# Author Correction: A Engineered immunogen binding to alum adjuvant enhances humoral immunity

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Correction to: *Nature Medicine* https://doi.org/10.1038/s41591-020-0753-3, published online 17 February 2020.

In the version of this article initially published, the procedure used was described incorrectly in fifth sentence of the final paragraph of Results ('cryoEM'), the legend to Fig. 6m,n ('CryoTEM') and the fifth sentence of the Author contributions section ('cryoTEM'). The correct procedure is 'TEM' (final paragraph of Results), 'Single-particle EM' (Fig. 6m,n legend) or 'TEM' (Author contributions). Also, one of the Methods sections and its references were missing; this is provided below. The errors have been corrected in the HTML and PDF versions of the article.

**Antibody isolation and EM**. IgG was purified from serum with protein A and then digested into Fab with papain. Purified Fab was added to BG505 SOSIP D664 MD39 mC trimer and complexes were purified using a GE Superose 6 column (GE HealthCare). Complexes were added to 400 mesh carbon-coated grids and stained with 2% uranyl formate. Grids of complexes made of Fab from serum collected at week 10 post immunization were imaged on a Tecnai F20 at 200 KeV using a 4k × 4k Gatan Ultrascan 4000 CCD. Complexes from week 18 post immunization were collected on a Tecnai Spirit at 120 KeV using a 4k × 4k TemCam F416 camera. Micrographs were collected with Leginon[62] and processed with Appion[63]. Particles were chosen using DoGpicker[64] and stacked, and initial 2D classes were made with MSA/MRA[65]. After removing classes with double particles or those not resembling trimers or protomers, unbinned particles were put into Relion[66], where 3D classification was performed to obtain maps of trimer and Fab complexes. Clean maps were then refined and put into Chimera[67] to segment and compare.

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Published online: 16 April 2020
https://doi.org/10.1038/s41591-020-0861-0