

Structure Factor Check

1YQ4

Title: AVIAN RESPIRATORY COMPLEX II WITH 3-NITROPROPIONATE AND UBIQ
Date: 01-FEB-05
PDB code: 1YQ4

Crystal

Cell parameters:

a: 69.59 Å b: 83.49 Å c: 288.59 Å
 α : 90.00 β : 90.00 γ : 90.00

Space group: P 21 21 21

Model

9291 atoms (575 water molecules)

Number of chains: 19

Volume not occupied by model: 52.5 %

 (for atomic model): 49.2 Å²

σ (B): 15.31 Å²

Matthews coefficient: 3.22

Corresponding solvent % : 61.53

Refinement

Program: CNS 1.1

Nominal resolution range: 56.4 – 2.33 Å

Reported R-factor: 0.202

Number of reflections used: 68868

Reported Rfree: 0.25

Sigma cut-off: N.A.

Structure Factors

Input

Nominal resolution range: 47.5 – 2.20 Å

Reflections in file: 77928

Unique reflections above 0: 77928

above 1 σ : 77181

above 3 σ : 58844

SF CHECK

Nominal resolution range: 47.5 – 2.33 Å

\05max. from input data, min. from author\05

Used reflections: 68868

Reflections out of resolution: 9060

Completeness: 94.4 %

R_{stand}(F) = $\langle \sigma(F) \rangle / \langle F \rangle$: 0.043

Anisotropic distribution of Structure Factors

ratio of eigen values: 0.8632 1.0000 0.6245

B_{overall} (by Patterson): 39.Å²

Optical resolution: 1.83 Å

Expected opt. resol. for complete data set: 1.83 Å

Estimated minimal error: 0.026 Å

Model vs. Structure Factors

R-factor for all reflections: 0.220

Correlation factor: 0.928

R-factor: 0.227

for $F > 2.0 \sigma$

nom. resolution range: 56.38 – 2.33 Å

reflections used: 68397

Rfree: 0.274

Nfree: 3313

R-factor without free-refl.: 0.224

Non free-reflections: 65084

<u> (error in coords by Luzzati plot): 0.290 Å

Estimated maximal error: 0.102 Å

DPI: 0.195 Å

Scaling

Scale: 0.905

Bdiff: -4.09

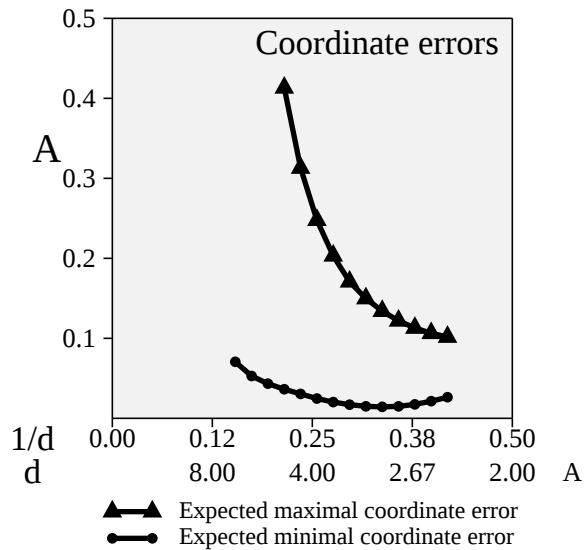
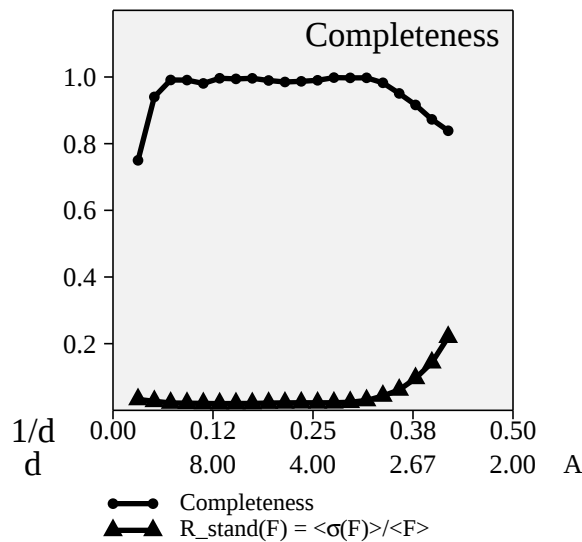
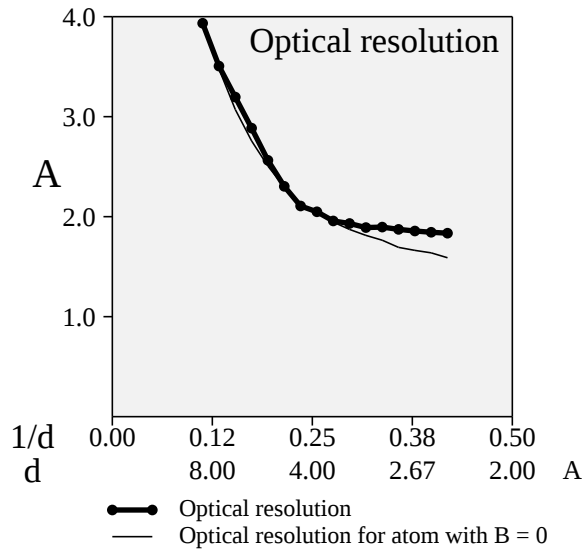
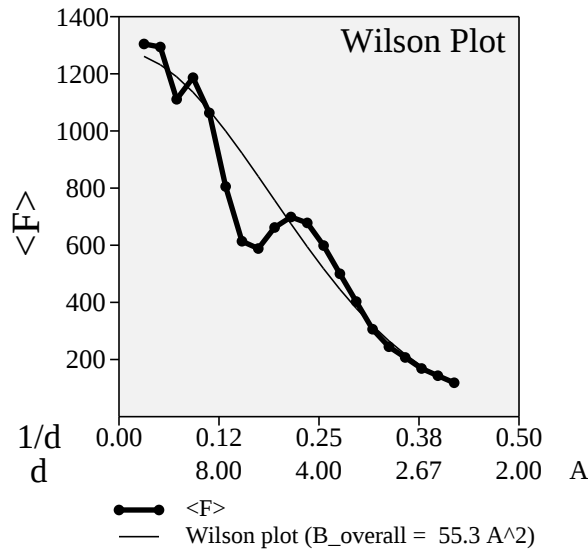
Anisothermal Scaling (Beta):

2.8026 4.0289 -1.9500 0.0000 0.0000 0.0000

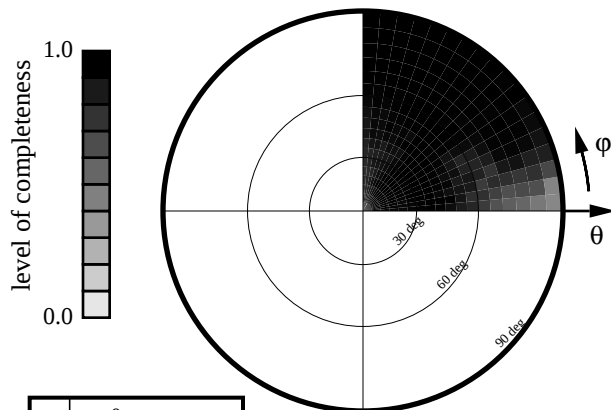
Solvent correction – Ks,Bs: 0.673 250.046

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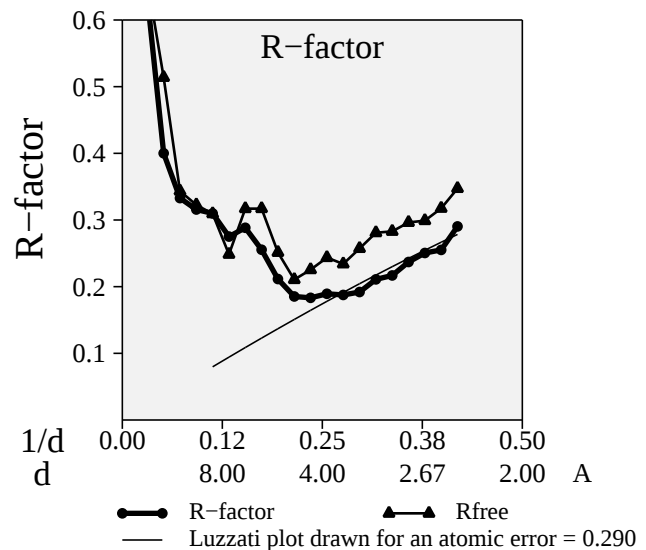


