V Y I G T</mark> D S G I	EEEVFIEASLTFI	I KEFAPEAPFVNGPGM
Y	Neodiprion_lecontei_NPV	H R P I V Y I G T D S G I	EEEVFIEASLTFI	IKEFAPEAPFVNGPGM
•	Neodiprion_sertifer_NPV	HRPIVYIGTDSG	DEDDVFIDASLTEI	IKEFAPEAPFVNGPGM

Fig. S2. Continued.

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Fig. S3. Limited structural similarity of the baculovirus polyhedrin with jelly-roll containing proteins. Cartoon representation of the top six Dali (1) hits (cf. Table S1 for details). By decreasing the *z* score, the hits are as follows: the capsid of the rice yellow mottle virus (*A*), the coat protein of coxsackievirus b3 (*B*), the coat protein of cucumber mosaic virus (*C*), the coat protein of the carnation mottle virus (*D*), the capsid protein of the tobacco necrosis virus (*E*), and the *Yersinia* pseudotuberculosis-derived mitogen (YPM) (*F*). (*G*) Baculovirus polyhedrin trimer is represented in the center of the figure for comparison. The asymmetrical unit is represented for the viral proteins [obtained from Viperdb2 (2)], and the biological unit is represented for YPM. A protein subunit is highlighted with a blue-green-yellow-red gradient from the N terminus to C terminus, and the rest of the molecules are shown in pale brown. The BIDG and CHEF β -sheets are also indicated.

1. Holm L, Kaariainen S, Rosenstrom P, Schenkel A (2008) Searching protein structure databases with DaliLite v. 3. Bioinformatics 24(23):2780-2781.

2. Carrillo-Tripp M, et al. (2009) VIPERdb2: An enhanced and web API enabled relational database for structural virology. Nucleic Acids Res 37(Database issue):D436-D442.



Fig. S4. Comparison of the electrostatic potential at the surface of baculovirus and cypovirus polyhedra. The electrostatic potential was calculated using APBS software [Baker NA, Sept D, Joseph S, Holst MJ, McCammon JA (2001) Electrostatics of nanosystems: Application to microtubules and the ribosome. *Proc Natl Acad Sci USA* 98:10037–10041] with standard settings (310 K, no ions, nonlinear Poisson–Boltzmann equation, 1.4-Å solvent radius, protein/solvent dielectric constants of 2.0 and 80.0, respectively). The structure of G25D AcMNPV polyhedrin was used here, and residues for which side chains could not be modeled were omitted from the calculations. The electrostatic potential is represented on the solvent-accessible surface by a red-white-blue gradient for the -10 to +10 kT range.

Table S1. Structural comparison

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	Origin	PDB ID	z score	rmsd	ldentity, %	Number of aligned residues, N _{algn}
Capsid of the rice yellow mottle virus	Sobemovirus	1f2n	6.3	6.1	8	115
Coxsackievirus coat protein	Picornaviridae	1cov	6.1	6.2	5	125
Cucumber mosaic virus coat protein	Bromoviridae	1f15	5.9	6.1	11	132
Carnation mottle virus coat protein	Tombusviridae	1opo	5.8	6.1	7	118
Tobacco necrosis virus capsid protein	Tobamovirus	1c8n	5.7	6.0	11	112
Yersinia pseudo-tuberculosis-derived mitogen	Yersinia (Enterobacteriaceae)	1pm4	5.6	2.9	12	85

This table lists the results of a Dali search for structural similarities between the WNPV polyhedrin and proteins from the PDB sorted according to *z* scores (*z* scores >5.5). Hits corresponding to orthologues in the same virus family are omitted for clarity (e.g., capsids of the numerous members of the *Picornaviridae* family).

