



BIOLOGICAL
CRYSTALLOGRAPHY

Volume 71 (2015)

Supporting information for article:

**Exploring the speed and performance of molecular replacement
with *AMPLE* using *QUARK ab initio* protein models**

**Ronan M. Keegan, Jaclyn Bibby, Jens Thomas, Dong Xu, Yang Zhang, Olga
Mayans, Martyn D. Winn and Daniel J. Rigden**

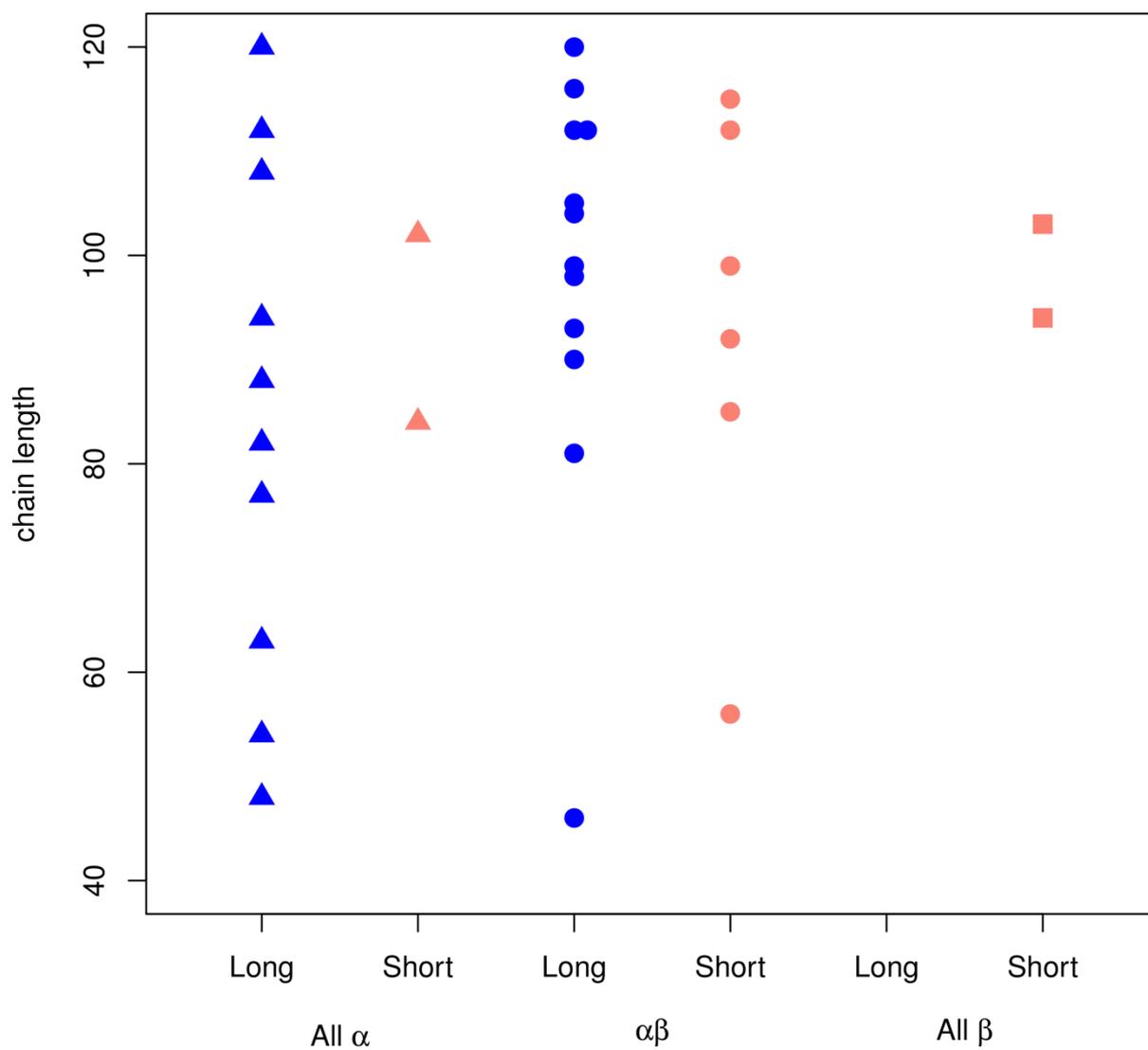


Figure S1 Secondary structure class and length of targets solved in either Run 3 ('Long' up to 12 hours Phaser) or Run 4 ('Short' 5 minutes Phaser) but not in the other.