Stereographic projection of the averaged radial completeness



	θ	ϕ
h	90.00	0.00
k	90.00	90.00
l	0.00	0.00

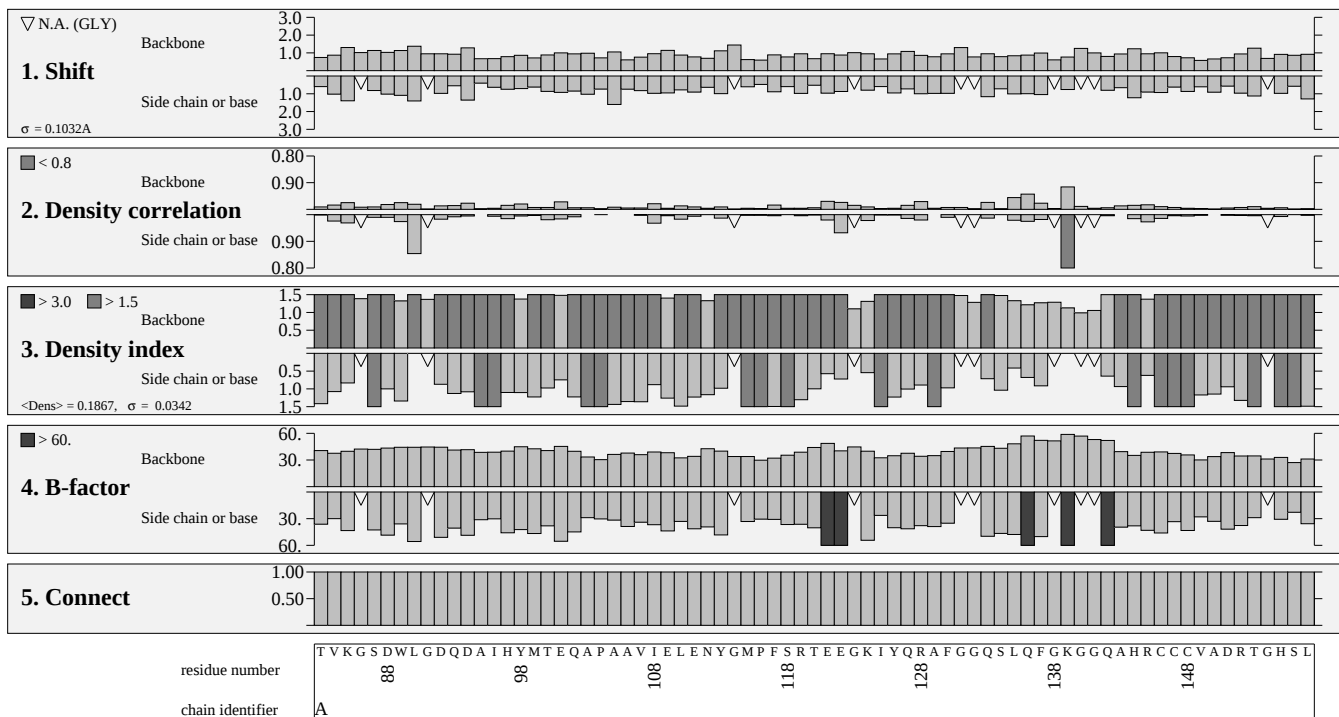
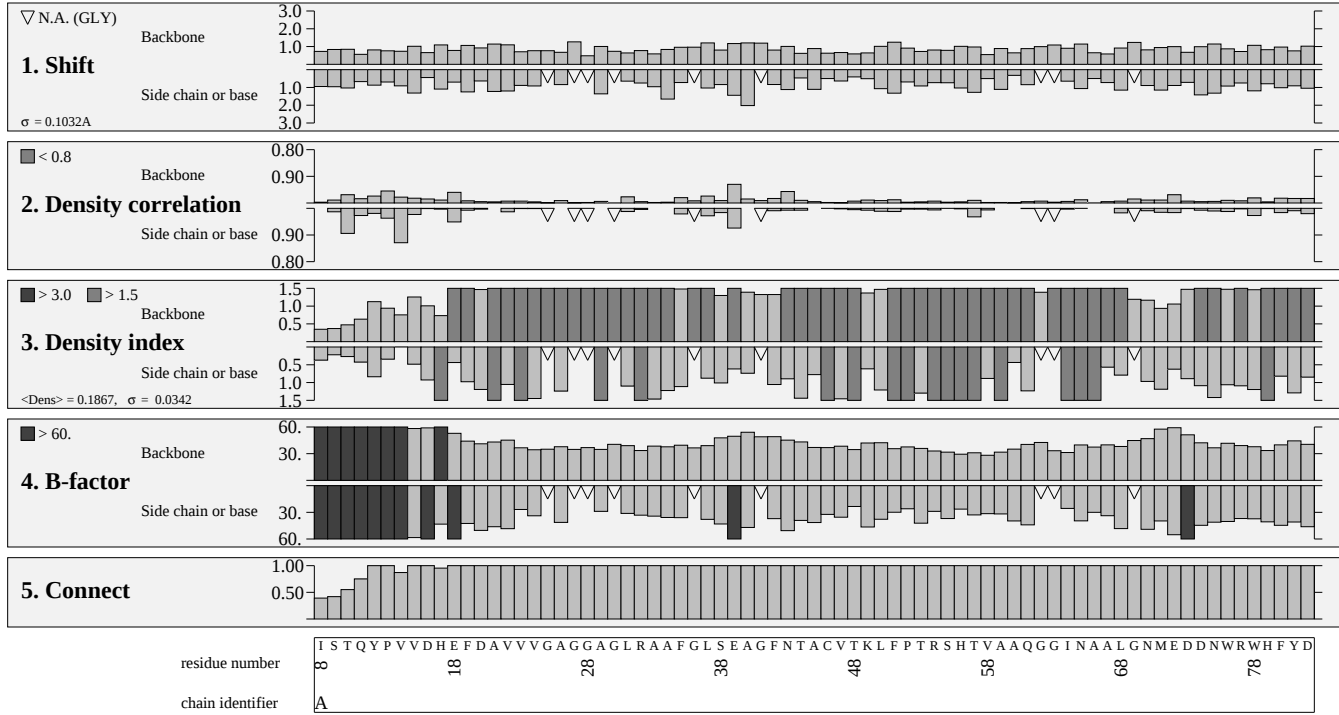
polar coordinates of the crystallographical axes



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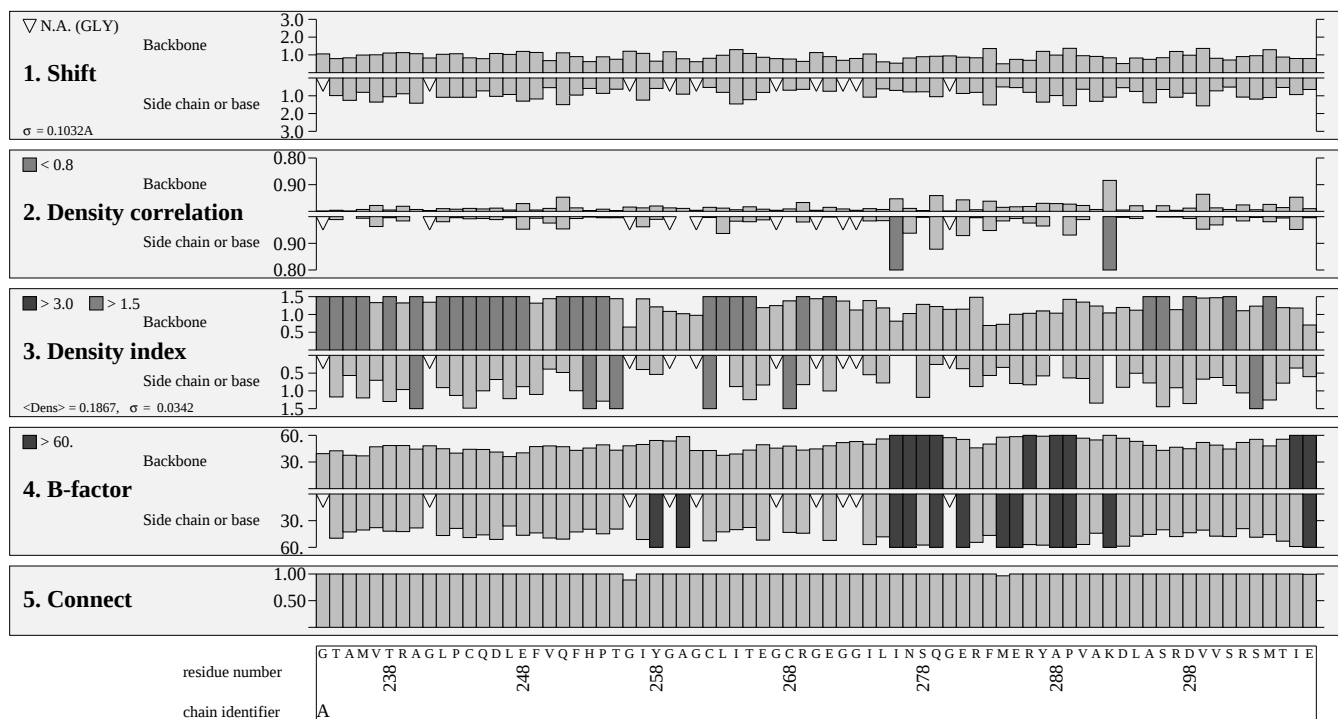
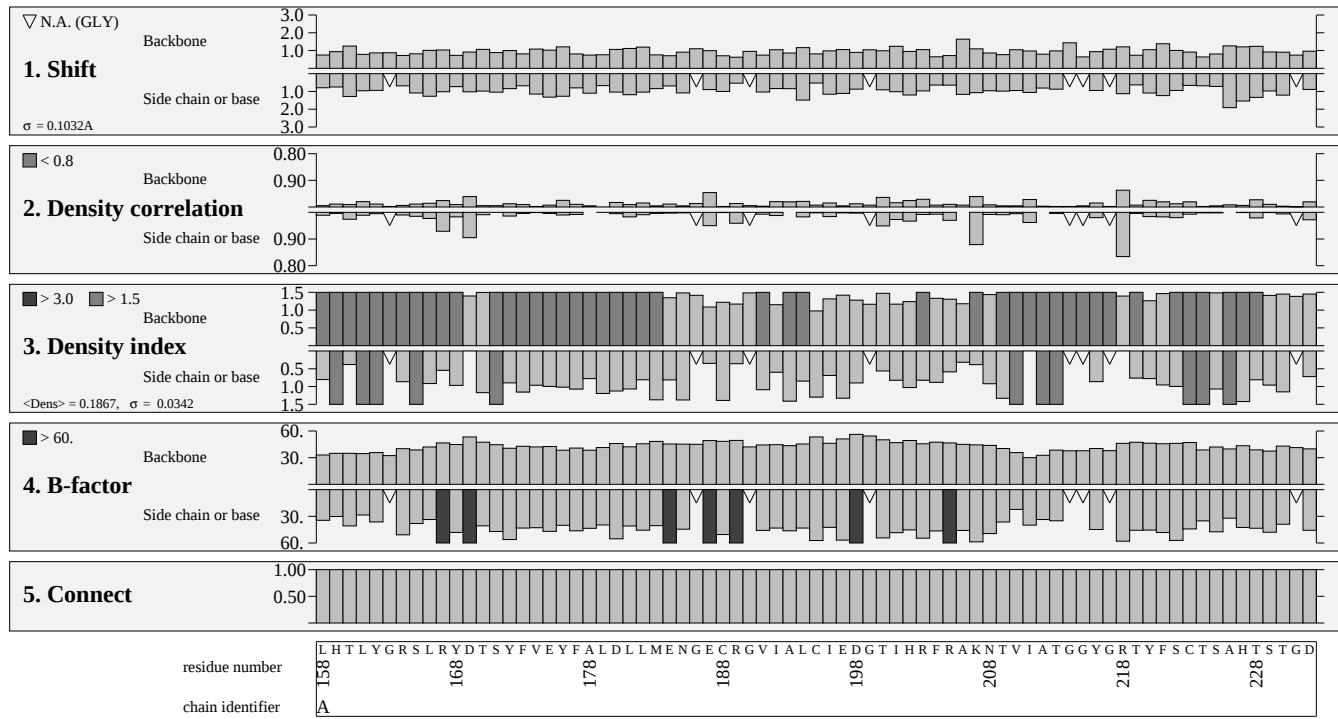
Local estimation



