

# Structure Factor Check

## 3L73

Title: CYTOCHROME BC1 COMPLEX FROM CHICKEN WITH TRIAZOLONE  
INHIBITOR  
Date: 27-DEC-09  
PDB code: 3L73

### Crystal

Cell parameters:

a: 171.50 A b: 182.93 A c: 241.03 A  
 $\alpha$ : 90.00  $\beta$ : 90.00  $\gamma$ : 90.00

Space group: P 21 21 21

### Structure Factors

#### Input

Nominal resolution range: 25.0 – 2.90 A  
 Reflections in file: 166720  
 Unique reflections above 0: 166720  
 above 1 $\sigma$ : 161882  
 above 3 $\sigma$ : 96414

#### SFCHECK

Nominal resolution range: 25.0 – 3.04 A  
\05max. from input data, min. from author\05  
 Used reflections: 145117  
 Reflections out of resolution: 21603  
 Completeness: 99.7 %  
 $R_{\text{stand}}(F) = \langle \sigma(F) \rangle / \langle F \rangle$  : 0.073  
 Anisotropic distribution of Structure Factors  
 ratio of eigen values: 1.0000 0.4474 0.4507  
 $B_{\text{overall}}$  (by Patterson): 53. A<sup>2</sup>  
 Optical resolution: 2.25 A  
 Expected opt. resol. for complete data set: 2.25 A  
 Estimated minimal error: 0.093 A

### Model

32645 atoms (19 water molecules)

Number of chains: 51  
 Volume not occupied by model: 62.4 %  
 $\langle B \rangle$  (for atomic model): 79.6 A<sup>2</sup>  
 $\sigma(B)$ : 18.27 A<sup>2</sup>  
 Matthews coefficient: 4.14  
 Corresponding solvent % : 70.03

### Model vs. Structure Factors

R-factor for all reflections: 0.306  
 Correlation factor: 0.851  
 R-factor: 0.307  
 for  $F > 2.0\sigma$   
 nom. resolution range: 24.97 – 3.04A  
 reflections used: 141488

Rfree: 0.335  
 Nfree: 2775  
 R-factor without free-refl.: 0.307  
 Non free-reflections: 138713  
 $\langle u \rangle$  (error in coords by Luzzati plot): 0.604 A  
 Estimated maximal error: 0.414 A  
 DPI: 0.376 A

#### Scaling

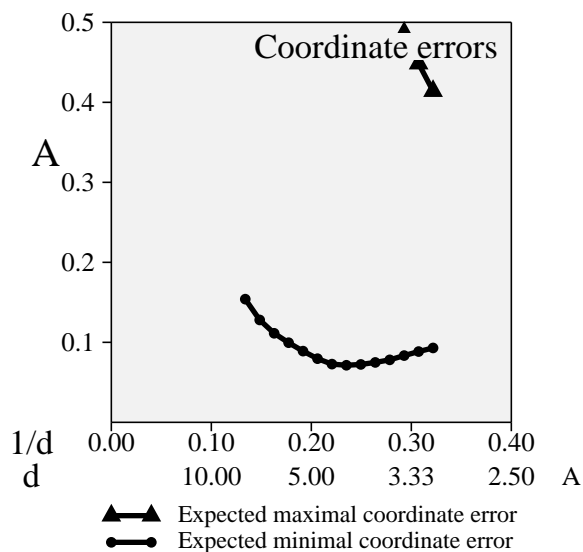
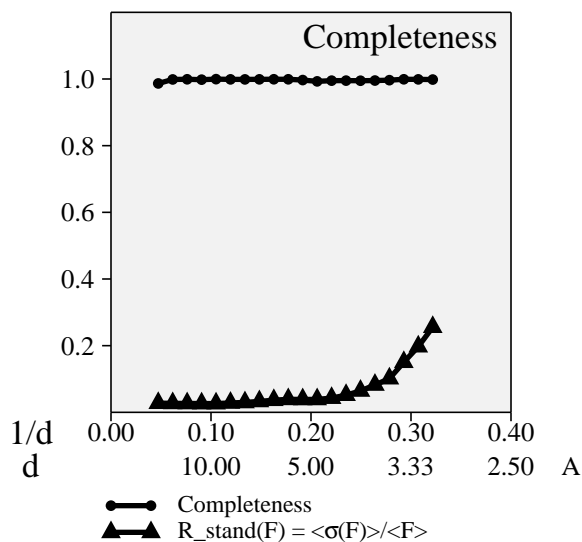
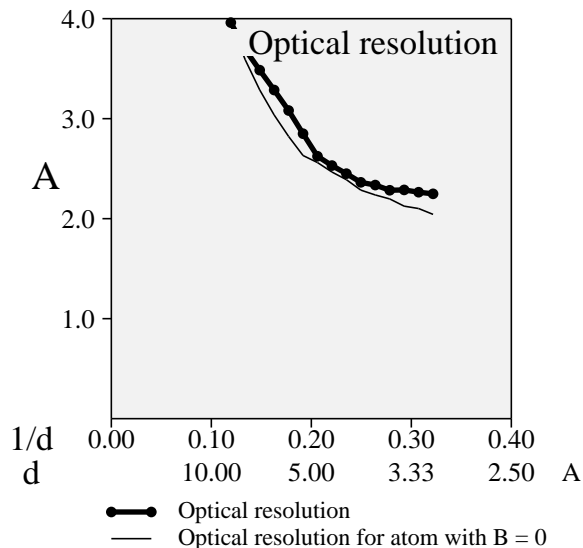
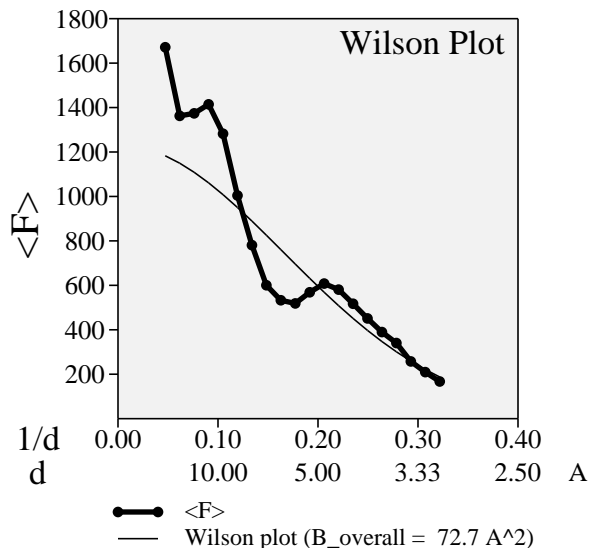
Scale: 0.483  
 Bdiff: -9.31  
 Anisothermal Scaling (Beta):  
 12.5073 -4.4573 -3.7911 0.0000 0.0000 0.0000  
 Solvent correction – Ks,Bs: 0.416 250.040

### Refinement

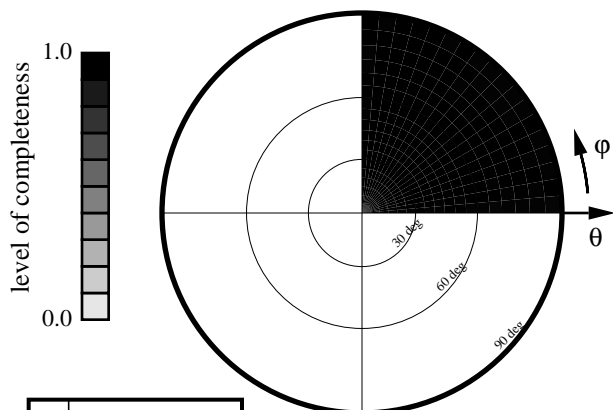
Program: CNS 1.1  
 Nominal resolution range: 25.0 – 3.04 A  
 Reported nominal resolution: 3.00 A  
 Reported R-factor: 0.259  
 Number of reflections used: 145117  
 Reported Rfree: 0.29  
 Sigma cut-off: N.A.

# Structure Factor Check

## 3L73

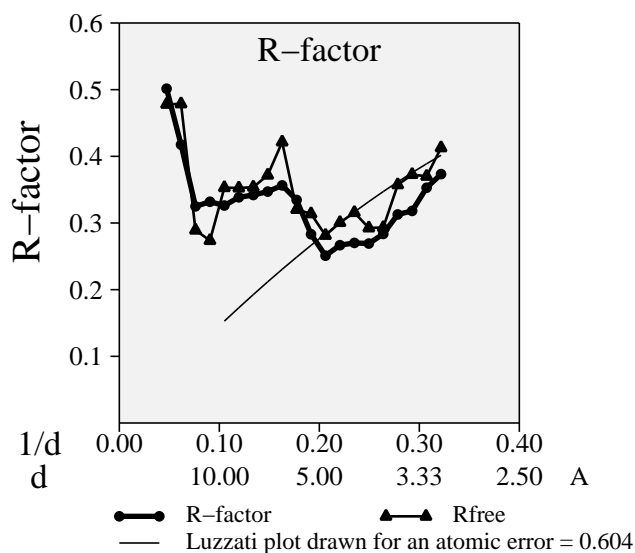


Stereographic projection of the averaged radial completeness



	$\theta$	$\phi$
h	90.00	0.00
k	90.00	90.00
l	0.00	0.00

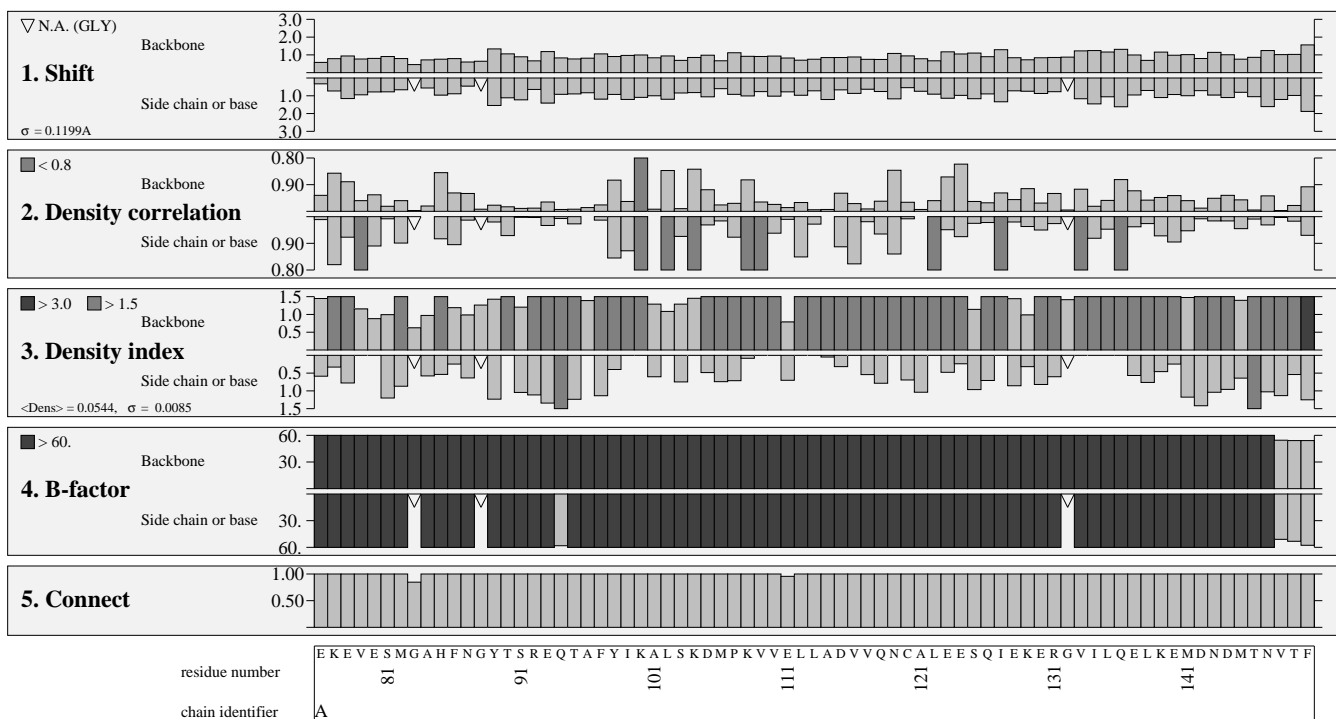
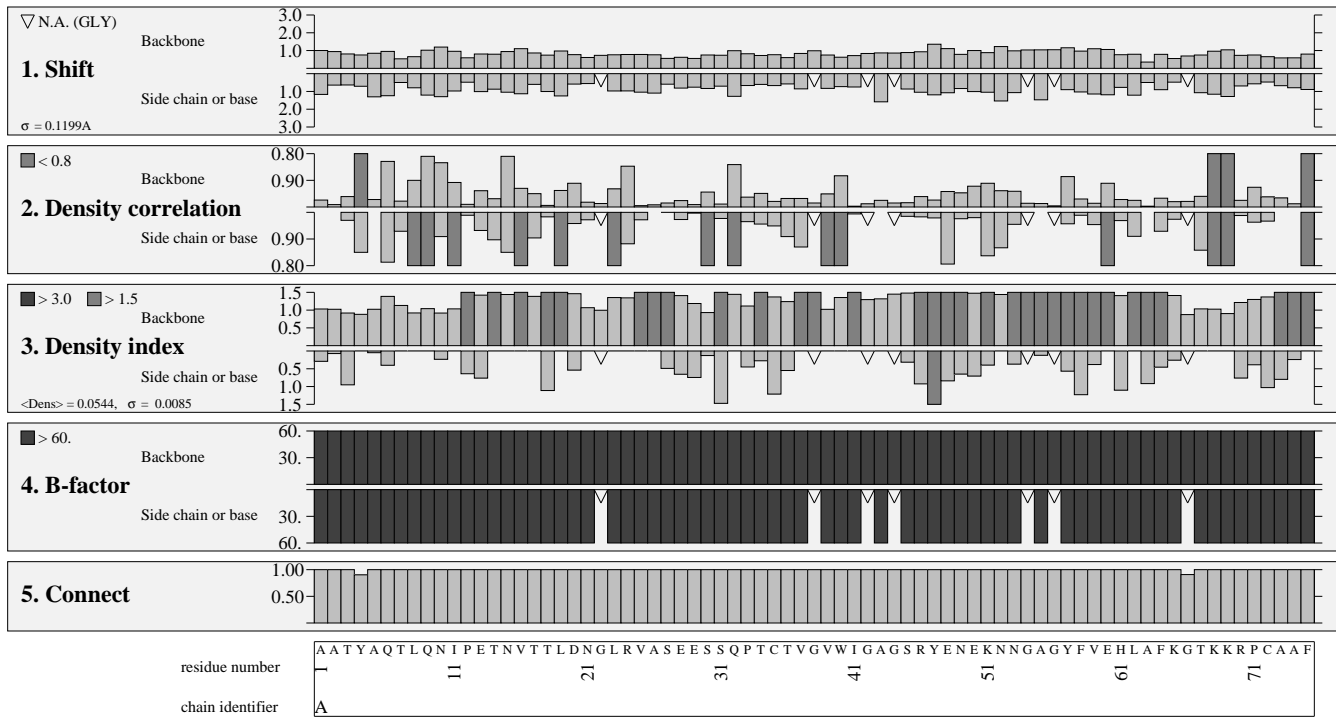
polar coordinates of the crystallographical axes



# Structure Factor Check

## 3L73

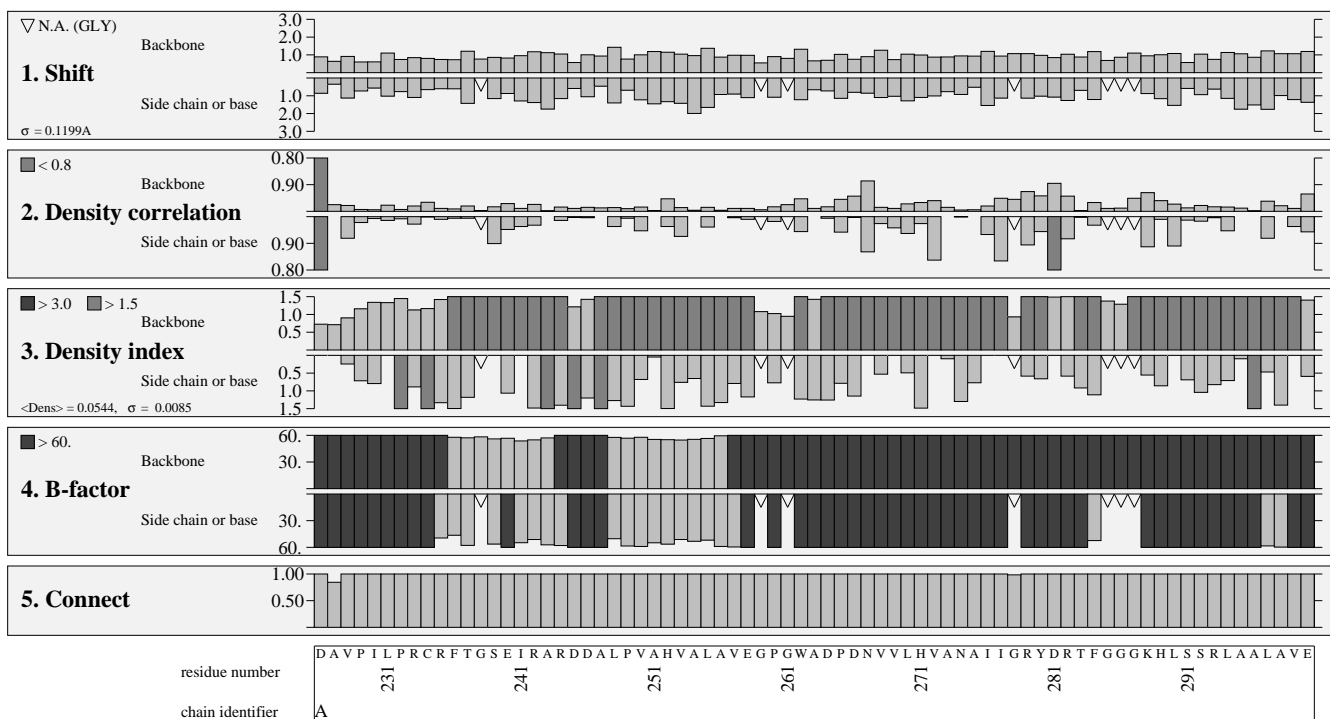
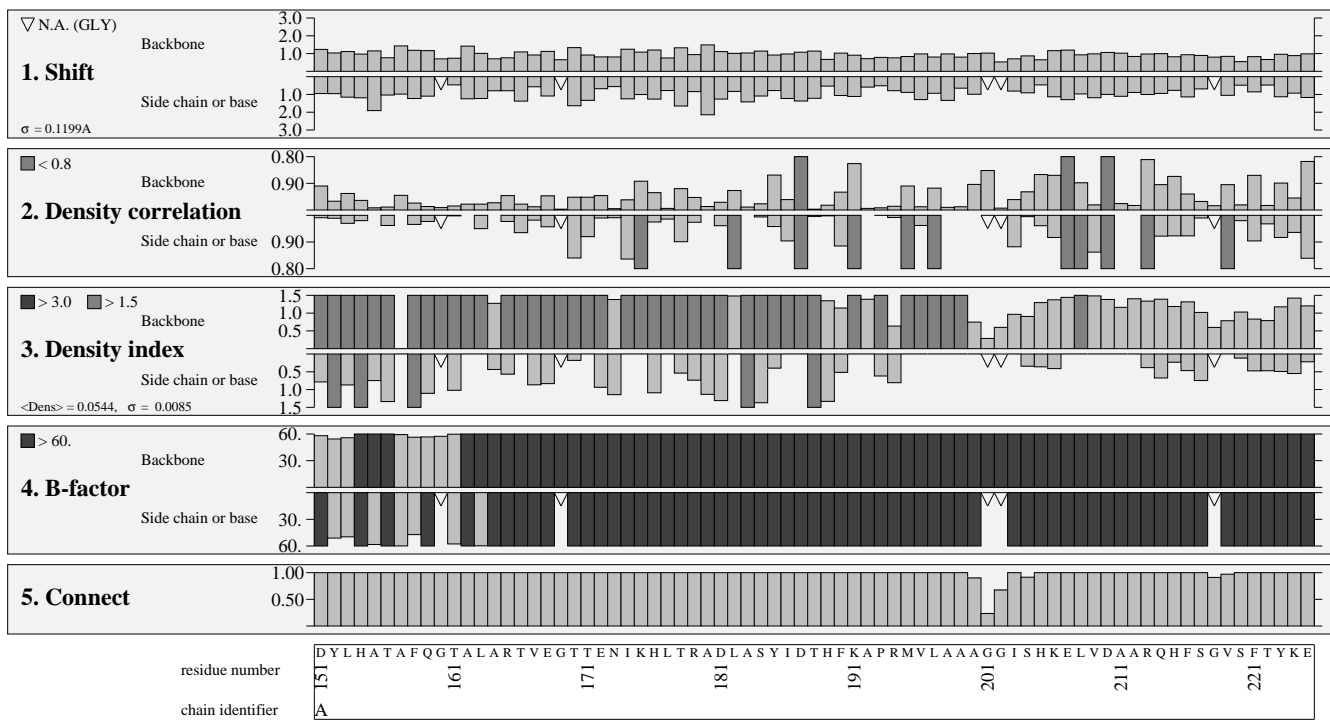
### Local estimation



