**Supporting Information**

# The cryo-EM structure of the *Rhodobacter sphaeroides* light-harvesting 2 complex at 2.1 Å

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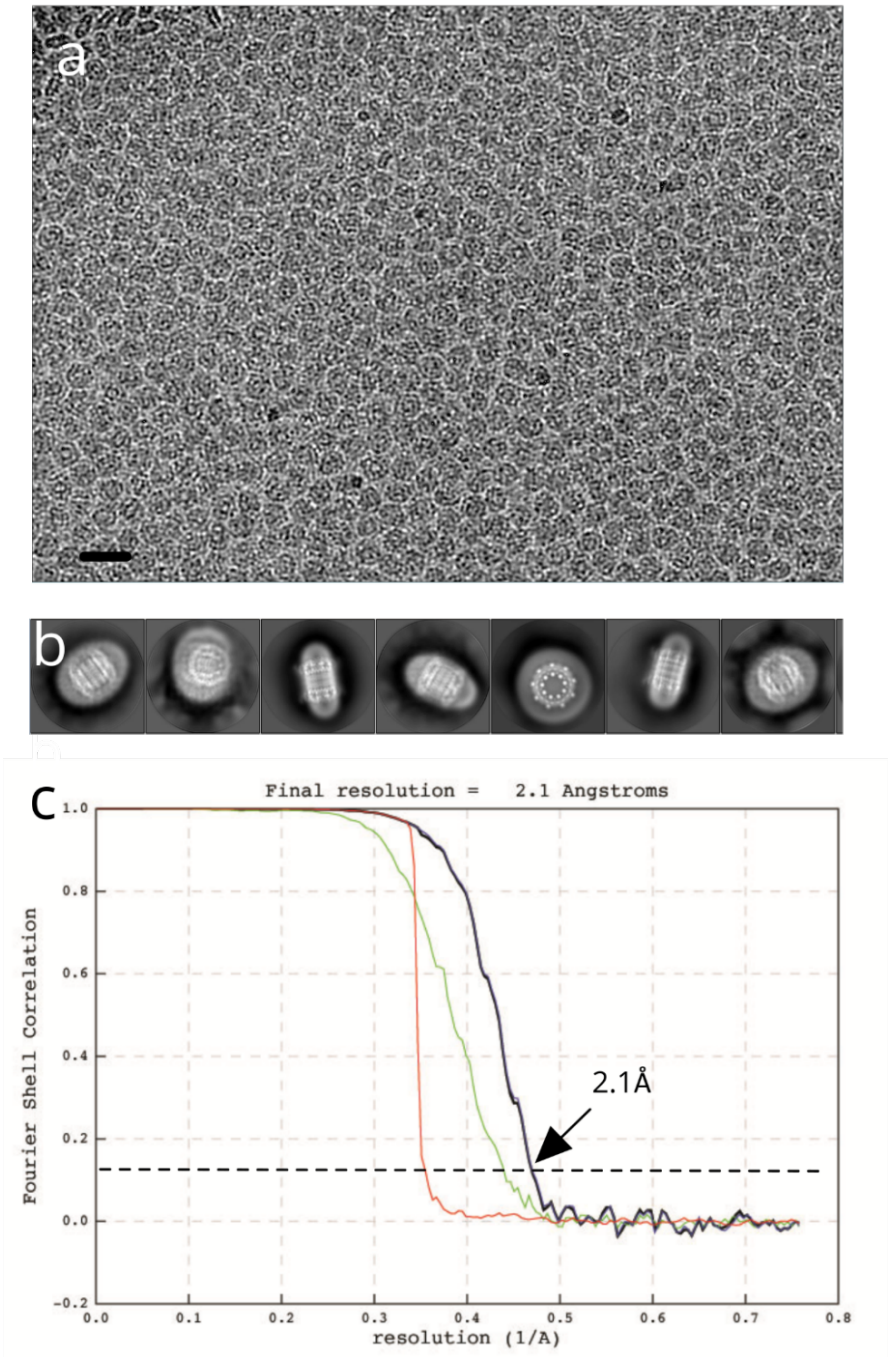


**Fig. S1**. Cryo-EM images of the LH2 complex from *Rba. sphaeroides* and resolution calculation of 3D map. a) A raw cryo-EM image of the LH2 molecules embedded in vitrified water. The image was 20 Å lowpass filtered with a sigma contrast of 3.0. Scale bar 10 nm. b) Selected 2D classes, showing different orientation of the LH2 molecules in the vitrified ice layer. The box size is 17.8 nm. c) Fourier shell correlation (FSC) curves of the CTF corrected (*black line*), masked (*blue solid line*), unmasked (*green line*), and phase randomized (*red line*) half-maps with C9 symmetry. The 0.143 cutoff is indicated by a dashed line.