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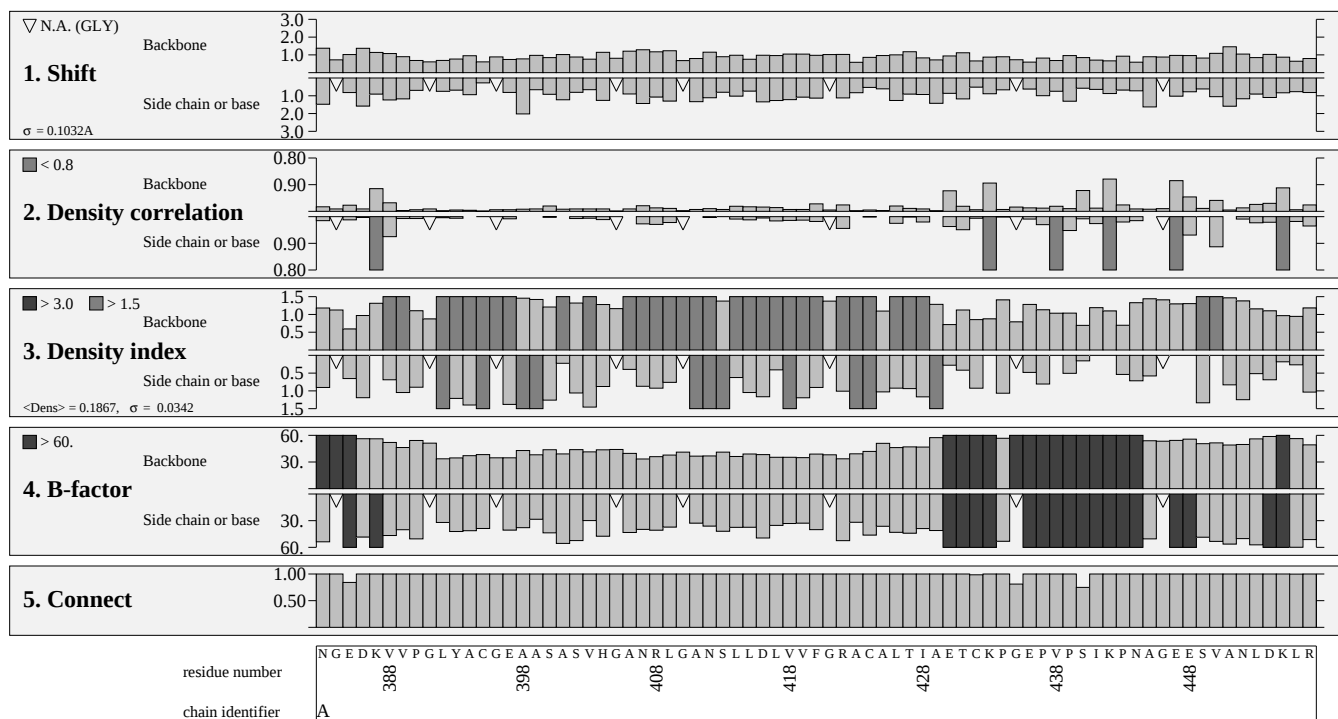
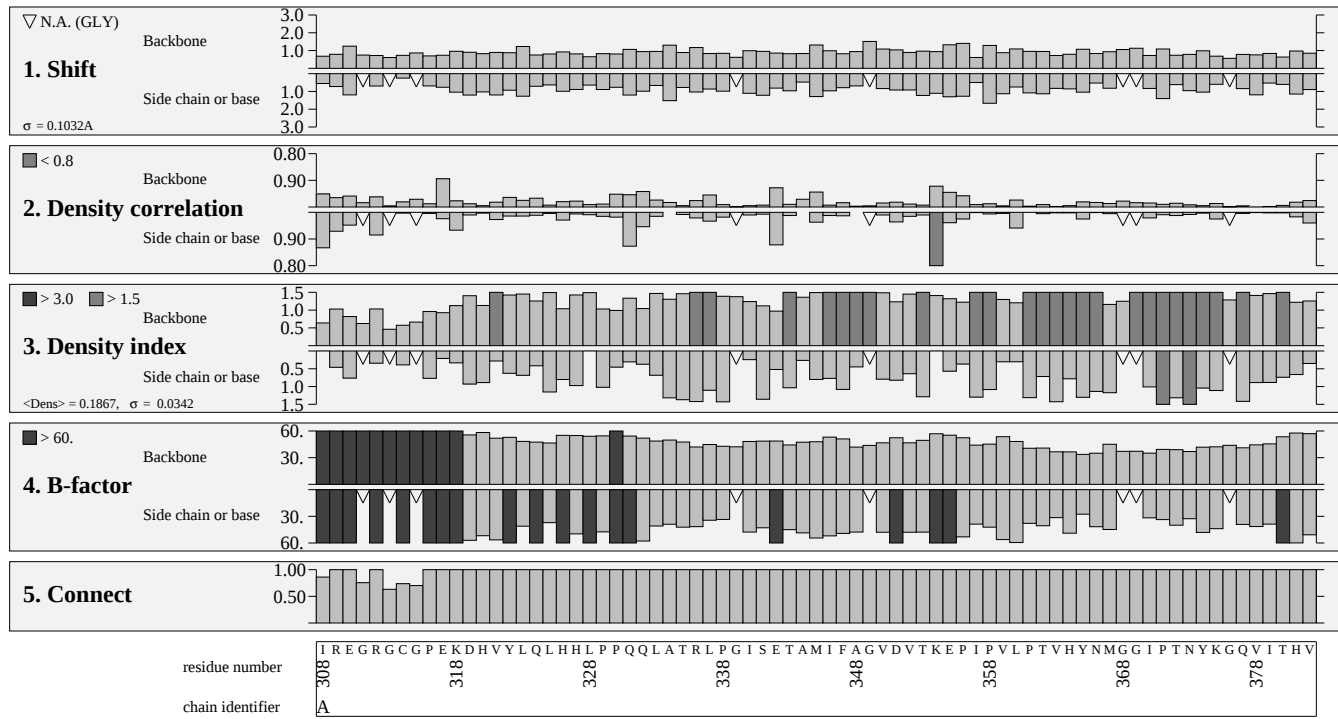
Local estimation (2)



