# Carbohydrate recognition by the antiviral lectin cyanovirin-N.

***Yukiji K. Fujimoto and David F. Green***

## Supplementary Material

## Energetic contributions of every residue in CVN for all systems studied

For the last 150 ns, we calculated the energetic contributions (electrostatic, van der Waals, and surface-area dependent) of every residue in CVN for all systems studied (Figure S1–S3). Each protein residue was partitioned into three groups — backbone carbonyl, backbone amino and side chain — and the sugars were partitioned into one group per hydroxyl. By separating the contributions of various chemical groups, it can provide us with more information as to where the energetic contributions are exactly coming from. In all three figures, we see only a handful of residues contribute to the binding free energy, while the rest are away from the binding interface. In almost all of the cases, each residue for all systems had similar energetic contributions within each category. However, the largest difference we see again comes from Arg 76.

## Time series of computed binding free energies for all simulations

To assess each simulation for every system a complete time series of the calculated binding free energies was plotted along with an analysis both of the overall distribution of energies and of any dependencies within the time series (Figure S4–S27). The analysis is shown both for the full 200 ns simulation and for the last 150 ns; for each system, six plots are given: (1) The energetic time series, with individual snapshot energies in black, and a moving-window average shown in red; (2) A histogram of the computed energies, along with a non-parametric estimate of the distribution function in blue, and a normal

distribution with the same mean and variance in red; (3) A quantile–quantile (Q–Q) plot comparing the observed distribution to an ideal normal distribution; and (4) Three autocorrelation functions, computed by sampling every 100 ps, 1 ns or 10 ns.

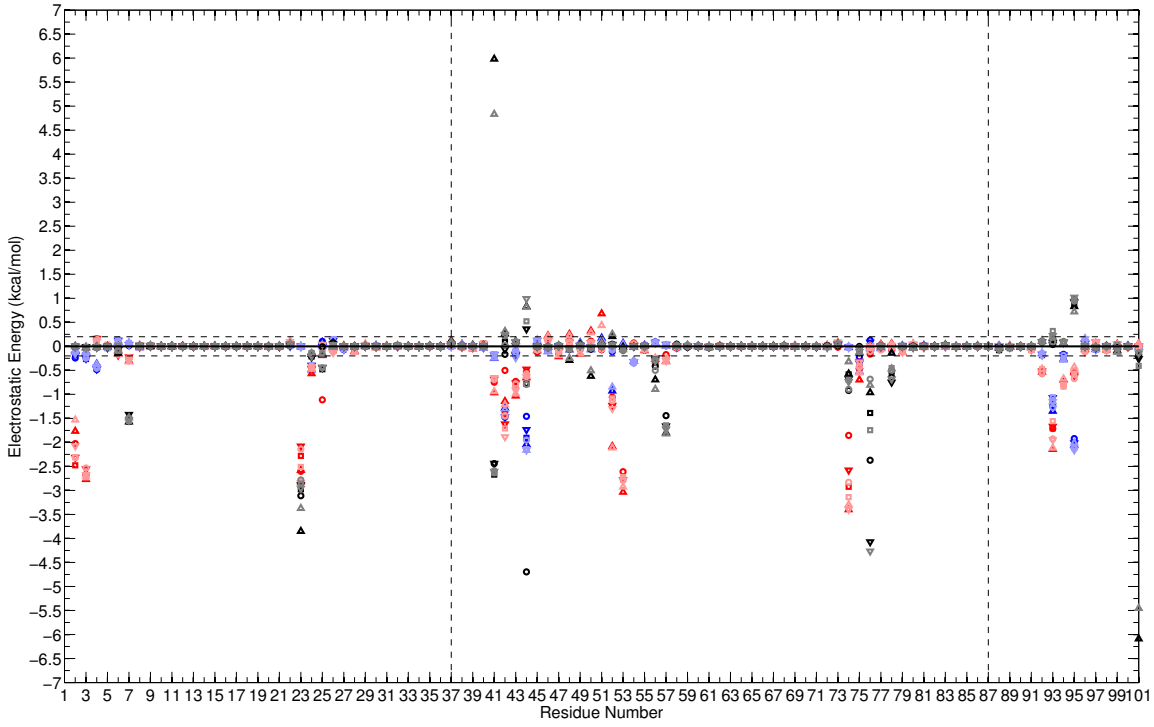



**Figure S1. Electrostatic contributions to binding free energy, by group.** Symbols are defined as follows: △, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,2)-$\alpha$-Man (internal orientation); ▽, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,2)-$\alpha$-Man (terminal orientation); □, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,3)-$\alpha$-Man; and ◯, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,6)-$\alpha$-Man. Blue symbols represent backbone amino groups, red symbols denote backbone carbonyl groups, and black symbols are used for protein side chains. Data from singly-bound simultions is shown in a lighter shade, and that from doubly-bound simulations in darker symbols. The vertical dashed lines mark the boundary between domains A and B. The horizontal dashed lines mark an estimate of the uncertainty in these data; values between the lines may be considered insignificantly different from zero.

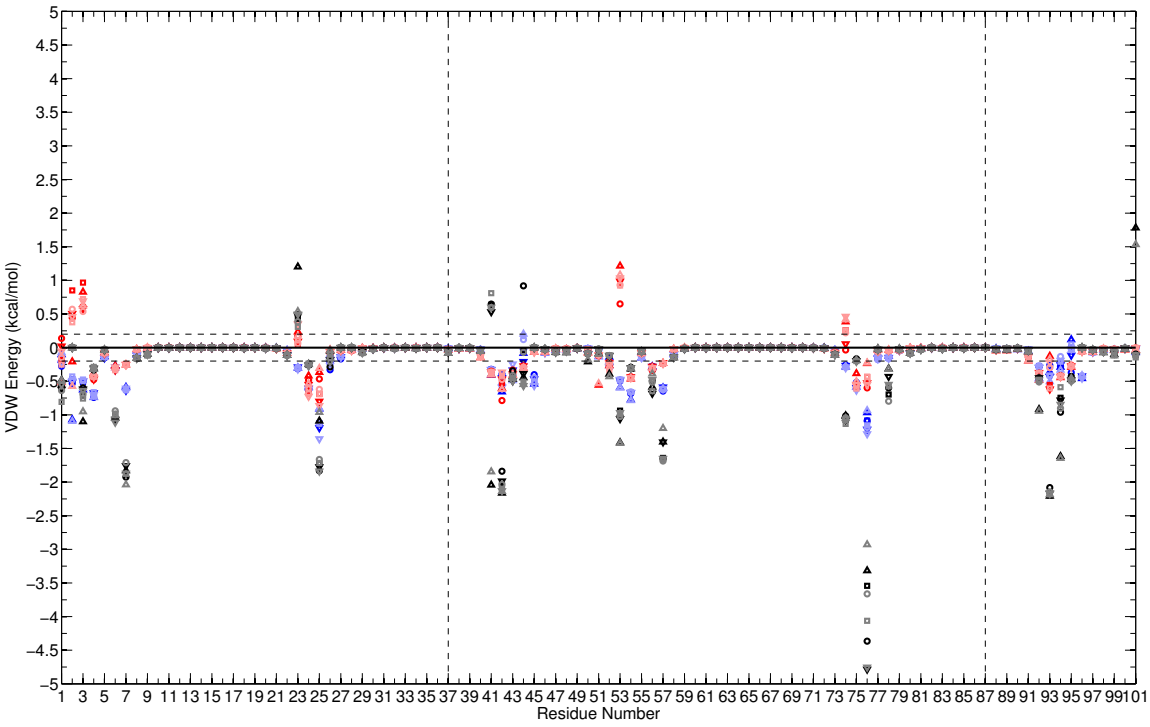



**Figure S2. Van der Waals contributions to binding free energy, by group.** Symbols are defined as follows: △, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,2)-$\alpha$-Man (internal orientation); ▽, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,2)-$\alpha$-Man (terminal orientation); □, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,3)-$\alpha$-Man; and ◯, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,6)-$\alpha$-Man. Blue symbols represent backbone amino groups, red symbols denote backbone carbonyl groups, and black symbols are used for protein side chains. Data from singly-bound simultions is shown in a lighter shade, and that from doubly-bound simulations in darker symbols. The vertical dashed lines mark the boundary between domains A and B. The horizontal dashed lines mark an estimate of the uncertainty in these data; values between the lines may be considered insignificantly different from zero.

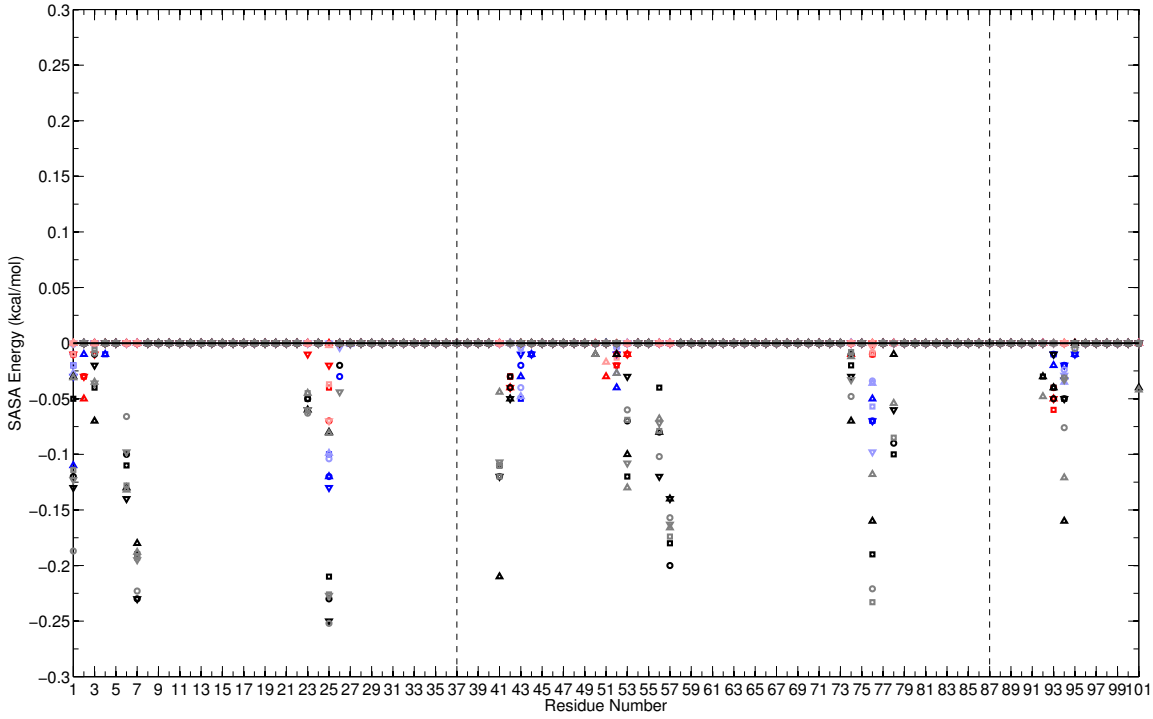



**Figure S3. Surface-area-dependent contributions to binding free energy, by group.** Symbols are defined as follows: △, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,2)-$\alpha$-Man (internal orientation); ▽, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,2)-$\alpha$-Man (terminal orientation); □, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,3)-$\alpha$-Man; and ◯, $\alpha$-Man-(1,2)-$\alpha$-Man-(1,6)-$\alpha$-Man. Blue symbols represent backbone amino groups, red symbols denote backbone carbonyl groups, and black symbols are used for protein side chains. Data from singly-bound simultions is shown in a lighter shade, and that from doubly-bound simulations in darker symbols. The vertical dashed lines mark the boundary between domains A and B. The horizontal dashed lines mark an estimate of the uncertainty in these data; values between the lines may be considered insignificantly different from zero.