# Structure Factor Check

## 3L73

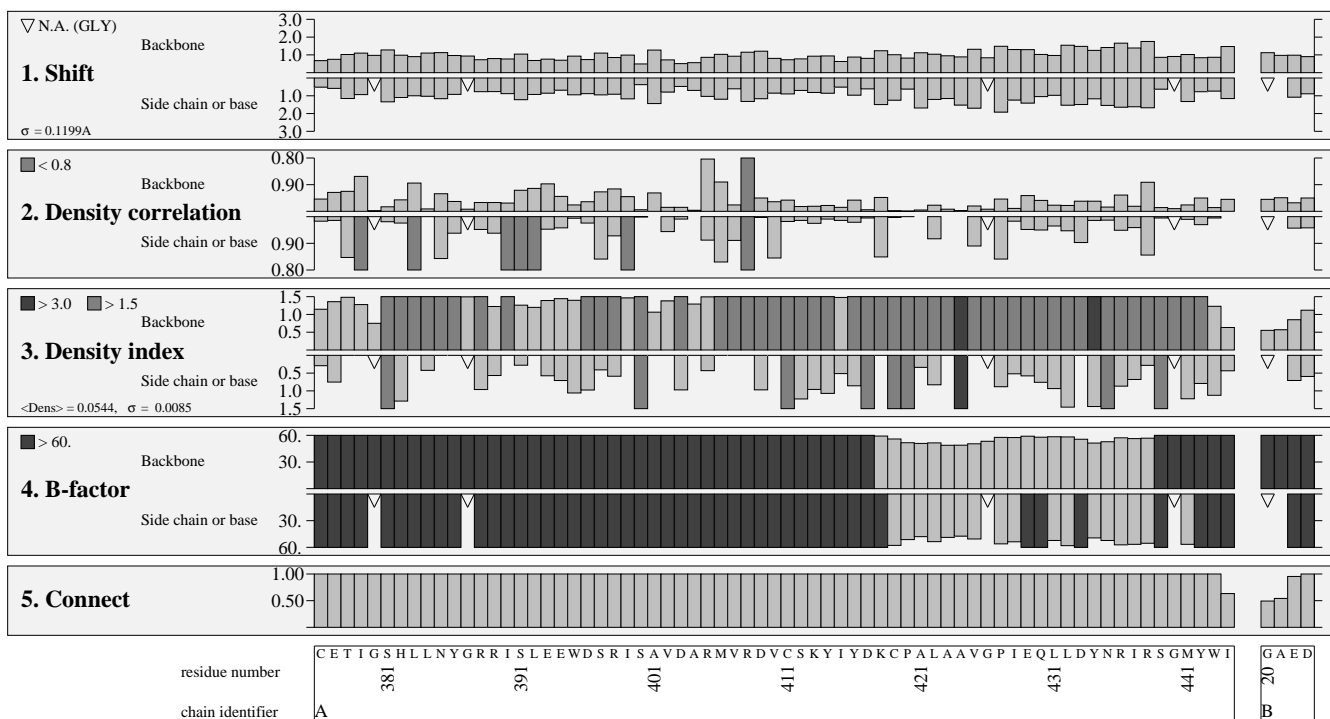
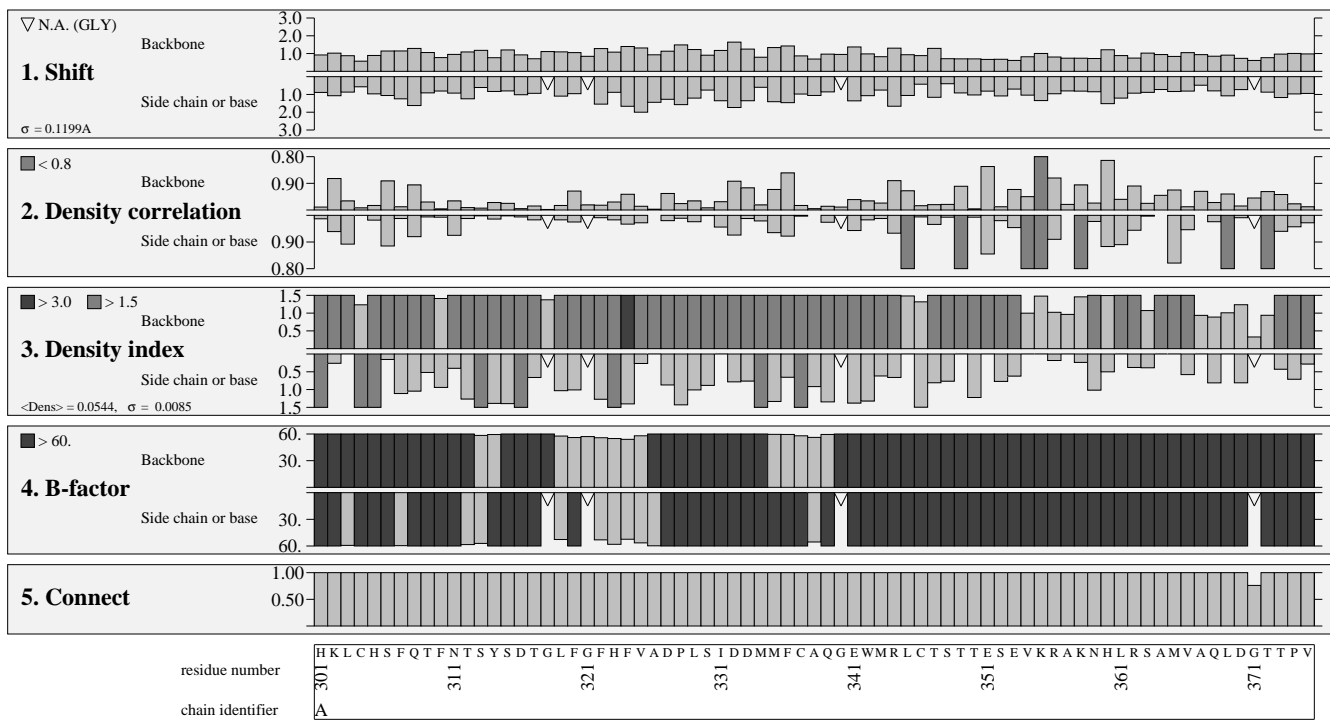
### Local estimation (2)



# Structure Factor Check

## 3L73

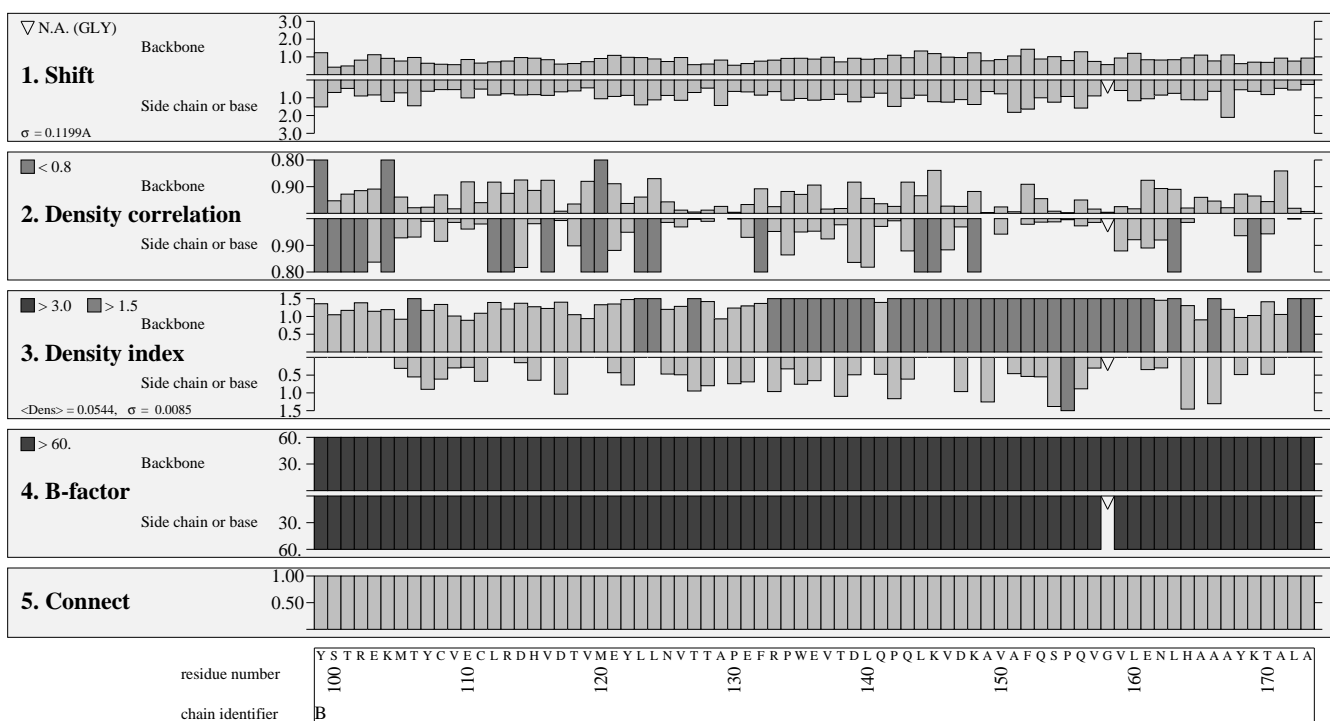
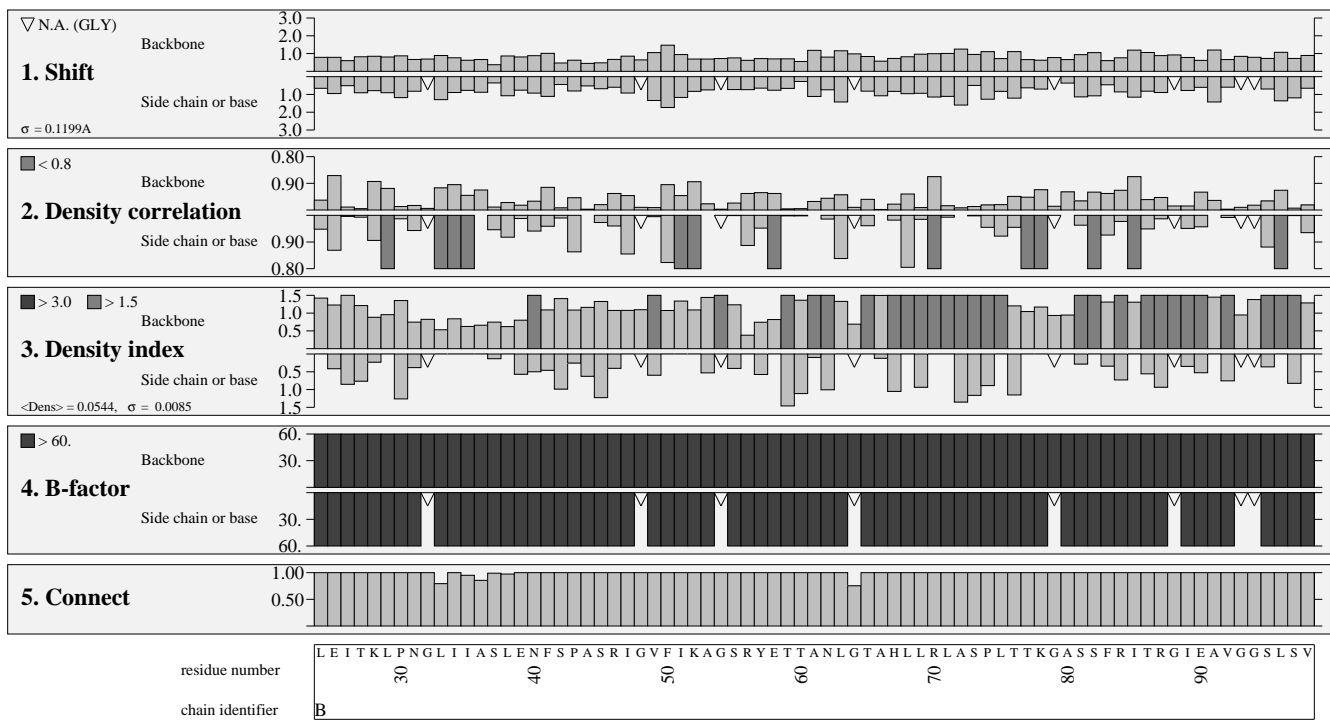
### Local estimation (3)



# Structure Factor Check

## 3L73

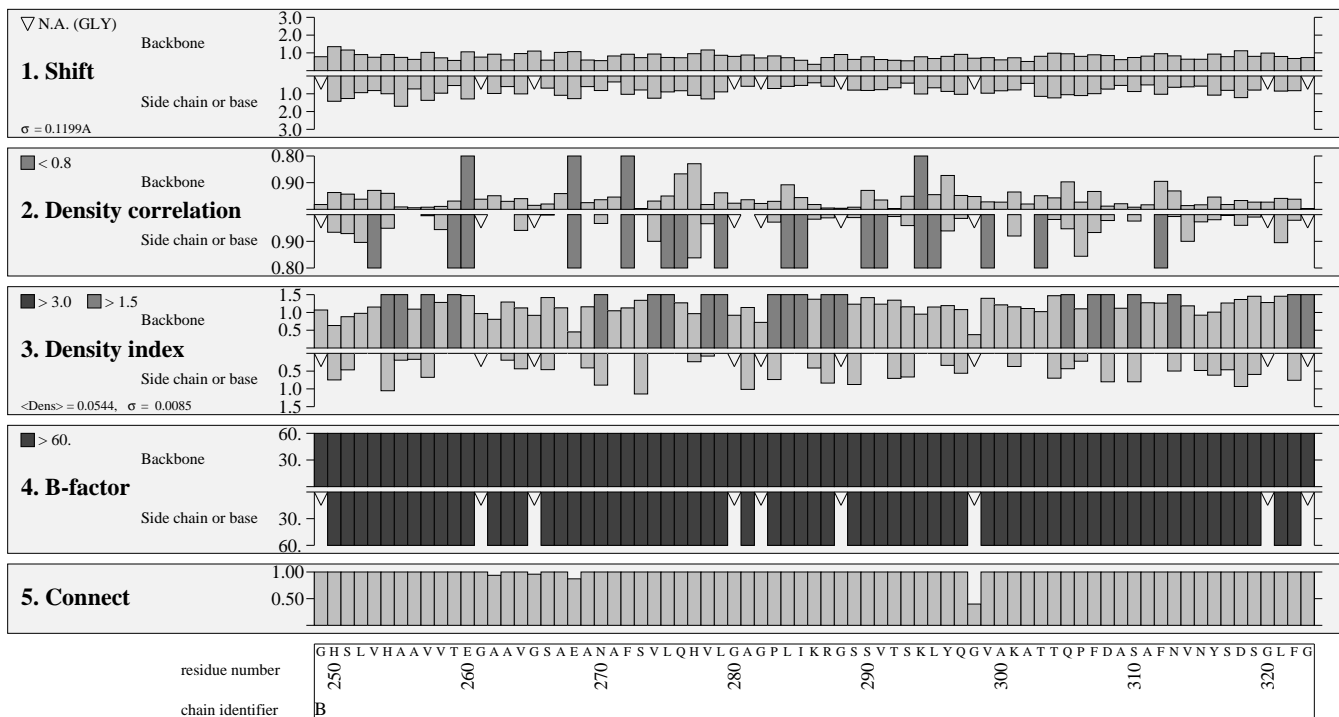
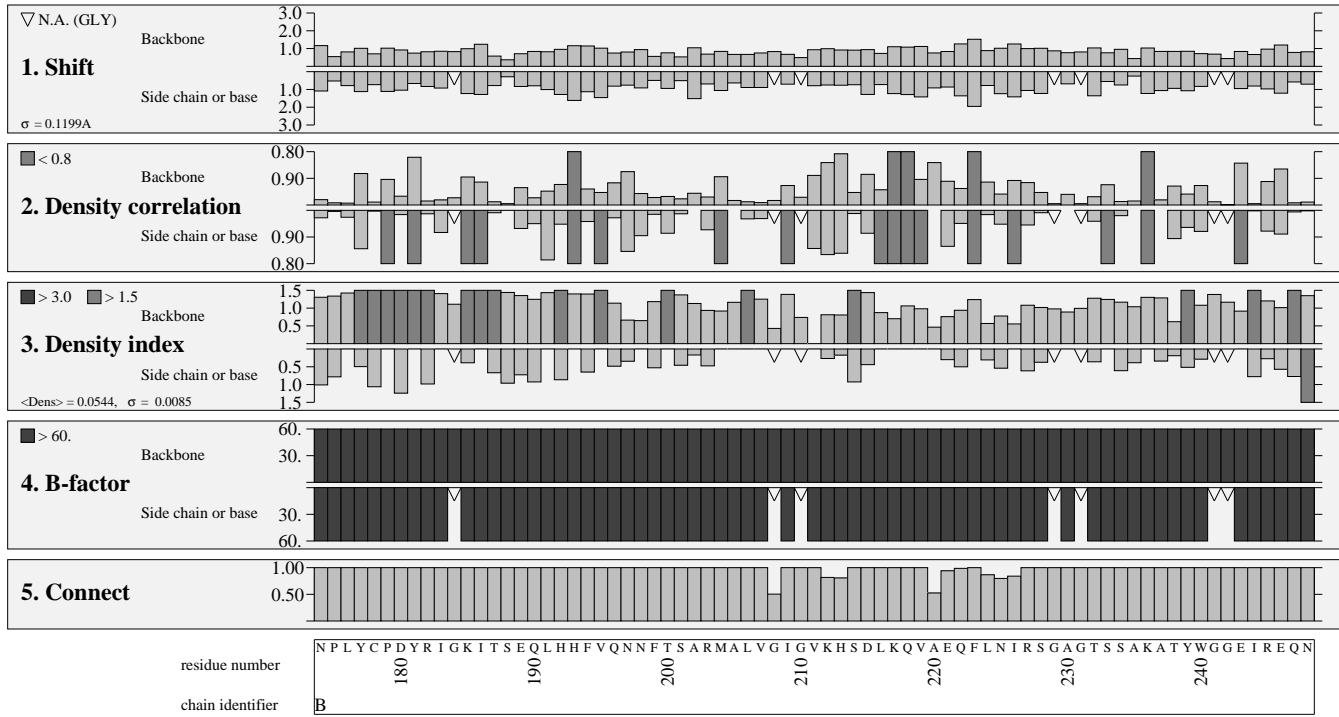
### Local estimation (4)



# Structure Factor Check

## 3L73

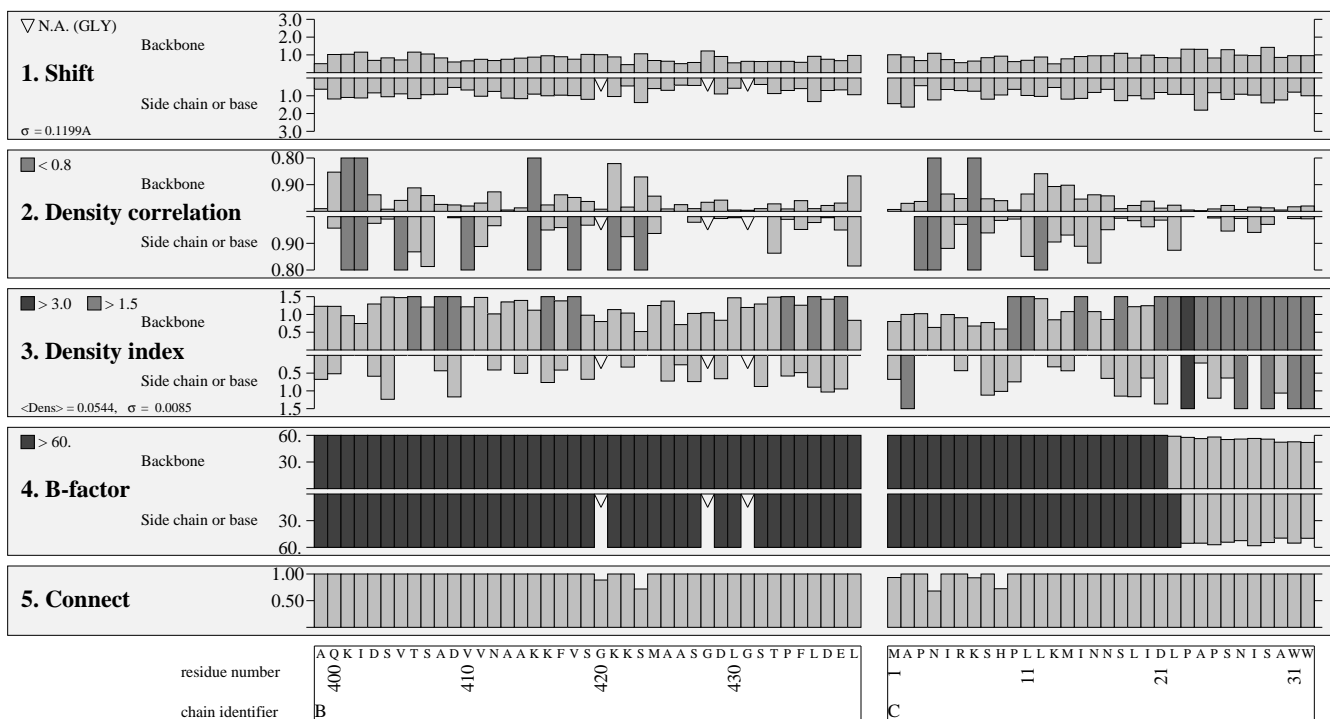
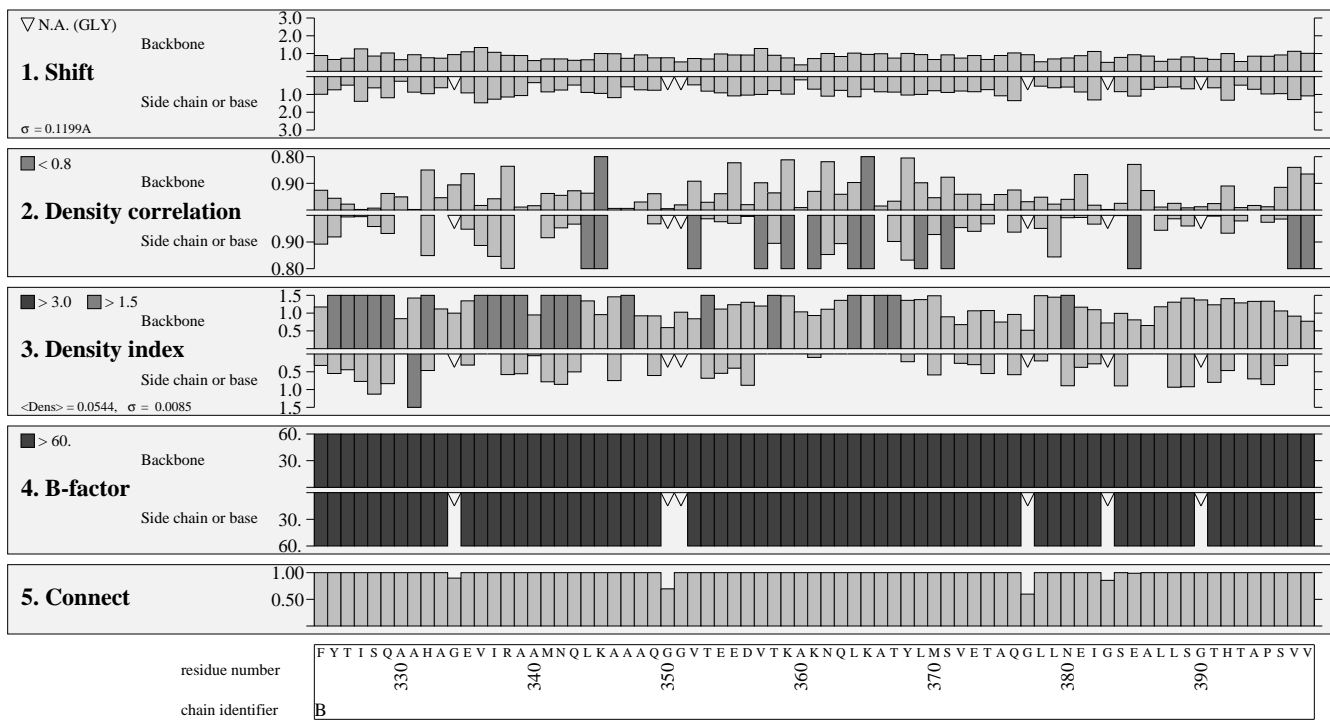
### Local estimation (5)



