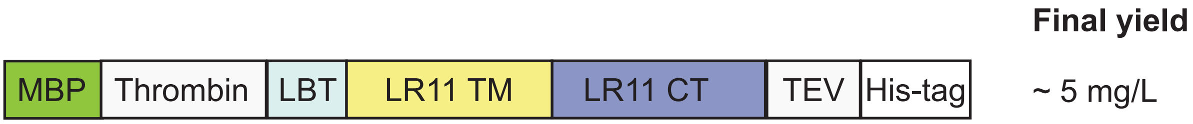


Figure S1: Expression construct and final yield of LR11 MTCT.
MBP: maltose binding protein. LBT: lanthanide binding tag. Both MBP and His-tag are removed for backbone assignment experiments.

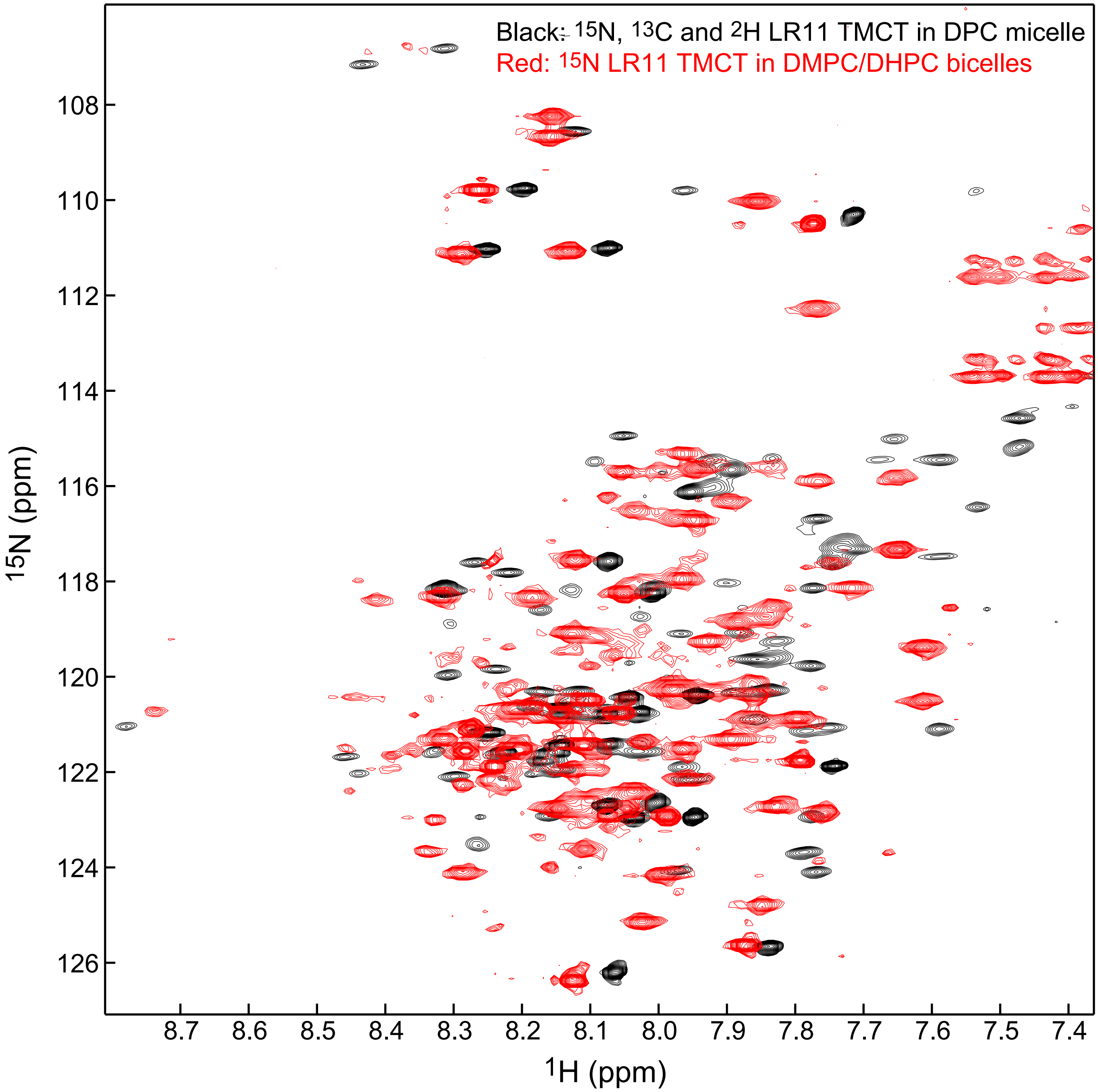


Figure S2a: Overlay of TROSY spectra of LR11 TMCT in DPC micelle and bicelles (q=0.3).