**Figure S4.**

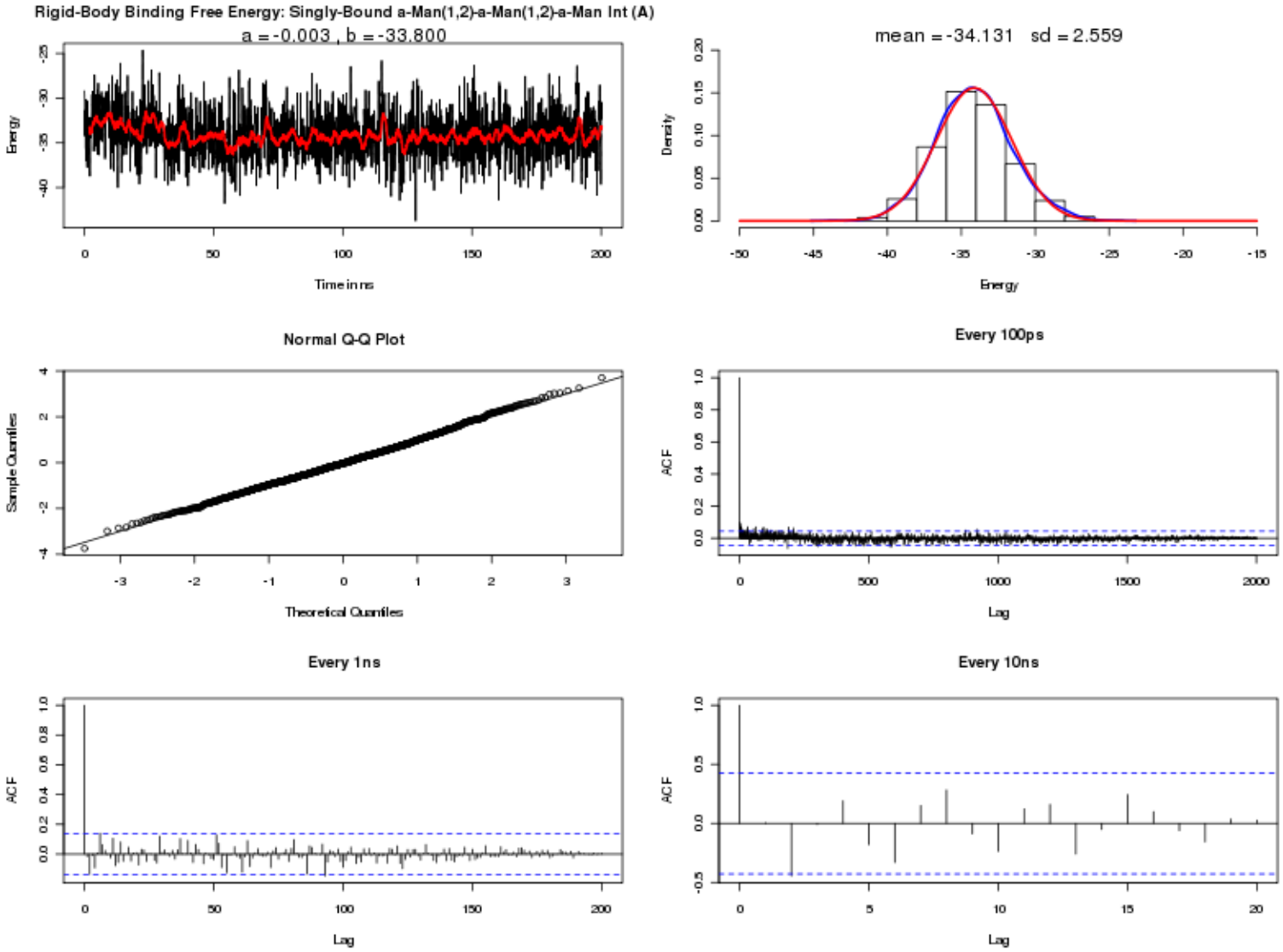

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,2)-a-Man Int (A)
a = -0.003 , b = -33.800
Energy
Time in ns
mean = -34.131 sd = 2.559
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S5.**

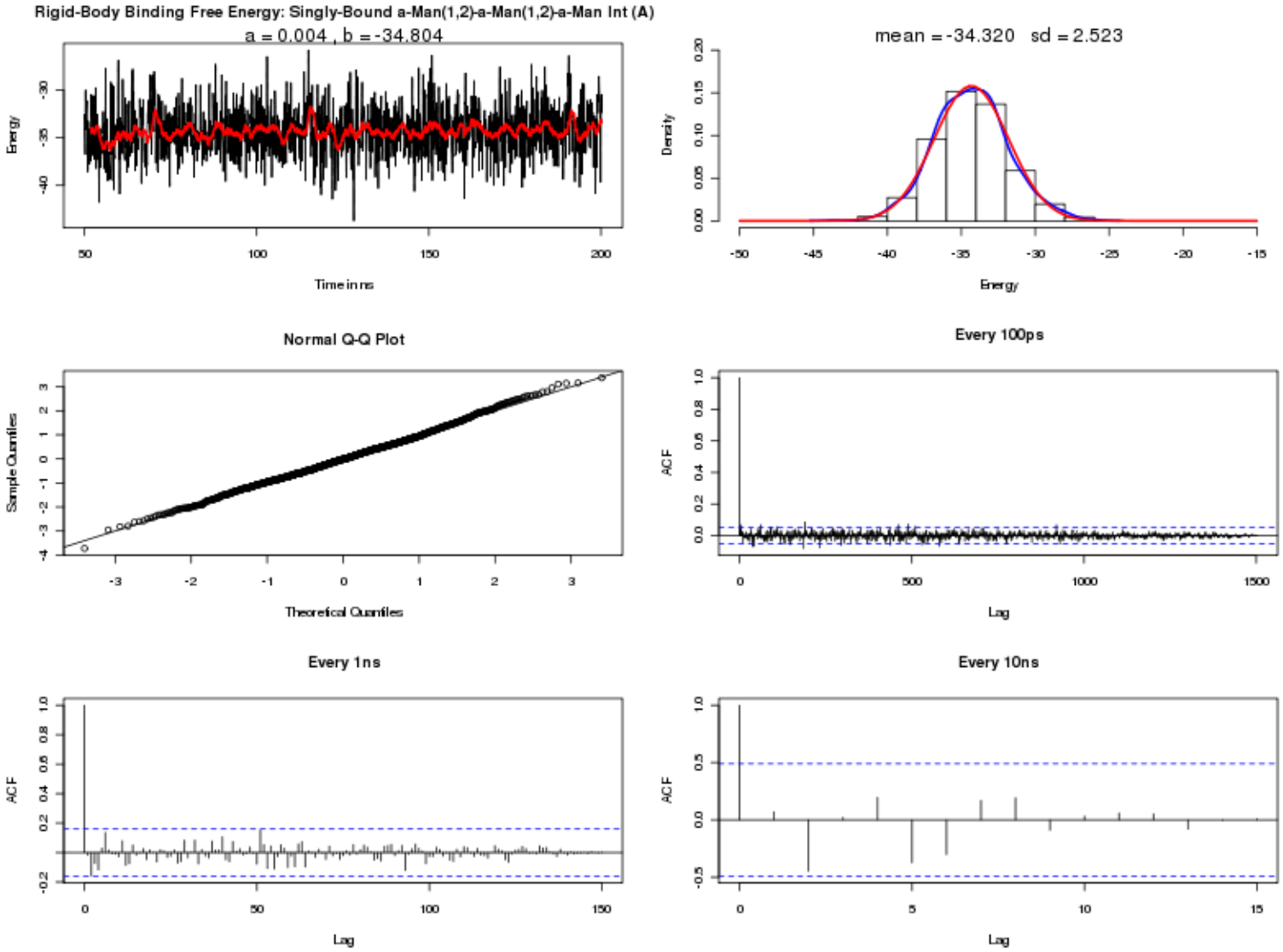

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,2)-a-Man Int (A)
a = 0.004 , b = -34.804
Energy
Time in ns
mean = -34.320 sd = 2.523
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S6.**

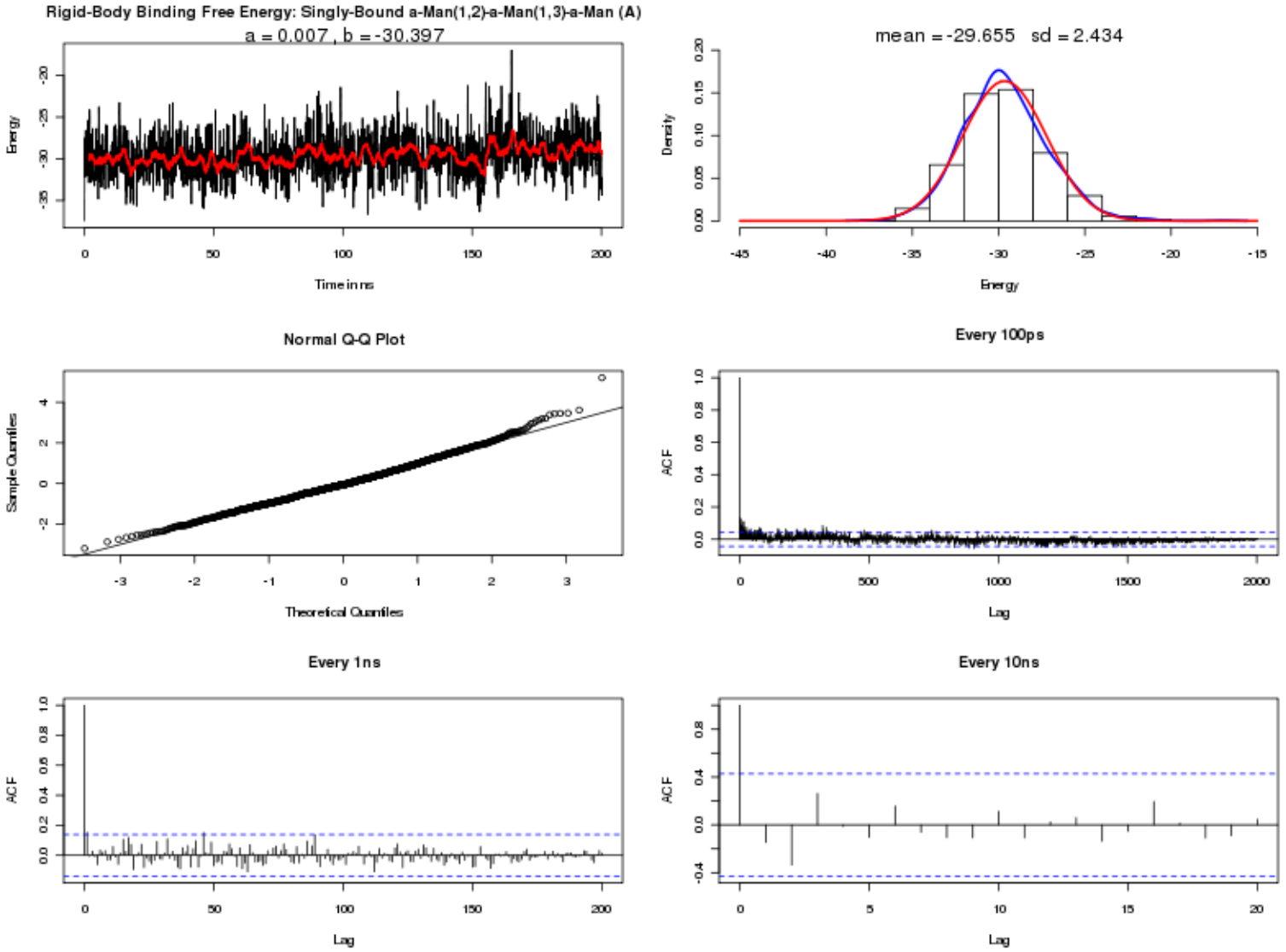

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,3)-a-Man (A)
a = 0.007 , b = -30.397
Energy
Time in ns
mean = -29.655 sd = 2.434
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S7.**

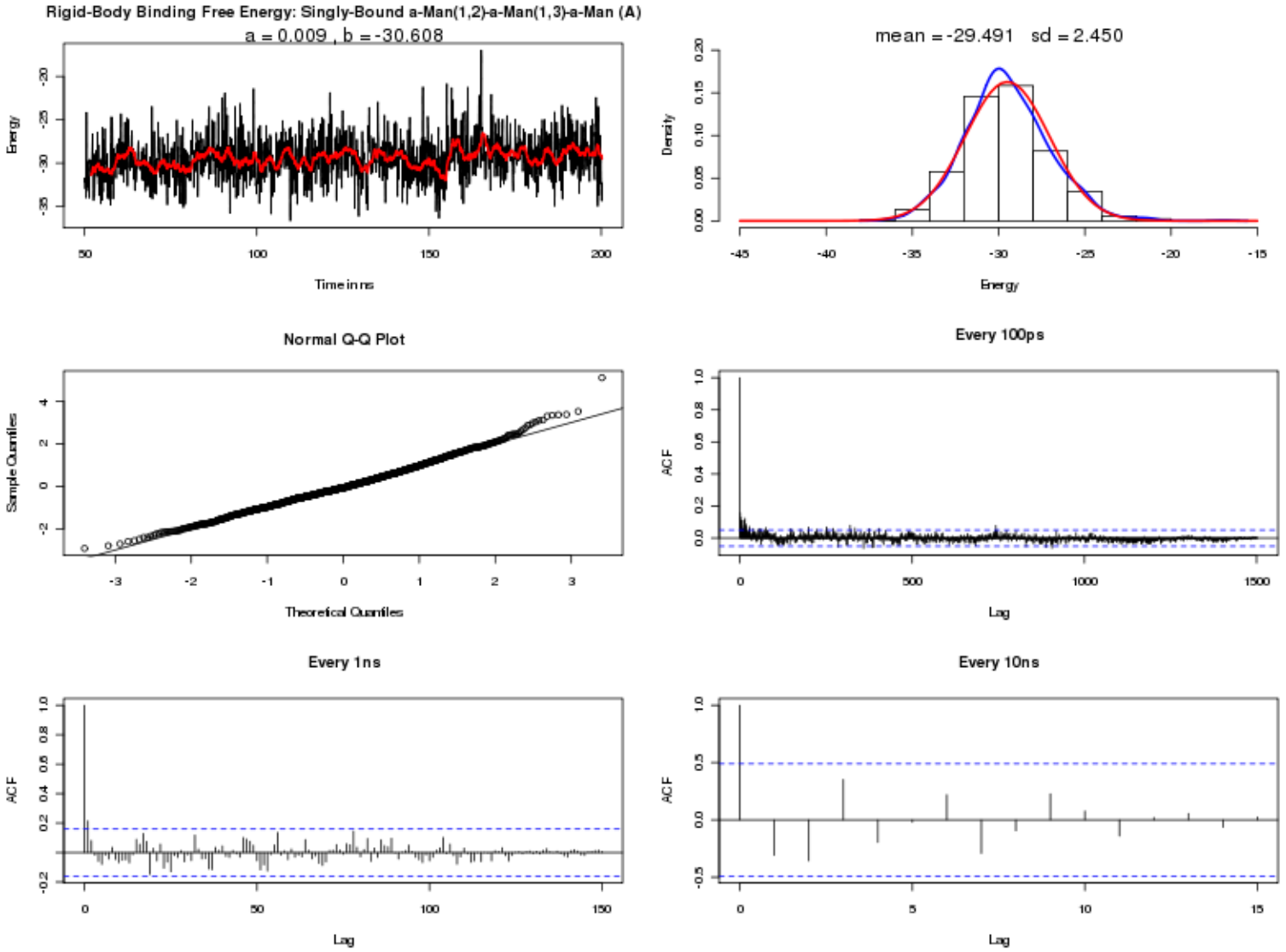

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,3)-a-Man (A)
a = 0.009 , b = -30.608
Energy
Time in ns
mean = -29.491 sd = 2.450
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S8.**

