

## Reporting Summary

Nature Portfolio wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Portfolio policies, see our [Editorial Policies](#) and the [Editorial Policy Checklist](#).

### Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- The exact sample size ( $n$ ) for each experimental group/condition, given as a discrete number and unit of measurement
- A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- The statistical test(s) used AND whether they are one- or two-sided  
*Only common tests should be described solely by name; describe more complex techniques in the Methods section.*
- A description of all covariates tested
- A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- For null hypothesis testing, the test statistic (e.g.  $F$ ,  $t$ ,  $r$ ) with confidence intervals, effect sizes, degrees of freedom and  $P$  value noted  
*Give  $P$  values as exact values whenever suitable.*
- For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- Estimates of effect sizes (e.g. Cohen's  $d$ , Pearson's  $r$ ), indicating how they were calculated

*Our web collection on [statistics for biologists](#) contains articles on many of the points above.*

### Software and code

Policy information about [availability of computer code](#)

Data collection

Facilities used for X-ray crystal data and cryo-EM data are noted in the text, HKL2000 was used for data collection

Data analysis

Software used for crystallography (HKL2000, CCP4, Phaser version 2.7.16, ROSETTA 3.12, PHENIX, 1.19.2, and COOT version 0.9), ChimeraX Version 1.3, cryo-EM (RELION2 and cryo-SPARC3.2), 3DVA available as part of cryo-SPARC, sequence comparisons (ClustalW 1.2.2 and Jalview 2.11), DLS and BIS-Ans (Zetasizer software version 3.30, softmax Pro v5.4, and GraphPad Prism v7.0) are reported in the main text/figure legends with appropriate references.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

### Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

Atomic coordinates and structure factors for the crystal structure of the GII.4 HOV VLP have been deposited in the Protein Data Bank with the accession code 7K6V. The cryo-EM structure of GII.4 HOV VLP has been deposited in the Protein Data Bank with the accession code PDB ID 7MRY and the Electron Microscopy Databank with the accession code EMD-23960. Source data are provided with this paper.

## Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

- Life sciences       Behavioural & social sciences       Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

## Life sciences study design

All studies must disclose on these points even when the disclosure is negative.

|                 |   |
|-----------------|---|
| Sample size     | <input type="text" value="we performed three technical replicates as noted in the manuscript"/> |
| Data exclusions | <input type="text" value="no data were excluded"/>  |
| Replication     | <input type="text" value="biochemical assays were replicated"/>                                 |
| Randomization   | <input type="text" value="no randomization was done"/>  |
| Blinding        | <input type="text" value="no blinding was necessary"/>  |

## Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

| Materials & experimental systems    |   | Methods                             |   |
|-------------------------------------|---|-------------------------------------|---|
| n/a                                 | Included in the study                                     | n/a                                 | Included in the study                           |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Antibodies            | <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq               |
| <input type="checkbox"/>            | <input checked="" type="checkbox"/> Eukaryotic cell lines | <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry         |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology and archaeology    | <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms      |                                     |   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants      |                                     |   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data                    |                                     |   |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Dual use research of concern     |                                     |   |

## Antibodies

|                 |  |
|-----------------|--|
| Antibodies used | <input type="text" value="Fab portion of an antibody NORO-320 (from Dr. Jim Crowe) obtained as described in our paper Alvarado et al. Nature Communications, 2021, https://doi.org/10.1038/s41467-021-24649-w"/> |
| Validation      | <input type="text" value="n/a"/>   |

## Eukaryotic cell lines

Policy information about [cell lines](#)

|  |  |
|--|--|
| Cell line source(s)  | <input type="text" value="HuNoV GII.4 VLP was expressed in Gibco Sf9 insect cells using Baylor College of Medicine core facility as noted in the manuscript"/> |
| Authentication   | <input type="text" value="Not-authenticated"/>   |
| Mycoplasma contamination   | <input type="text" value="cell lines were tested for mycoplasma contamination in a regular basis and found to negative"/>                                      |
| Commonly misidentified lines<br>(See <a href="#">ICLAC</a> register) | <input type="text" value="none"/>  |