# Structure Factor Check

## 3L73

### Local estimation (6)

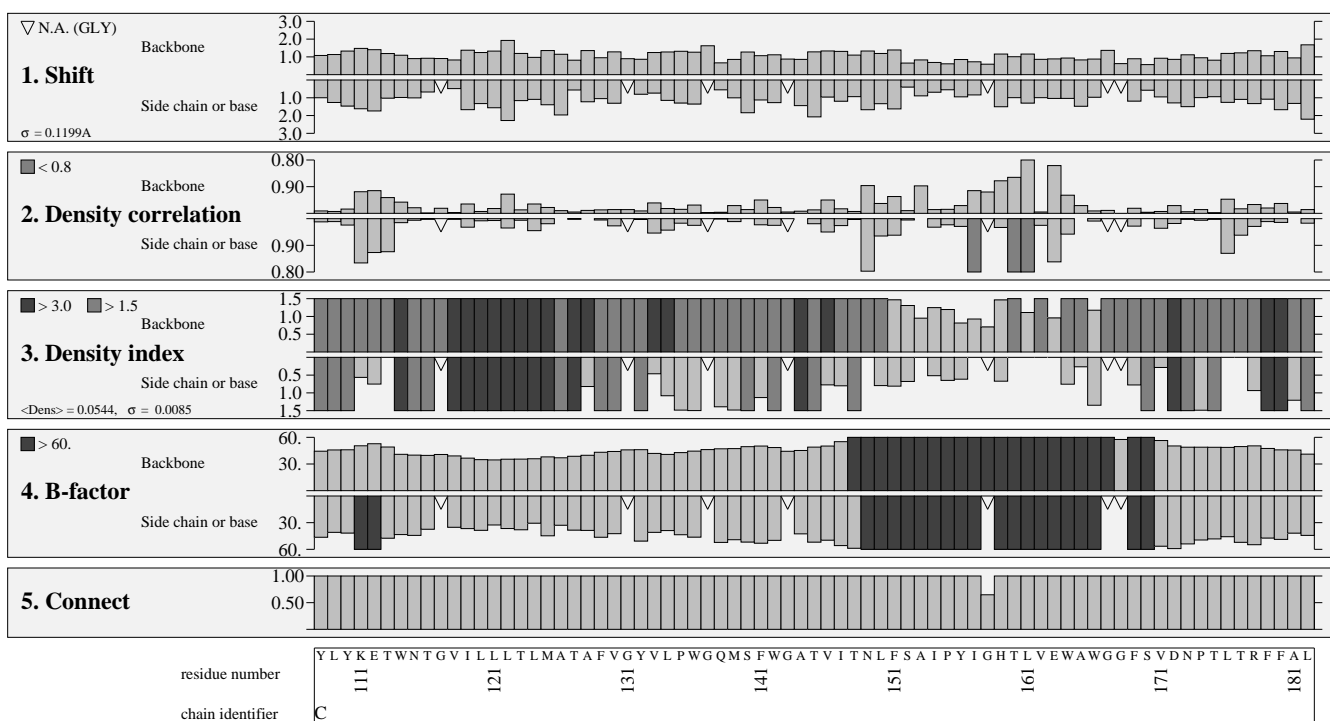
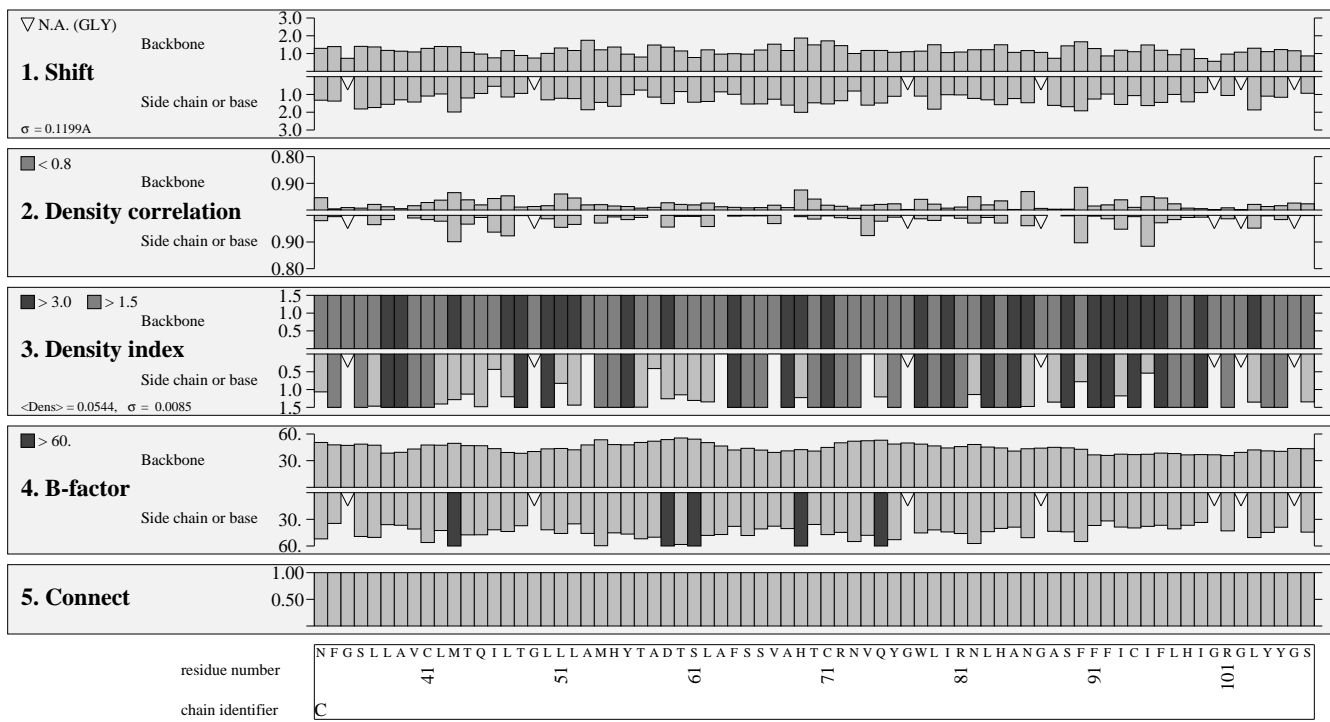




# Structure Factor Check

## 3L73

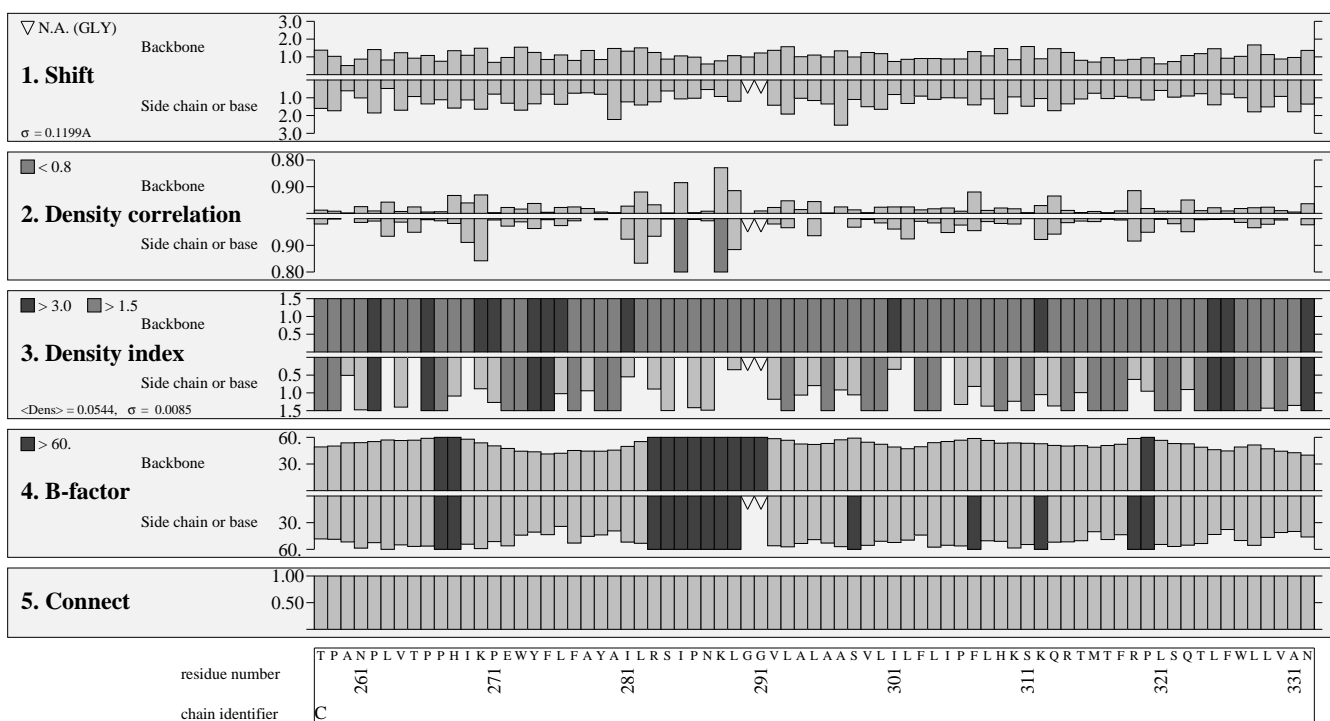
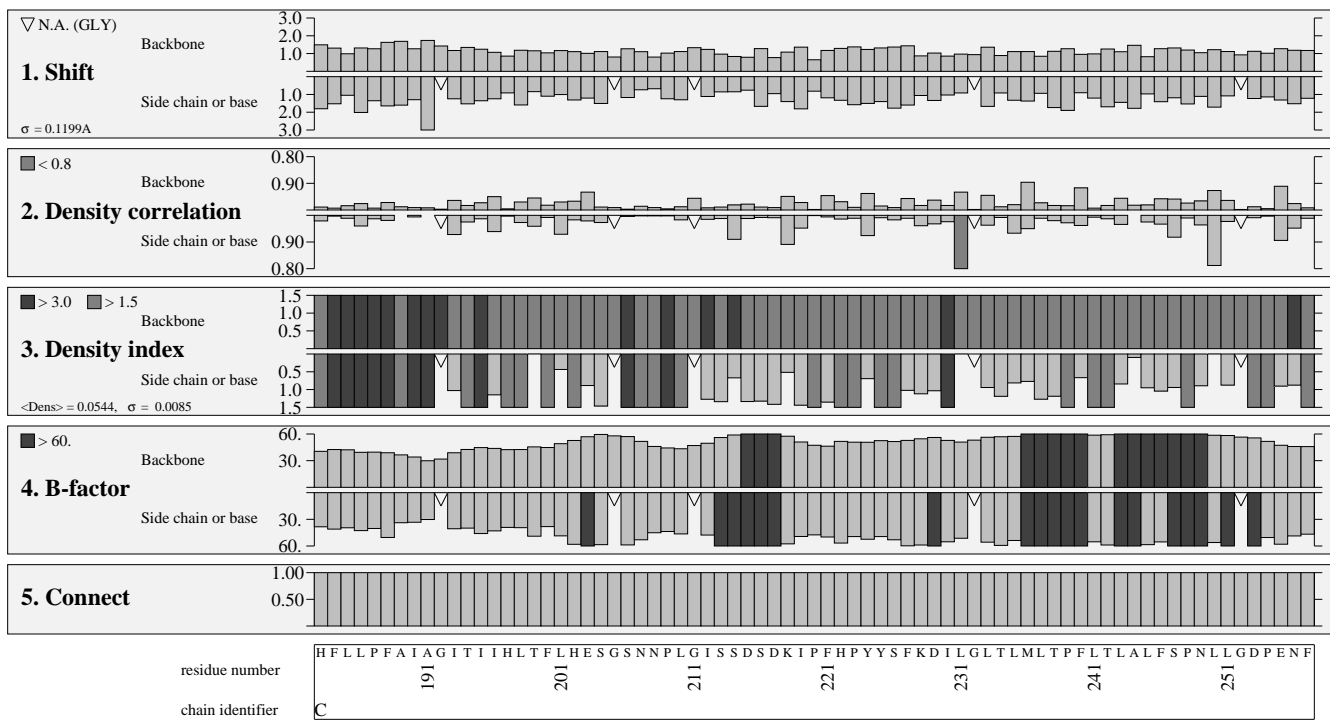
### Local estimation (7)



# Structure Factor Check

## 3L73

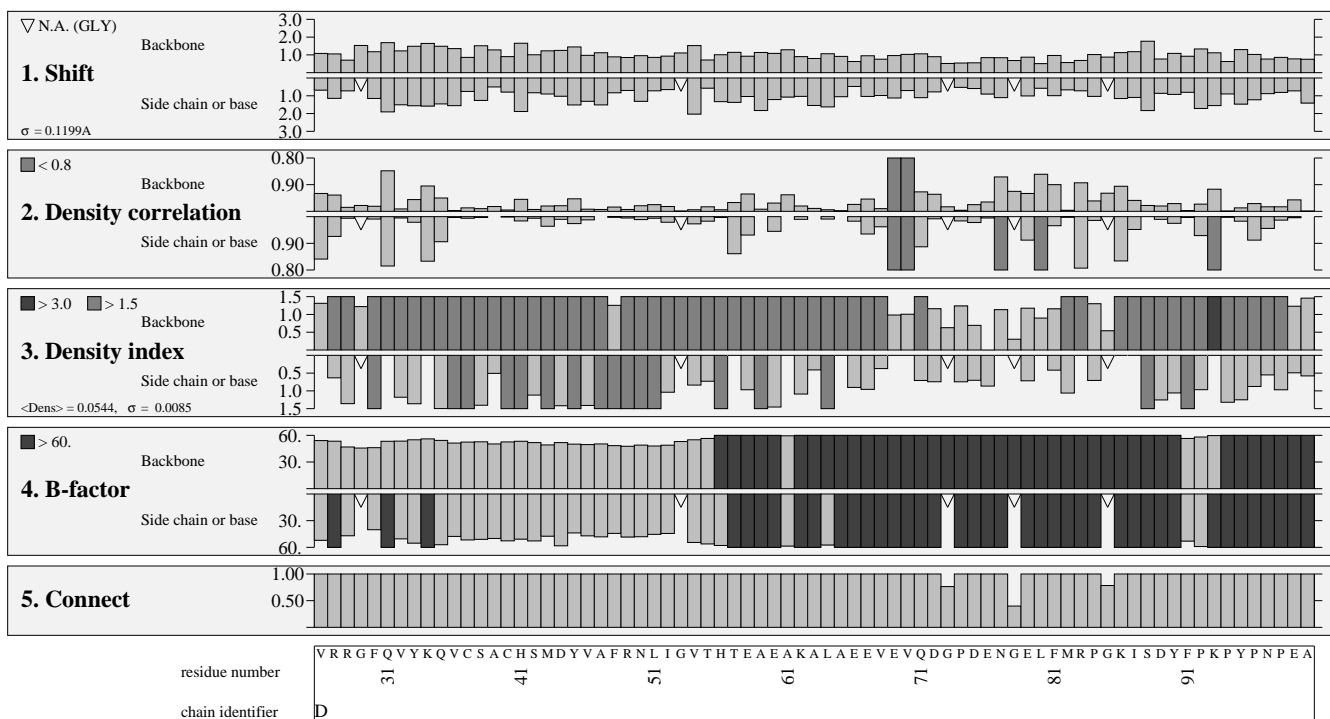
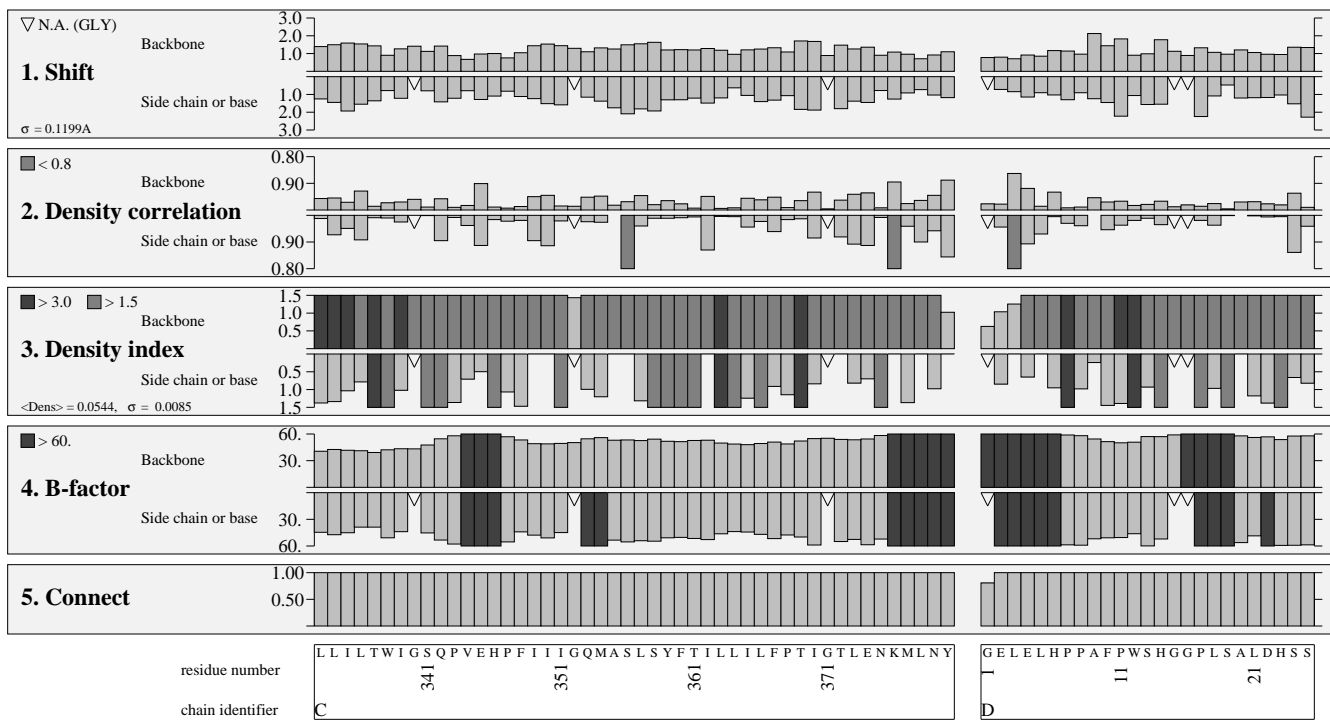
### Local estimation (8)



# Structure Factor Check

## 3L73

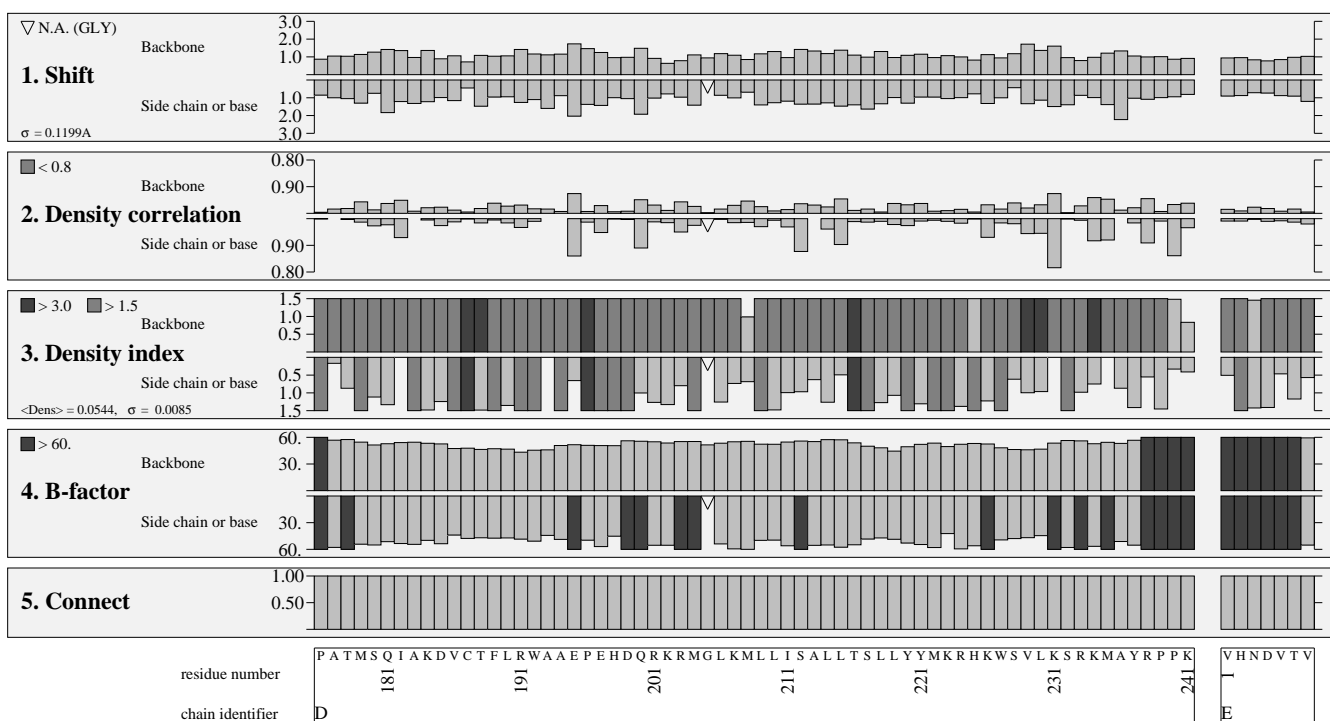
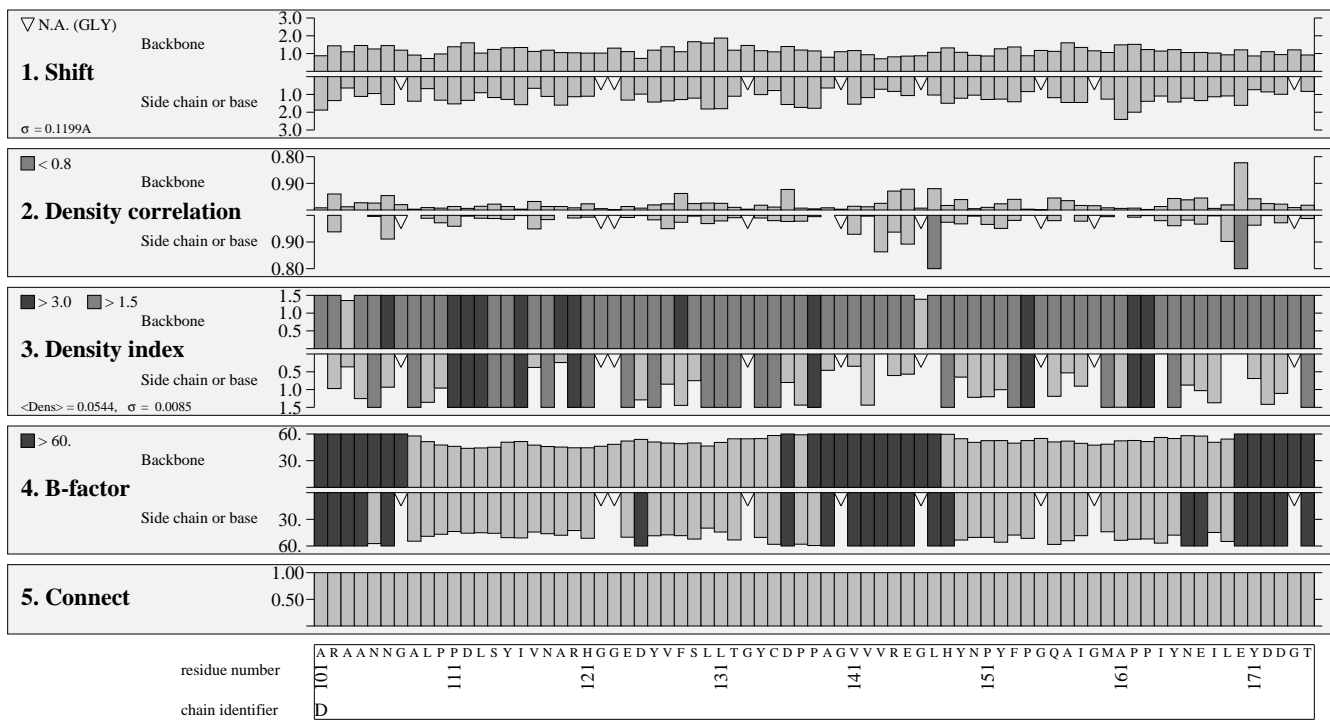
### Local estimation (9)