Structure Factor Check

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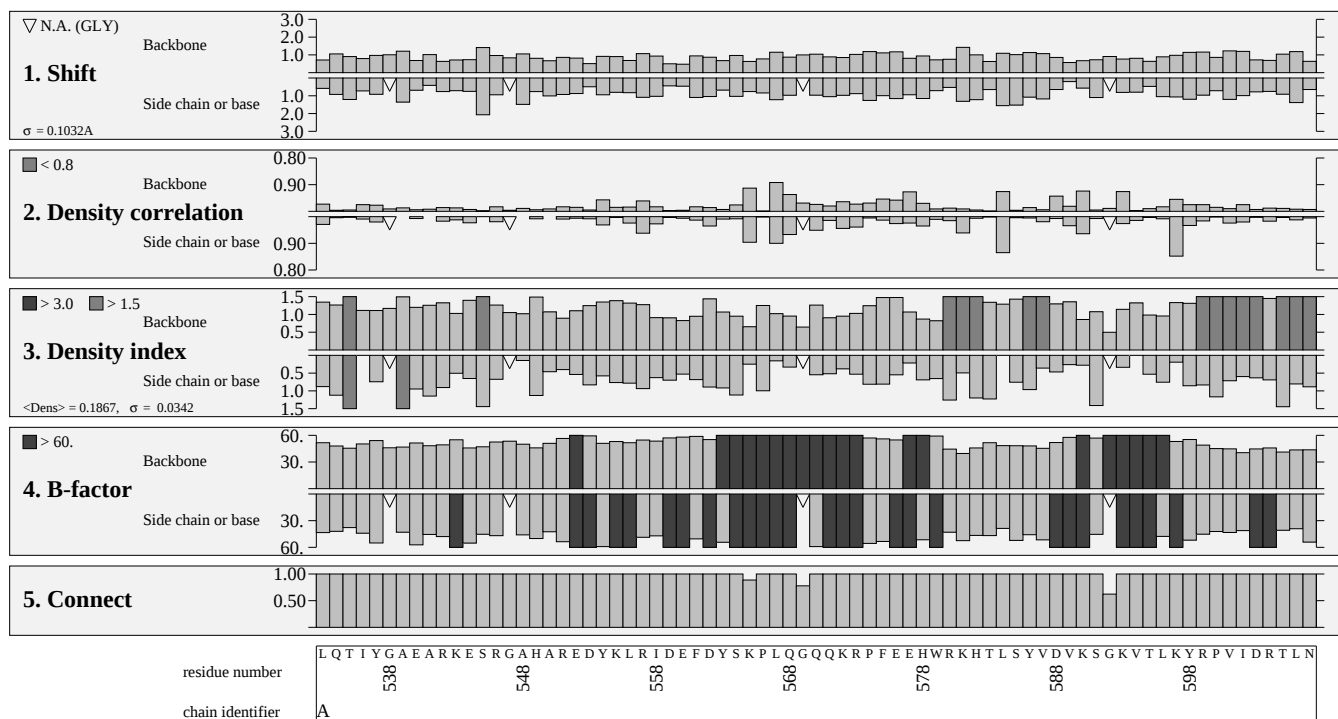
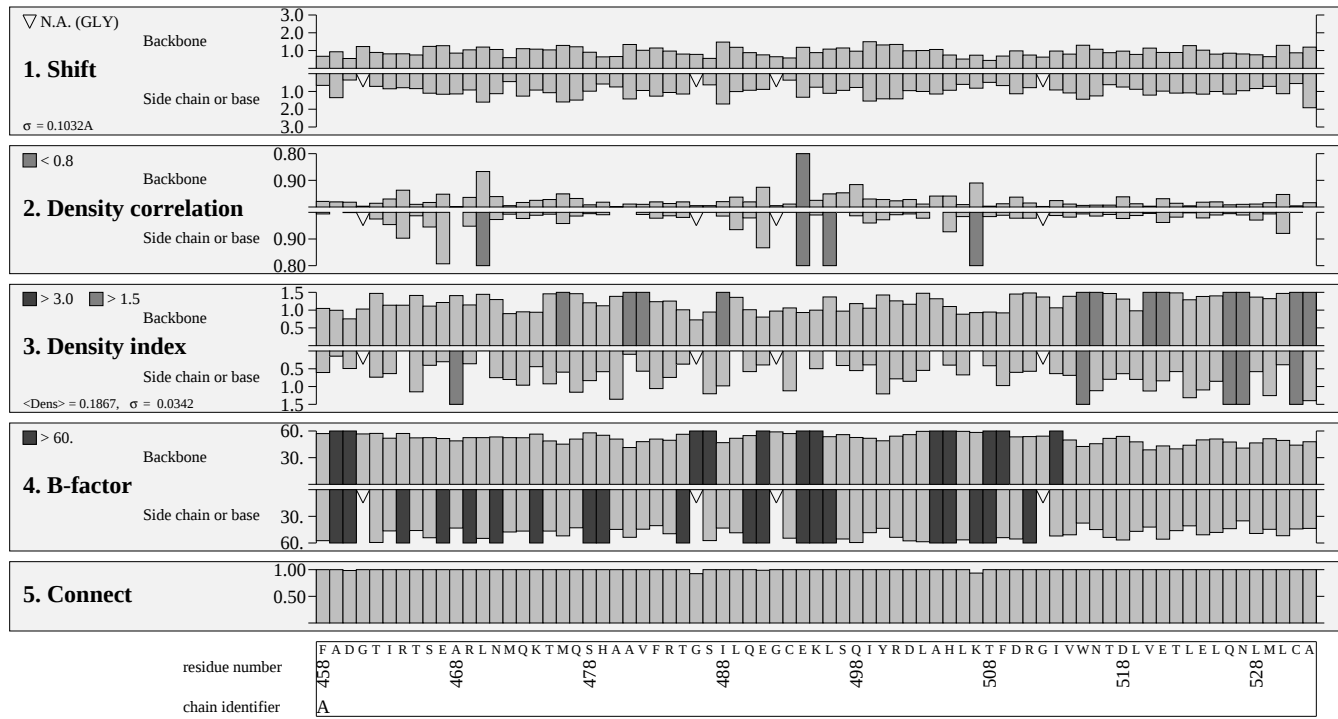
Local estimation (3)



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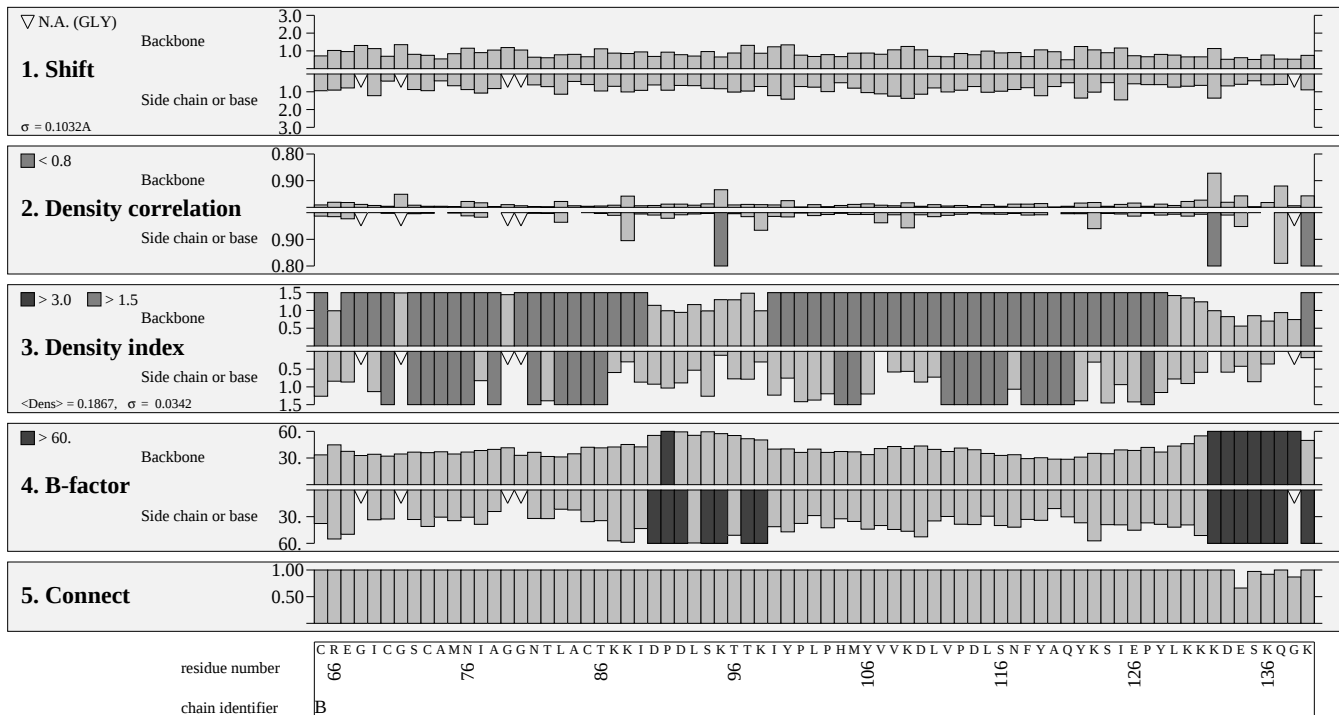
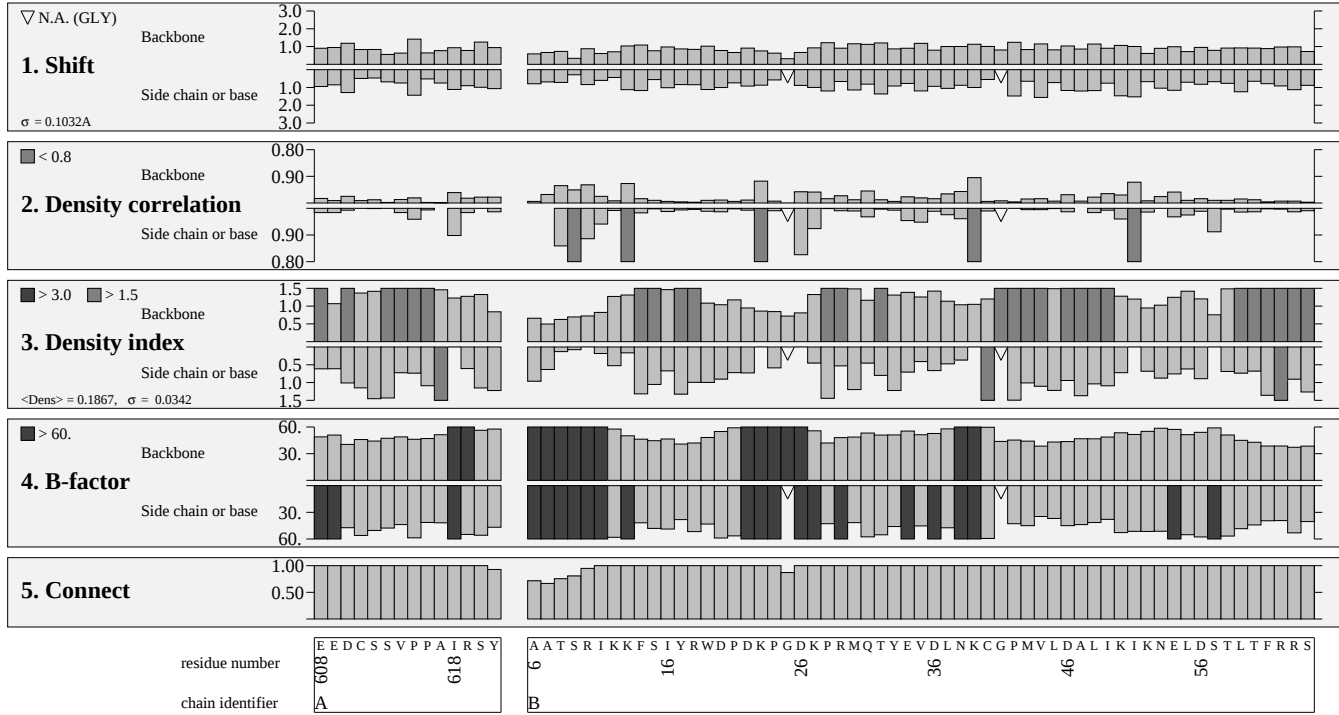
Local estimation (4)