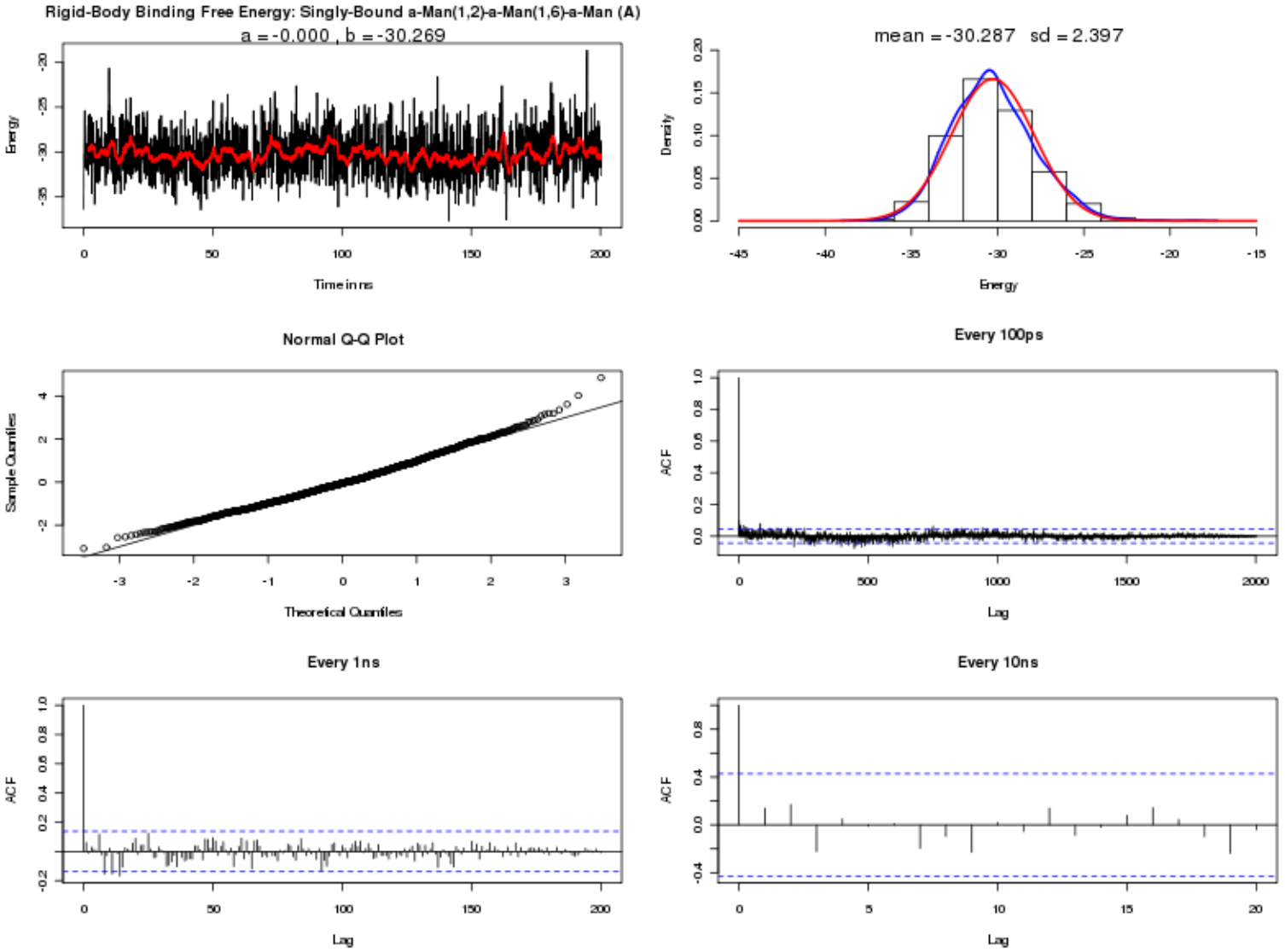

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,6)-a-Man (A)
a = -0.000 , b = -30.269
Energy
Time in ns
mean = -30.287 sd = 2.397
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S9.**

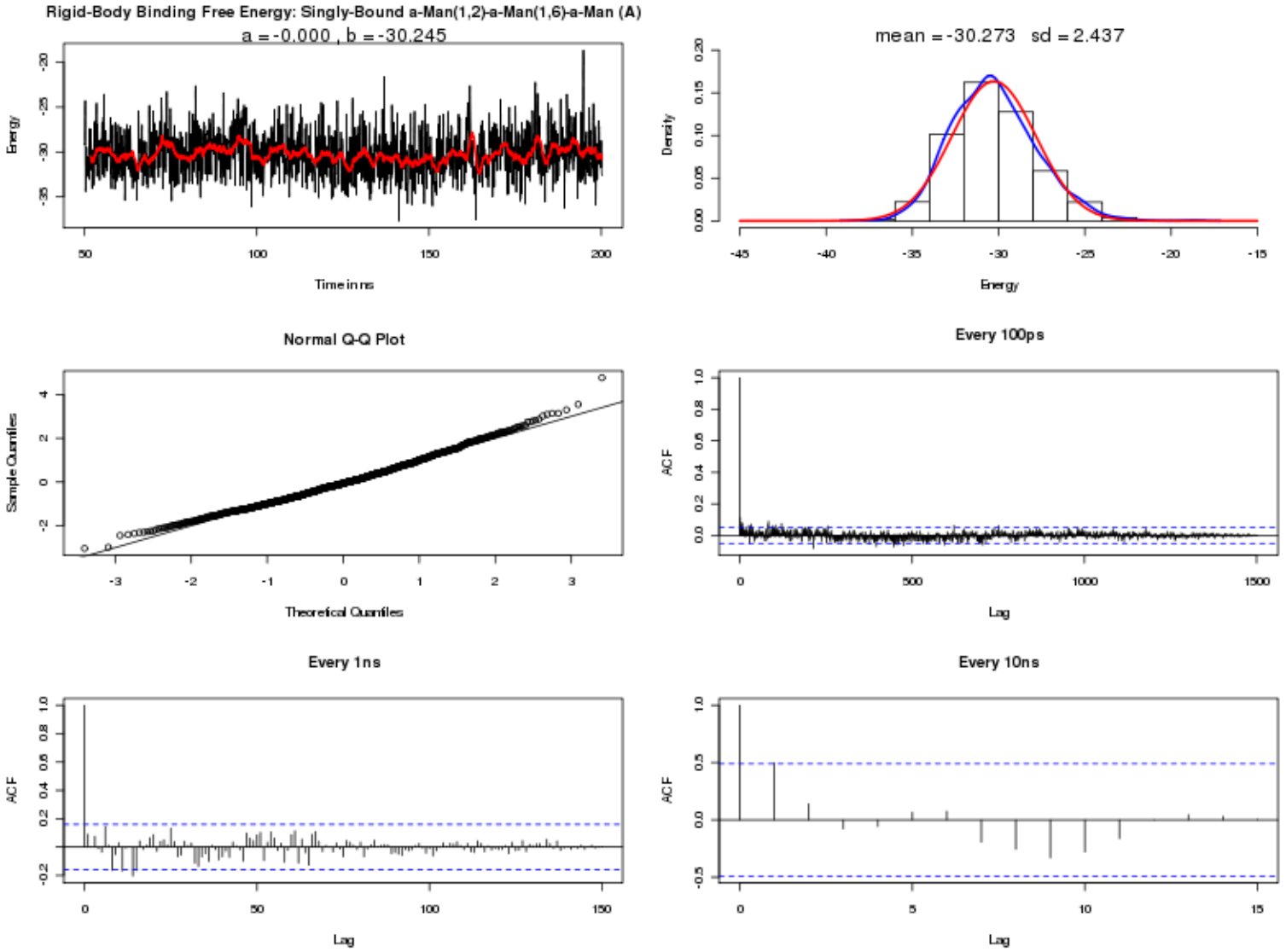

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,6)-a-Man (A)
a = -0.000 , b = -30.245
Energy
Time in ns
mean = -30.273 sd = 2.437
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S10.**

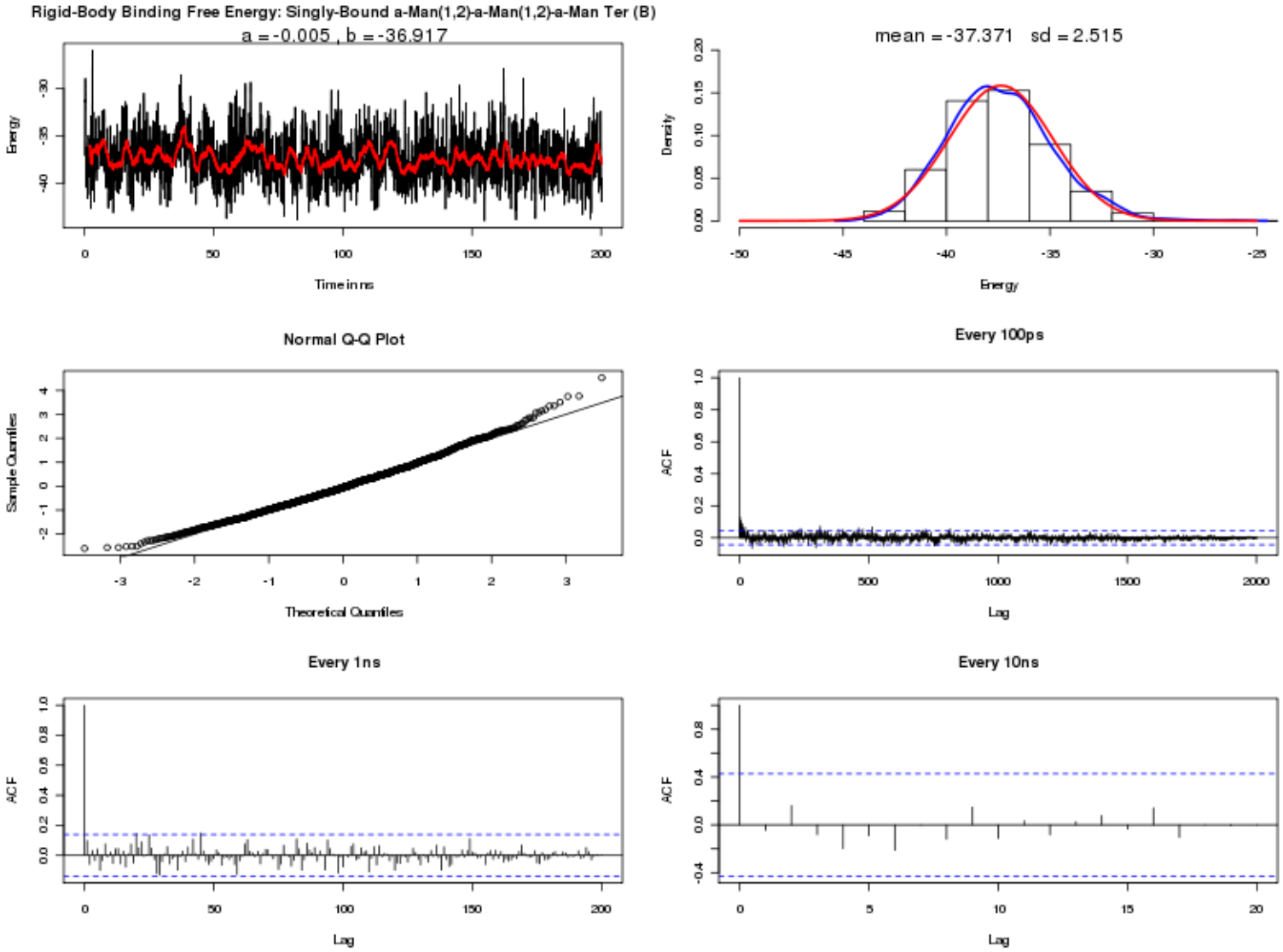

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,2)-a-Man Ter (B)
a = -0.005 , b = -36.917
Energy
Time in ns
mean = -37.371 sd = 2.515
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S11.**