# Structure Factor Check

## 3L73

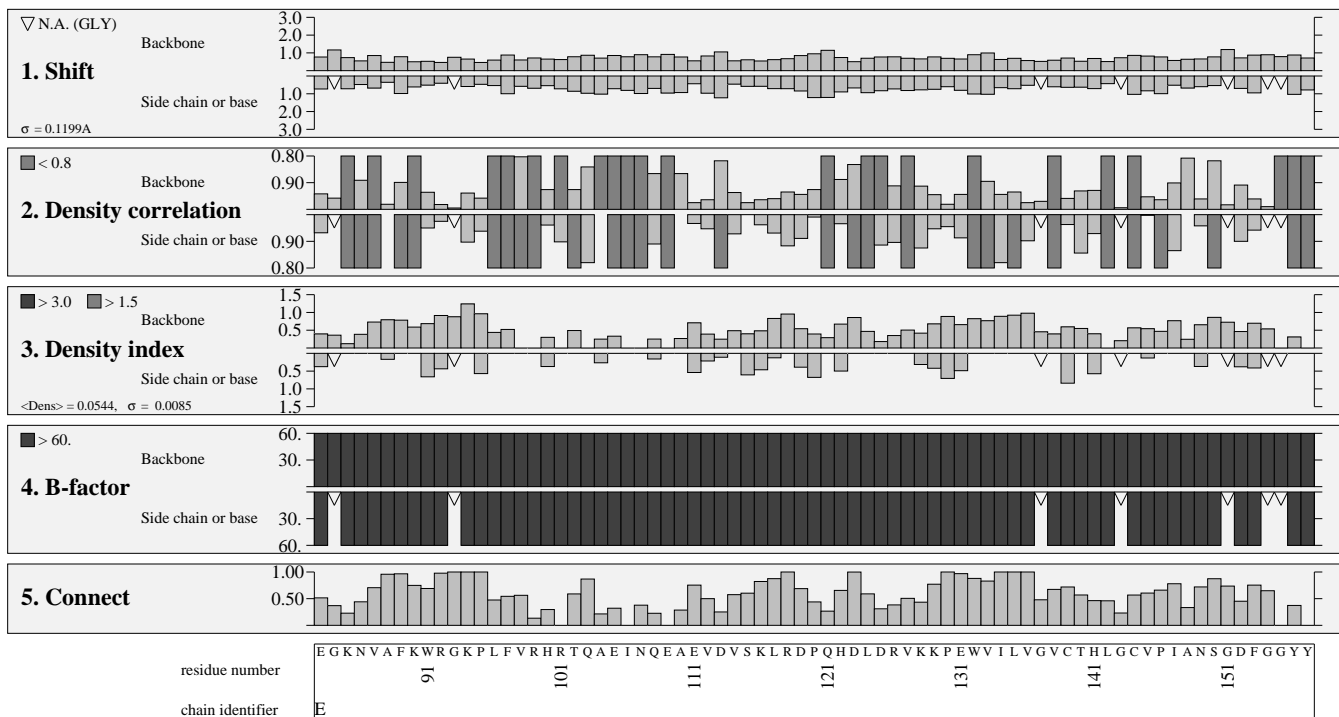
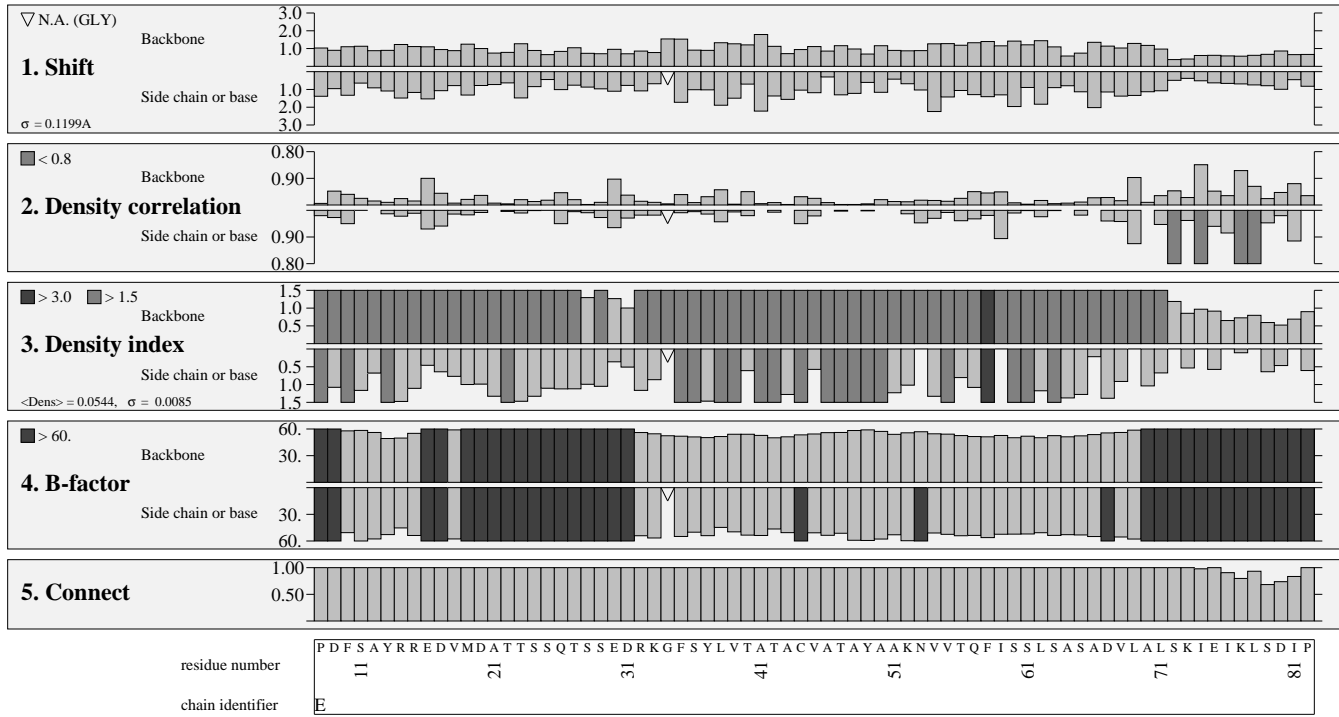
### Local estimation (10)



# Structure Factor Check

## 3L73

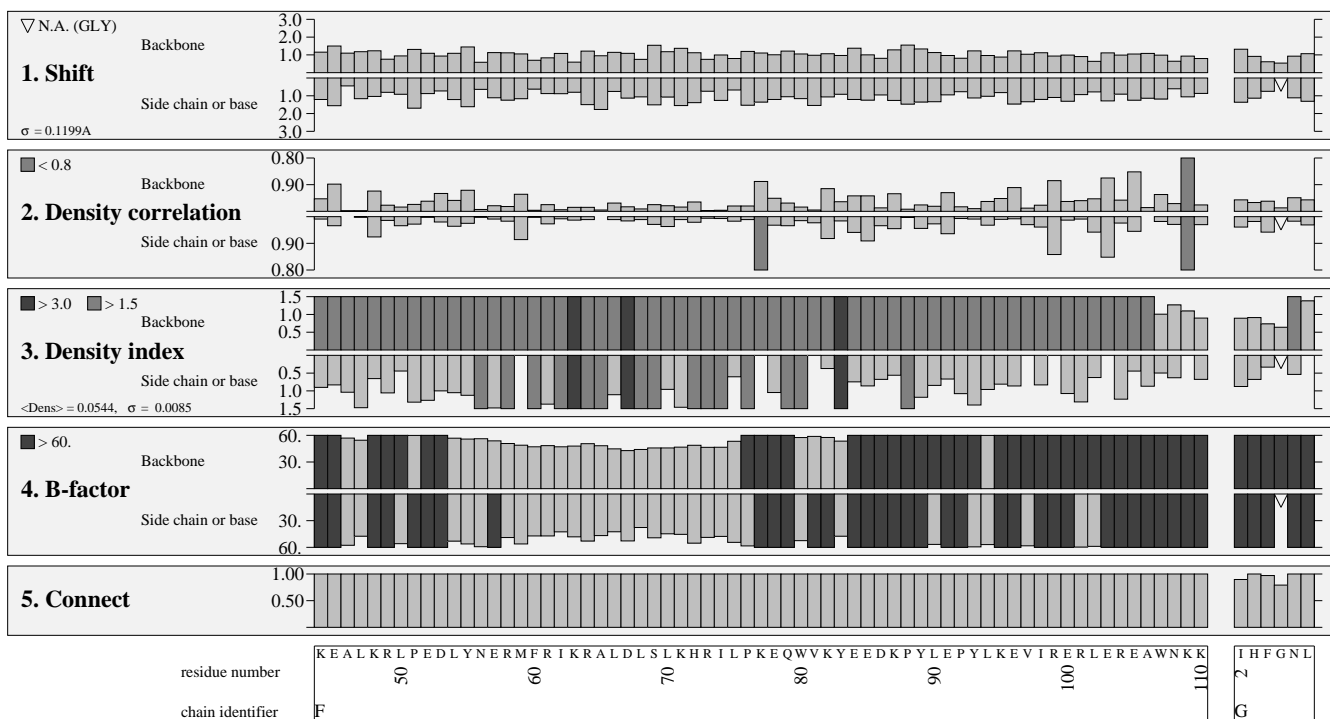
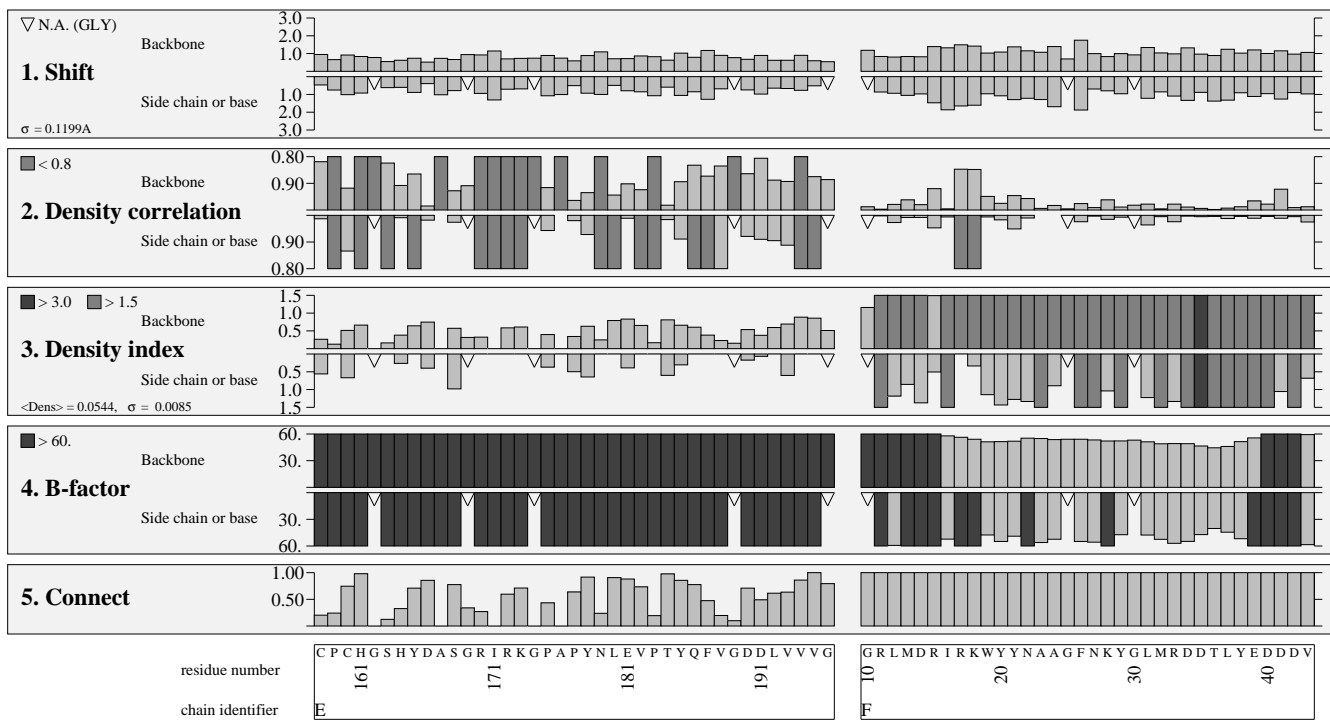
### Local estimation (11)



# Structure Factor Check

## 3L73

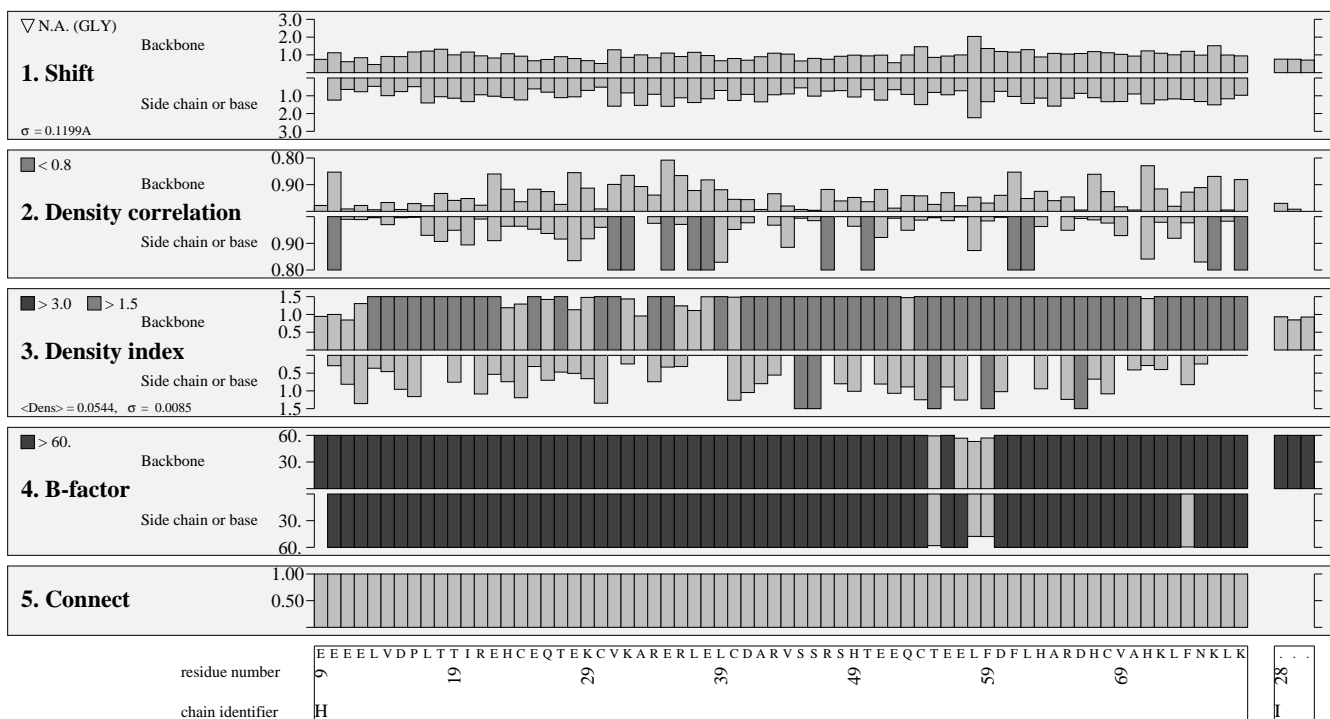
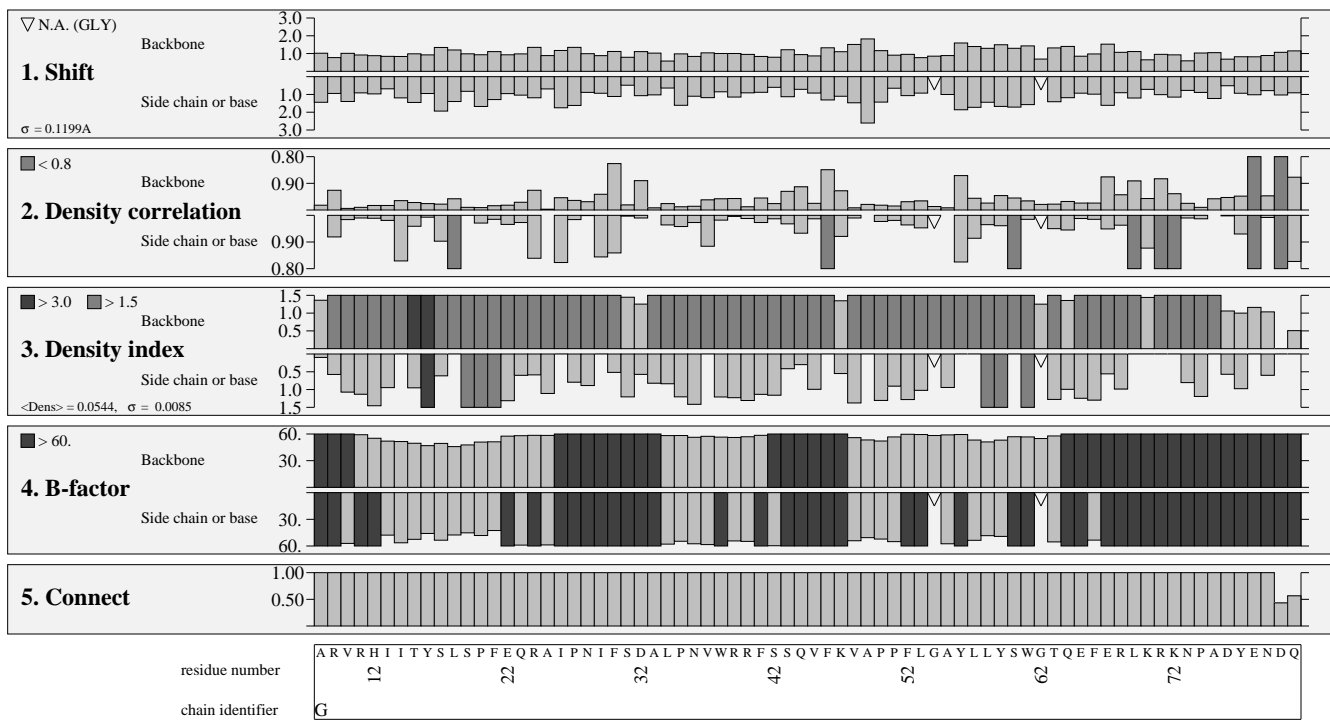
### Local estimation (12)