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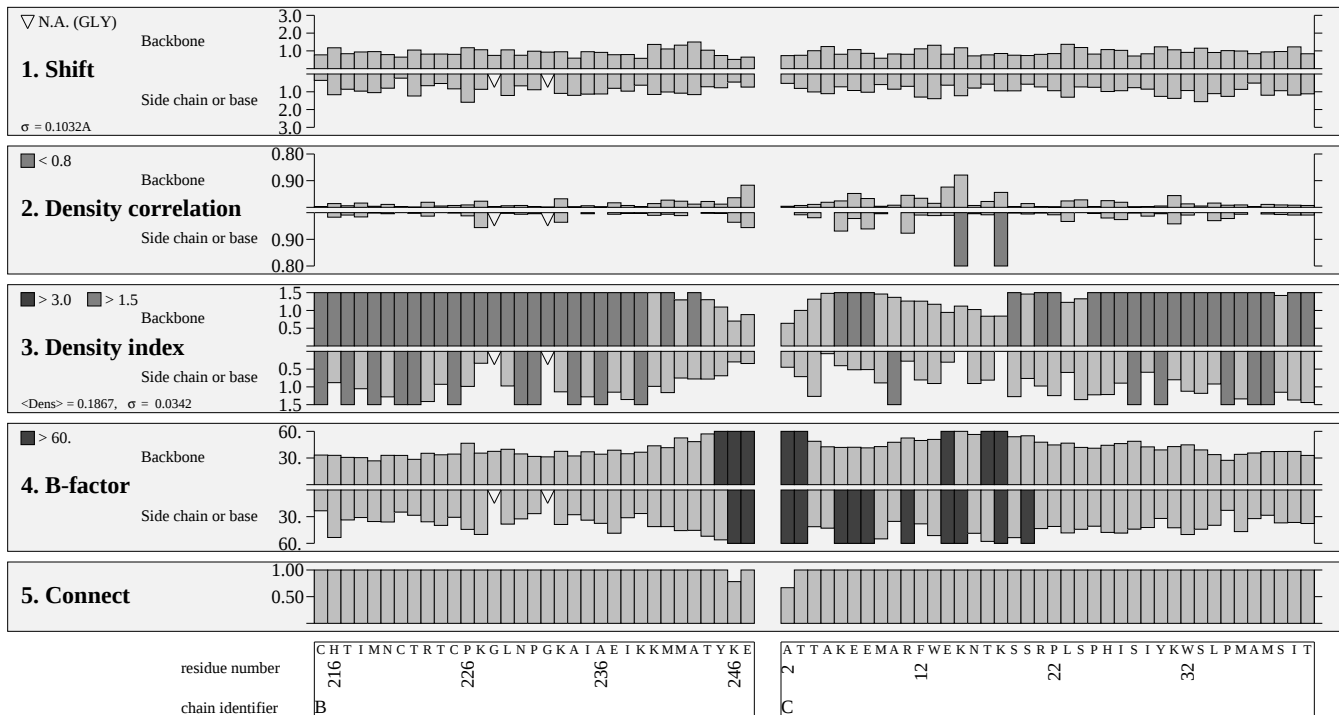
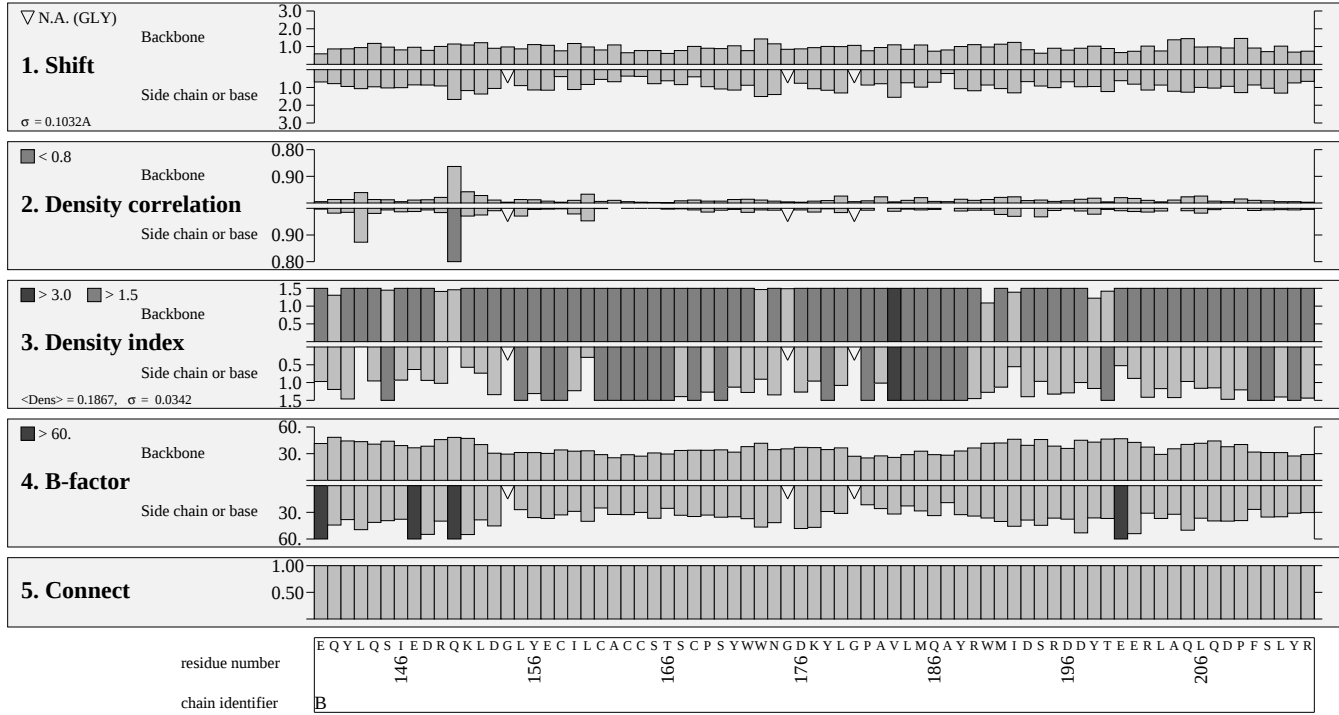
Local estimation (5)



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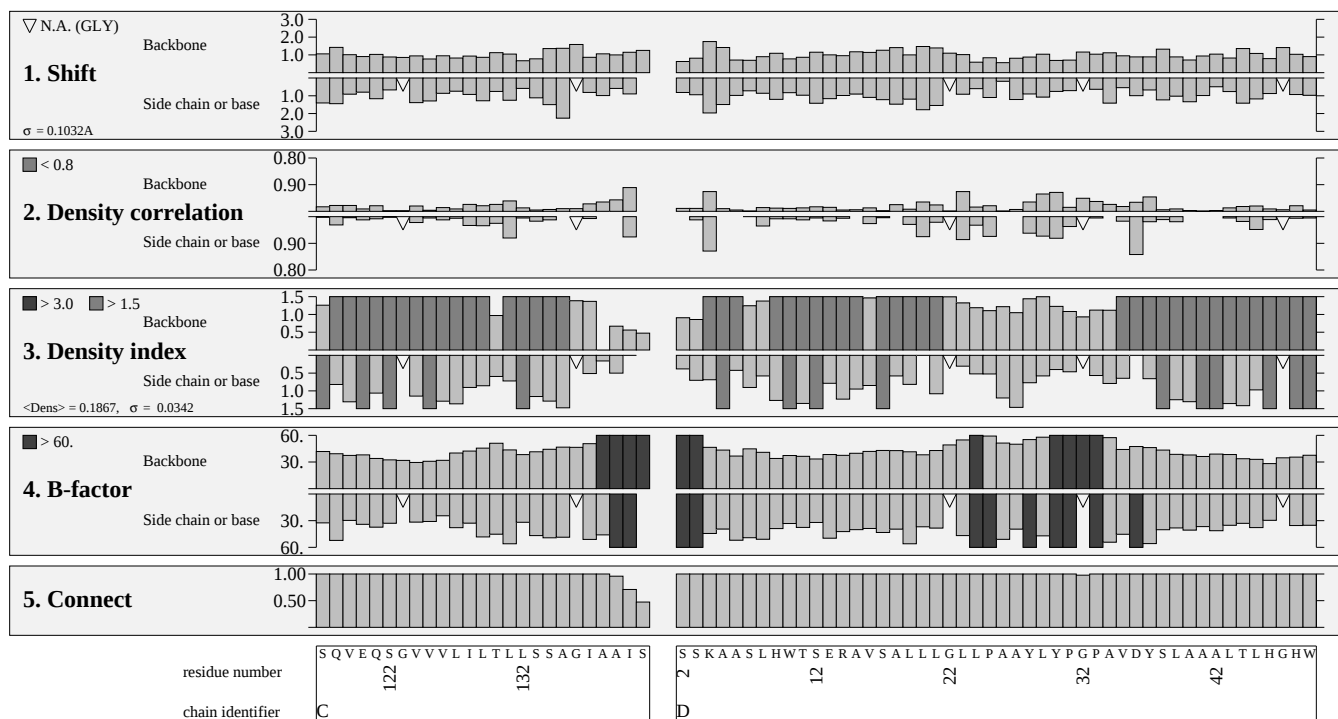
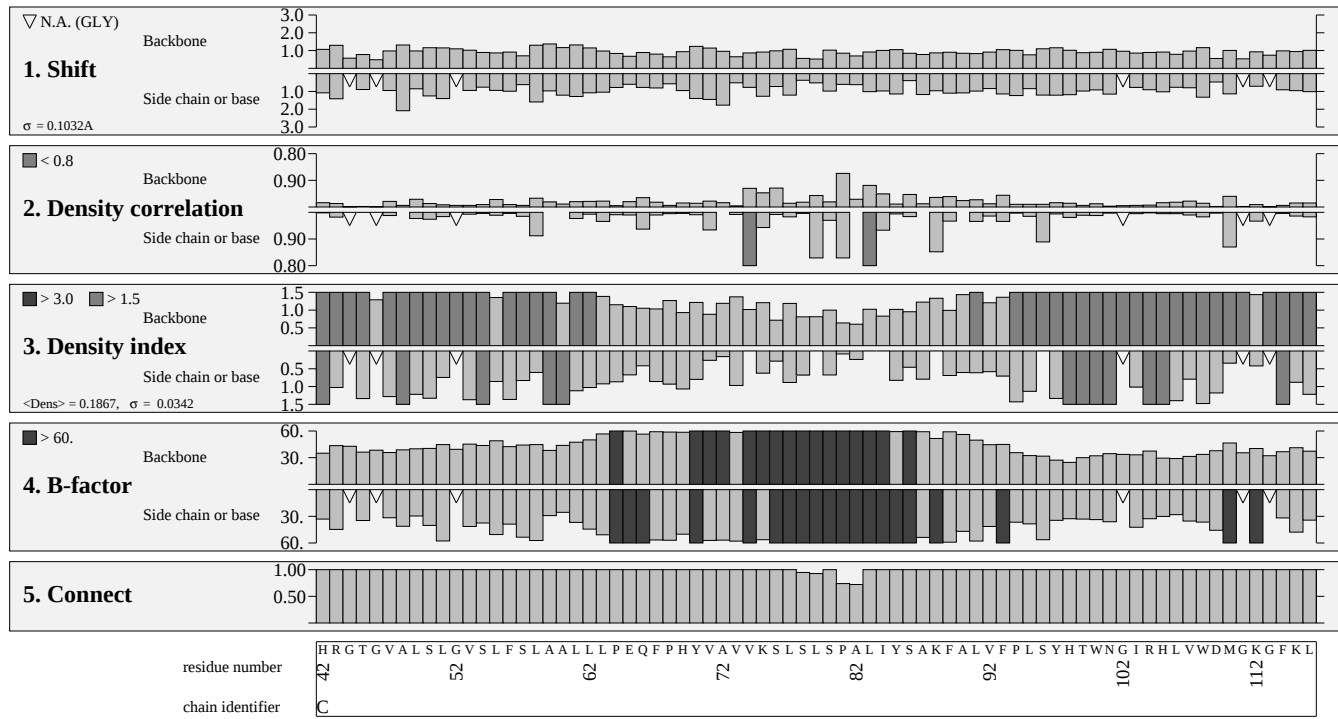
Local estimation (6)