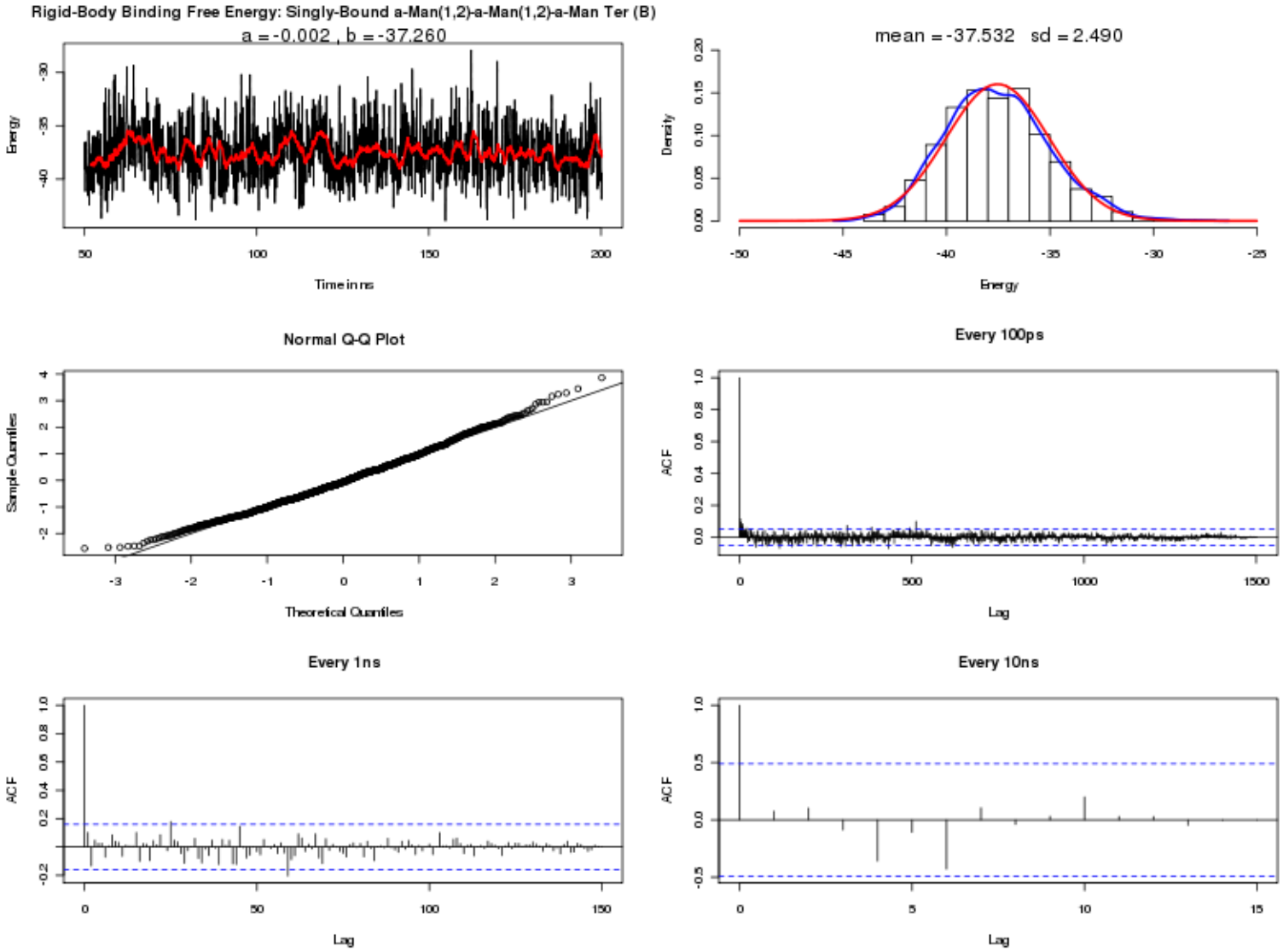

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,2)-a-Man Ter (B)
a = -0.002 , b = -37.260
Energy
Time in ns
mean = -37.532 sd = 2.490
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S12.**

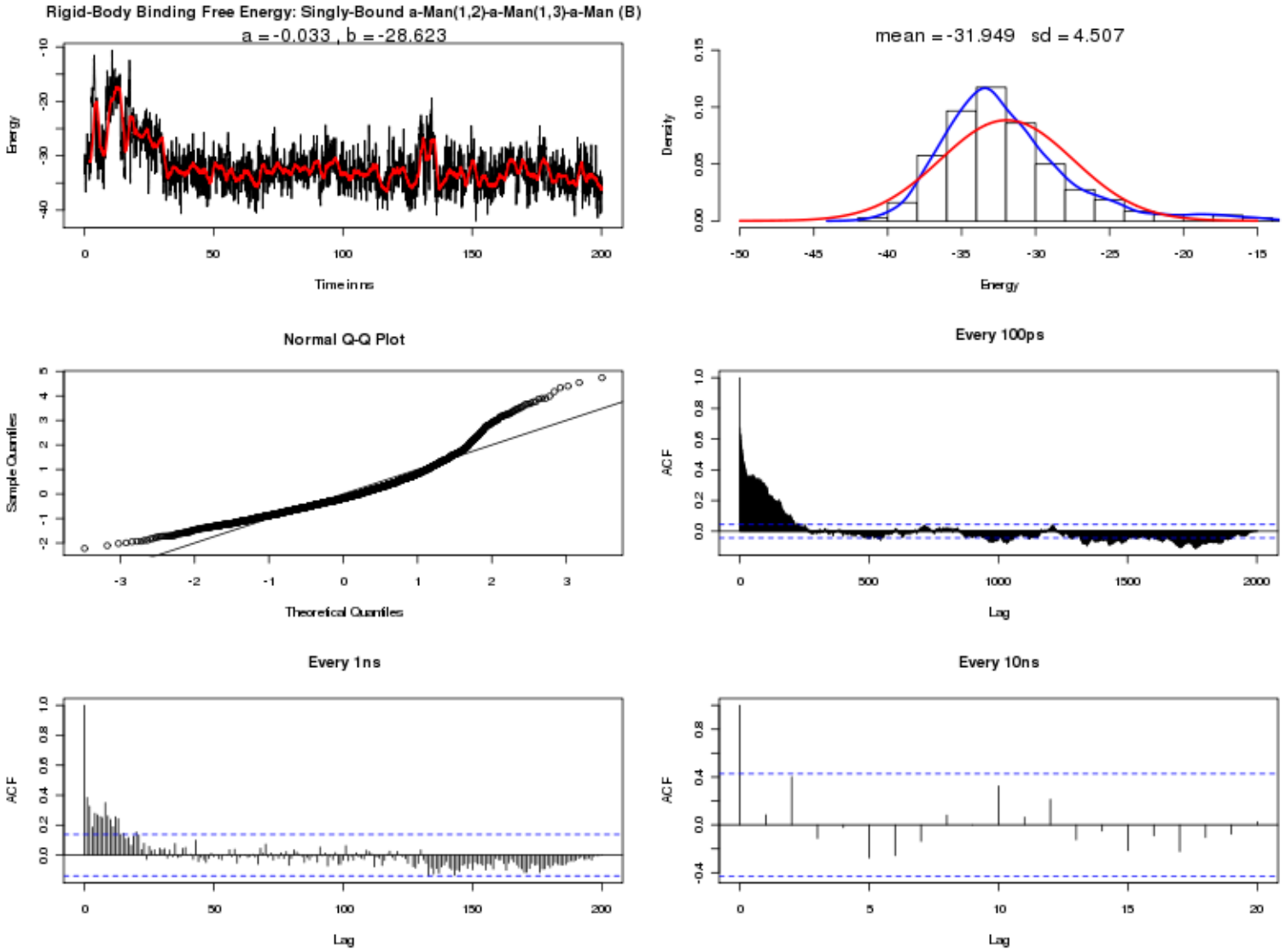

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,3)-a-Man (B)
a = -0.033 , b = -28.623
Energy
Time in ns
mean = -31.949 sd = 4.507
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S13.**

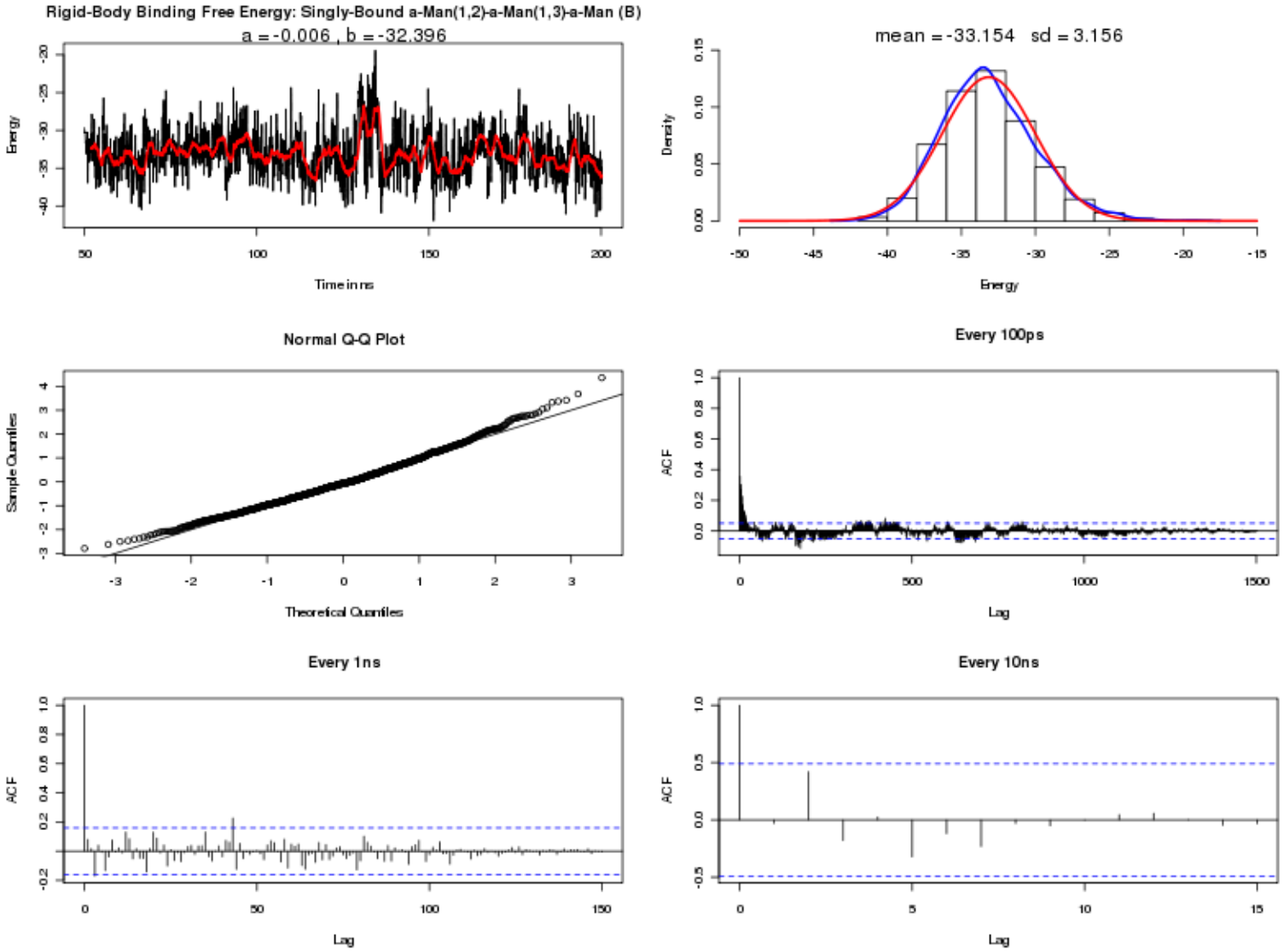

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,3)-a-Man (B)
a = -0.006 , b = -32.396
Energy
Time in ns
mean = -33.154 sd = 3.156
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S14.**

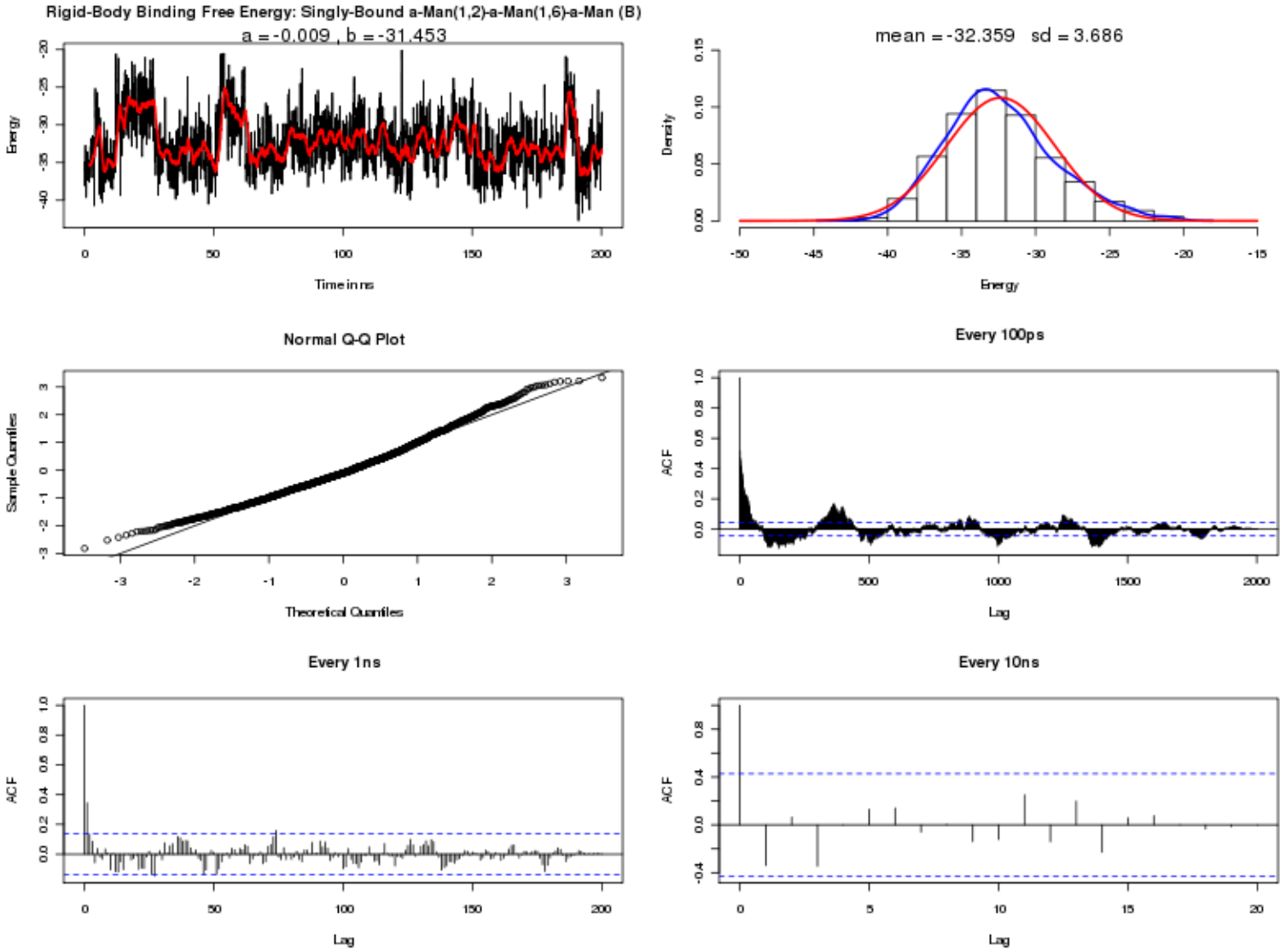

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,6)-a-Man (B)
a = -0.009 , b = -31.453
Energy
Time in ns
mean = -32.359 sd = 3.686
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S15.**