# Structure Factor Check

## 3L73

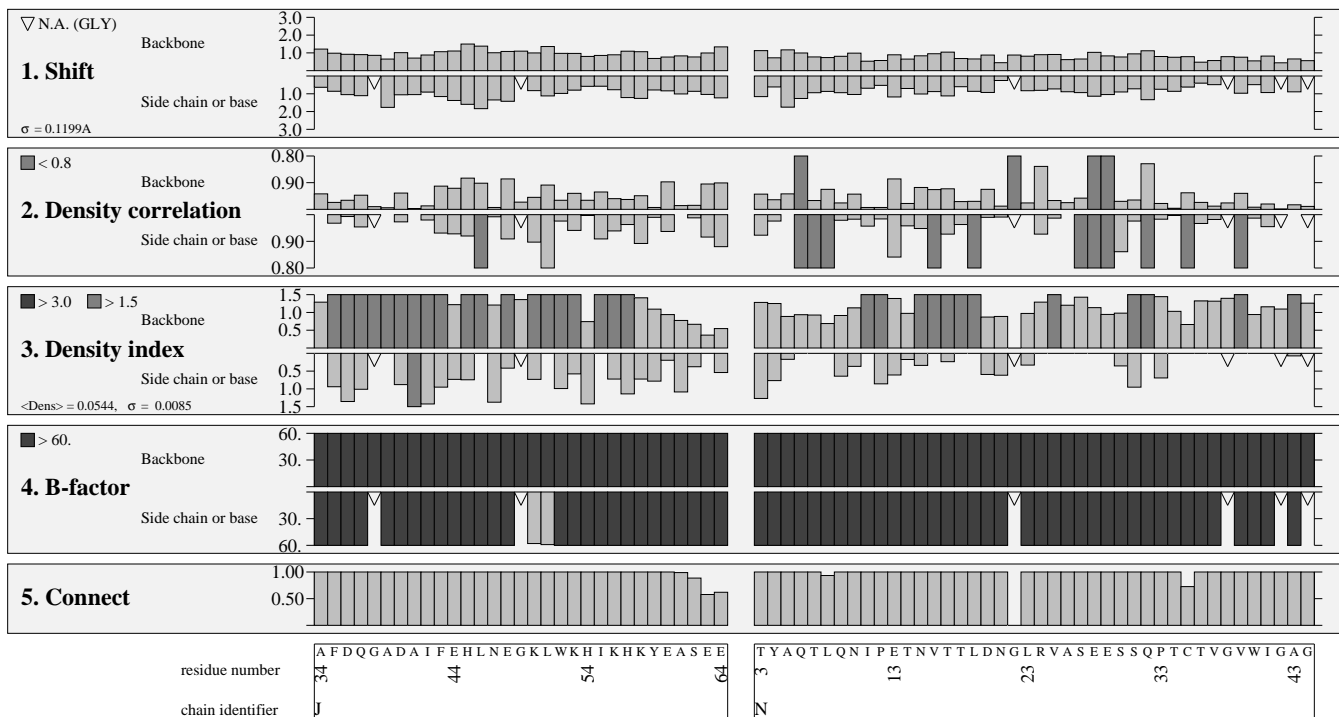
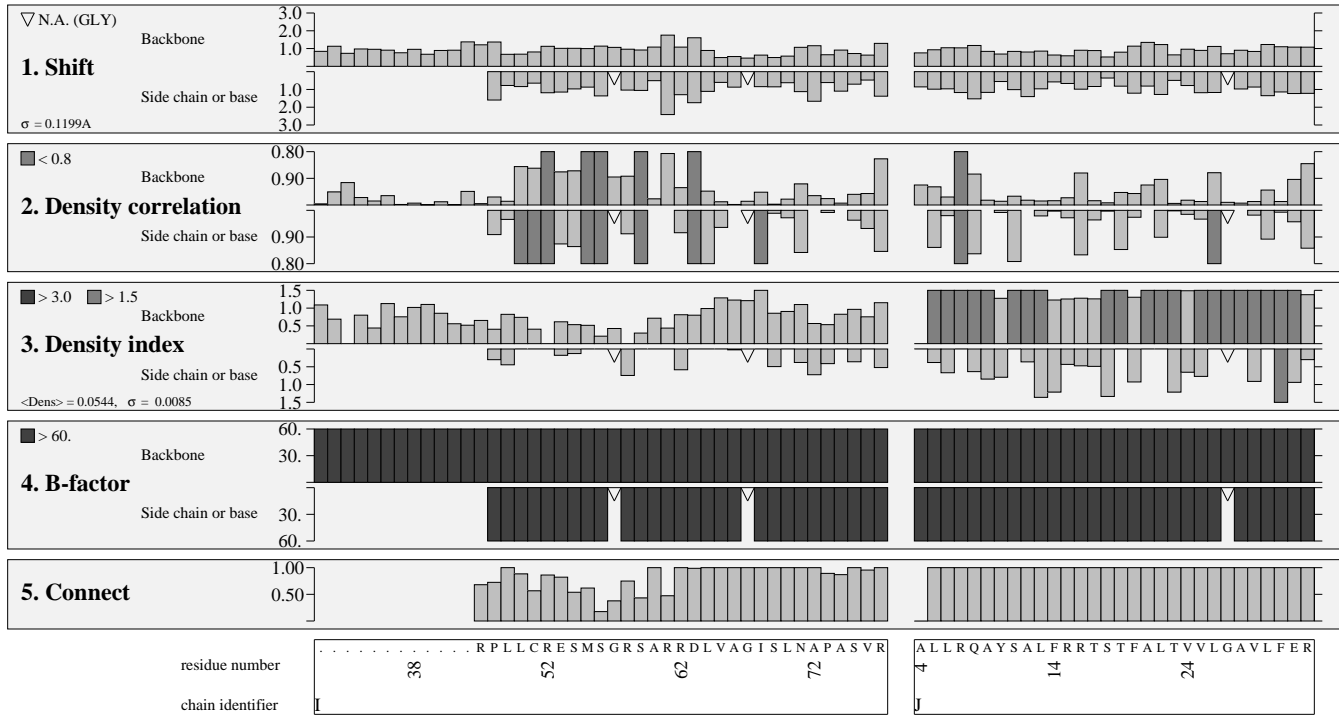
### Local estimation (13)



# Structure Factor Check

## 3L73

### Local estimation (14)

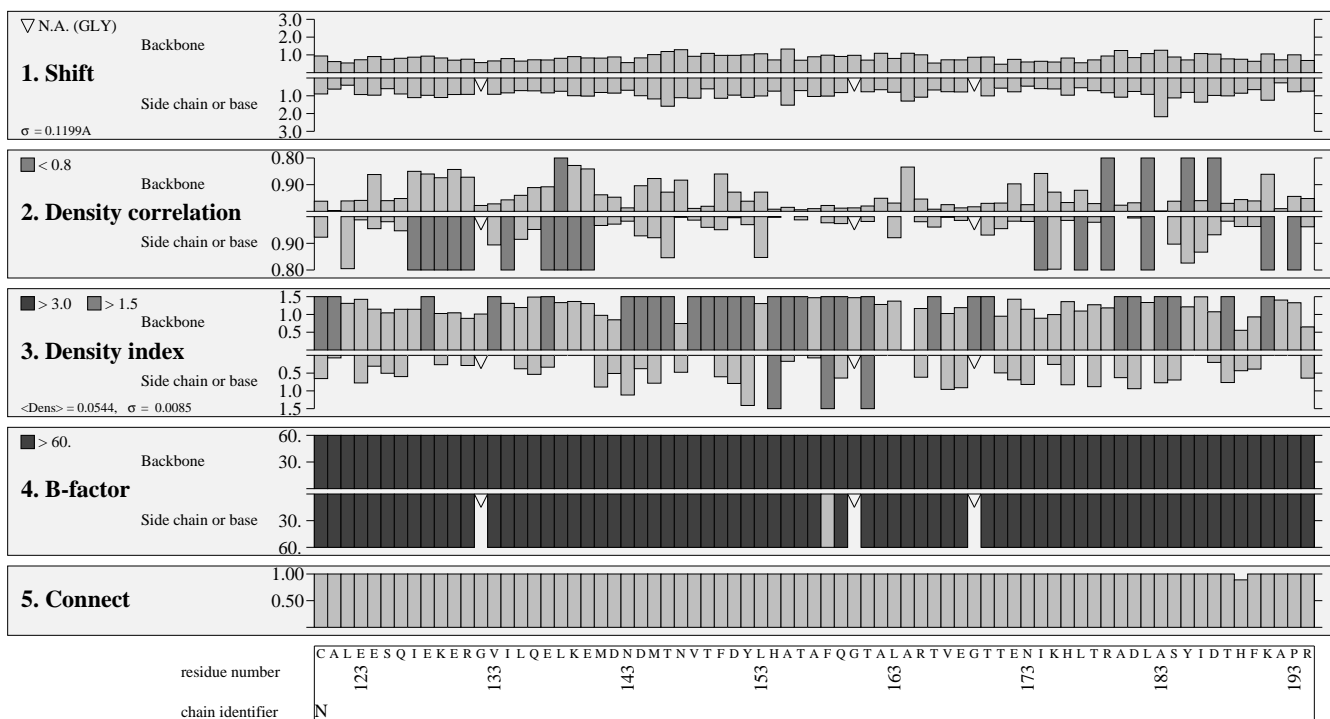
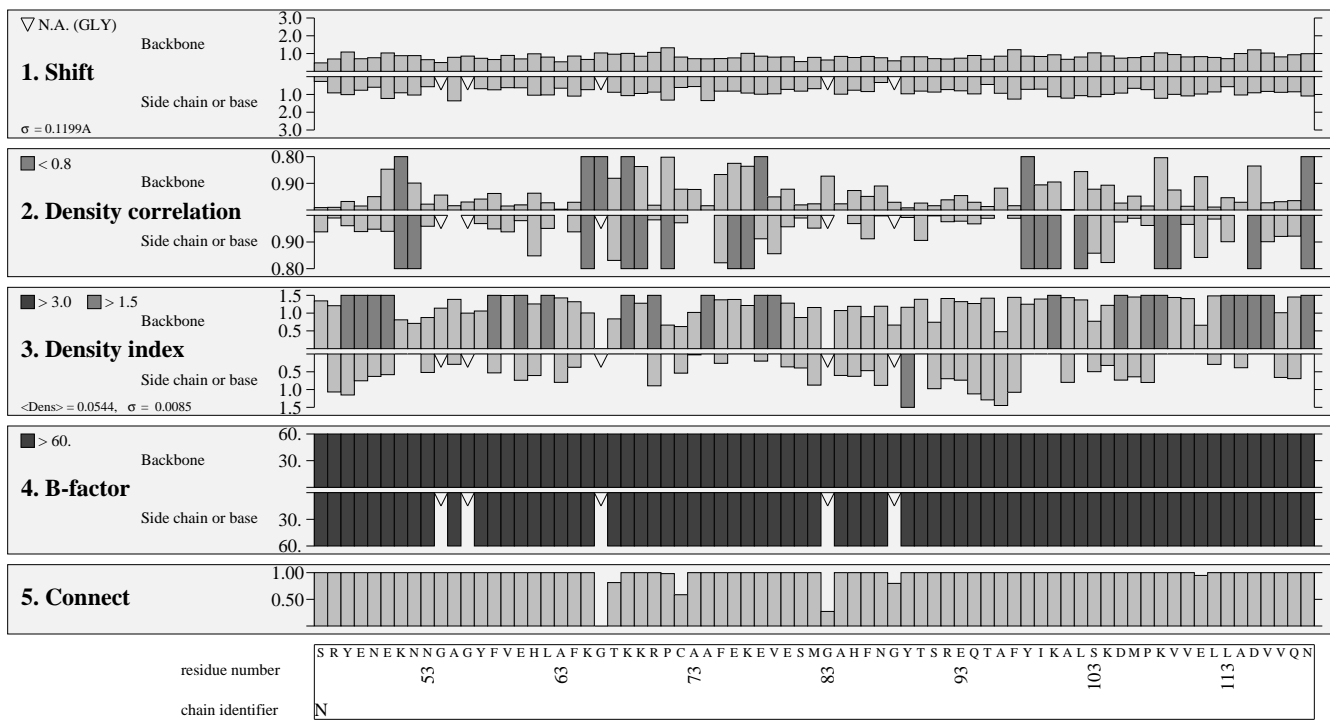




# Structure Factor Check

## 3L73

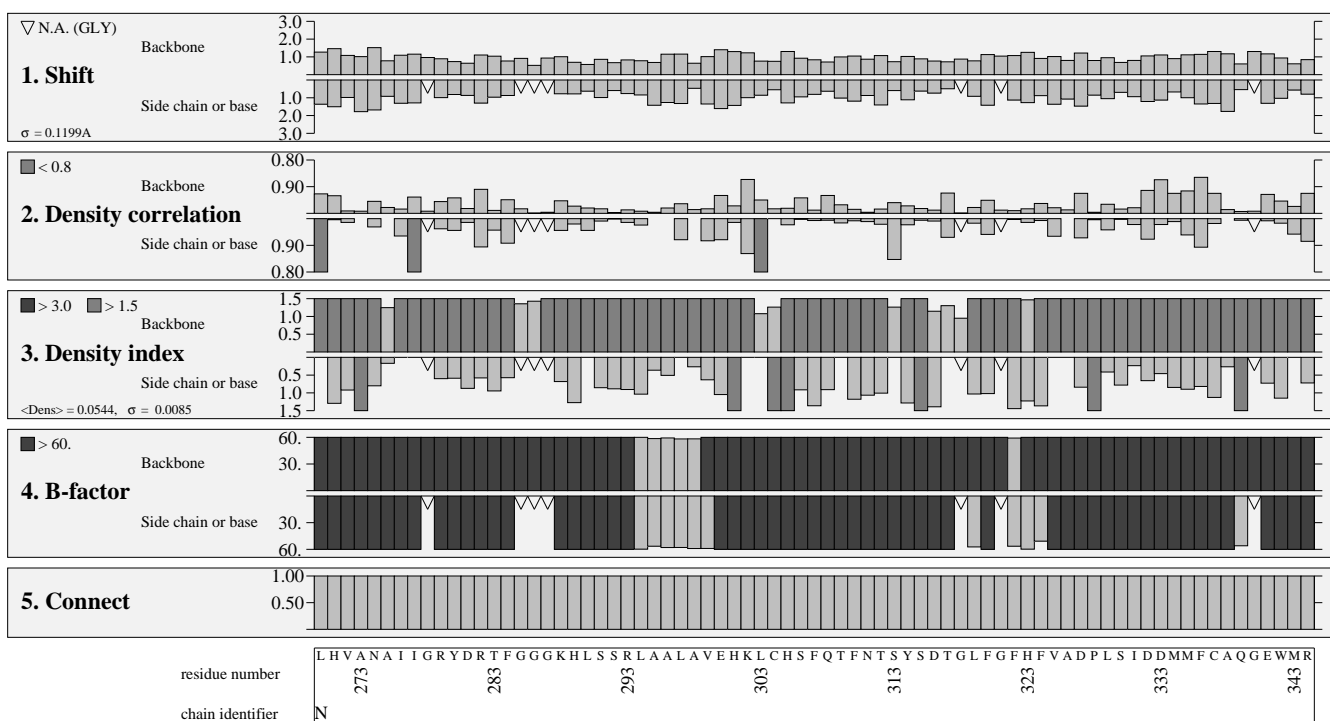
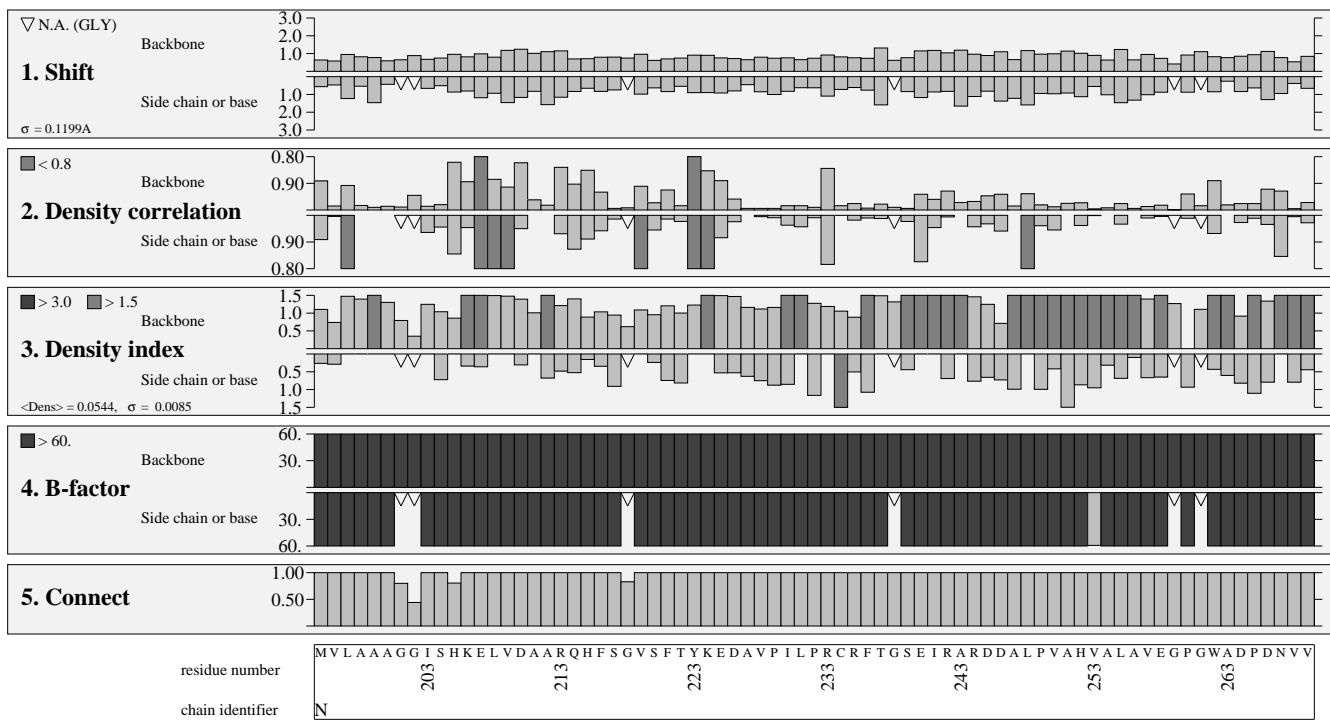
### Local estimation (15)



# Structure Factor Check

## 3L73

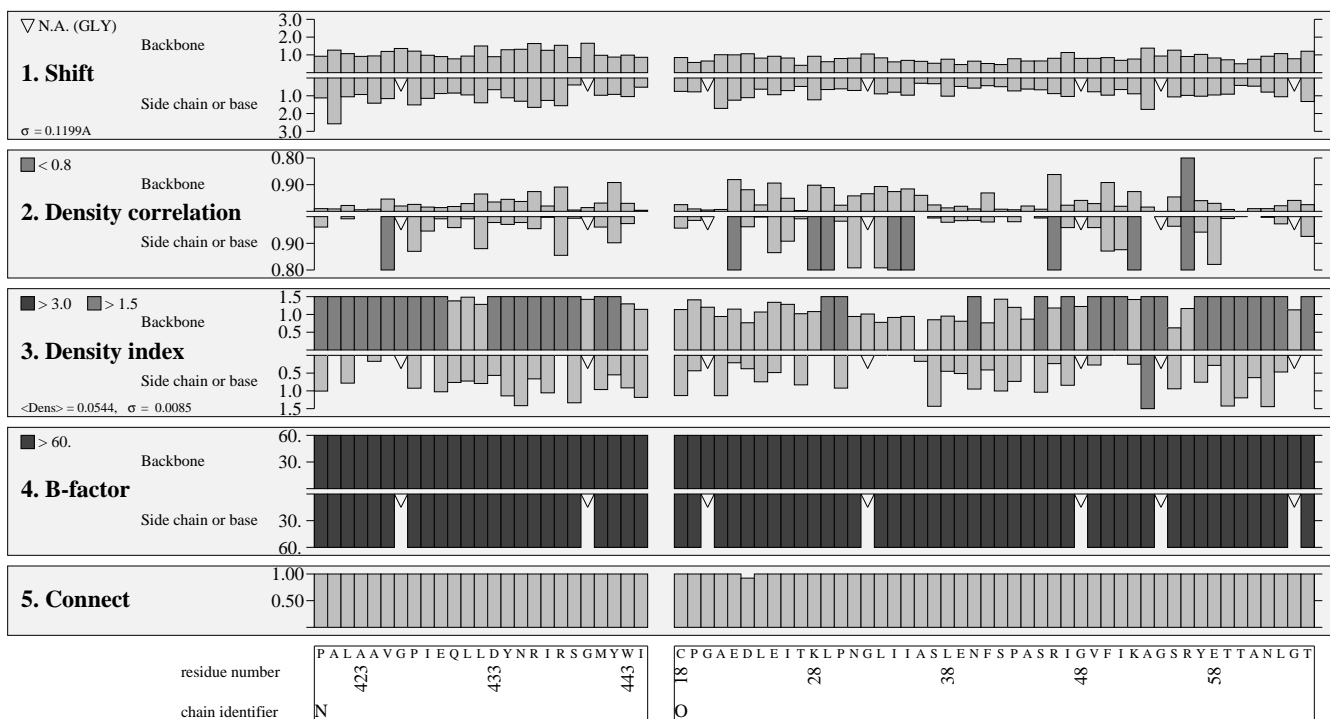
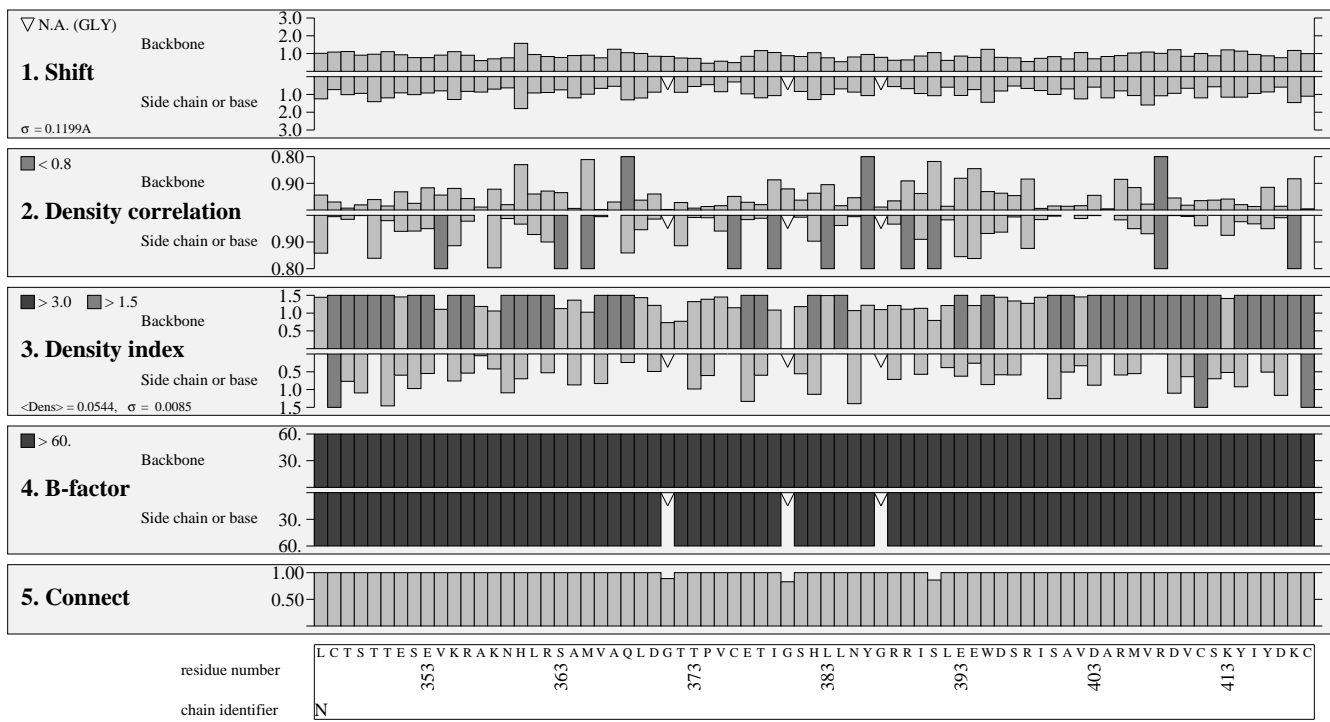
### Local estimation (16)



