

# Structure Factor Check

## 1PPJ

Title: BOVINE CYTOCHROME BC1 COMPLEX WITH STIGMATELLIN AND ANTIMYCI  
 Date: 16-JUN-03  
 PDB code: 1PPJ

### Crystal

Cell parameters:

a: 128.53 A    b: 168.75 A    c: 231.53 A  
 $\alpha$ : 90.00     $\beta$ : 90.00     $\gamma$ : 90.00

Space group: P 21 21 21

Number of NCS-operators: 1  
 NC-symmetry only for information

### Structure Factors

#### Input

Nominal resolution range: 93.5 – 2.10 A  
 Reflections in file: 285058  
 Unique reflections above 0: 285058  
                                   above 1 $\sigma$ : 278499  
                                   above 3 $\sigma$ : 213616

#### SFCHECK

Nominal resolution range: 93.5 – 2.10 A  
\05max. from input data, min. from author\05  
 Used reflections: 285058  
 Completeness: 97.6 %  
 $R_{\text{stand}}(F) = \langle \sigma(F) \rangle / \langle F \rangle$  : 0.079  
 Anisotropic distribution of Structure Factors  
     ratio of eigen values: 1.0000 0.7563 0.6853  
 B\_overall (by Patterson): 39.A<sup>2</sup>  
 Optical resolution: 1.75 A  
 Expected opt. resol. for complete data set: 1.75 A  
 Estimated minimal error: 0.029 A

### Model

33549 atoms (1370 water molecules)  
 Number of chains: 51  
 Volume not occupied by model: 42.7 %  
 $\langle B \rangle$  (for atomic model): 49.8 A<sup>2</sup>  
 $\sigma(B)$ : 16.04 A<sup>2</sup>  
 Matthews coefficient: 2.67  
 Corresponding solvent % : 53.62

### Model vs. Structure Factors

R-factor for all reflections: 0.250  
 Correlation factor: 0.931  
 R-factor: 0.253  
     for  $F > 2.0\sigma$   
         nom. resolution range: 93.53 – 2.10A  
         reflections used: 278714  
 Rfree: 0.274  
 Nfree: 13882  
 R-factor without free-refl.: 0.252  
 Non free-reflections: 264832  
 $\langle u \rangle$  (error in coords by Luzzati plot): 0.322 A  
 Estimated maximal error: 0.104 A  
 DPI: 0.189 A