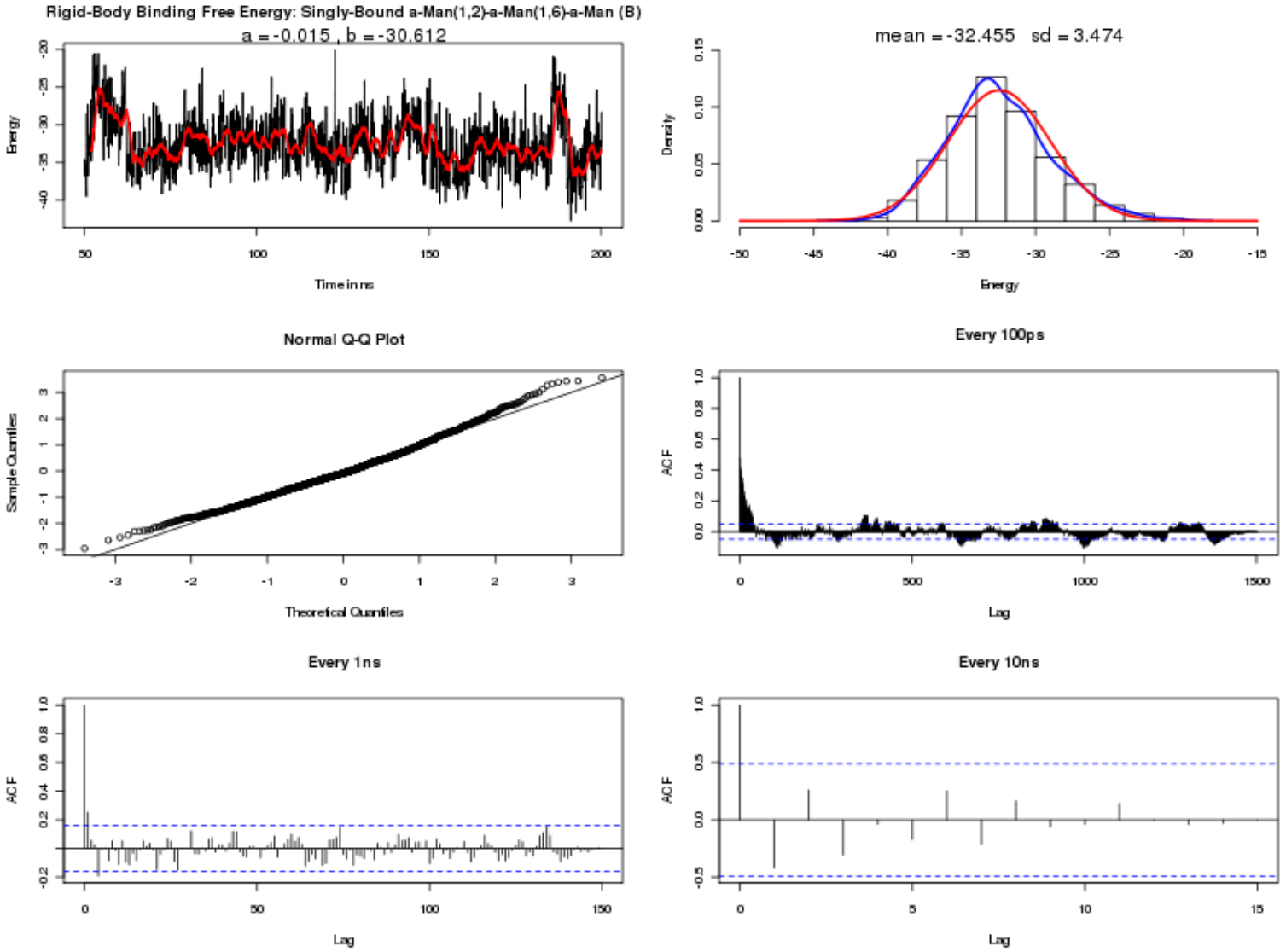

Rigid-Body Binding Free Energy: Singly-Bound a-Man(1,2)-a-Man(1,6)-a-Man (B)
a = -0.015 , b = -30.612
Energy
Time in ns
mean = -32.455 sd = 3.474
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S16.**

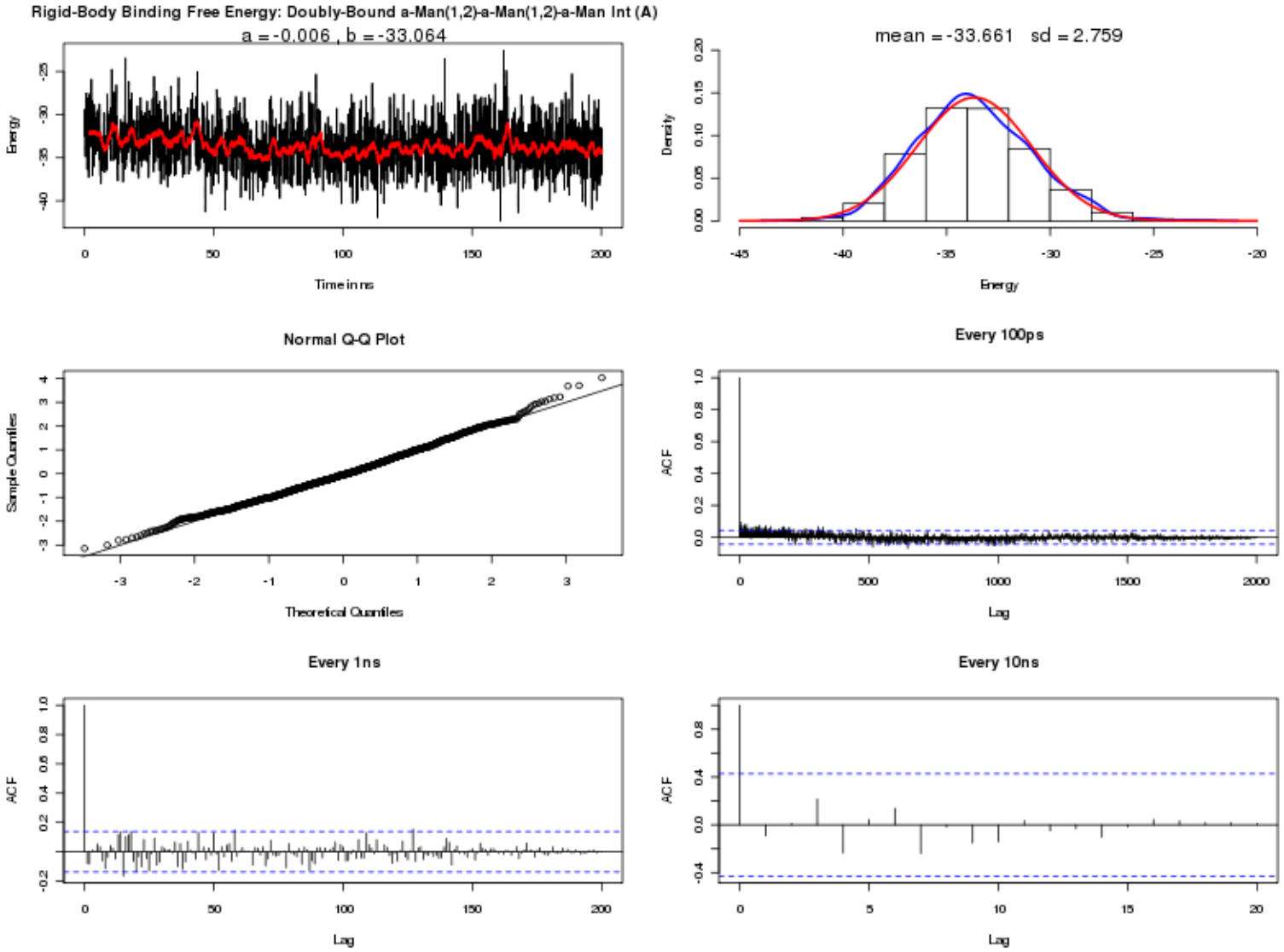

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,2)-a-Man Int (A)
a = -0.006 , b = -33.064
Energy
Time in ns
mean = -33.661 sd = 2.759
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S17.**

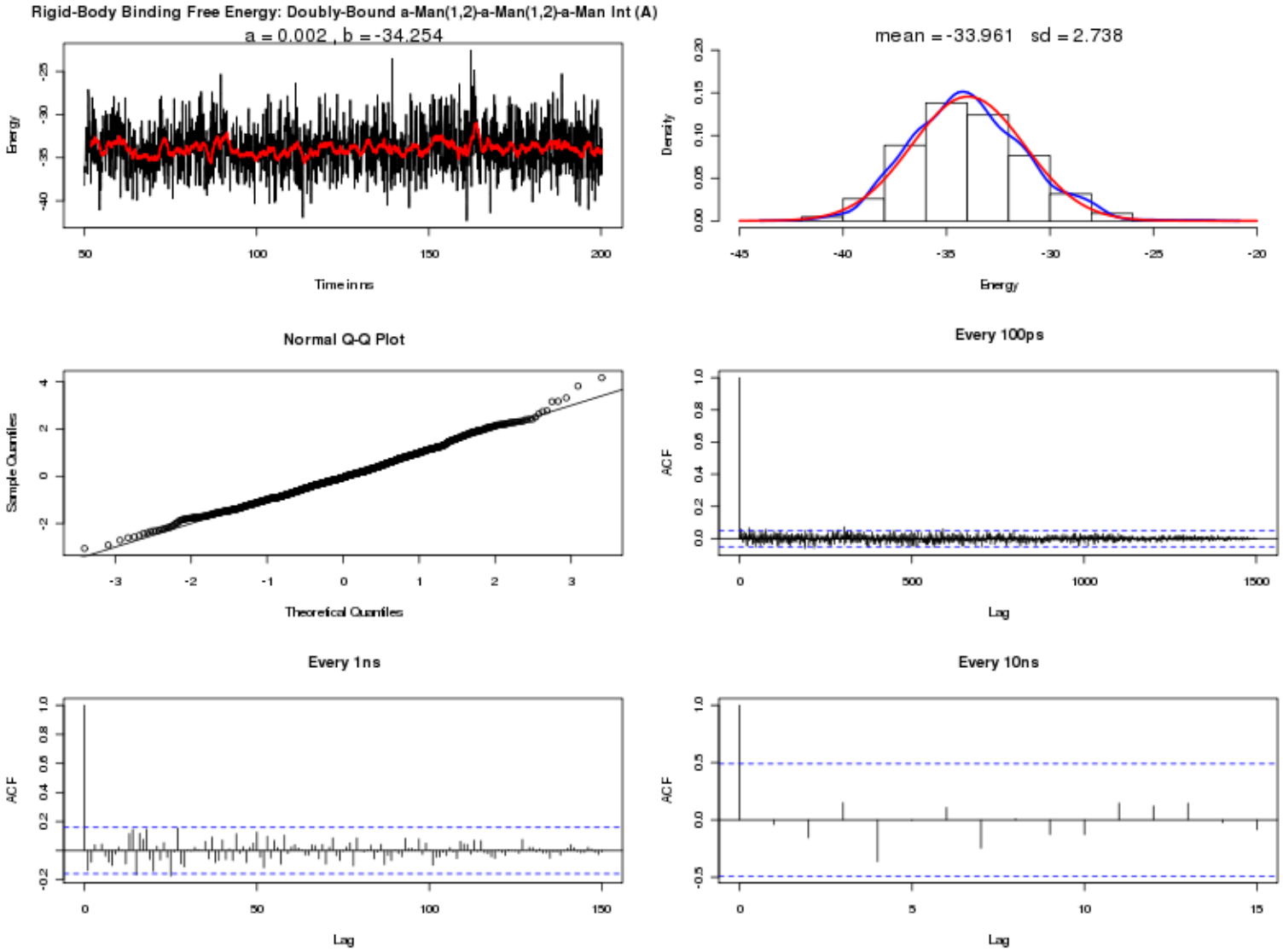

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,2)-a-Man Int (A)
a = 0.002 , b = -34.254
Energy
Time in ns
mean = -33.961 sd = 2.738
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S18.**