# Structure Factor Check

## 3L73

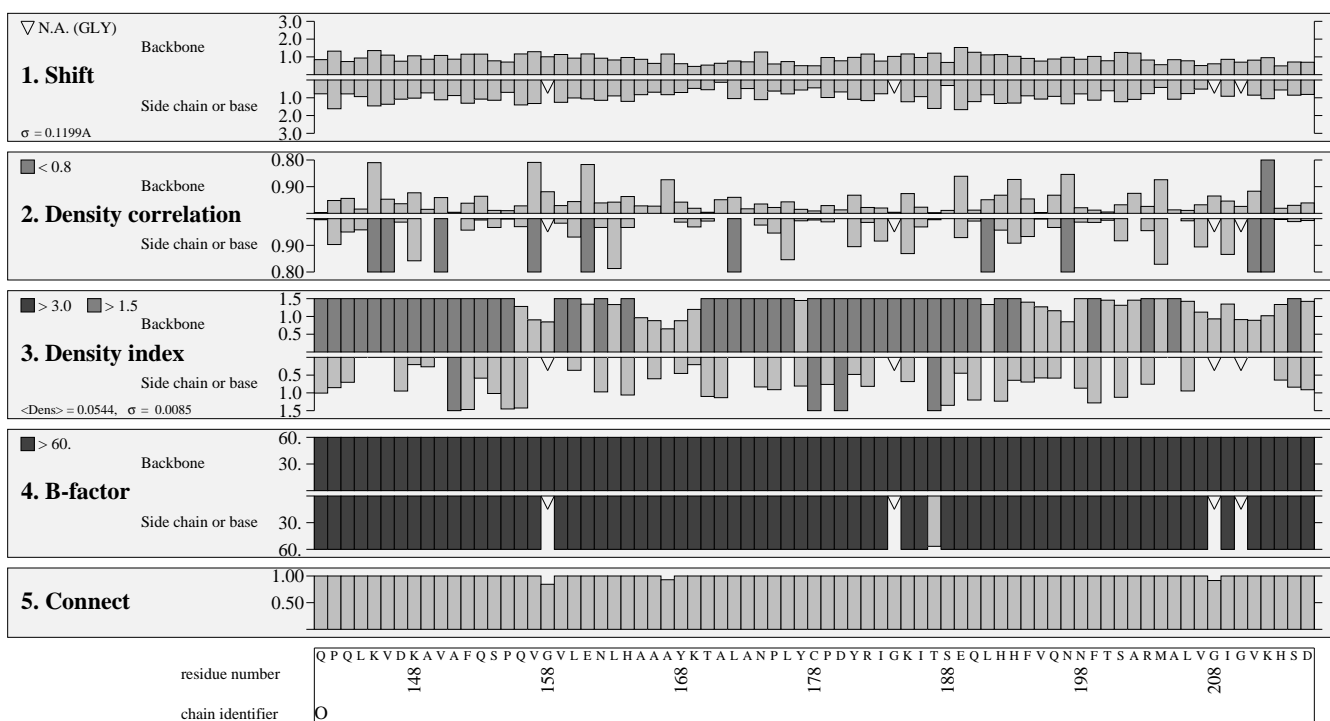
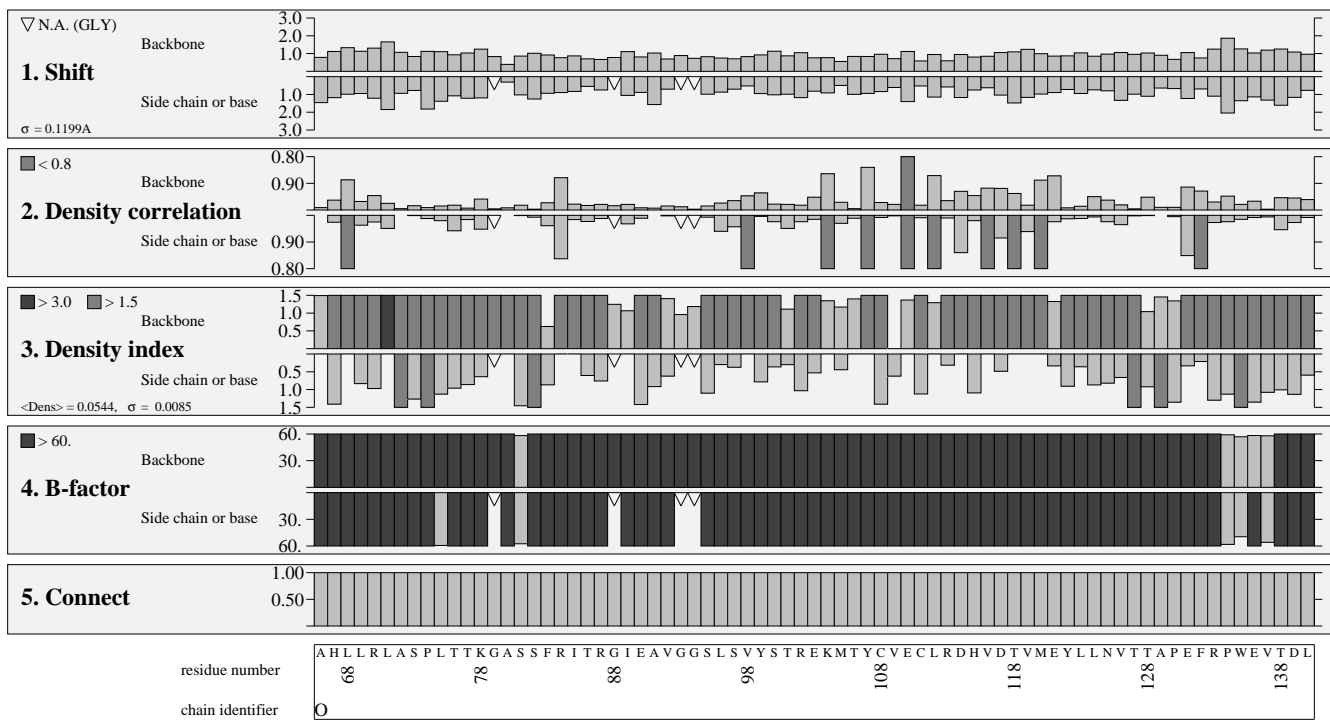
### Local estimation (17)



# Structure Factor Check

## 3L73

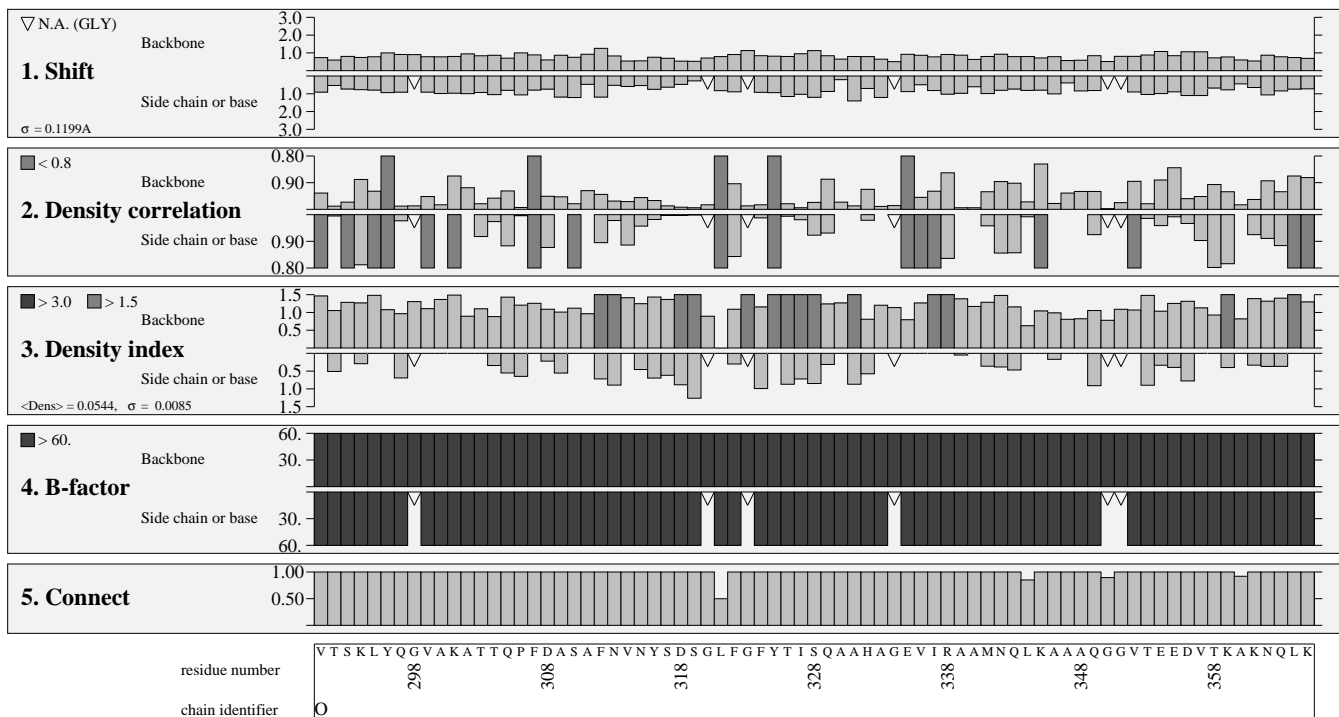
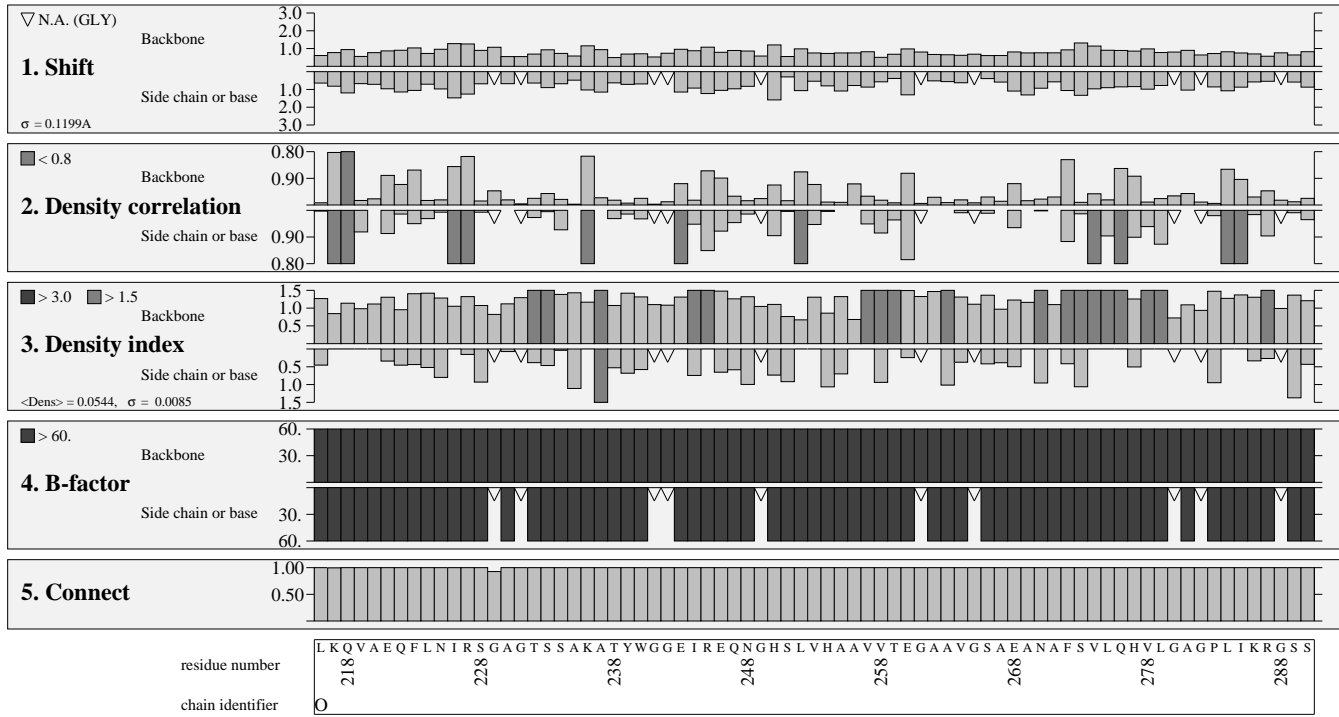
### Local estimation (18)



# Structure Factor Check

## 3L73

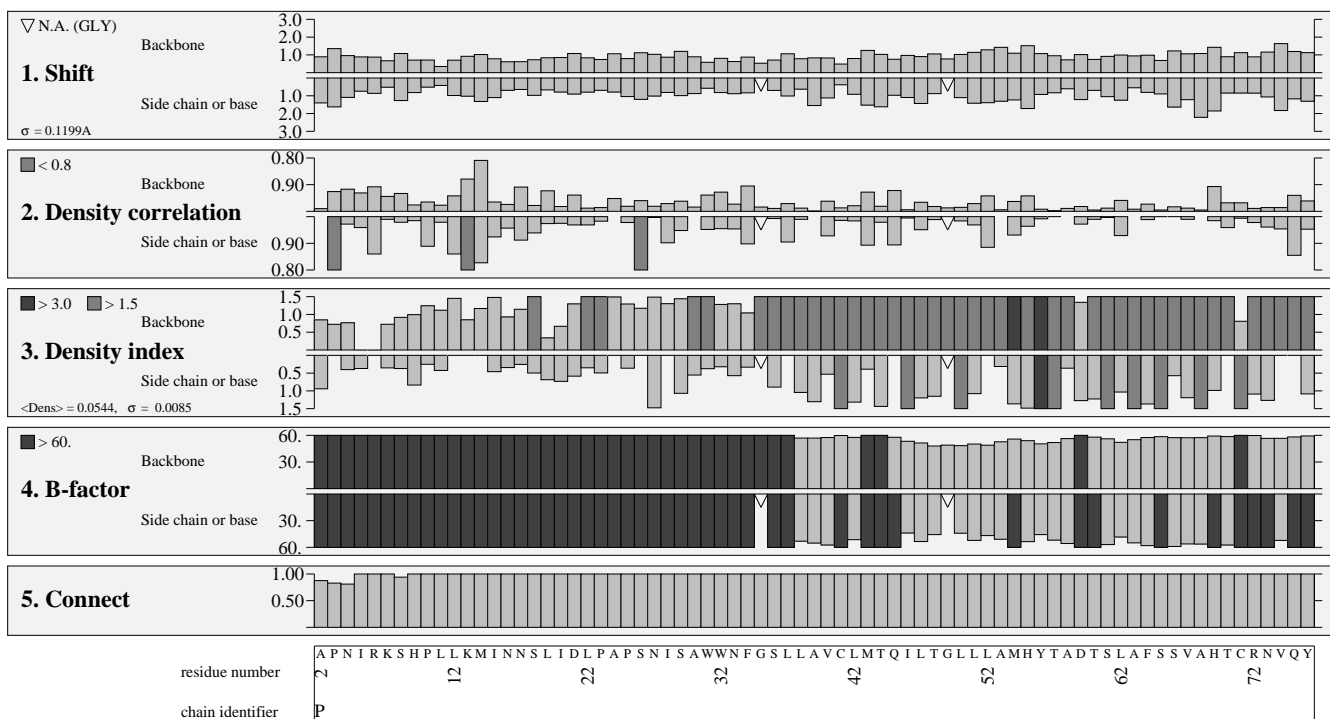
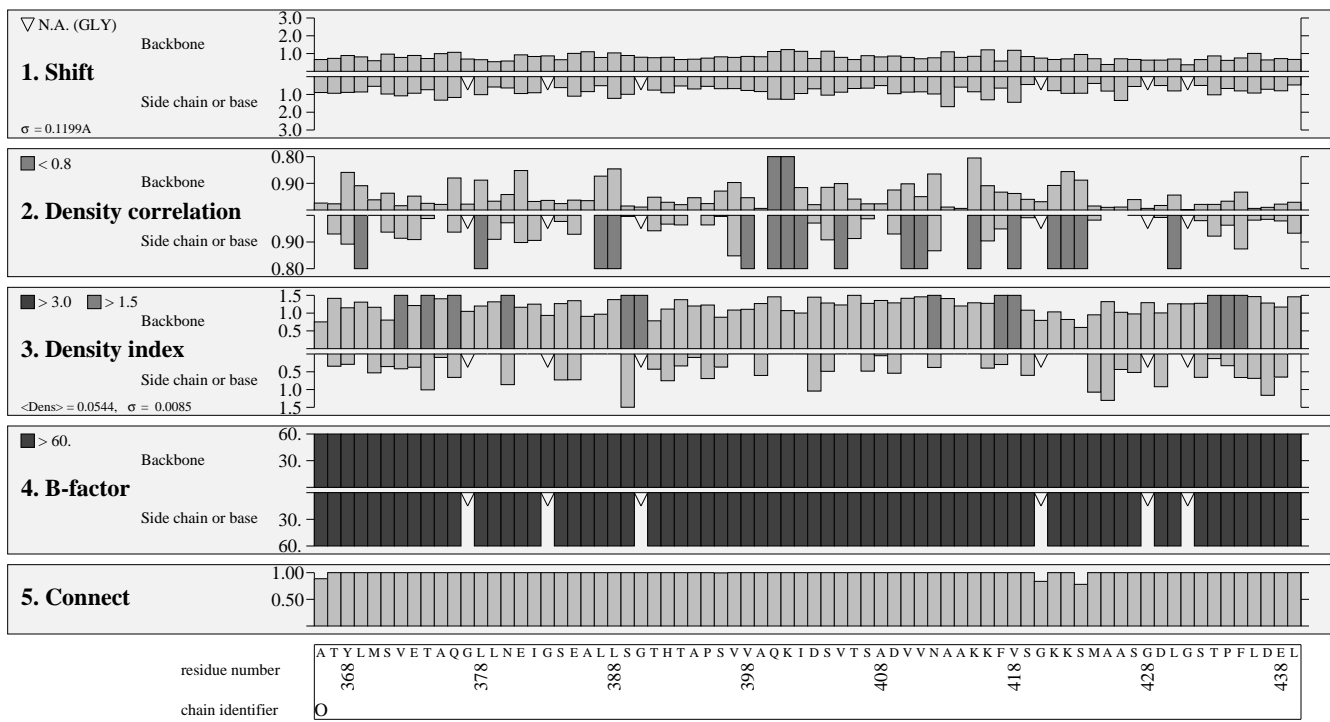
### Local estimation (19)



# Structure Factor Check

## 3L73

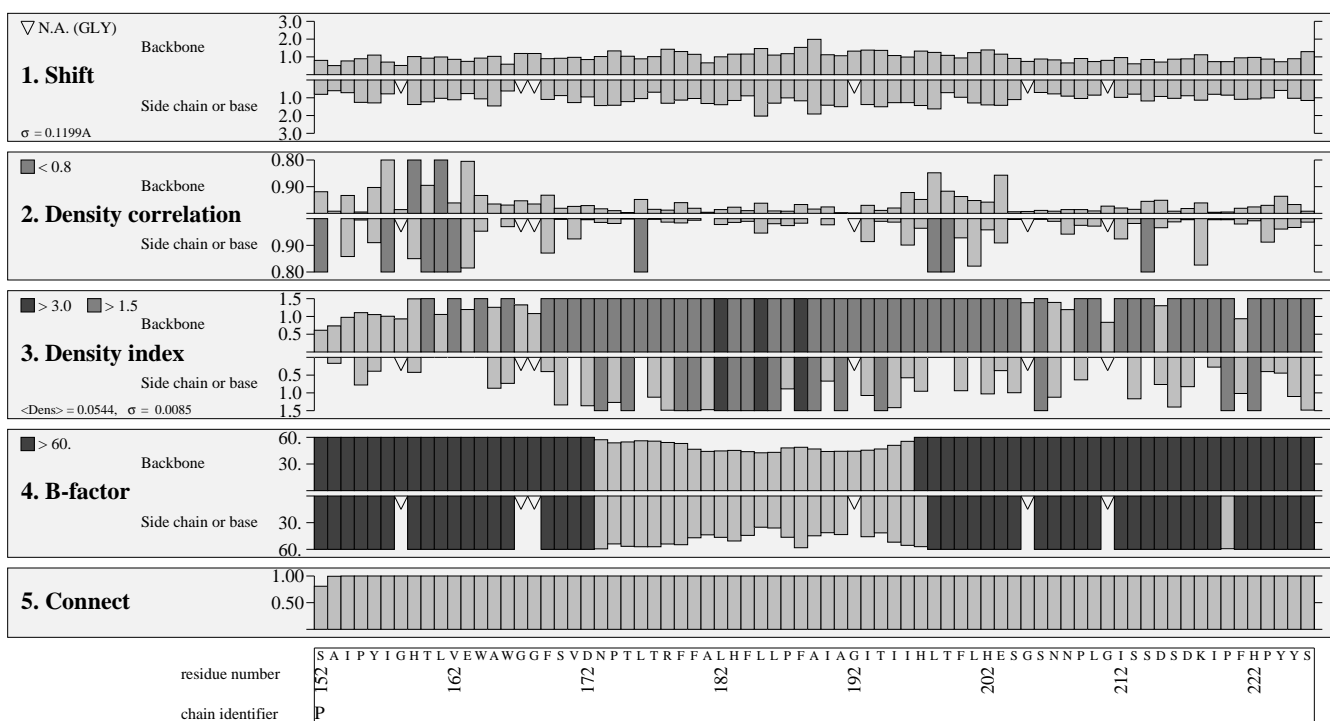
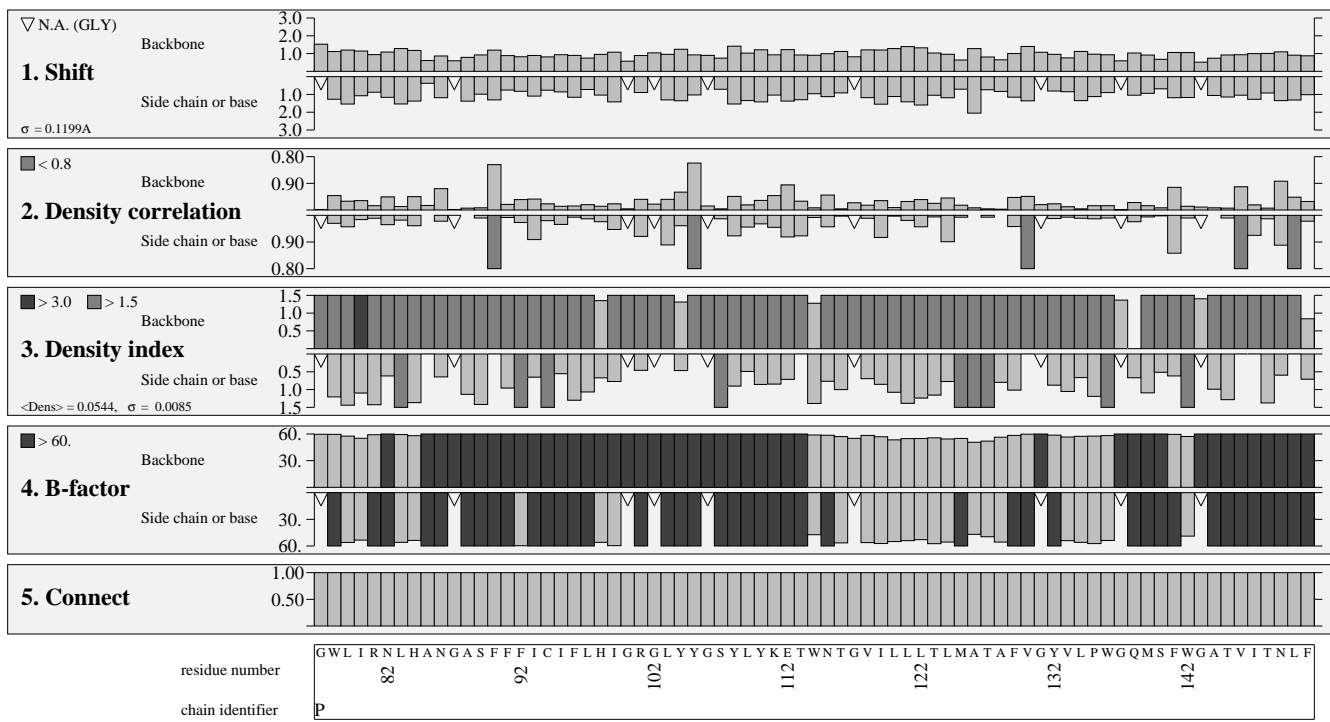
### Local estimation (20)



