

## Supplemental material

Savich et al., <https://doi.org/10.1085/jgp.201812210>

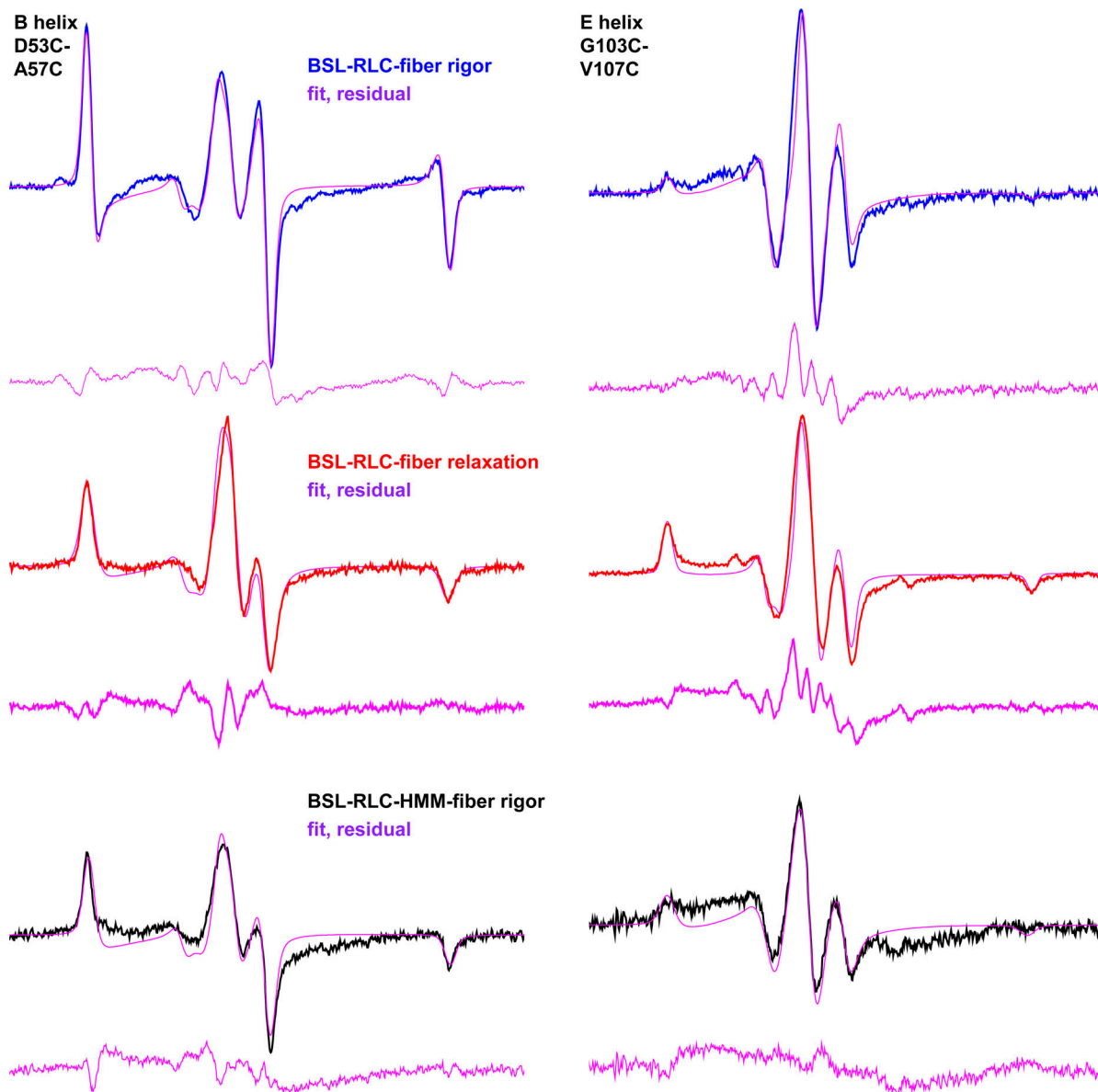


Figure S1. EPR data on BSL-RLC-fiber in rigor (blue), BSL-RLC-fiber in relaxation (red), and BSL-RLC-HMM-fiber in rigor (black). Fits and residuals are in magenta. Static limit was assumed during fitting. The field sweep width shown is 100 G.