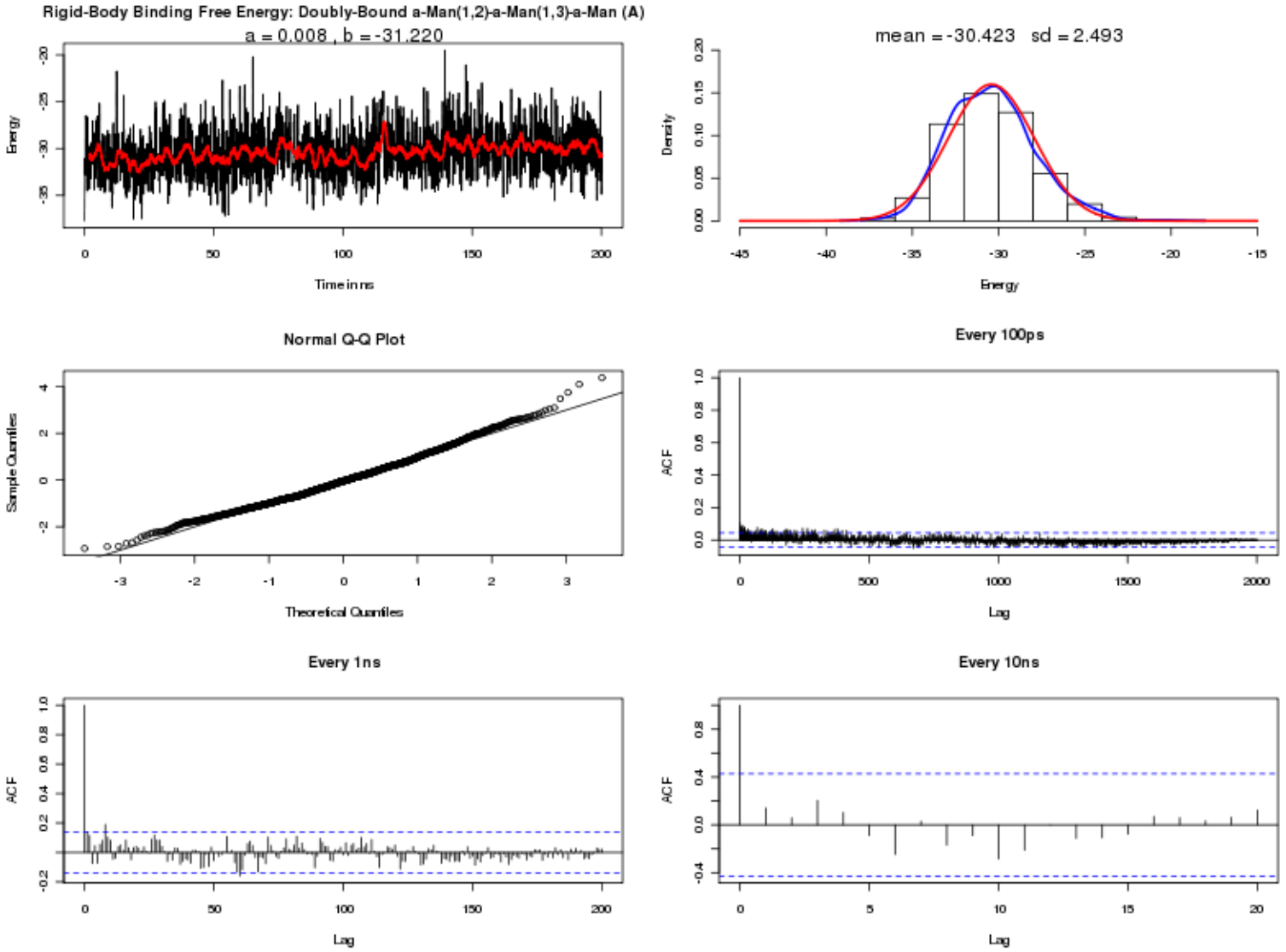

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,3)-a-Man (A)
a = 0.008 , b = -31.220
Energy
Time in ns
mean = -30.423 sd = 2.493
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S19.**

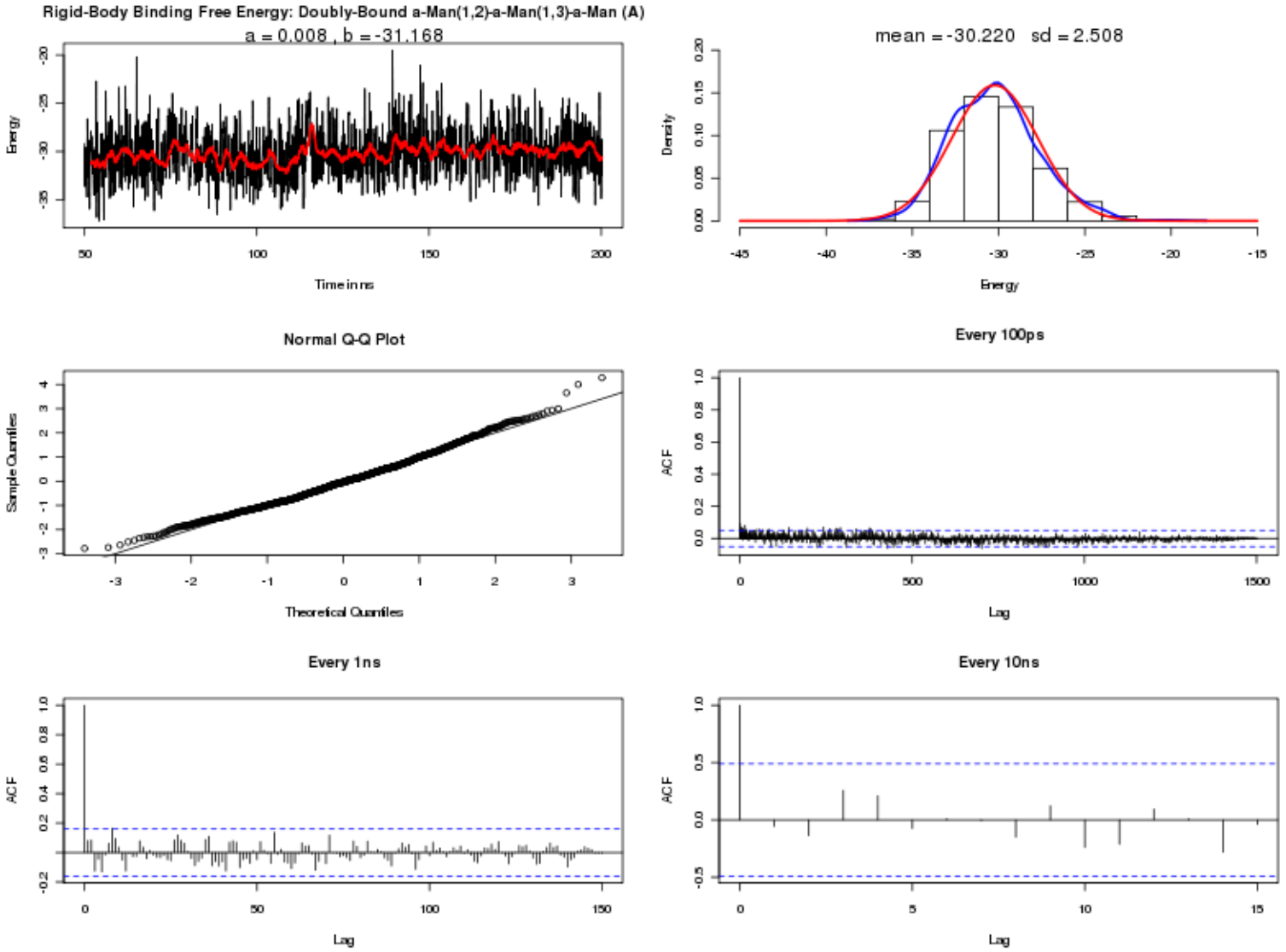

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,3)-a-Man (A)
a = 0.008 , b = -31.168
Energy
Time in ns
mean = -30.220 sd = 2.508
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S20.**

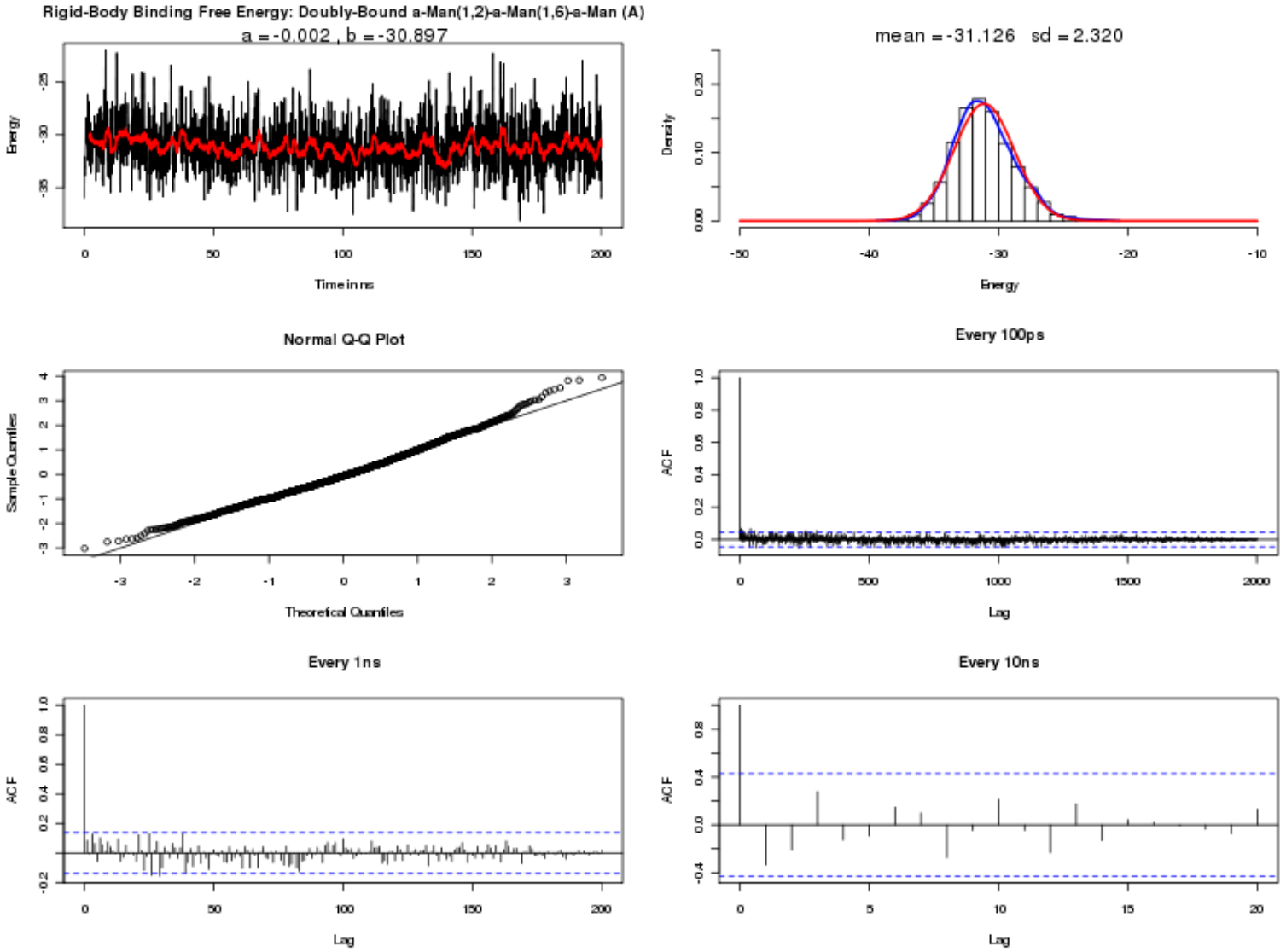

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,6)-a-Man (A)
a = -0.002 , b = -30.897
Energy
Time in ns
mean = -31.126 sd = 2.320
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S21.**