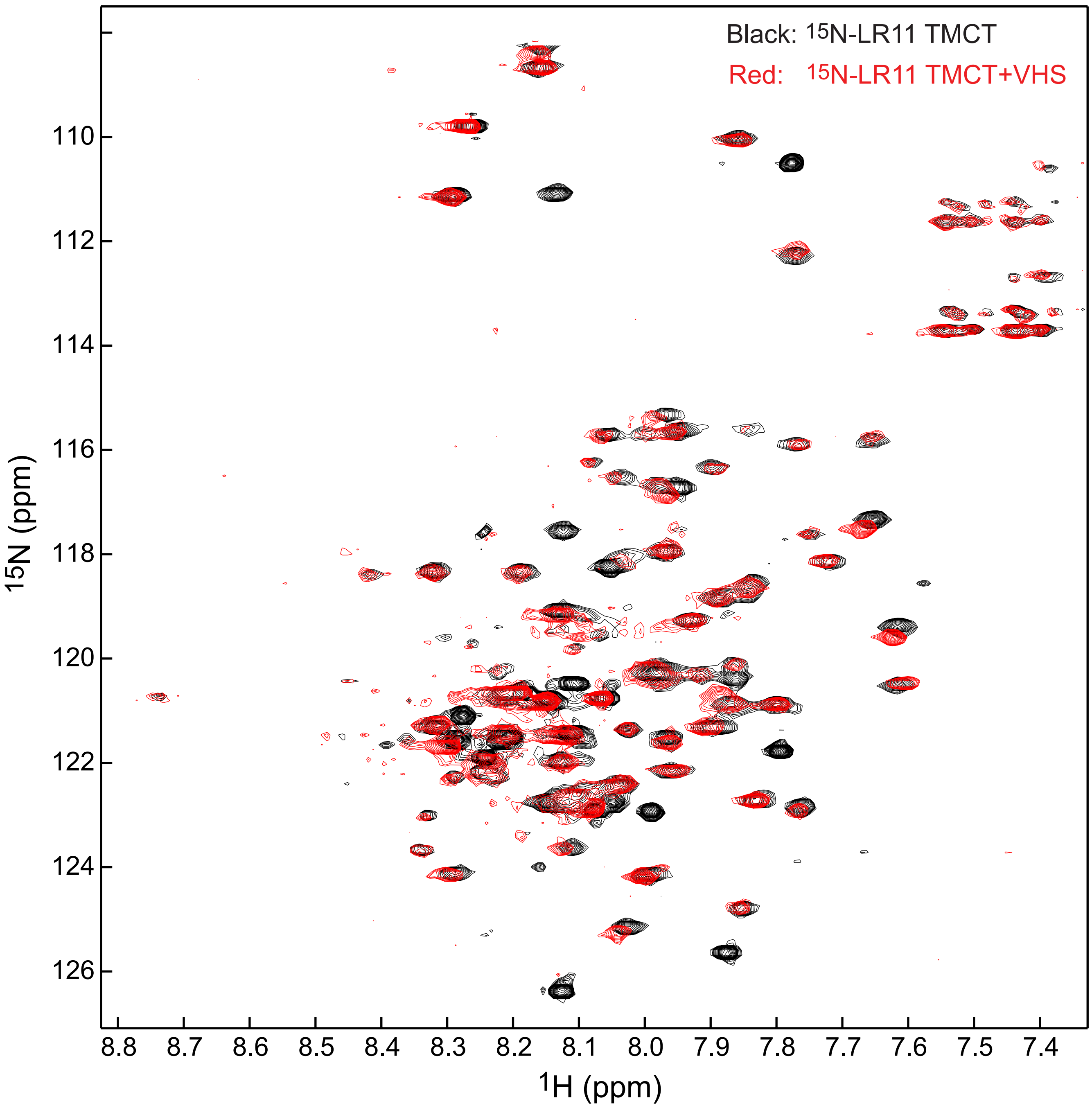