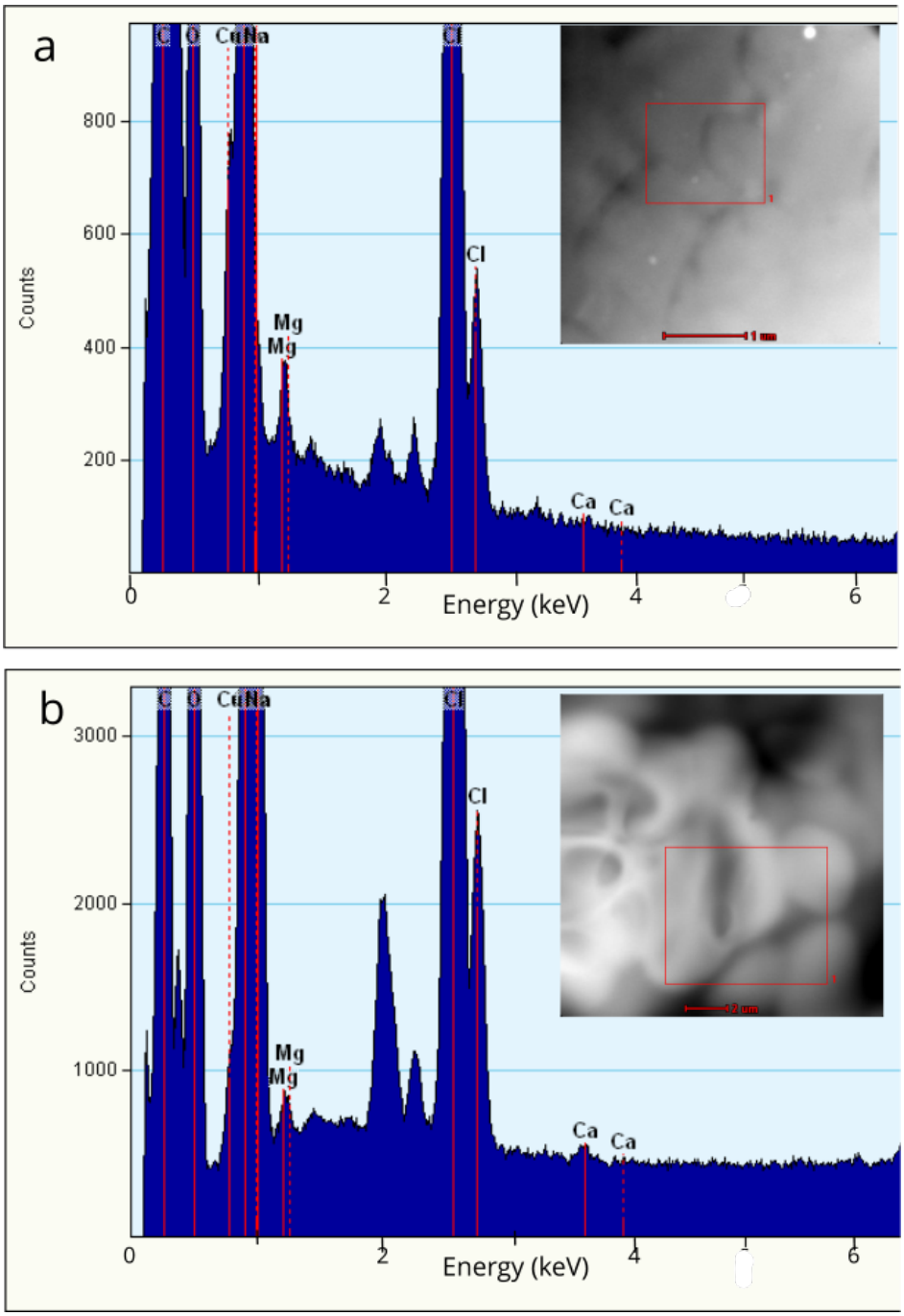


**Fig. S2**. Qualitative determination of metal ions in the LH2 complexes from *Rbl. acidophilus* and *Rba. sphaeroides* by energy dispersive X-ray analysis (EDX*)*. a, An EDX spectrum from the LH2 of *Rbl. acidophilus***.** Peak positions of magnesium and calcium are indicated. The insert shows a scanned area indicated by a red square with a scale bar. b, EDX spectrum from the LH2 of *Rba. sphaeroides.*