#### Scaling

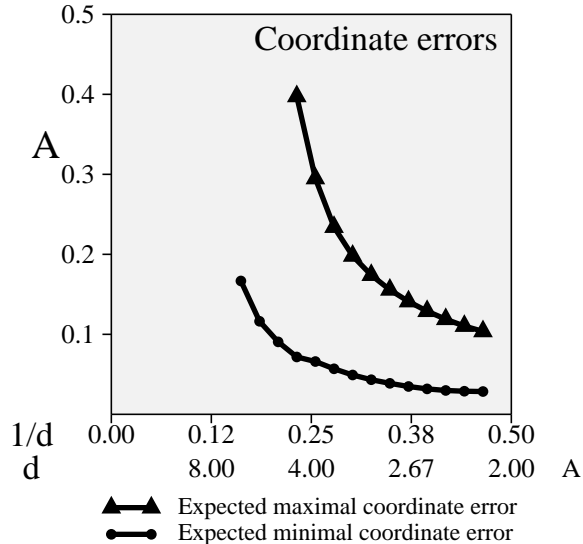
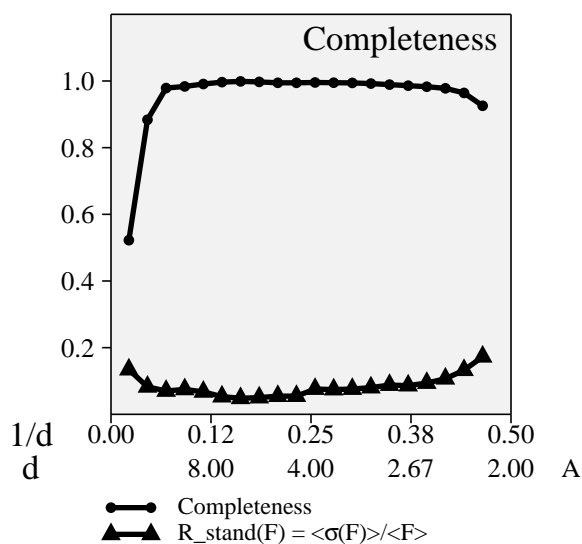
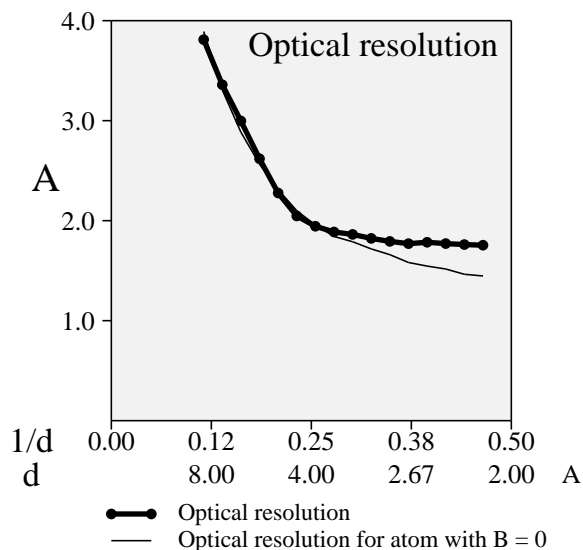
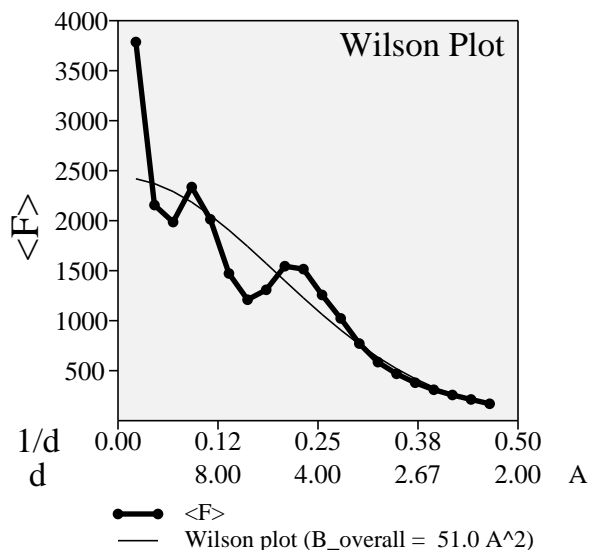
Scale: 1.011  
 Bdiff: -4.22  
 Anisothermal Scaling (Beta):  
     4.0086 0.5538 -0.7789 0.0000 0.0000 0.0000  
 Solvent correction – Ks,Bs: 0.841 250.032

### Refinement

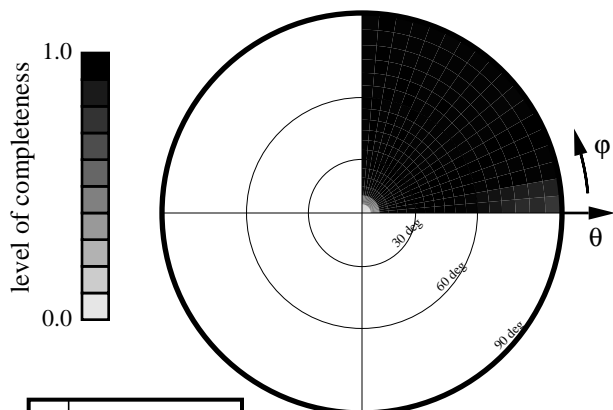
Program: CNS 1.1  
 Nominal resolution range: 93.5 – 2.10 A  
 Reported R-factor: 0.224  
 Number of reflections used: 285060  
 Reported Rfree: 0.26  
 Sigma cut-off: N.A.