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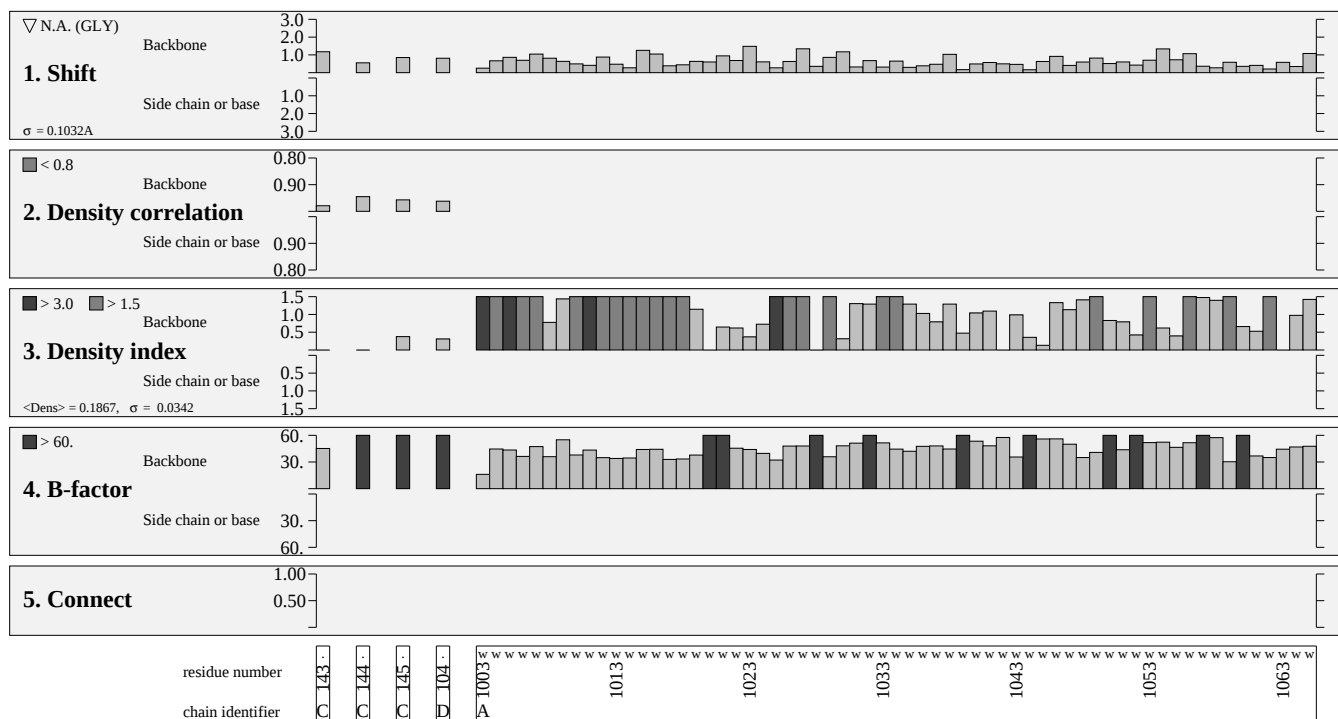
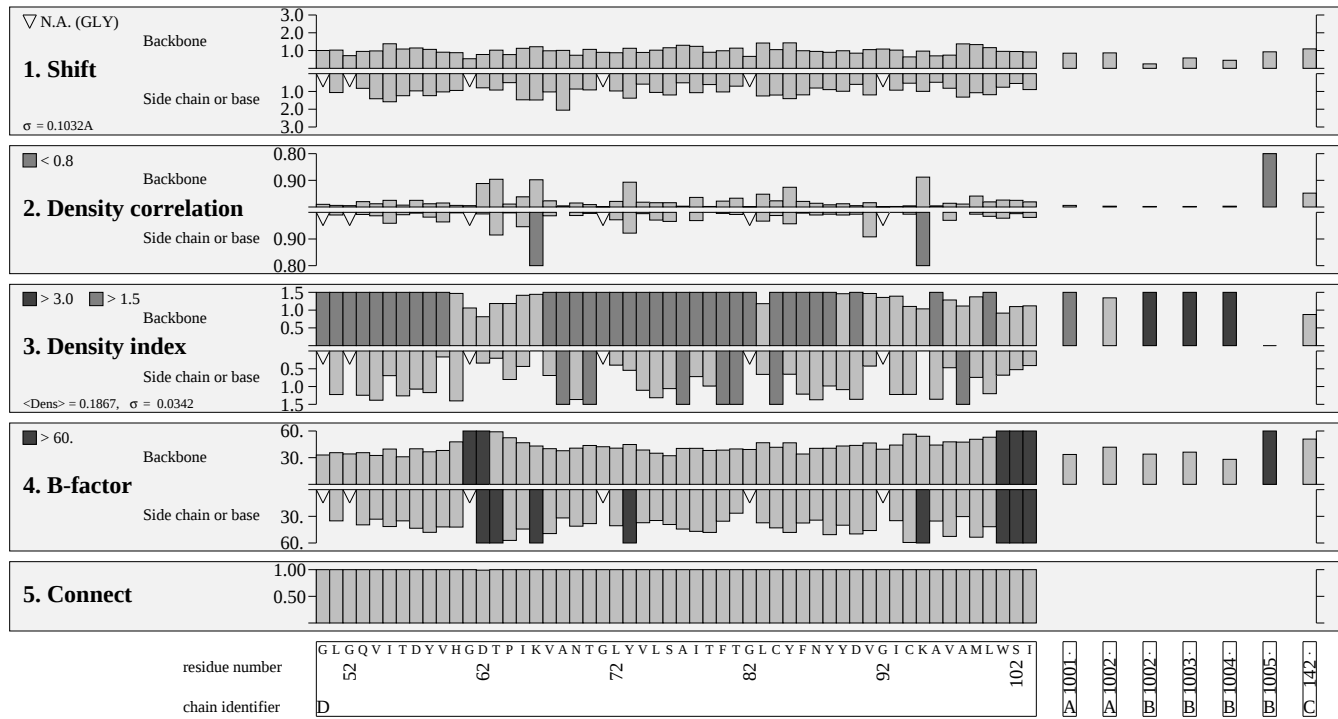
Local estimation (7)