# Structure Factor Check

## 3L73

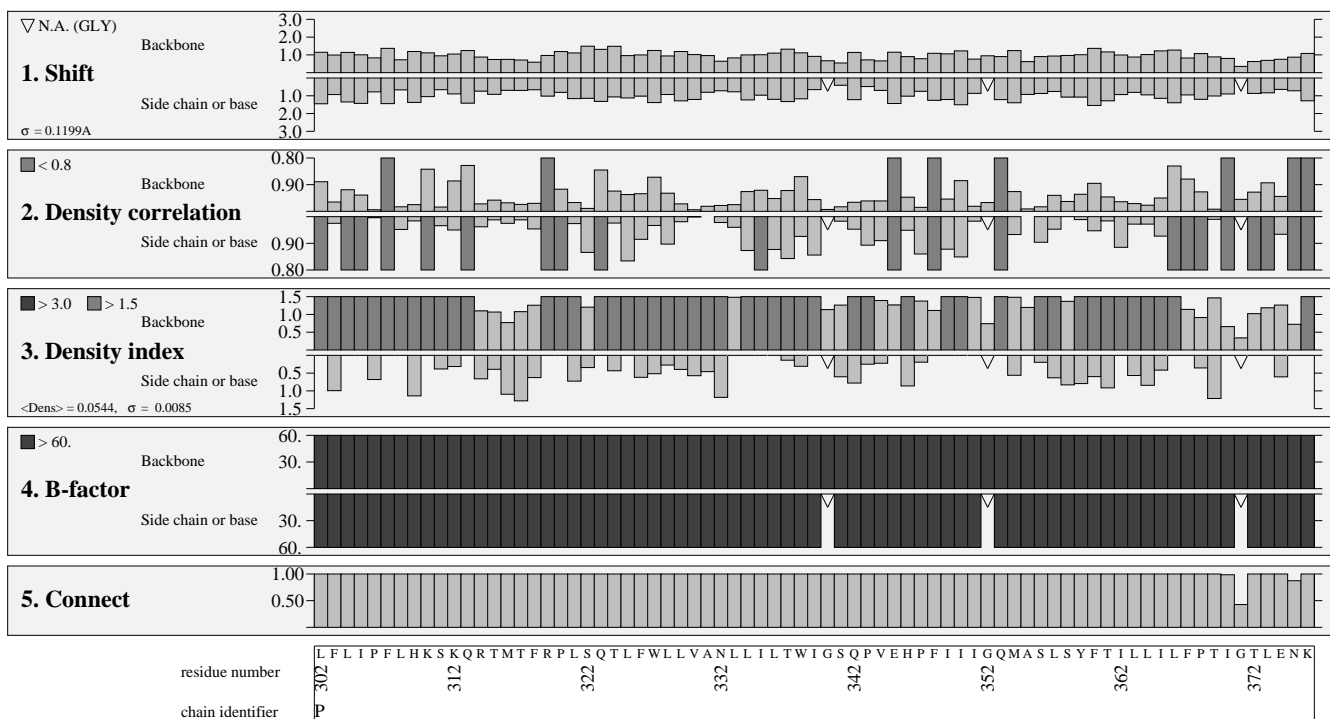
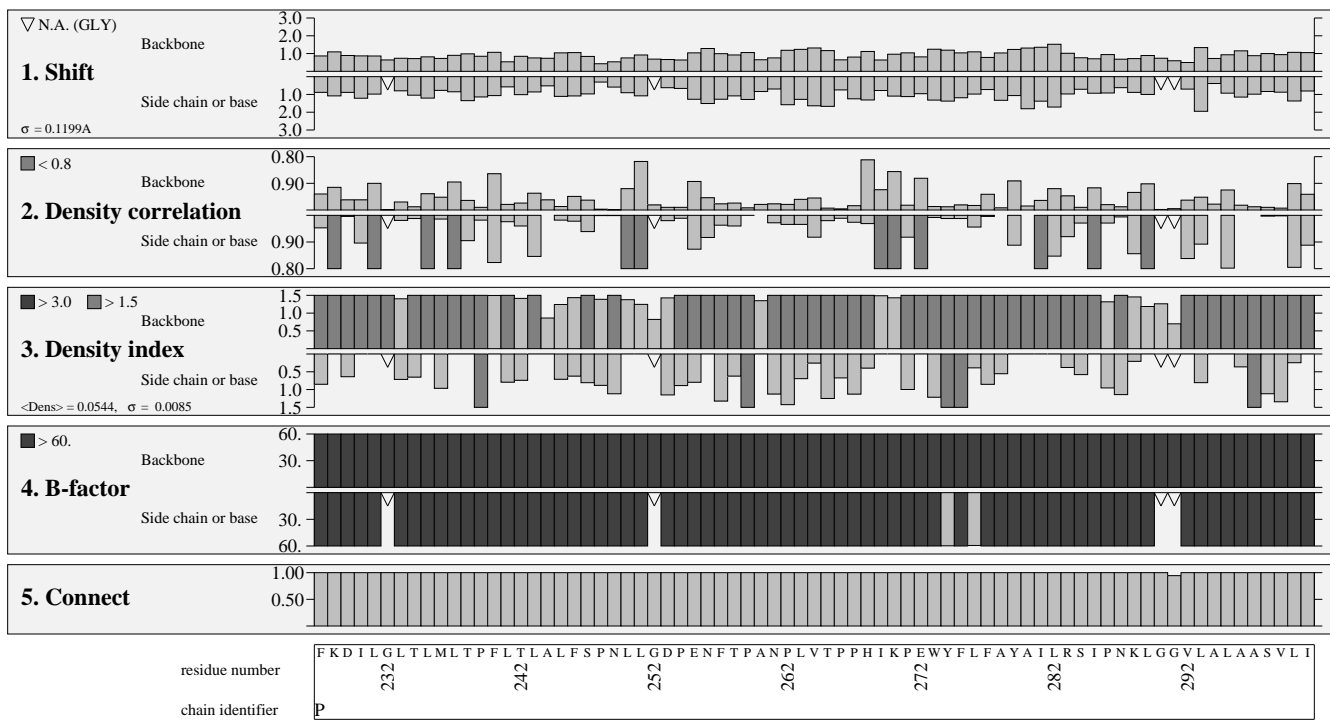
### Local estimation (21)



# Structure Factor Check

## 3L73

### Local estimation (22)

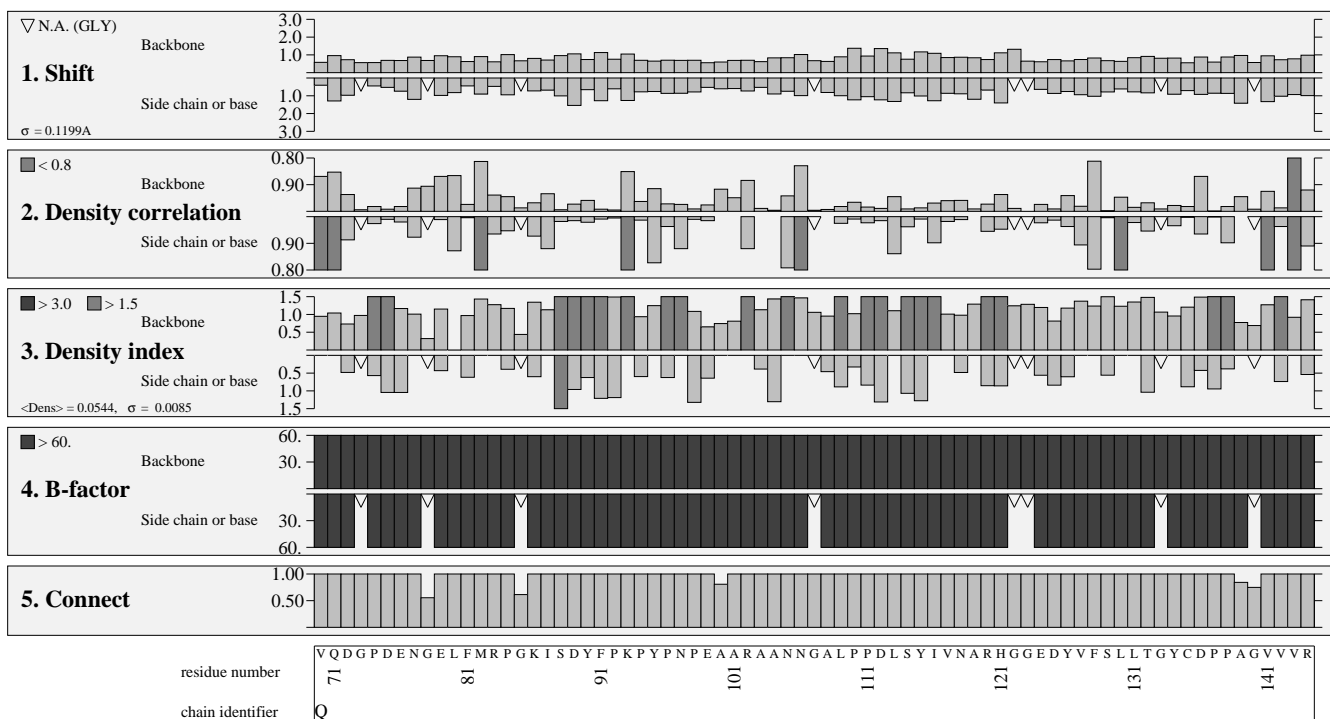
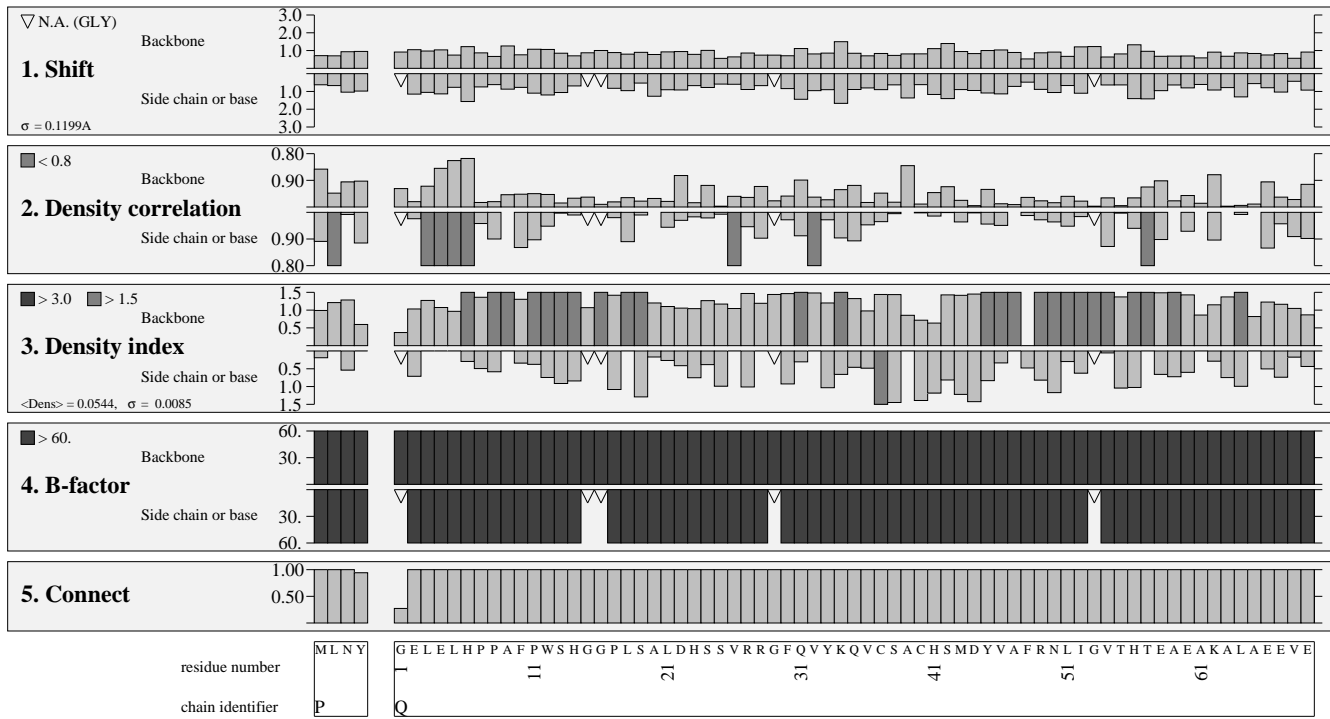




# Structure Factor Check

## 3L73

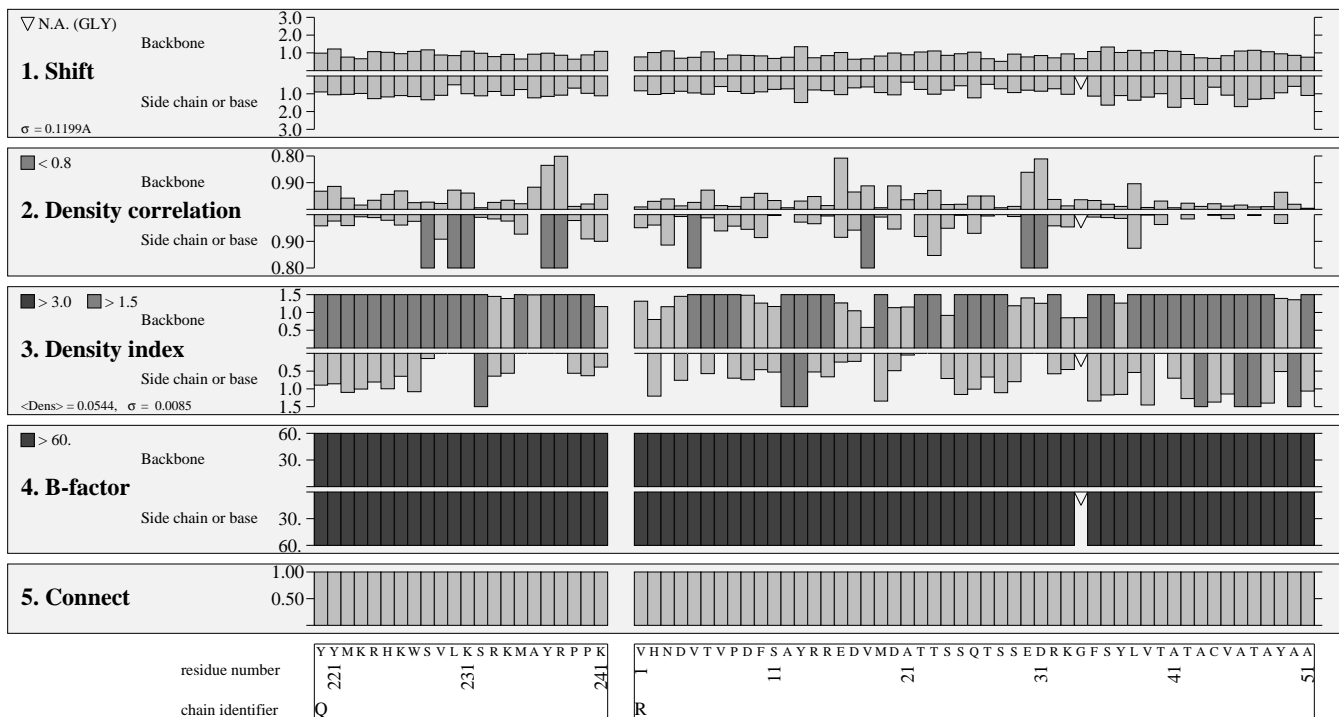
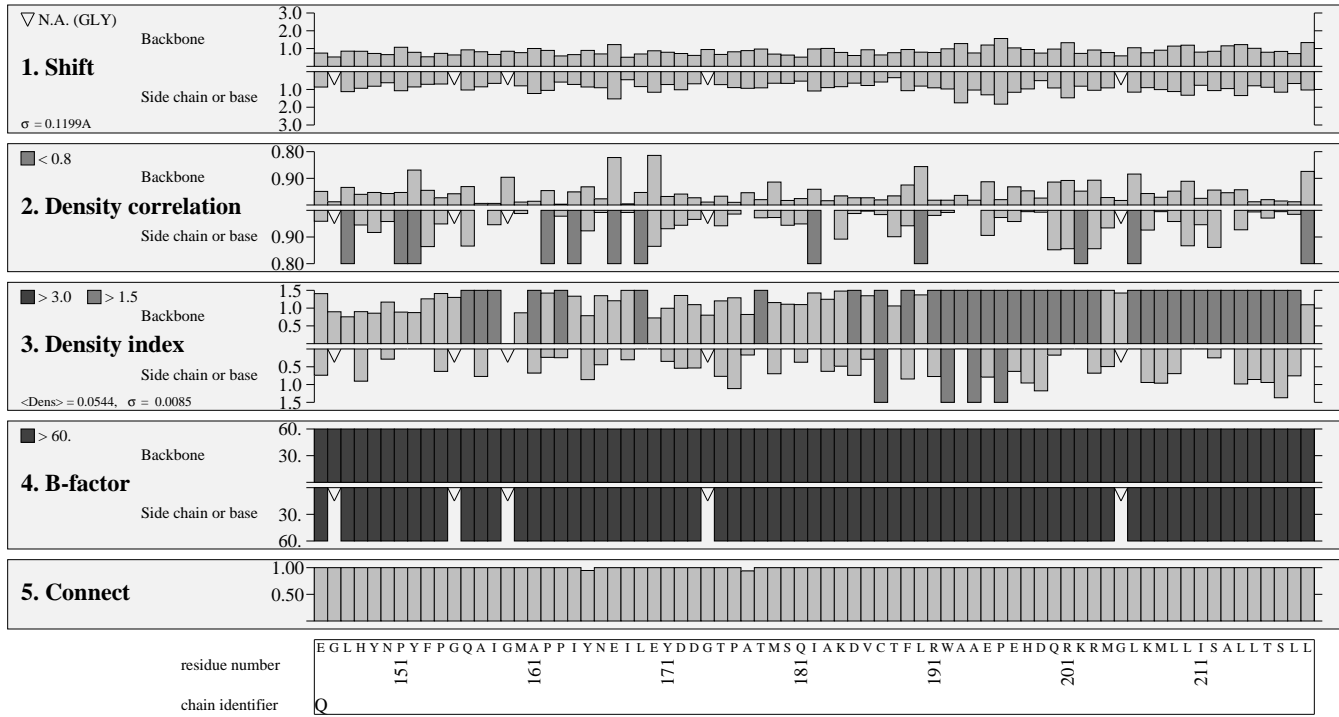
### Local estimation (23)