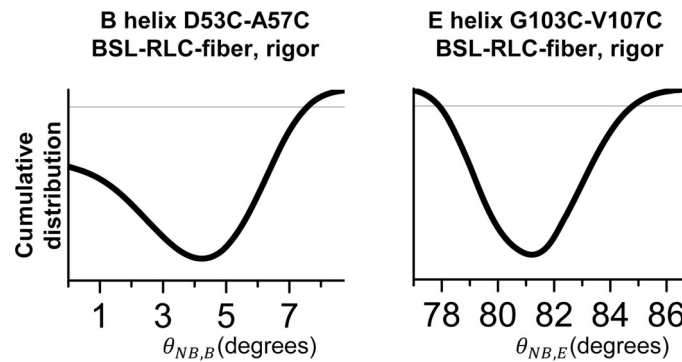


Figure S2. **The cumulative distribution function of the F-ratio distribution, comparing the ratio of the residual sum of squares of the fits with the residual sum of squares of the best fit.** The 95% intervals are depicted by horizontal lines. The confidence interval for helix B is flatter on the left-hand side, as compared with helix E. This happens due to the vanishing of the derivatives of the  $g$  and  $A$  tensors (Eqs. S2 and S3)  $\frac{\partial g}{\partial \theta_{NB}}$  and  $\frac{\partial A}{\partial \theta_{NB}}$  at the turning points ( $\theta_{NB} = 0^\circ, 90^\circ$ ). Since those tensors define the spectral position of a given probe orientation (Eq. S1), the EPR spectrum is not sensitive to orientation near the turning points. However, the symmetry of the resonance position  $B_{res}(-\theta_{NB}) = B_{res}(\theta_{NB})$  restricts  $\theta_{NB} > 0^\circ$  for the B helix, which brings the angular resolution for the probes on both helices to  $4^\circ$ .

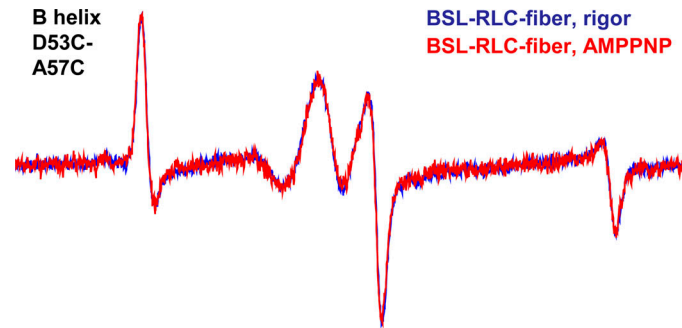


Figure S3. **The effect of 5 mM AMPPNP (red) on a BSL-RLC-fiber labeled on the B helix in rigor (blue) during EPR.** The field sweep width is 100 G.

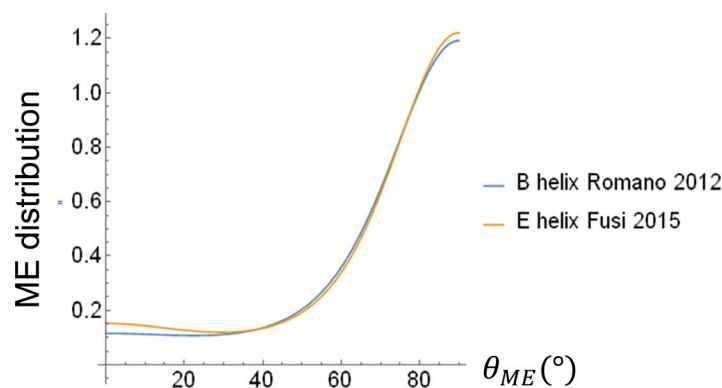


Figure S4. **The ME distributions (calculated according to Eqs. S4–S7) for the B and E helix calculated from reported order in fluorescence polarization experiments.** The B and helix E orienting potentials (reproduced here from digitized figures using GetData GraphDigitizer, v.2.26) are  $-0.296 P_2(\cos \alpha) + 0.118 P_4(\cos \alpha)$  (Romano et al., 2012) and  $-0.293 P_2(\cos \alpha) + 0.127 P_4(\cos \alpha)$  (Fusi et al., 2015), respectively, where  $\alpha$  is the angle between the BR dipole and the muscle fiber,  $p_n(x)$  is the  $n$ th order Legendre polynomial, and the coefficients are the respective order parameters. Since  $P_2(\cos \alpha)$  varies from 1 to  $-0.5$  as  $\alpha$  goes from  $0^\circ$  to  $90^\circ$ , and  $P_2(\cos \alpha)$  varies from +1 to  $-0.43$  as  $\alpha$  goes from  $0^\circ$  to  $50^\circ$ ; such a small difference in the order parameters between the B and E helices yields indistinguishable ME distributions.