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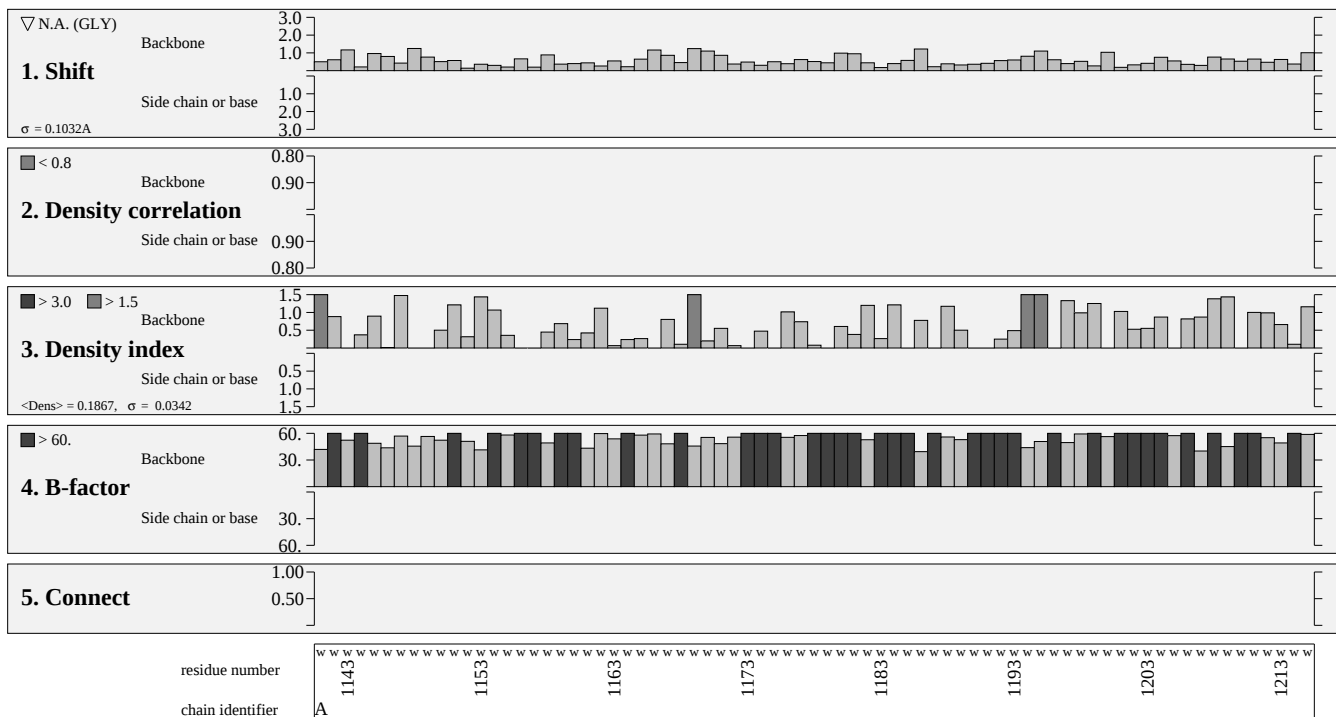
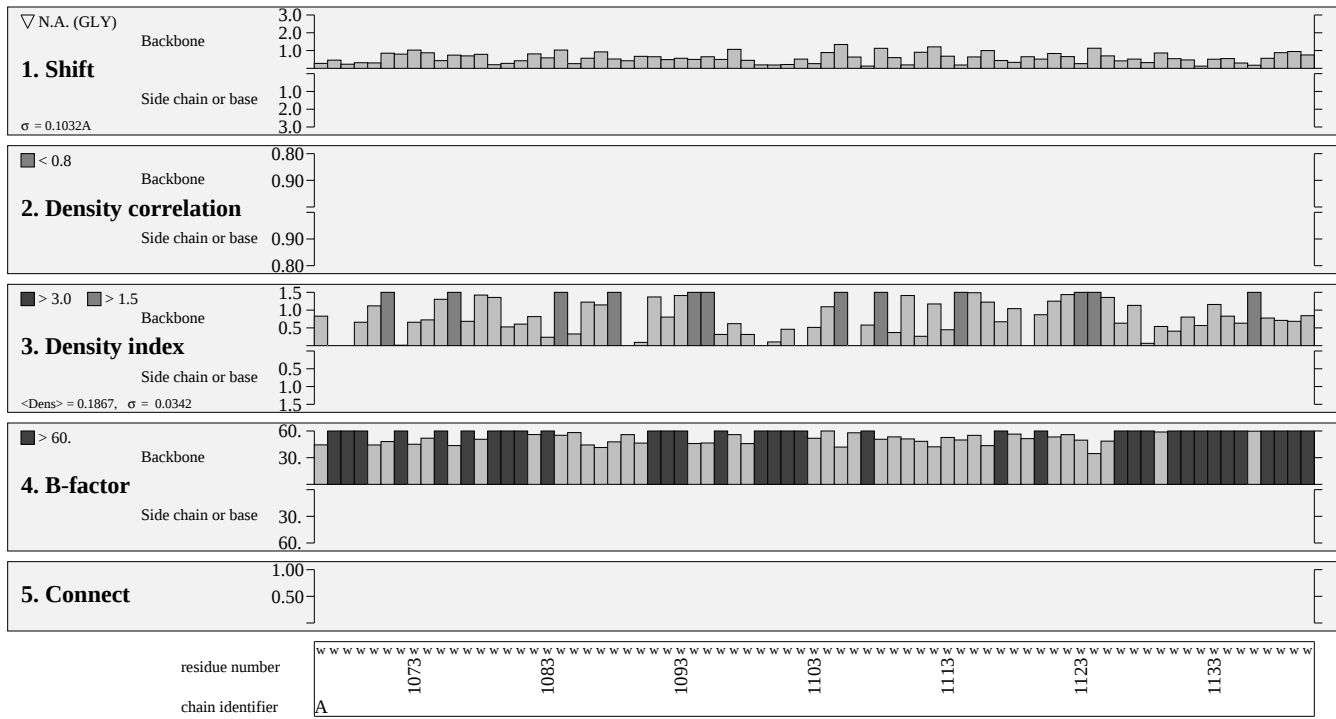
Local estimation (8)



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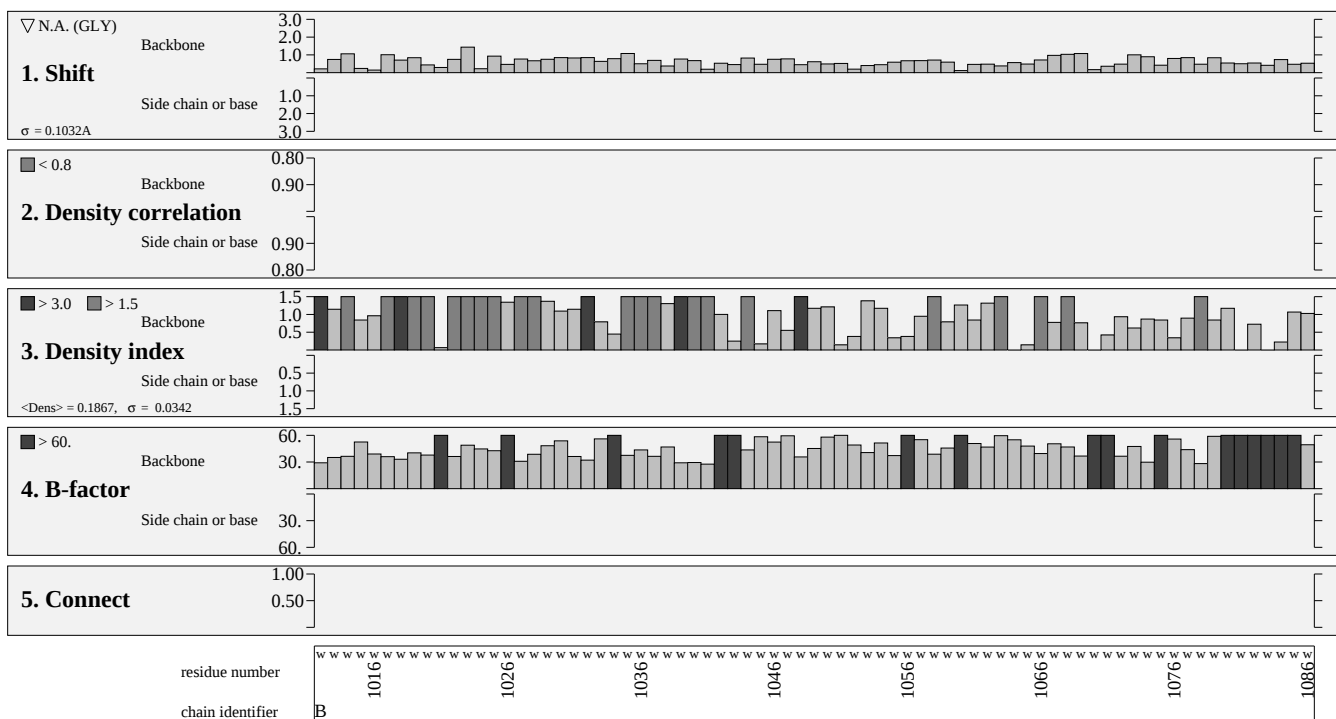
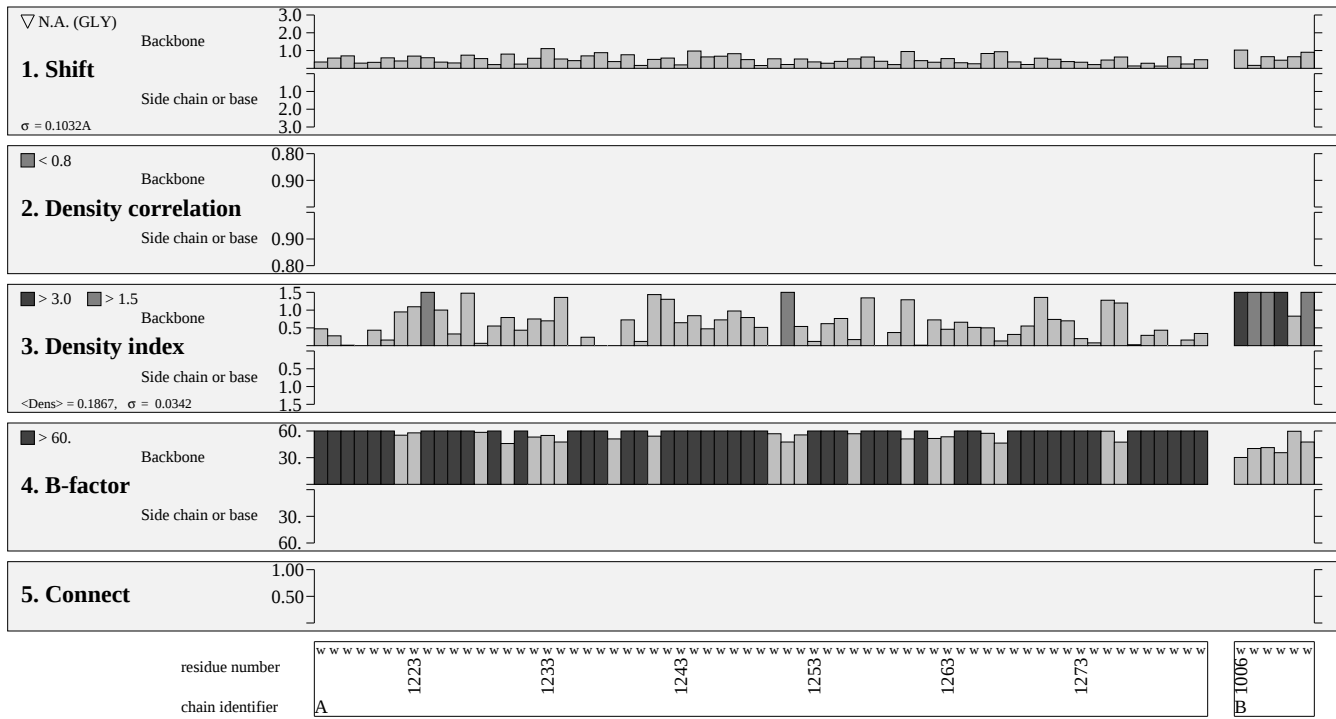
Local estimation (9)



