

**Supplementary information, Table S1 X-ray data collection, processing and refinement**

**statistics**

| <b>Statistics</b>                          | <b>NS2B-G4SG4-NS3pro</b>                 |
|--------------------------------------------|------------------------------------------|
| Data collection                            |                                          |
| Wavelength (Å) .....                       | 0.97853                                  |
| Resolution limit (Å).....                  | 50.00-2.60 (2.64-2.60)*                  |
| Space group.....                           | <i>P</i> 4 <sub>1</sub> 2 <sub>1</sub> 2 |
| Cell parameters                            |                                          |
| a, b, c (Å).....                           | 55.2, 55.2, 250.1                        |
| $\alpha = \beta = \gamma (^{\circ})$ ..... | 90                                       |
| No. of unique reflections.....             | 12503 (569)                              |
| Completeness (%).....                      | 99.9 (99.8)                              |
| Redundancy.....                            | 11.1 (9.5)                               |
| R <sub>merge</sub> (%).....                | 10.8 (0.00**)                            |
| R <sub>pim</sub> (%).....                  | 4.0 (64.9)                               |
| Sigma cutoff .....                         | 0                                        |
| <i>I</i> / $\sigma$ ( <i>I</i> ) .....     | 17.0 (1.2)                               |
| <i>CC</i> <sub>1/2</sub> .....             | 1 (0.72)                                 |
| Refinement                                 |                                          |
| Resolution range(Å) .....                  | 39.04-2.60 (2.69-2.60)                   |
| R <sub>work</sub> (%) .....                | 22.4                                     |
| R <sub>free</sub> (%).....                 | 27.3                                     |
| Rmsd from ideal geometry                   |                                          |
| Bonds (Å) .....                            | 0.019                                    |
| Angles (°).....                            | 2.0                                      |
| Avg B factor (Å <sup>2</sup> ).....        | 104.8                                    |
| Protein.....                               | 104.8                                    |

\* Numbers in the brackets are for the highest resolution shell.

\*\* R<sub>>=1</sub>