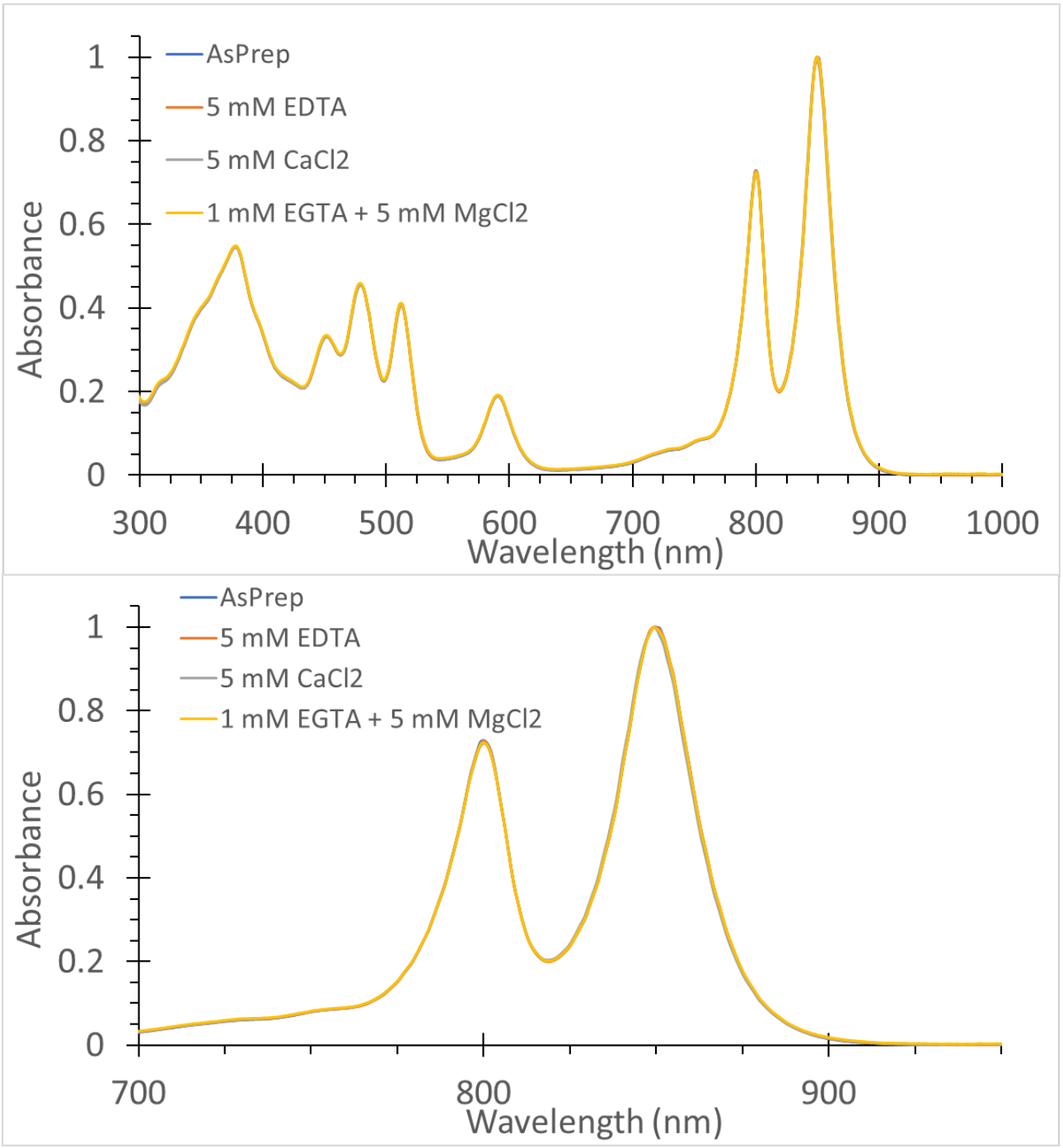


**Fig. S3**. Absorbance spectra of the LH2 complexes of *Rba. sphaeroides,* recorded from 300 to 1000 nm, with the 700-950 nm region expanded in the lower set of spectra. The spectra of the complexes were unaffected by treatments with EDTA, $CaCl_2$ or EGTA and $MgCl_2$, and so were superimposable.