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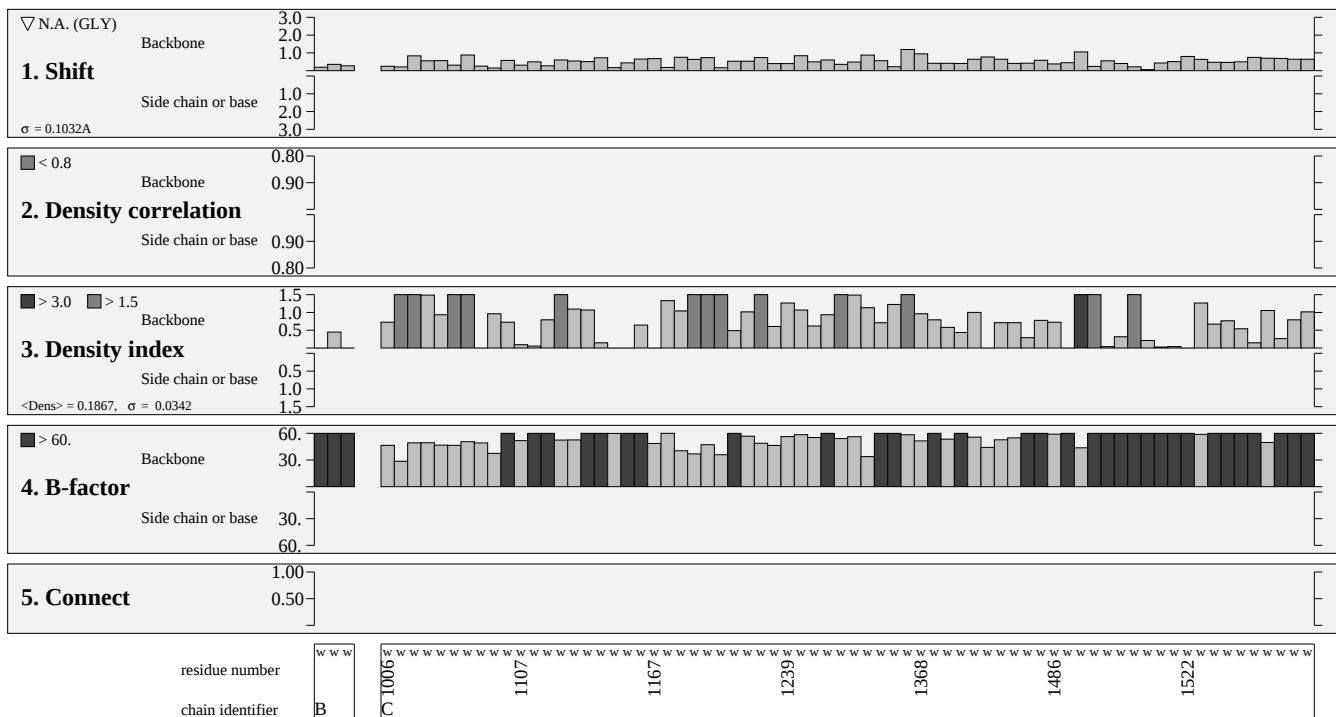
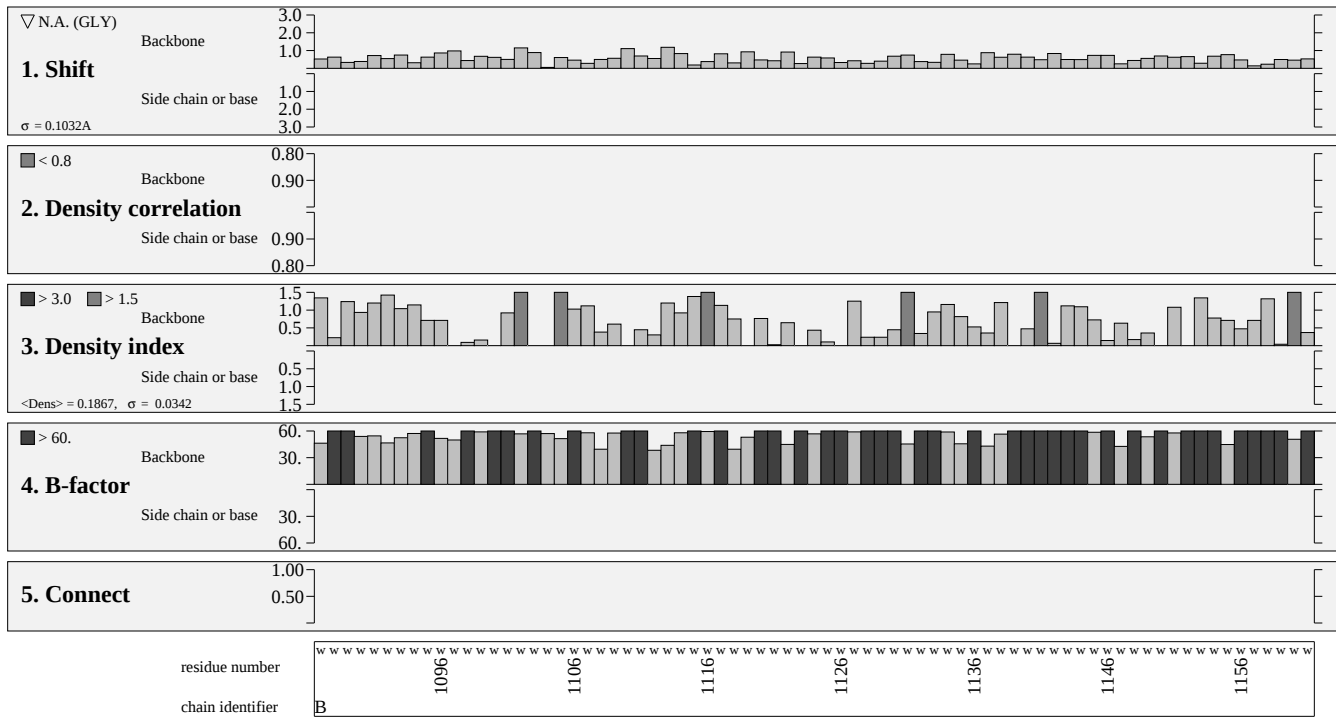
Local estimation (10)



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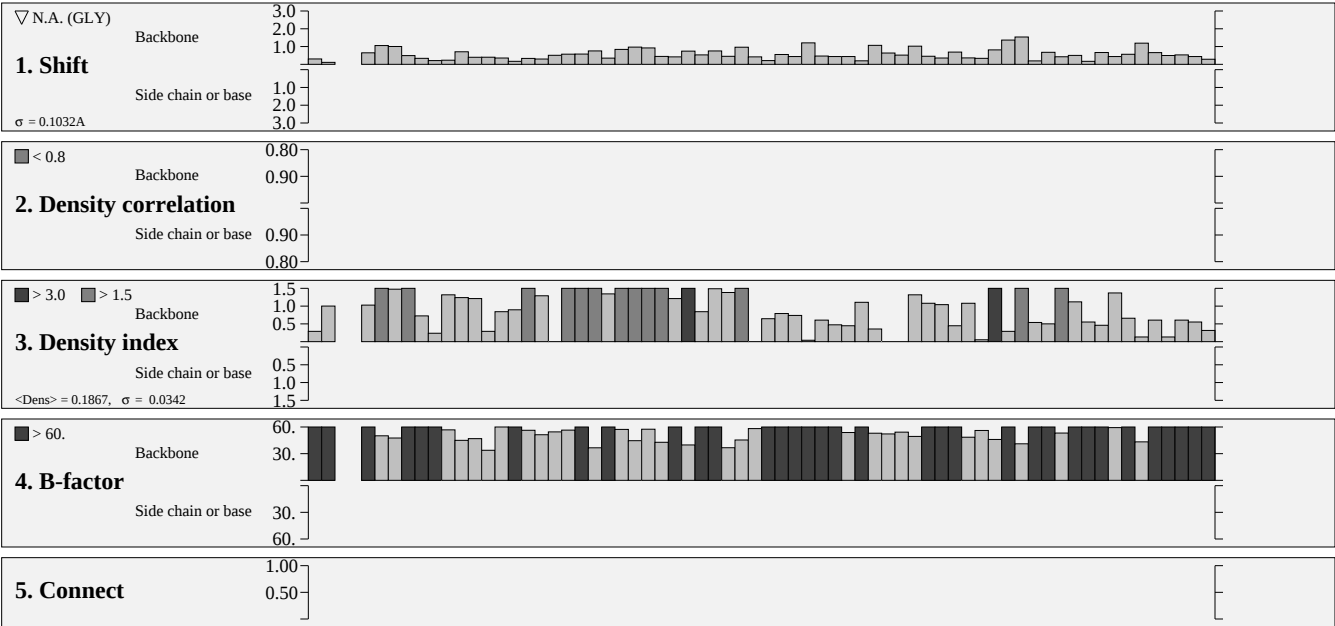
Local estimation (11)



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Local estimation (12)



residue number	1583	1040	1155	1261	1321	1403	1478	1576
chain identifier	C	D						