Table S2. Data collection and phasing statistics

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-		SoMot	SoMot2	SoMot2	V 1/1	
	G25D ACIVINEV	Seivier	SelvietZAg	SelvietSPt	KI/12	
Data collection						
Space group	123	123	123	123	123	123
Cell dimensions						
a = b = c, A	103.158	103.207	103.136	103.20	103.242	103.515
Resolution, Å	2.8 (2.95–2.8)	2.92 (3.07–2.92)	2.90 (3.06–2.90)	2.80 (2.95–2.80)	2.40 (2.53–2.40)	2.90 (3.06–2.90)
R _{merge}	10.6 (20.2)	9.3 (34.1)	21.5 (53.8)	9.3 (21.1)	9.0 (28.3)	13.6 (68.1)
Mean, l/ σ l	13.1 (4.5)	10.7 (3.6)	9.7 (4.0)	8.3 (3.6)	7.6 (3.2)	4.4 (1.9)
Completeness, %	98.1 (93.9)	97.2 (93.5)	95.4 (94.4)	84.2 (76.5)	89.1 (93.4)	35.3 (24.8)
Redundancy	5.7 (2.2)	4.6 (4.2)	10.6 (7.4)	1.9 (1.5)	2.0 (1.9)	1.3 (1.1)
Phasing						
Heavy-atom sites/occupancy B	HA1	HA1	HA1	HA1	HA1	
	0.74/47.4	0.70/36.5	0.96/54.2	0.72/45.8	0.68/20.1	
		HA2	HA2	HA2	HA2	HA2
		0.71/37.5	0.66/25.9	0.71/22.8	0.61/25.6	0.76/42.9
		HA3	HA3	HA3	HA3	HA3
		0.85/67.4	0.79/41.4	0.72/44.3	0.75/62.4	0.67/14.1
		HA4	HA4	HA4	HA4	HA6
		0.54/68.3	0.38/53.1	1.29/155.1	0.56/70.1	0.70/49.7
					HA5	HA7
					0.28/23.1	0.59/29.9
						HA8
						2.21/174.3
FOM 18.2–2.8 Å (3.4–2.8 Å)						
Acentric	0.44 (0.29)					
Centric	0.50 (0.33)					
Phasing power acentric/centric		0.97/0.76	1.00/0.86	1.14/1.01	1.54/1.39	1.03/0.75

Highest resolution shell is shown in parenthesis.

HA1 (0.593, 0.911, 0.175), HA2 (0.617, 0.874, 0.091), HA3 (0.335, 0.128, 0.258), HA4 (0.406, 0.416, 0.108), HA5 (0.577, 0.230, 0.411), HA6 (0.942, 0.773, 0.307), HA7 (0.468, 0.870, 0.452), HA8 (0.310, 0.732, 0.275).

Table S3. Data collection and refinement statistics

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	G25D AcMNPV			
Data collection				
No. crystals	5	19		
Space group	123	123		
Cell dimensions				
a = b = c, A	103.183	102.437		
Resolution, Å	20–2.30 (2.42–2.30)	30–2.17 (2.29–2.17)		
R _{merge} , %	14.8 (54.6)	34.9 (*)		
R _{pim} , %	6.1 (23.0)	9.2 (36.7)		
Mean, $I/\sigma I$	10.2 (3.8)	8.0 (2.3)		
Completeness, %	99.7 (99.1)	99.9 (100.0)		
Redundancy	6.6 (6.3)	15.0 (14.5)		
Refinement				
Resolution, Å	18.84–2.30 (2.57–2.30)	20.91–2.17 (2.43–2.17)		
No. reflections	8,240 (811)	9,620 (947)		
R _{work} /R _{free}	16.05/21.40	16.12/18.99		
	(16.38/23.46)	(19.05/22.44)		
No. atoms	1,655	1,710		
Protein	1,577	1,619		
lons	1 $ imes$ ethylene glycol	$1 imes SO_4^{2-}$		
Water	74	86		
B-factors				
Protein	24.08	20.83		
Water	31.70	31.55		
rmsd				
Bond lengths, Å	0.008	0.008		
Bond angles, °	1.04	1.04		

*R_{merge} values higher than 100% are reported as 0.000 by Scalepack. Given the large number of crystals and high redundancy, R_{pim} is a more appropriate measure of data quality than R_{merge} (see *Methods* for details on the processing strategy).