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Erratum

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Soohee Chung, Gerhard Frank, Herbert Zuber & Donald A. Bryant. *Genes encoding two chlorosomes components from the green sulfur bacteria* Chlorobium vibrioforme *strain 8327D and* Clorobium tepidum

Because of the poor quality of the original printing, Fig. 1, which appeared in the above-mentioned publication on page 266, has been reprinted below.

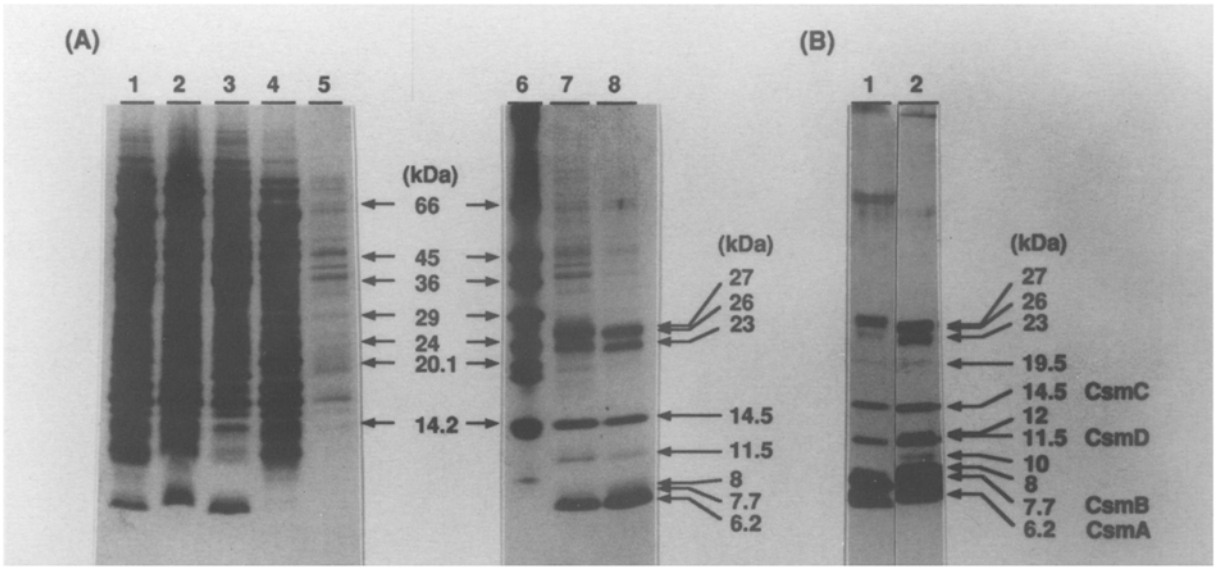

Fig. 1. Protein composition of chlorosomes from *Cb. tepidum* as determined by polyacrylamide gel electrophoresis. A. Coomassie-blue stained gel of selected fractions from chlorosome isolation by the method of Gerola and Olson (1986) and chlorosomes from combined procedures (see 'Materials and methods'). Lane 1, whole cell extract of *Cb. tepidum* after cell disruption; Lane 2, cell debris pellet obtained by centrifugation of whole-cell extract at 12,000 × *g*; Lane 3, pellet and Lane 4, supernatant, from 200,000 × *g* centrifugation of supernatant fraction obtained after 12,000 × *g* centrifugation of whole-cell extract; Lane 5, high-density fraction (probably cytoplasmic membranes) from sucrose gradient centrifugation of resuspended chlorosome and membrane fraction (Lane 3). The CsmA and CsmB polypeptides are clearly visible in Lanes 1–3; note the absence of CsmA and CsmB proteins in Lane 4. Lane 6, molecular mass standards (a-lactalbumin, 14.2 kDa; soybean trypsin inhibitor, 20.1 kDa; trypsinogen, 24 kDa; carbonic anhydrase, 29 kDa; glyceraldehyde-3-phosphate dehydrogenase, 36 kDa; ovalbumin, 45 kDa; bovine serum albumin, 66 kDa); Lane 7, chlorosome fraction obtained by sucrose gradient centrifugation, 300 µg BChl *c*; Lane 8, chlorosome fraction obtained by a combination of the methods of Feick and coworkers (Feick et al. 1982; Feick and Fuller 1984) and Gerola and Olson (1986, see 'Materials and methods'), 500 µg BChl *c*. B. Silver-stained gel of chlorosome proteins. Lane 1, Chlorosome fraction from sucrose gradient centrifugation, 10 µg BChl *c*; Lane 2, chlorosome fraction prepared as described for Lane 8 above, 50 µg BChl *c*. Some proteins identified by N-terminal amino acid sequencing (also see Table 1) are indicated at the right along with apparent molecular masses.