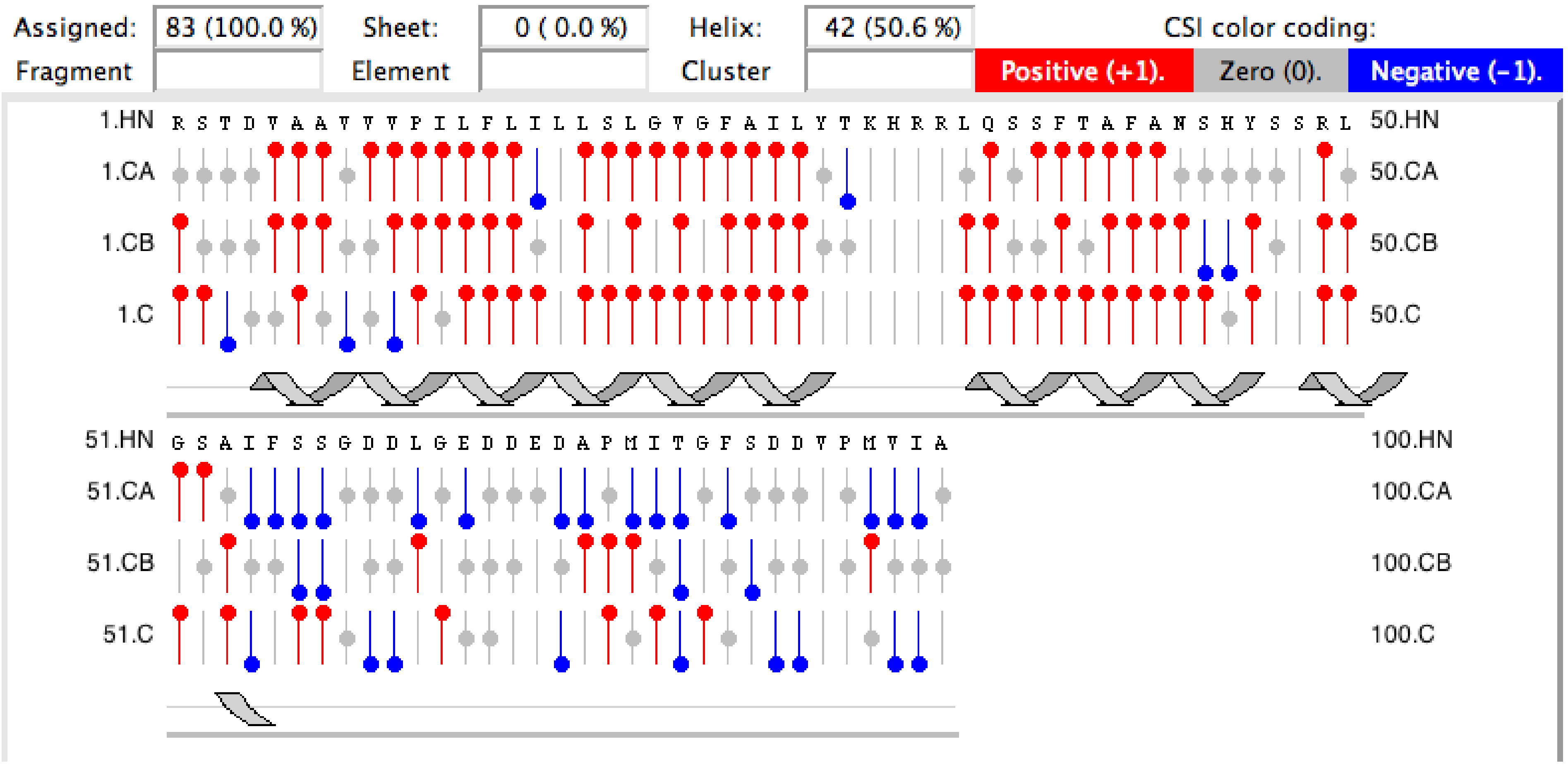