# Structure Factor Check

## 3L73

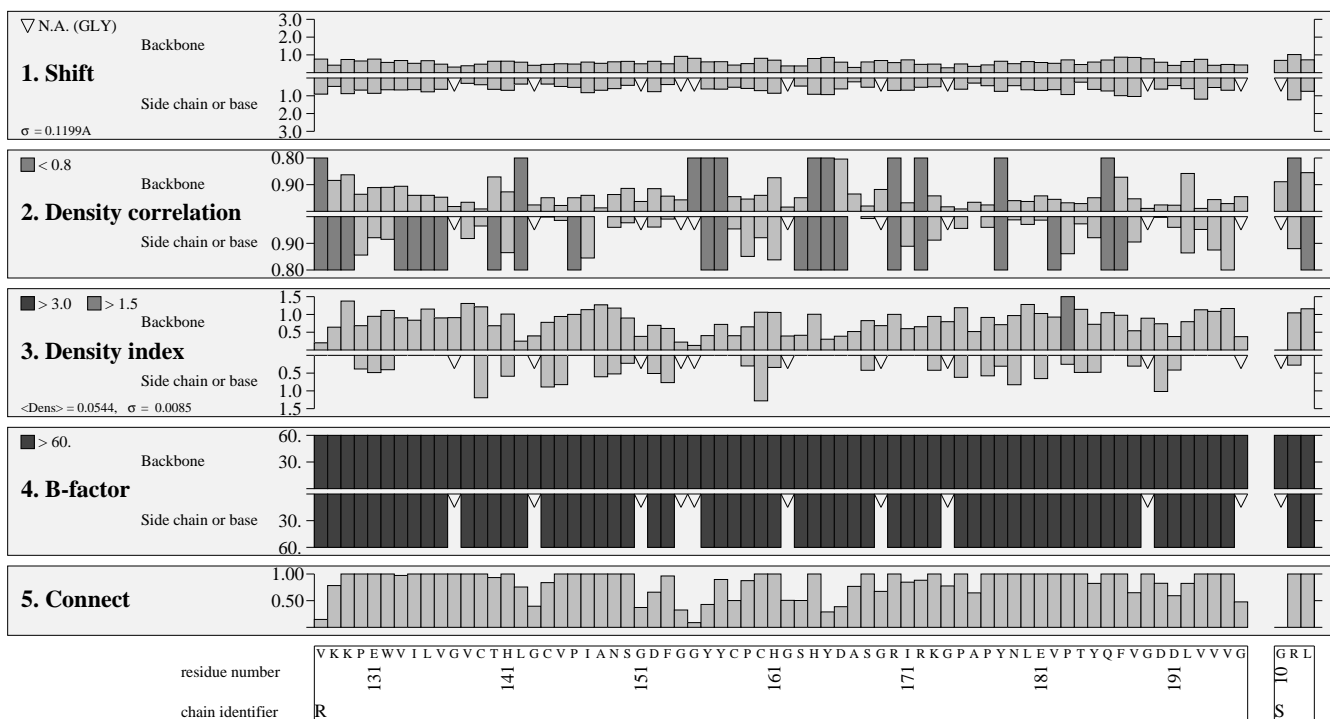
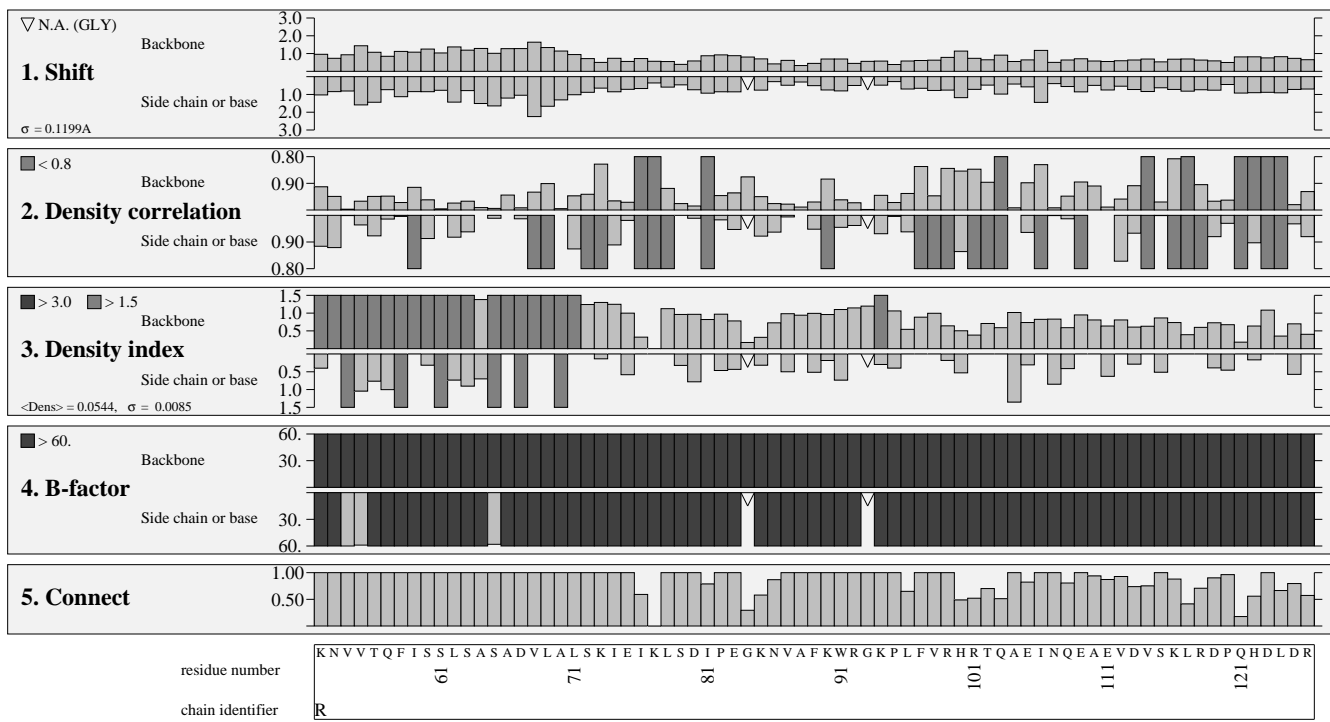
### Local estimation (24)



# Structure Factor Check

## 3L73

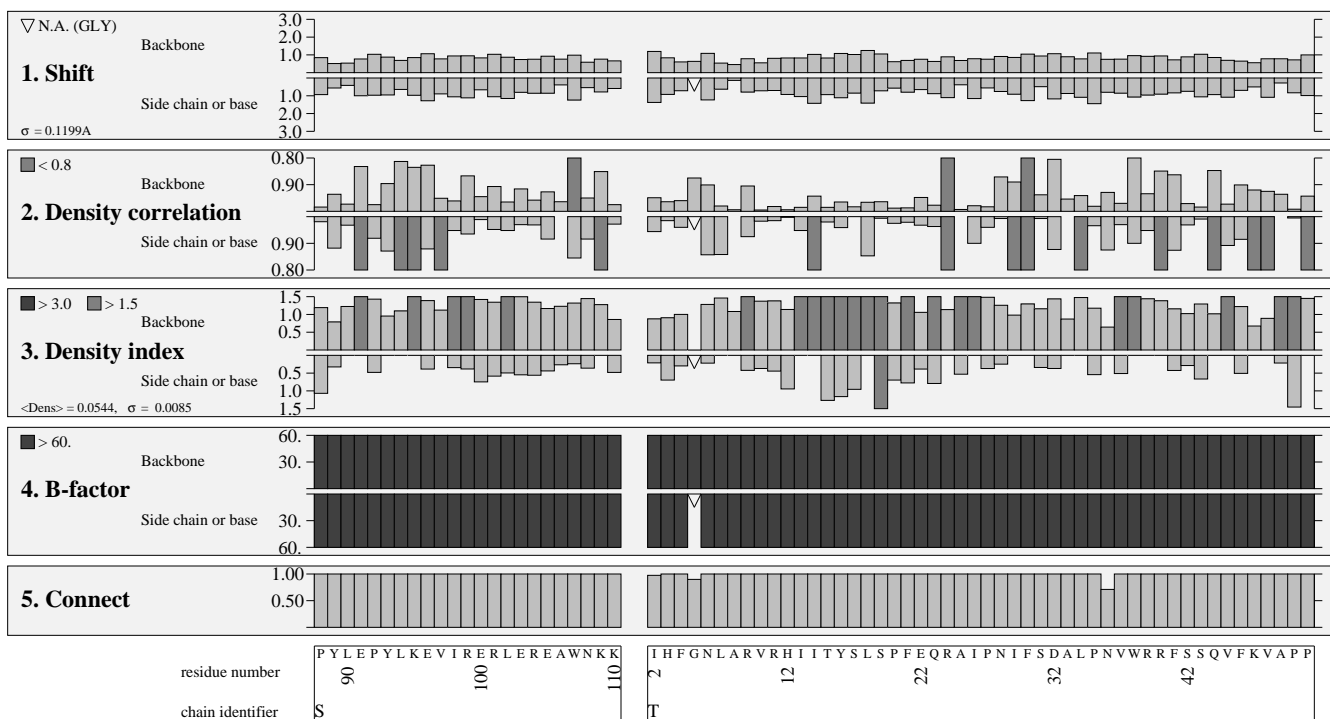
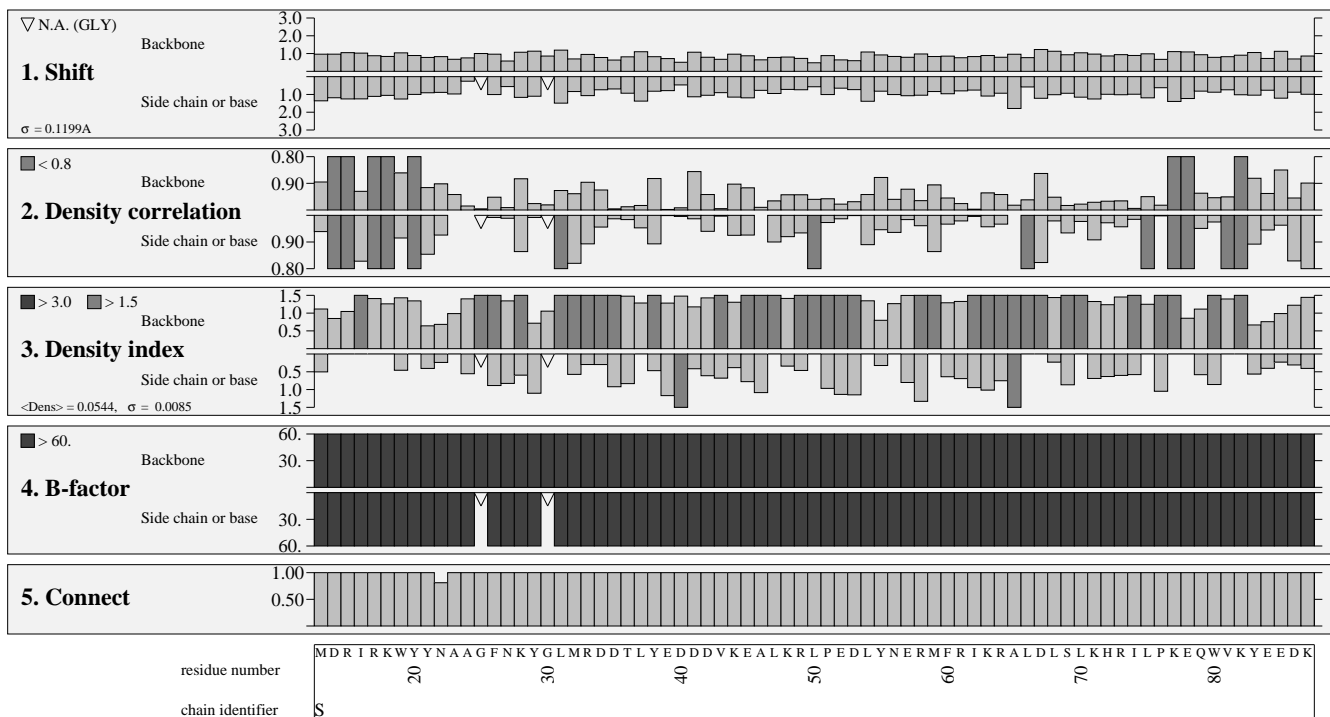
### Local estimation (25)



# Structure Factor Check

## 3L73

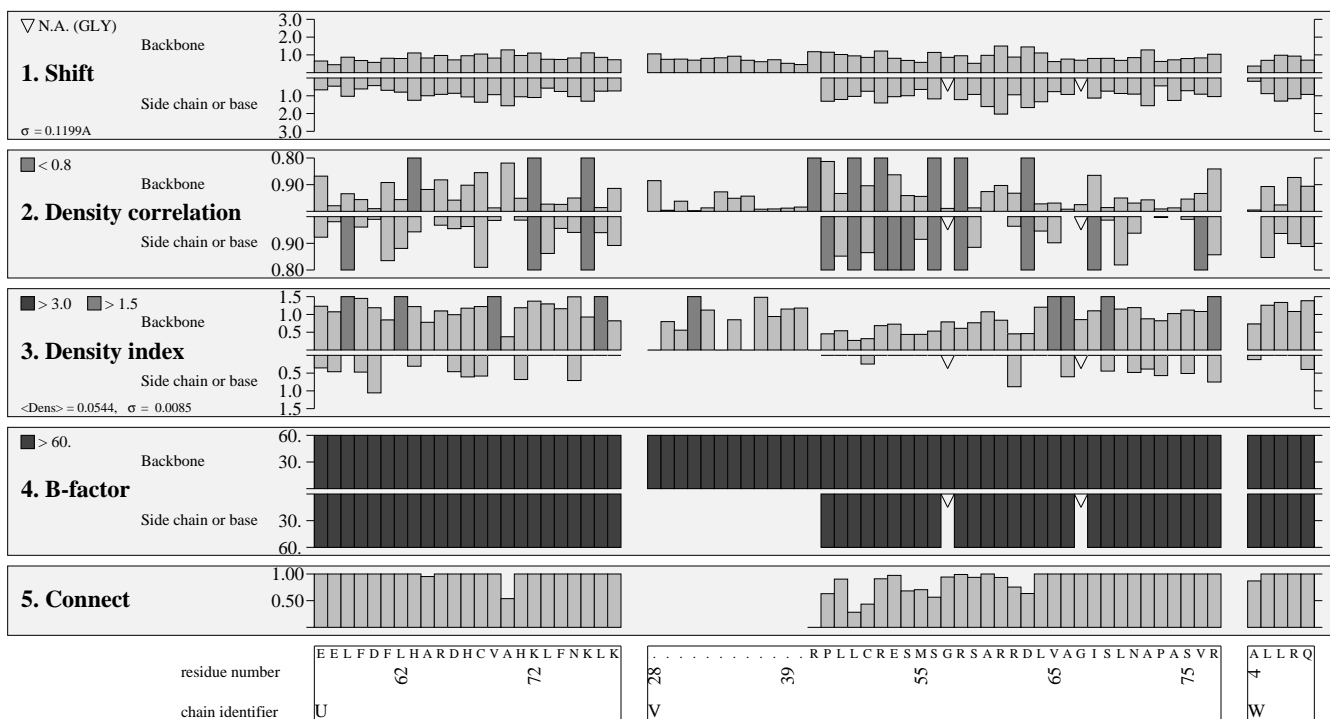
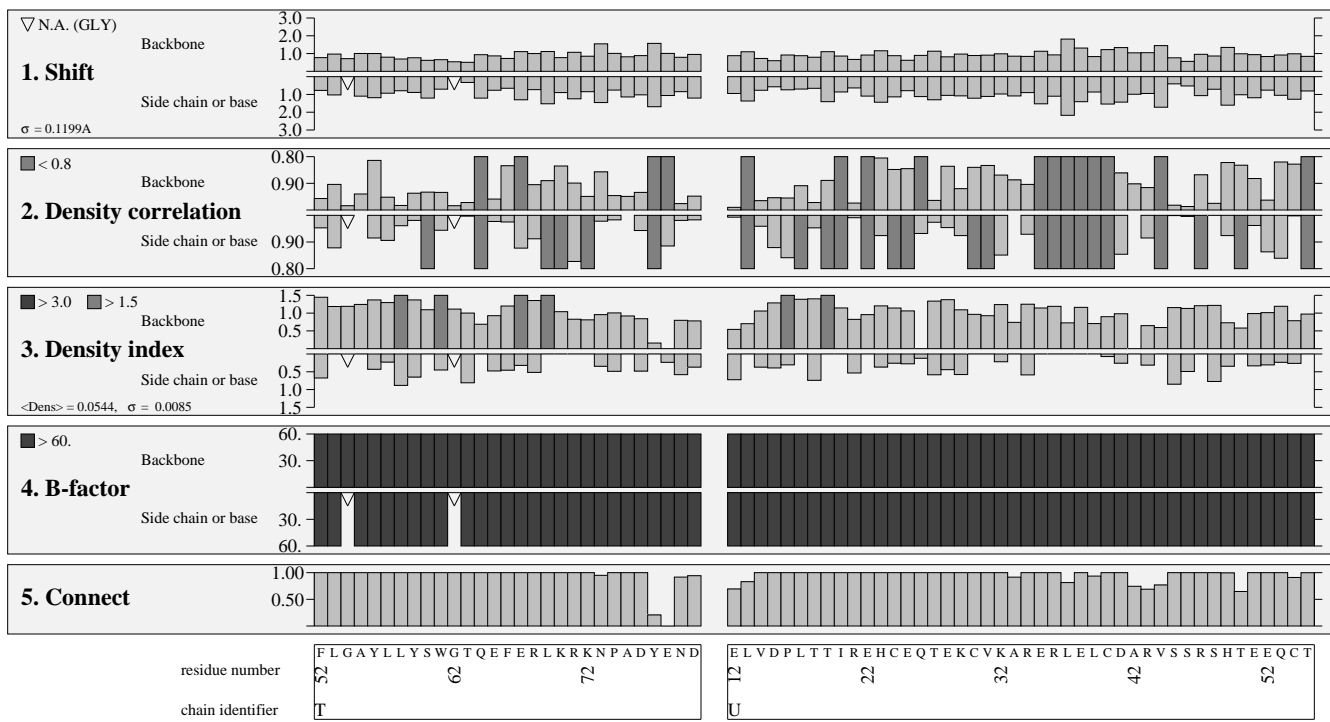
### Local estimation (26)



# Structure Factor Check

## 3L73

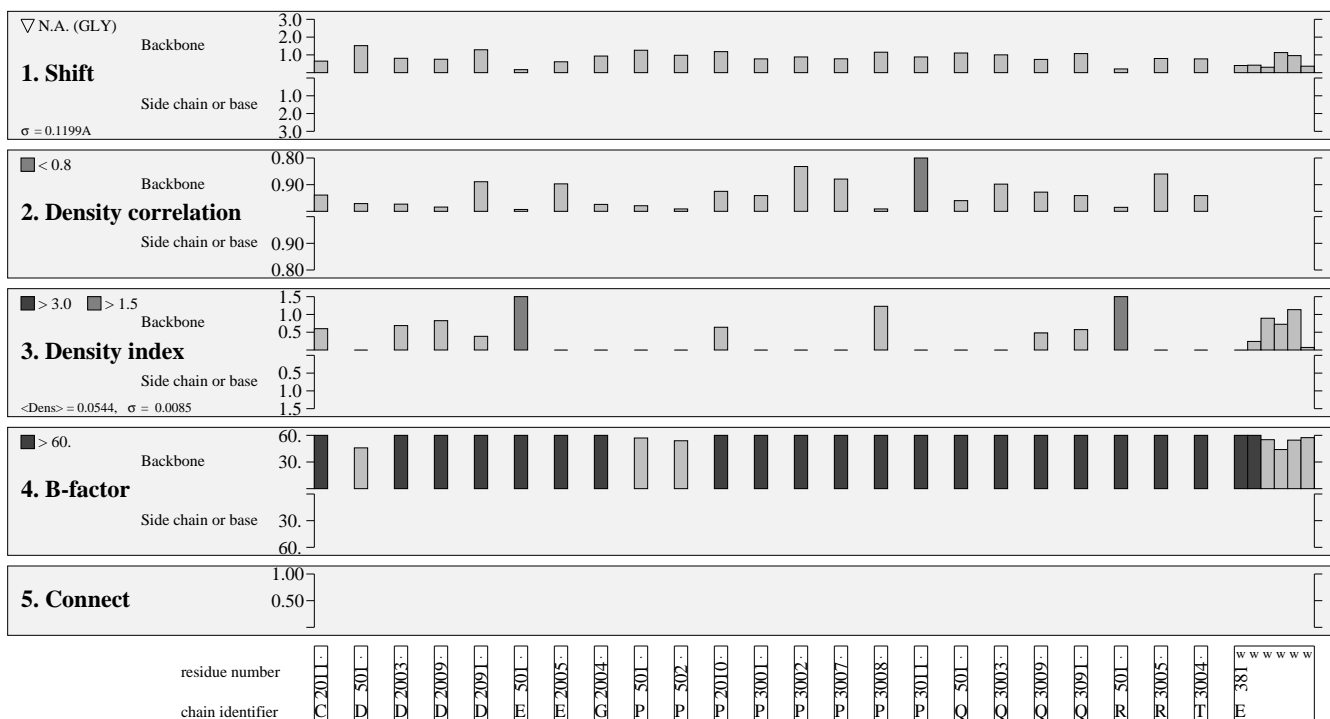
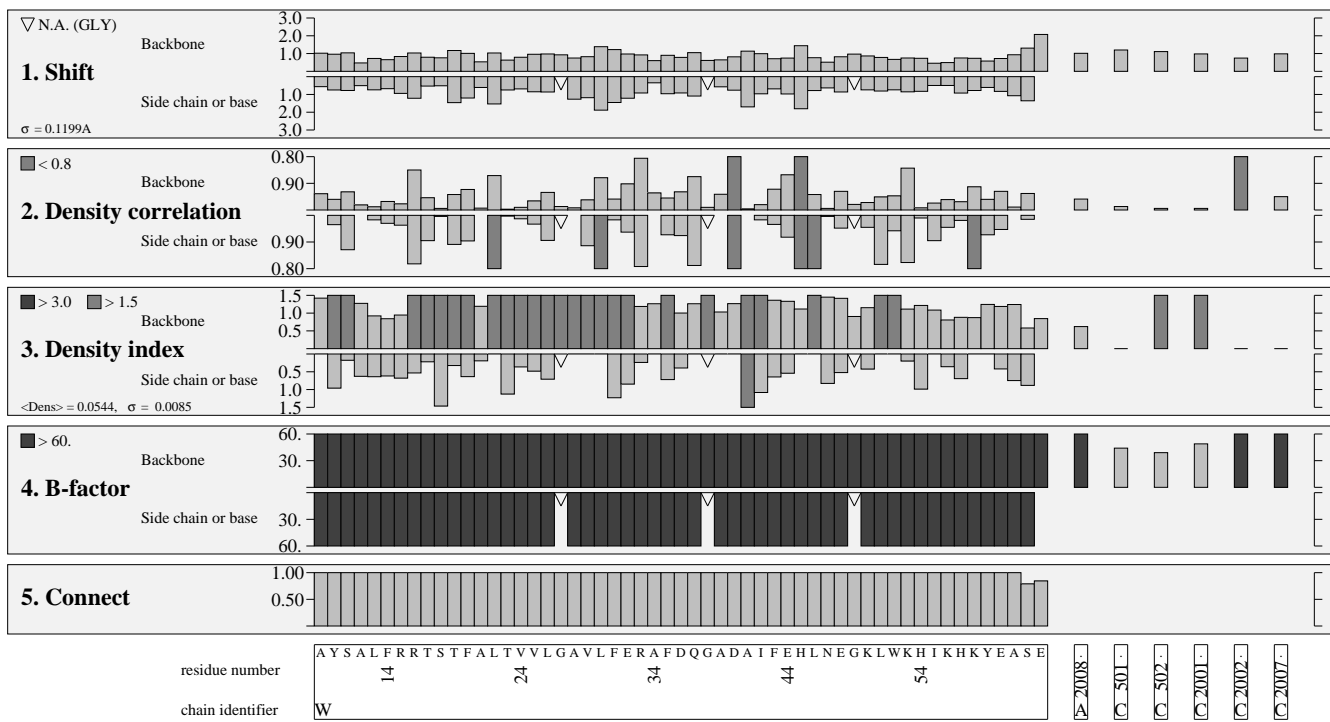
### Local estimation (27)



# Structure Factor Check

## 3L73

### Local estimation (28)



# Structure Factor Check

## 3L73

### Local estimation (29)



residue number    

w w w w w w w w w w w w w w w w
382

chain identifier    

E
---