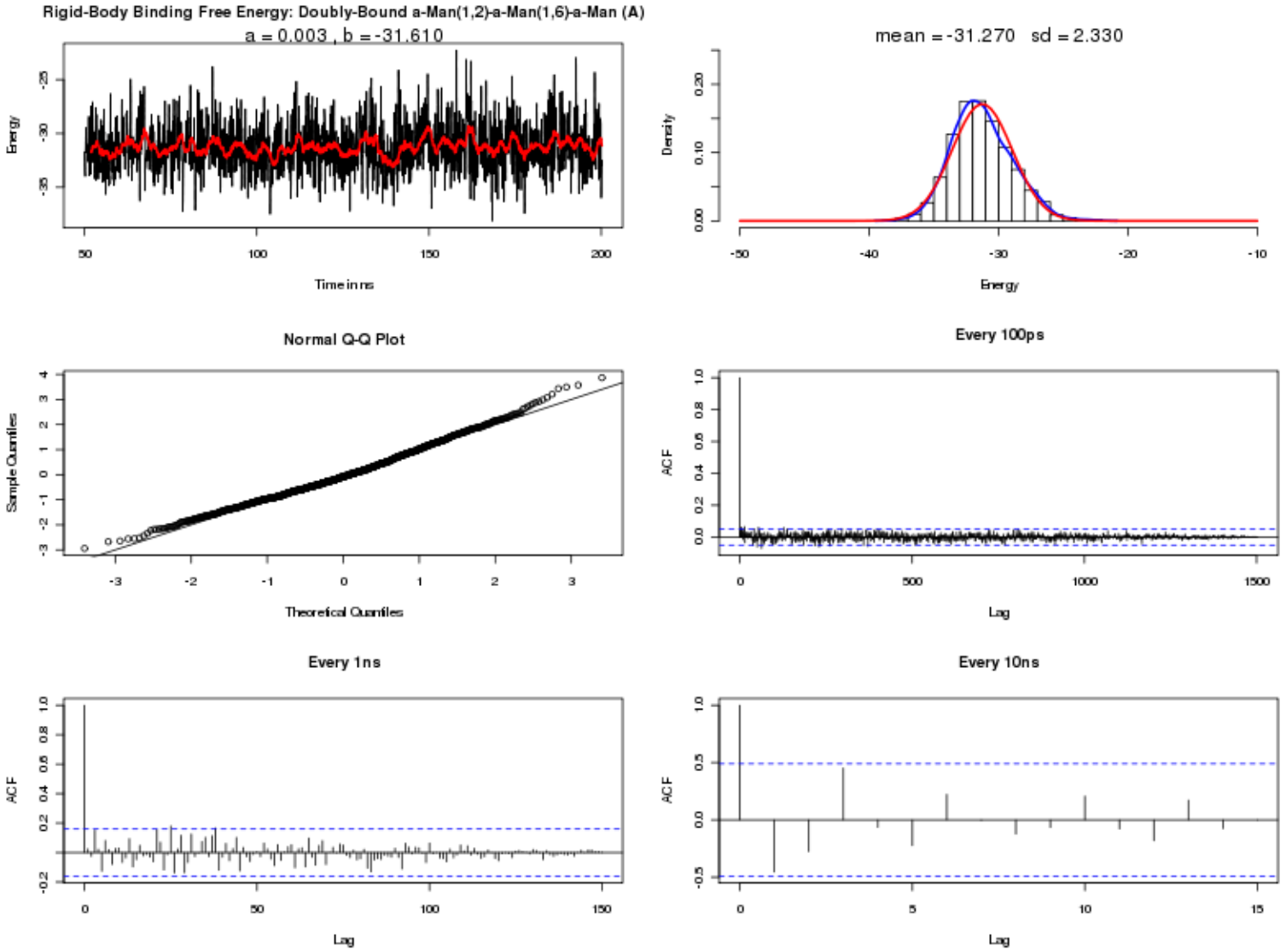

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,6)-a-Man (A)
a = 0.003 , b = -31.610
Energy
Time in ns
mean = -31.270 sd = 2.330
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S22.**

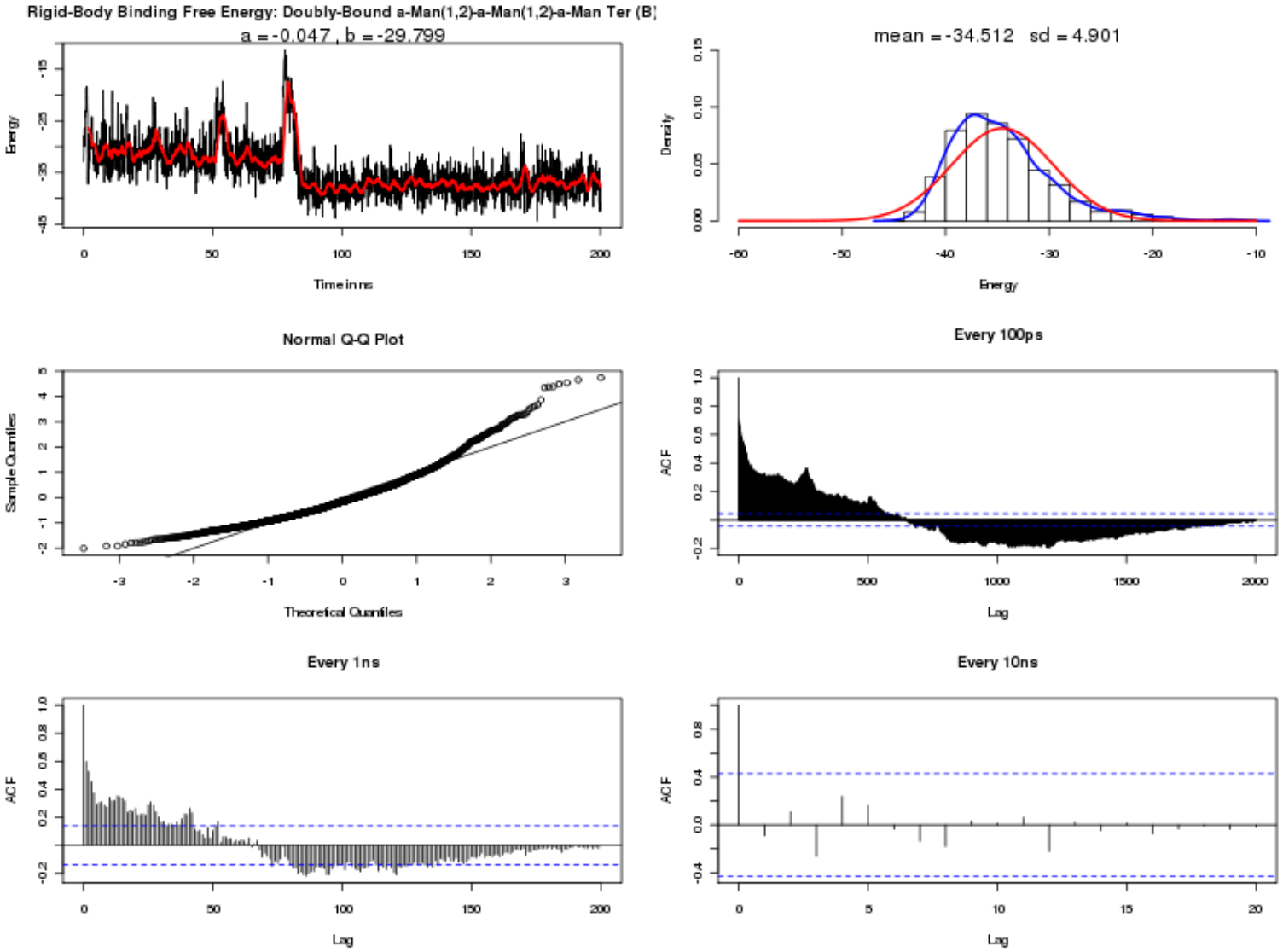

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,2)-a-Man Ter (B
a = -0.047 , b = -29.799
Energy
Time in ns
mean = -34.512 sd = 4.901
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S23.**

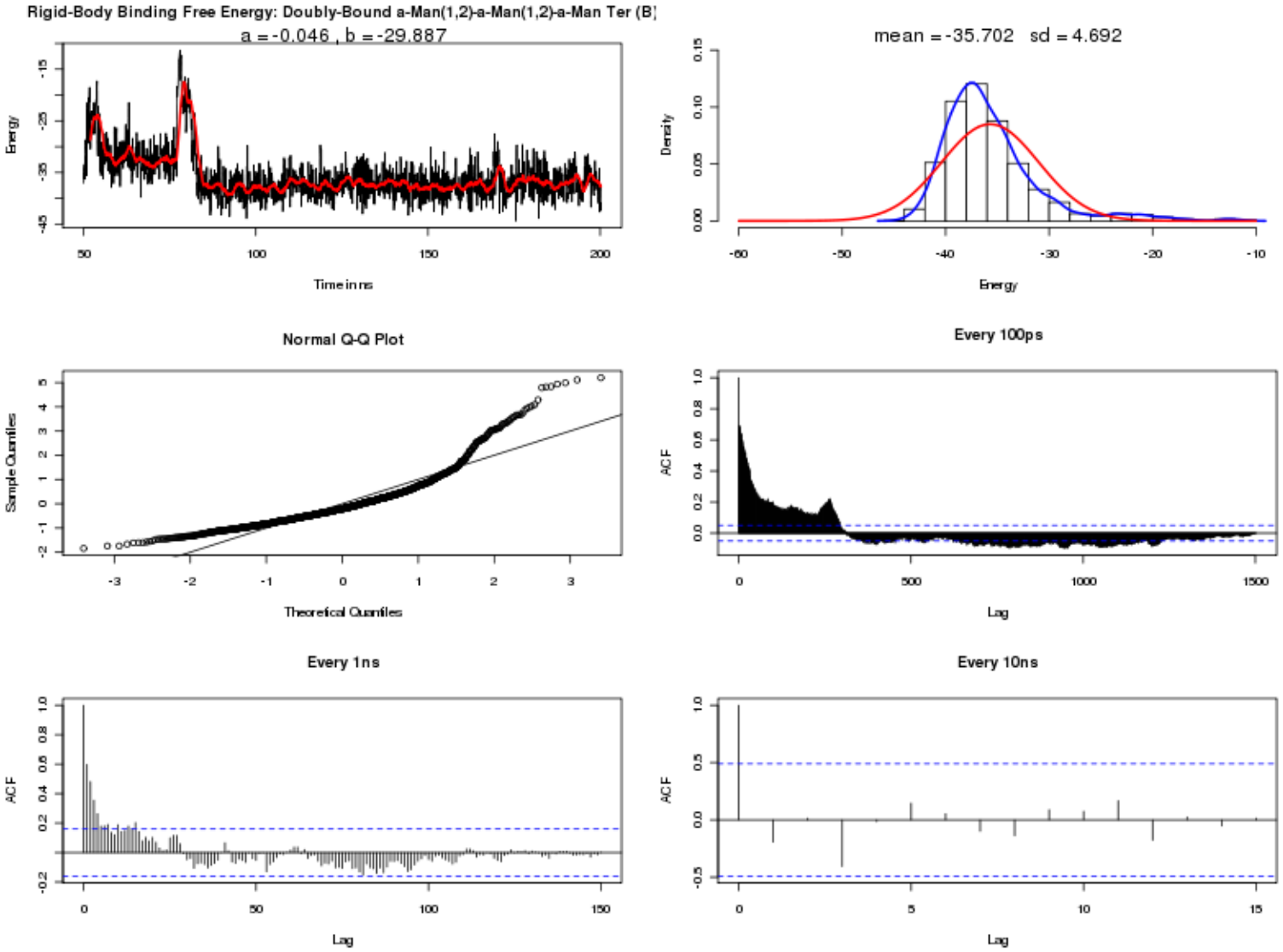

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,2)-a-Man Ter (B
a = -0.046 , b = -29.887
Energy
Time in ns
mean = -35.702 sd = 4.692
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S24.**

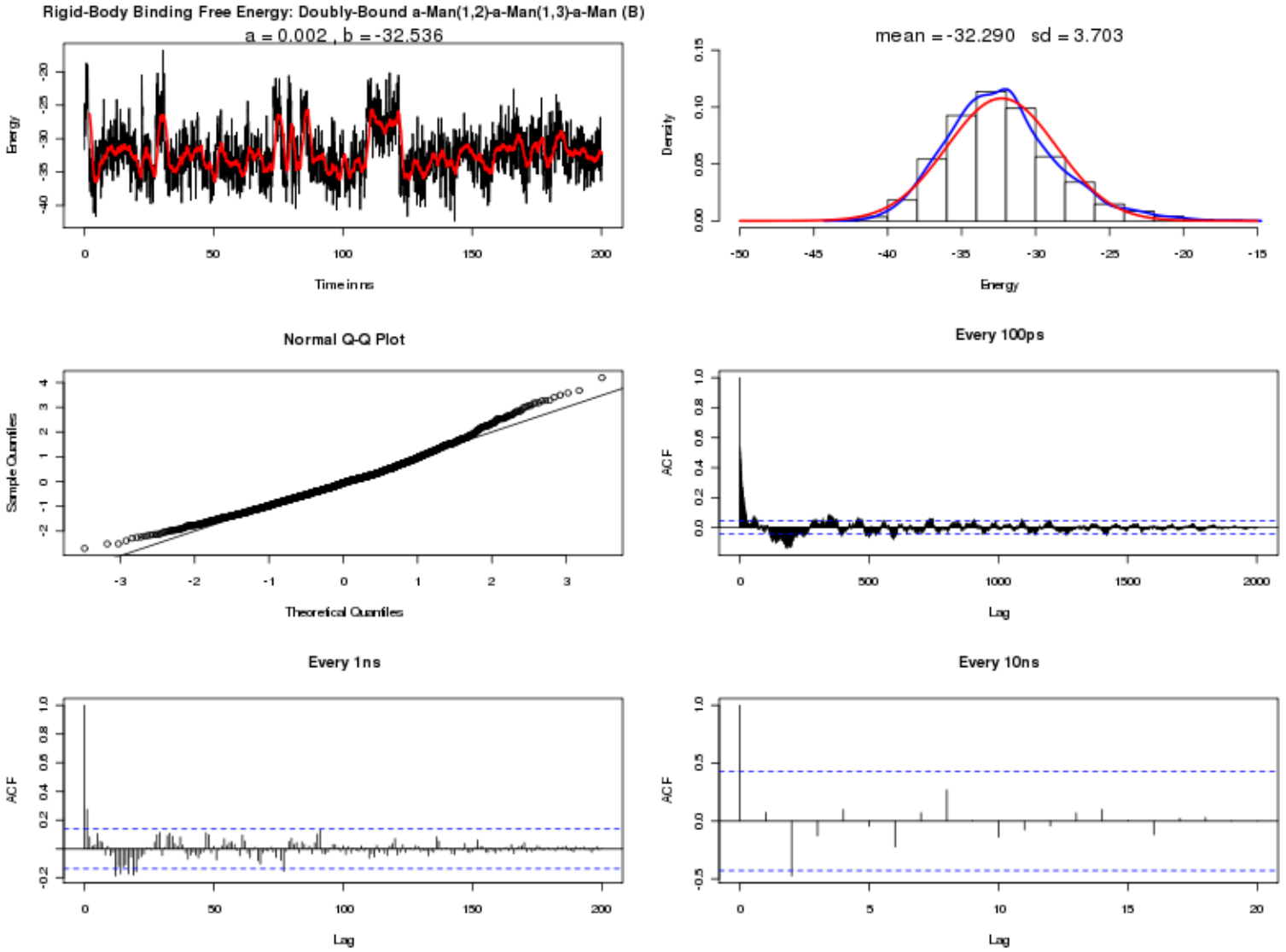

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,3)-a-Man (B)
a = 0.002 , b = -32.536
Energy
Time in ns
mean = -32.290 sd = 3.703
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S25.**