Figure S2b: TROSY spectra of ^{15}N-LR11 TMCT in 12% DMPC/DHPC (q=0.3) solution at 850 MHz spectrometer with and without the VHS domain of the GGA protein. GGA is an adpator protein involved in LR11 intracellular trafficking (Jacobsen et al. 2002, FEBS Lett. 511: 155-158).



Assigned: 83 (100.0 %)

Sheet: 0 (0.0 %)

Helix: 42 (50.6 %)

Fragment

Element

Cluster

CSI color coding:

Positive (+1). Zero (0). Negative (-1).

Figure S3: Chemical shift index (CSI) analysis of C’, C_{α}, and C_{β} chemical shifts of LR11 TMCT.

Table S1: Predicted backbone torsion angles of LR11 TMCT using assigned chemical shifts of N, C^{α}, C^{β}, and C' in DPC solution by the TALOS+ program.

```
VARS   RESID RESNAME PHI PSI DPHI DPSI DIST S2 COUNT CS_COUNT CLASS
FORMAT %4d %s %8.3f %8.3f %8.3f %8.3f %8.3f %5.3f %2d %2d %s

   1 R 9999.000 9999.000    0.000    0.000    0.000 0.000  0  8 None
   2 S -121.639  139.493   33.967   35.223   28.279 0.632 10 12 Warn
   3 T  -62.871  -43.087    6.802    7.823   30.904 0.717 10 12 Good
   4 D  -64.655  -40.324    4.724    6.939   24.992 0.812 10 12 Good
   5 V  -61.251  -46.812    7.637    5.987   22.102 0.855 10 12 Good
   6 A  -61.796  -33.611    5.020   12.671   22.364 0.864 10 12 Good
   7 A  -61.642  -29.575    7.857    7.901   24.540 0.866 10 12 Good
   8 V  -87.788  -29.510   22.135   19.183   33.695 0.879 10 12 Good
   9 V  -62.343  -44.490   11.627    8.641   38.241 0.899 10 12 Good
  10 V  -57.283  -49.013    9.122    6.502   67.345 0.910 10 11 Good
  11 P  -58.765  -32.217    3.726    7.351   50.077 0.906 10 11 Good
  12 I  -69.461  -35.619    8.229   10.015   40.895 0.900 10 11 Good
  13 L  -65.211  -39.149    8.314    9.304   21.082 0.895 10 12 Good
  14 F  -61.870  -45.733    4.441    7.094   19.693 0.884 10 12 Good
  15 L  -60.857  -45.270    5.661    5.810   22.277 0.861 10 12 Good
  16 I  -70.985  -36.867    8.025    8.858   67.231 0.846 10  8 Good
  17 L  -67.543  -26.787   10.026   25.214   86.538 0.835 10  7 Good
  18 L  -63.943  -41.482    4.025    2.855   66.985 0.845 10  6 Good
  19 S  -66.878  -41.258   10.673    3.739   37.931 0.845 10 10 Good
  20 L  -65.636  -42.763    5.571    8.732   33.385 0.851 10 10 Good
  21 G  -61.207  -42.609    3.807    7.687   27.950 0.857 10 11 Good