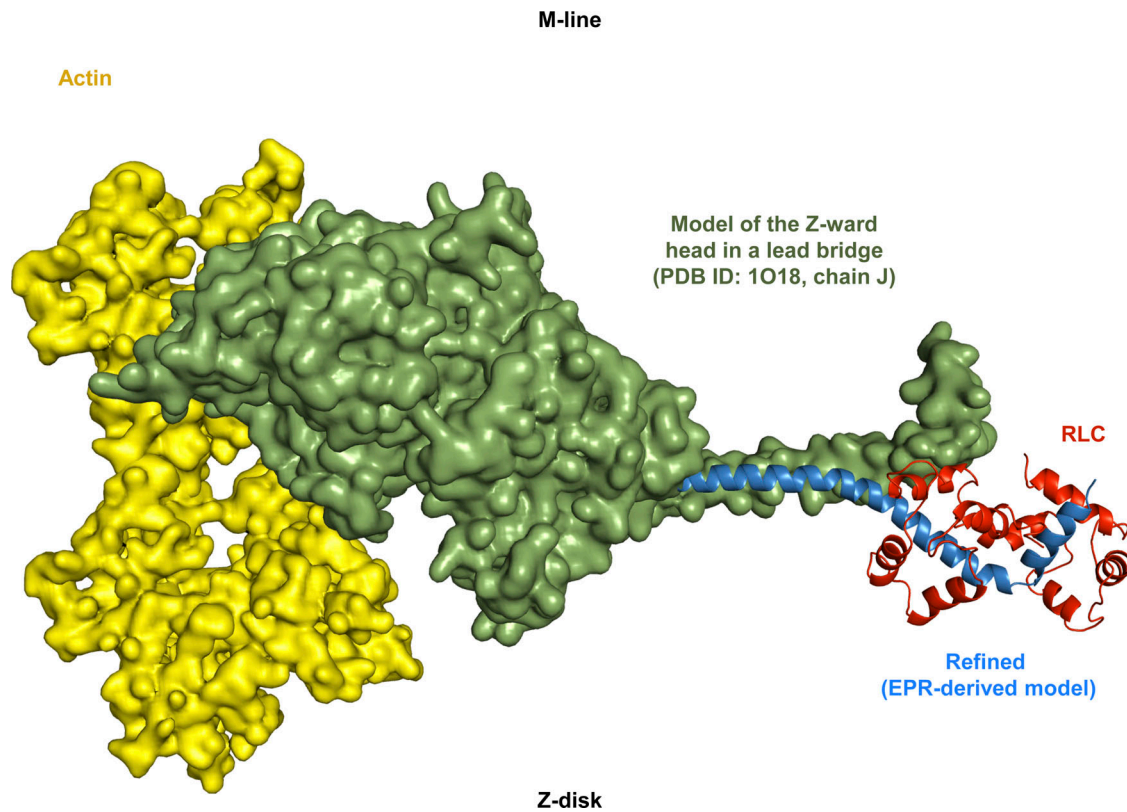


Figure S5. **Alignment of the EPR-derived model (blue lever arm helix, red RLC) with the Z-ward head (green) of the lead bridge in the 7-nm-resolution model derived from insect flight muscle tomography.** From PDB accession number 1O18, chain J (Chen et al., 2002). Actin is shown in yellow and RLC in red. The alignment was done via the lower 50-kD domain.

Table S1. **Fitting parameters of the oriented fiber experiments**

	$\theta_{NB}(\circ)$	$\sigma(\circ)$	Mole fraction
<b>B helix (53-57)</b>			
RLC-fiber rigor (first component)	$4 \pm 4$	$9 \pm 3$	$0.11 \pm 0.02$
RLC-fiber rigor (second component)	$22 \pm 15$	>38	$0.89 \pm 0.02$
RLC-fiber relaxation (single component)	$18 \pm 14$	>38	—
RLC-HMM-fiber rigor (single component)	$32 \pm 14$	>38	—
<b>E helix (103-107)</b>			
RLC-fiber rigor (first component)	$81 \pm 4$	$11 \pm 3$	$0.54 \pm 0.03$
RLC-fiber (second component)	$86 \pm 18$	>38	$0.46 \pm 0.03$
RLC-fiber relaxation (single component)	$51 \pm 15$	>38	—
RLC-HMM-fiber rigor (first component)	$81 \pm 4$	$11 \pm 3$	$0.25 \pm 0.03$
RLC-HMM-fiber rigor (second component)	$88 \pm 16$	>38	$0.75 \pm 0.03$

Errors are propagated from 95% confidence intervals imposed on the simulated fit error surface.