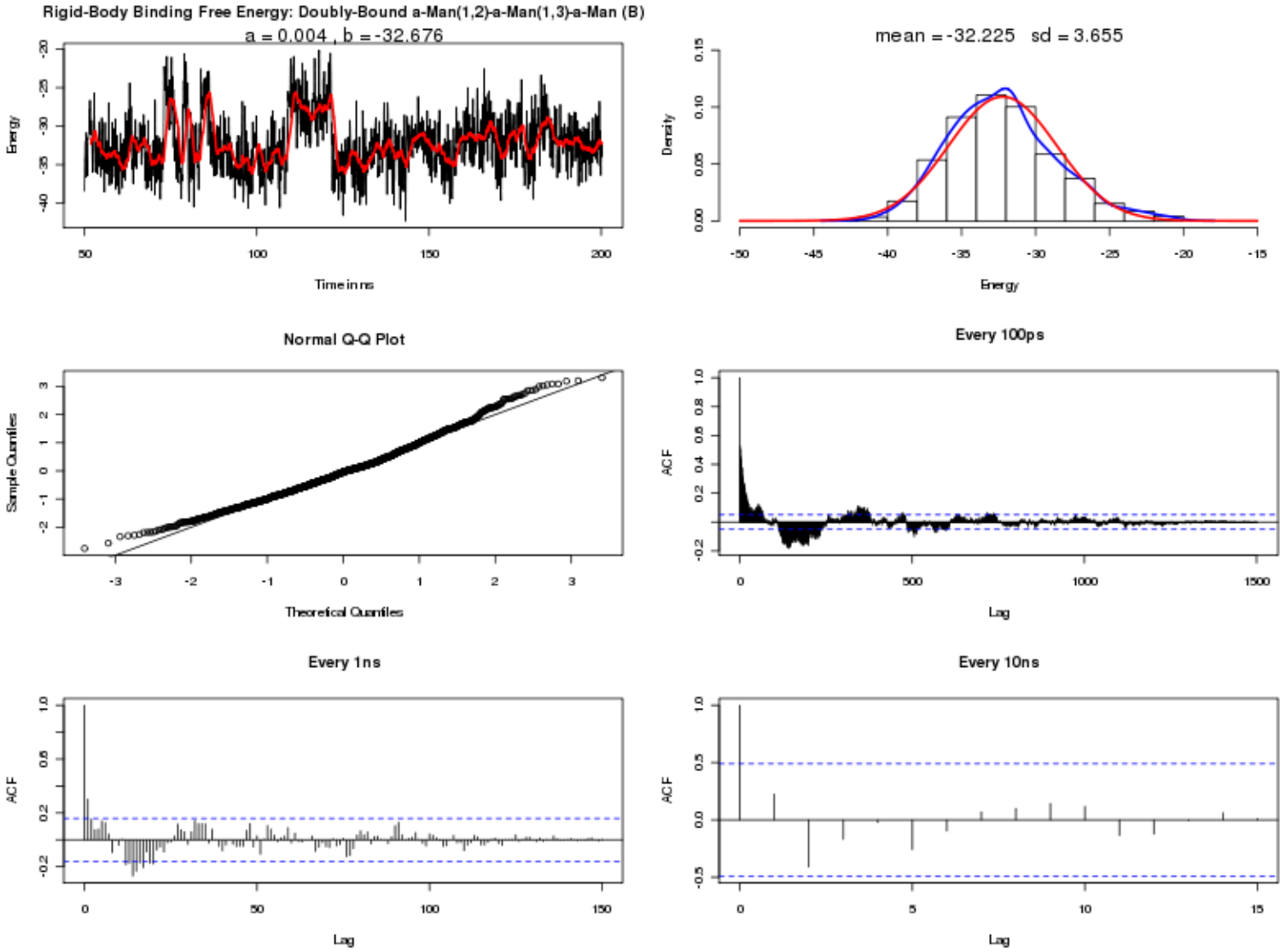

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,3)-a-Man (B)
a = 0.004 , b = -32.676
Energy
Time in ns
mean = -32.225 sd = 3.655
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S26.**

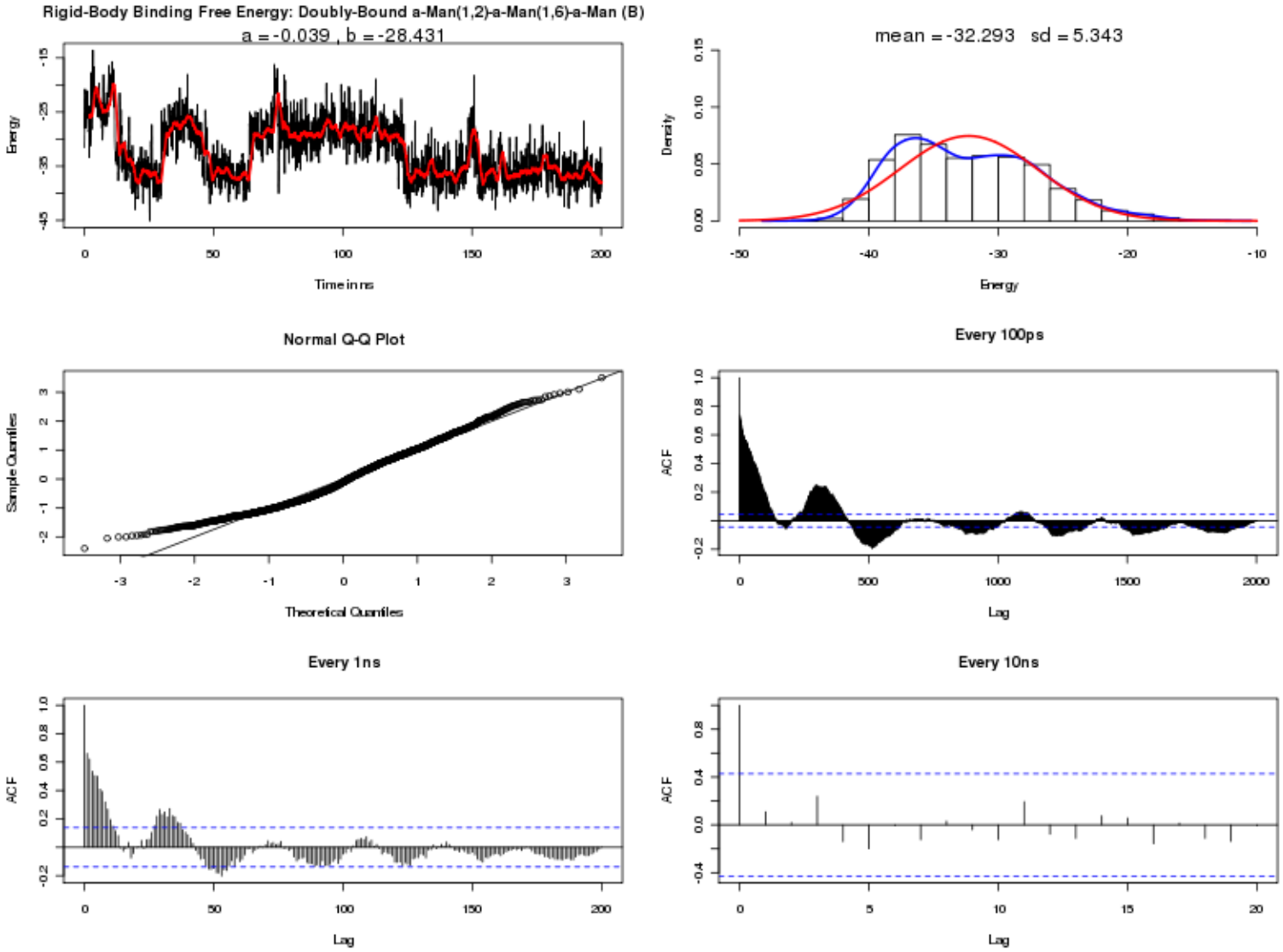
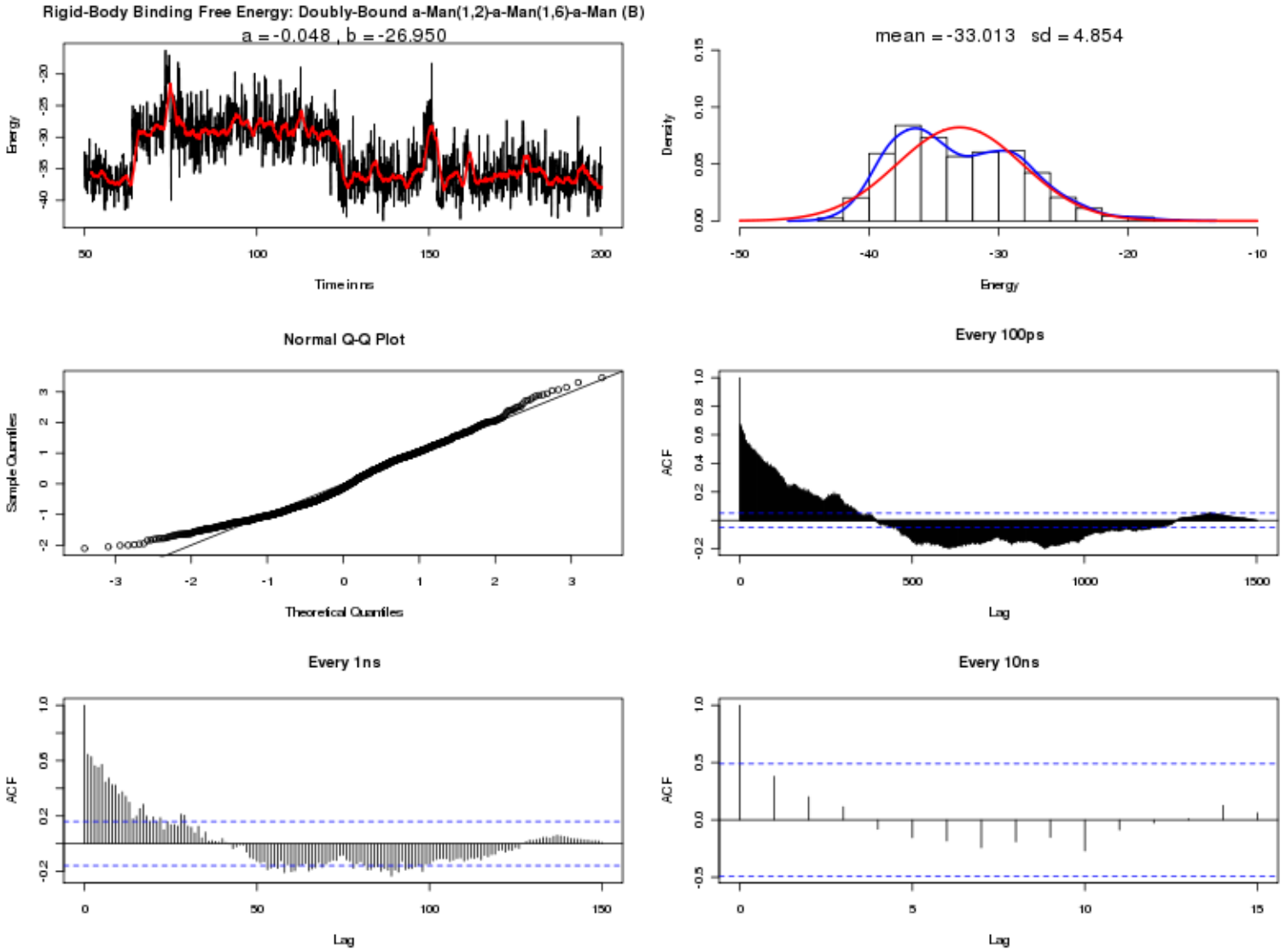

Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,6)-a-Man (B)
a = -0.039 , b = -28.431
Energy
Time in ns
mean = -32.293 sd = 5.343
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag

**Figure S27.**


Rigid-Body Binding Free Energy: Doubly-Bound a-Man(1,2)-a-Man(1,6)-a-Man (B)
a = -0.048 , b = -26.950
Energy
Time in ns
mean = -33.013 sd = 4.854
Density
Energy
Normal Q-Q Plot
Sample Quantiles
Theoretical Quantiles
Every 100ps
ACF
Lag
Every 1ns
ACF
Lag
Every 10ns
ACF
Lag