  22 V  -61.722  -44.934    3.373    4.369   35.367 0.872 10 10 Good
  23 G  -61.071  -41.834    3.050    4.721   28.544 0.884 10 11 Good
  24 F  -65.144  -42.513    6.289    6.900   26.628 0.894 10 11 Good
  25 A  -66.155  -37.884    6.226    9.134   18.457 0.899 10 12 Good
  26 I  -65.680  -45.207    4.161    4.367   17.515 0.883 10 12 Good
  27 L  -61.354  -41.426    5.531    4.737   28.801 0.838 10 11 Good
  28 Y  -72.841  -26.140   15.305   16.634   41.201 0.698 10 10 Good
  29 T  -89.553  -15.215   17.482   27.637   92.748 0.639  7  6 Warn
  30 K 9999.000 9999.000    0.000    0.000    0.000 0.000  0  3 None
  31 H 9999.000 9999.000    0.000    0.000    0.000 0.000  0  0 None
  32 R 9999.000 9999.000    0.000    0.000    0.000 0.000  0  0 None
  33 R 9999.000 9999.000    0.000    0.000    0.000 0.000  0  3 None
  34 L  -62.534  -35.943    7.882   32.900   73.943 0.688 10  7 Good
  35 Q  -59.975  -39.614    6.851    9.972   30.001 0.718 10 11 Good
  36 S  -63.672  -40.202    3.596   12.471   19.691 0.771 10 12 Good
  37 S  -62.907  -38.521    4.034    3.492   20.904 0.806 10 12 Good
  38 F  -69.639  -38.929   17.504   12.123   20.822 0.829 10 12 Good
  39 T  -60.064  -42.002    7.139    7.022   20.258 0.851 10 12 Good
  40 A  -62.700  -36.883    7.571    8.460   19.124 0.843 10 12 Good
  41 F  -64.563  -43.446    6.273    8.305   19.127 0.817 10 12 Good
  42 A  -62.453  -34.613    9.455   12.504   19.049 0.764 10 12 Good
  43 N  -75.730  -25.581   16.967   20.147   22.719 0.728 10 12 Good
  44 S  -83.836  -34.523   10.146   13.983   65.628 0.721 10 11 Good
  45 H  -92.044  -27.790   25.009   17.127   47.608 0.740 10 11 Good
  46 Y  -70.330  -36.699   13.439    9.888   54.348 0.732 10 10 Good
  47 S  -73.001  -31.767   15.827   18.376   87.013 0.721 10  7 Good
  48 S  -70.143  -25.742   19.504   31.201  104.312 0.714 10  6 Good
  49 R  -61.775  -35.833    4.687   15.268   62.120 0.767 10  7 Good
  50 L  -67.063  -31.975    6.823   10.519   37.315 0.771 10 10 Good
  51 G  -62.584  -35.149    4.420   11.724   36.612 0.773 10 10 Good
  52 S  -69.030  -34.777   13.063   14.937   35.184 0.762 10 10 Good
  53 A  -71.538  -28.640   11.507   28.946   27.569 0.741 10 11 Good