### EPR equations

The position of resonance in an EPR experiment at a given orientation  $\theta_{NB}$ ,  $\phi_{NB}$  of a spin label  $\pi$  orbital is given by

$$B_{res} = \frac{h\nu}{\mu_B g(\theta_{NB}, \phi_{NB})} - m_I A(\theta_{NB}, \phi_{NB}), \quad (S1)$$

where  $h$  is the Planck constant,  $\nu$  is the microwave frequency,  $\mu_B$  is the Bohr magneton,  $m_I$  is the  $N^{14}$  nuclear quantum number ( $-1, 0, 1$ ),  $g(\theta_{NB}, \phi_{NB})$ , and  $A(\theta_{NB}, \phi_{NB})$  are Zeeman and hyperfine tensors whose eigenvalues determine anisotropy of the system:

$$g^2(\theta_{NB}, \phi_{NB}) = g_x^2 \sin^2 \theta_{NB} \cos^2 \phi_{NB} + g_x^2 \sin^2 \theta_{NB} \sin^2 \phi_{NB} + g_z^2 \cos^2 \theta_{NB}, \quad (S2)$$

and

$$A^2(\theta_{NB}, \phi_{NB}) = A_x^2 \sin^2 \theta_{NB} \cos^2 \phi_{NB} + A_x^2 \sin^2 \theta_{NB} \sin^2 \phi_{NB} + A_z^2 \cos^2 \theta_{NB}. \quad (S3)$$

### ME equations

Once  $\langle P_2(\cos\alpha) \rangle$  and  $\langle P_4(\cos\alpha) \rangle$  are obtained in an experiment, there is a continuum of orientational distribution functions that yield  $\langle P_2(\cos\alpha) \rangle$  and  $\langle P_4(\cos\alpha) \rangle$ . The ME distribution function maximizes informational entropy and thus yields the broadest distribution that serves as a low-resolution approximation of the angular distribution of the probe. The ME distribution is defined as

$$f(a, \lambda_2, \lambda_4) = Z(\lambda_2, \lambda_4)^{-1} \exp[-\lambda_2 P_2(\cos\alpha) - \lambda_4 P_4(\cos\alpha)], \quad (S4)$$

where  $\lambda_2, \lambda_4$  are Lagrange multipliers and  $Z(\lambda_2, \lambda_4)$  is a normalization factor:

$$Z(\lambda_2, \lambda_4) = \int_0^\pi d\alpha \exp[-\lambda_2 P_2(\cos\alpha) - \lambda_4 P_4(\cos\alpha)] \sin \alpha. \quad (S5)$$

We determine  $\lambda_2, \lambda_4$  by

$$\langle P_2(\cos\alpha) \rangle = \int_0^\pi d\alpha P_2(\cos\alpha) f(a, \lambda_2, \lambda_4) \sin \alpha, \quad (S6)$$

and

$$\langle P_4(\cos\alpha) \rangle = \int_0^\pi d\alpha P_4(\cos\alpha) f(a, \lambda_2, \lambda_4) \sin \alpha. \quad (S7)$$

### References

- Chen, L.F., H. Winkler, M.K. Reedy, M.C. Reedy, and K.A. Taylor. 2002. Molecular modeling of averaged rigor crossbridges from tomograms of insect flight muscle. *J. Struct. Biol.* 138:92–104. [https://doi.org/10.1016/S1047-8477\(02\)00013-8](https://doi.org/10.1016/S1047-8477(02)00013-8)
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- Romano, D., B.D. Brandmeier, Y.B. Sun, D.R. Trentham, and M. Irving. 2012. Orientation of the N-terminal lobe of the myosin regulatory light chain in skeletal muscle fibers. *Biophys. J.* 102:1418–1426. <https://doi.org/10.1016/j.bpj.2012.02.010>