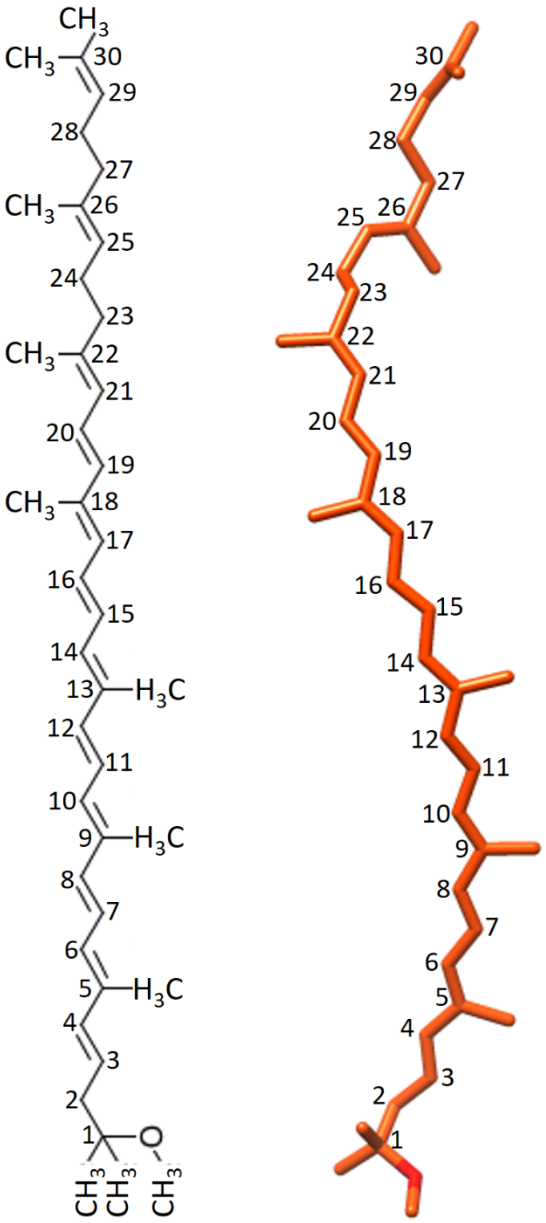

**Fig. S4**. Numbering of carbons in spheroidene, shown in diagram form (left) and in the all-*trans* conformation (right) adopted within the LH2 complex.

Table S1: Cryo-EM data acquisition, model refinement and validation statistics.

| | |
|---|---|
| **Protein source** | Photosynthetic bacterium |
| **Data collection and processing** | |
| Microscope | ThermoFisher Titan Krios G2 |
| Voltage (kV) | 300 |
| Camera | Gatan BioQuantum K3 |
| Energy filter | Yes |
| Energy filter slit width | 20 eV |
| Magnification | 130,000 |
| Defocus range (μm) | -0.8 to -2.2 |
| Mean defocus (μm) | -1.8 |
| Pixel size (Å) | 0.66 |
| Electron flux ($e^-$/ Å$^2$/s) | 1.37 |
| Electron fluence ($e^-$/ Å$^2$) | 41.6 |
| Exposure time (sec/frame) | 0.034 |
| Electron fluence per frame (e/ Å$^2$/frame) | 1.04 |
| Number of frames per movie | 40 |
| Number of movies used | 3138 |
| Initial no. particle images | 1,719,688 |
| Final no. particle images | 519,005 |
| Symmetry imposed | C9 |
| Local resolution range | 2.0 to 2.5 |
| Resolution of unmasked reconstruction (Å, FSC=0.143) | 2.3 |
| Resolution of masked reconstruction (Å, FSC=0.143) | 2.1 |
| Specimen temperature | ~80K |
| Particle box size | (512 px)$^2$ |
| **Refinement and validation** | |
| Refinement package | COOT, ISOLDE, PHENIX |
| Initial model | PDB 1NKZ |
| Model resolution (Å, FSC=0.5) | 2.1 |
| Map sharpening B factor (Å$^2$) | -77.06 |
| **Model composition** | |
| Non-hydrogen atoms | 9500 |
| Protein residues | 873 |
| Molecular weight (kD) | 134.7 |
| Protein B factor (Å$^2$) | 11.2 |
| **RMS deviations** | |
| Bond length (Å) | 0.004 |
| Bond angle ($^0$) | 0.941 |
| **Validation** | |
| MolProbity score | 1.11 |
| Clashscore | 3.20 |
| Rotamer outliers (%) | 0.00 |
| EMRinger score | 7.90 |
| Cb deviations (%) | 0.00 |
| CaBLAM outliers (%) | 0.00 |
| **Ramachandran plot** | |
| Favoured (%) | 100.00 |
| Allowed (%) | 0.00 |
| Disallowed (%) | 0.00 |
| Ramachandran Z-score | 3.14 |
| **PDB ID** | 7PBW |
| **EMDB ID** | 13307 |