  54 I  -74.103  -33.141   13.813   15.352   31.860 0.720 10 11 Good
  55 F  -98.173   -1.787   10.043   16.892   39.053 0.662 10 11 Good
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56 S  -93.955  146.863   32.841   21.060   41.436 0.562 10 11 Dyn
57 S  -80.507  148.522   25.833   12.794   39.926 0.529  6 11 Dyn
58 G   91.010   10.075   12.630   19.314   61.793 0.552 10 11 Dyn
59 D  -81.895  137.175   72.752   45.467   33.178 0.632 10 11 Warn
60 D -105.959    0.219   20.639   24.921   28.413 0.606 10 11 Good
61 L  -67.388  142.950   56.215   14.443   46.108 0.424 10 10 Dyn
62 G   93.838   -9.700   14.437   14.862   88.198 0.414 10 10 Dyn
63 E  -79.267  139.997   70.627   44.274   38.697 0.465 10 11 Dyn
64 D  -76.847  123.252   64.434   58.034   28.486 0.701  6 11 Warn
65 D  -71.259  -29.926   26.661   24.688   67.886 0.753 10  8 Good
66 E  -76.636  -27.406   24.708   18.322   54.158 0.711 10  8 Warn
67 D  -86.525  132.142   67.493   20.159   52.673 0.677  8  8 Warn
68 A  -70.528  141.416    9.302   15.537   63.573 0.583 10 10 Dyn
69 P  -70.459  153.003    6.169    9.884   50.103 0.551 10 10 Dyn
70 M  -93.912  131.479   26.945   19.440   43.898 0.512 10 11 Dyn
71 I -101.764  127.454   33.603   22.180   27.779 0.532 10 12 Dyn
72 T  -83.769  148.417   22.764   17.038   38.785 0.480 10 11 Dyn
73 G   89.094    3.693   12.954   18.528   46.261 0.418 10 11 Dyn
74 F  -90.202  137.023   59.668   31.840   35.936 0.417 10 10 Dyn
75 S  -93.121  119.664   30.316   26.261   30.703 0.495 10 11 Dyn
76 D  -94.069  -18.472   19.892   27.721   37.420 0.650 10 11 Good
77 D  -77.542  127.140   61.253   28.349   68.177 0.728  9  8 Warn
78 V -104.922  124.099   20.498   16.264   92.039 0.718 10  6 Good
79 P  -67.030  147.798    8.753    8.428   78.397 0.544 10  6 Dyn
80 M  -97.325  128.190   26.817   16.250   47.823 0.489 10 10 Dyn
81 V  -91.466  137.863   24.075   15.079   23.275 0.388 10 12 Dyn
82 I  -93.938  121.604   23.608   10.351   32.727 0.341 10 11 Dyn
83 A 9999.000 9999.000    0.000    0.000    0.000 0.000  0  7 None
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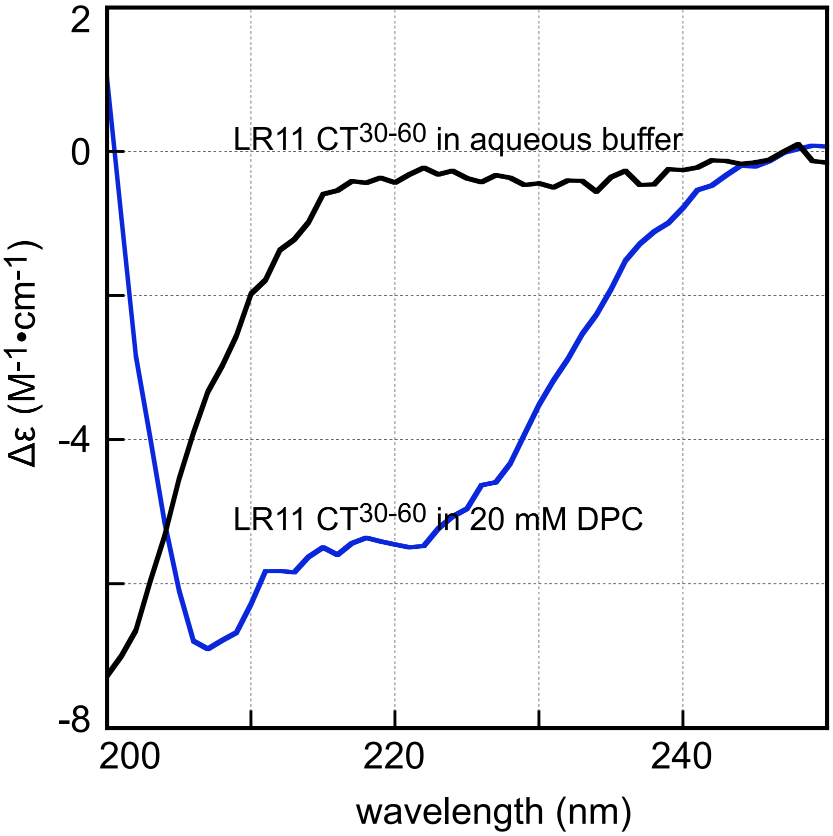

Figure S4: CD spectra of LR11 CT^{30-60} peptide in aqueous solution and DPC micelles.