# Structure Factor Check

## 1PPJ

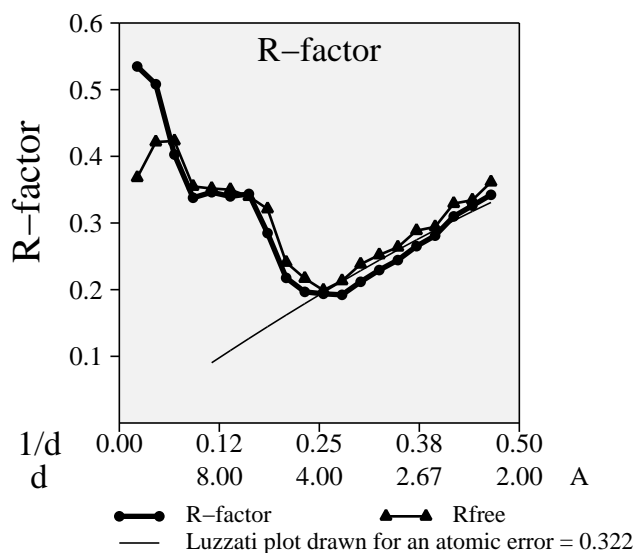


Stereographic projection of the averaged radial completeness



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

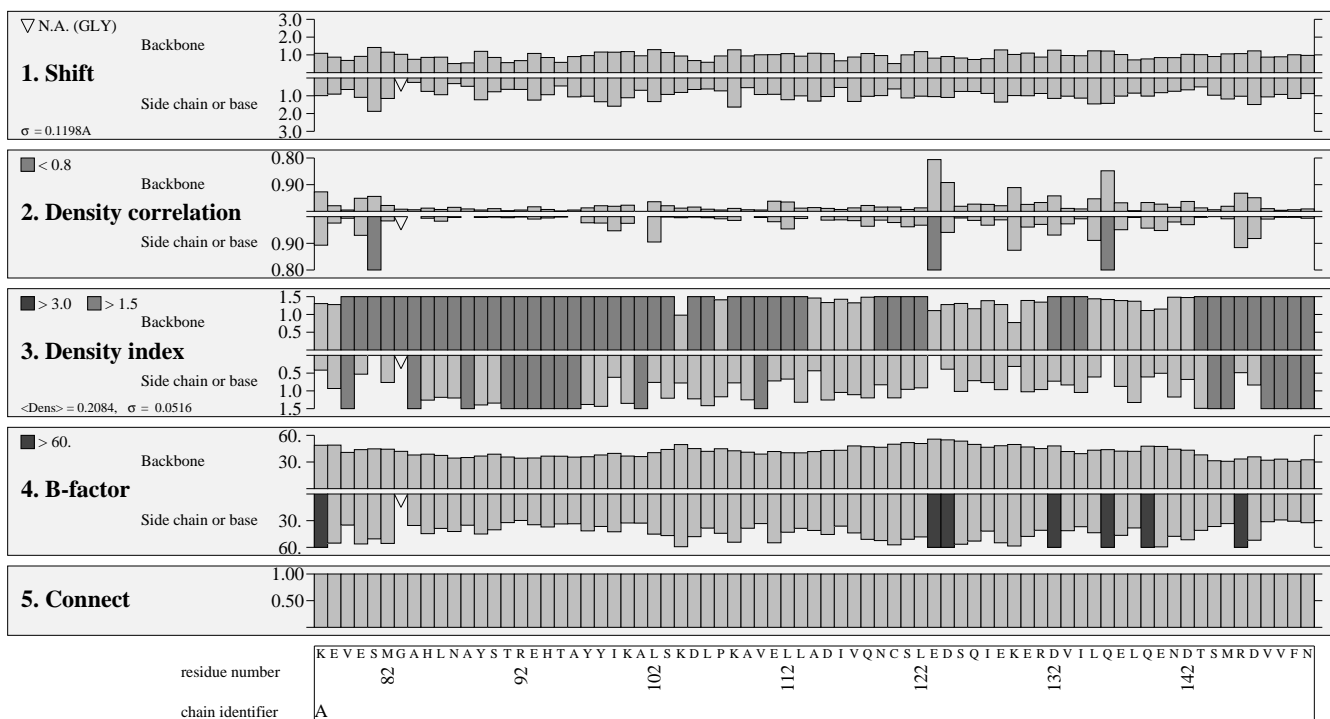
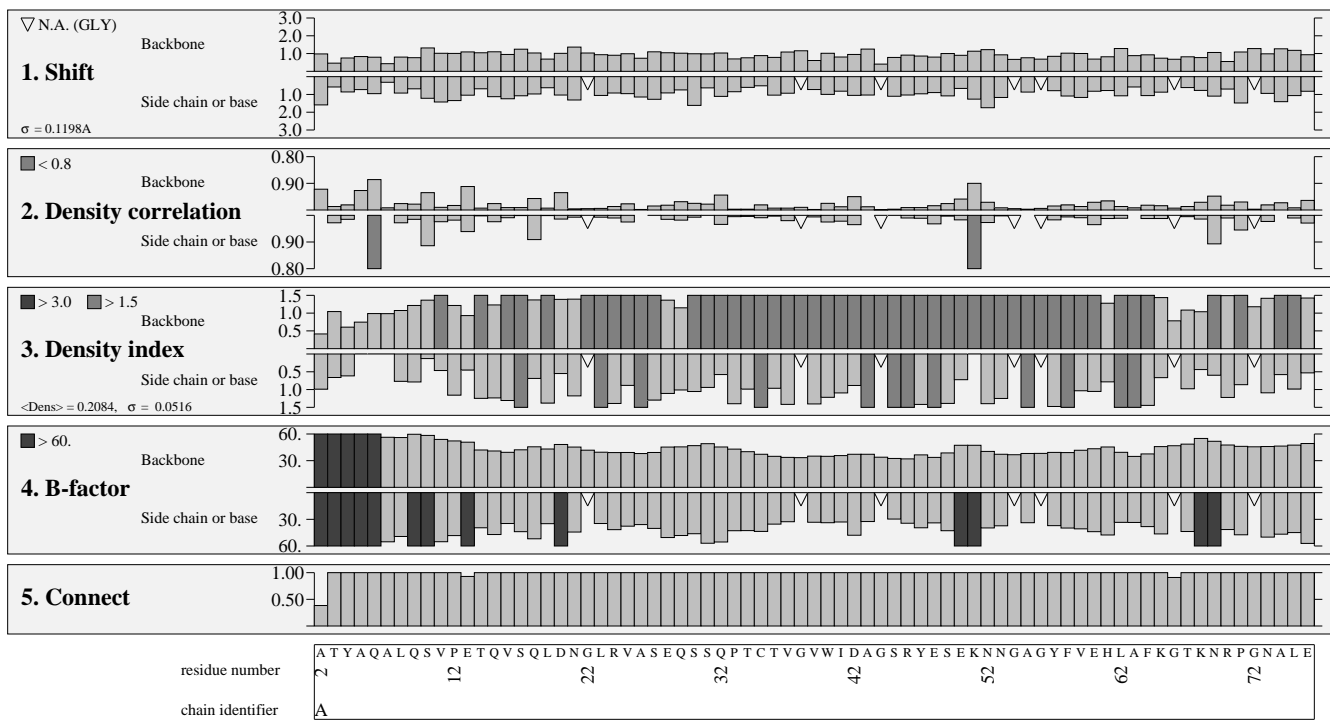
polar coordinates of the crystallographical axes



# Structure Factor Check

## 1PPJ

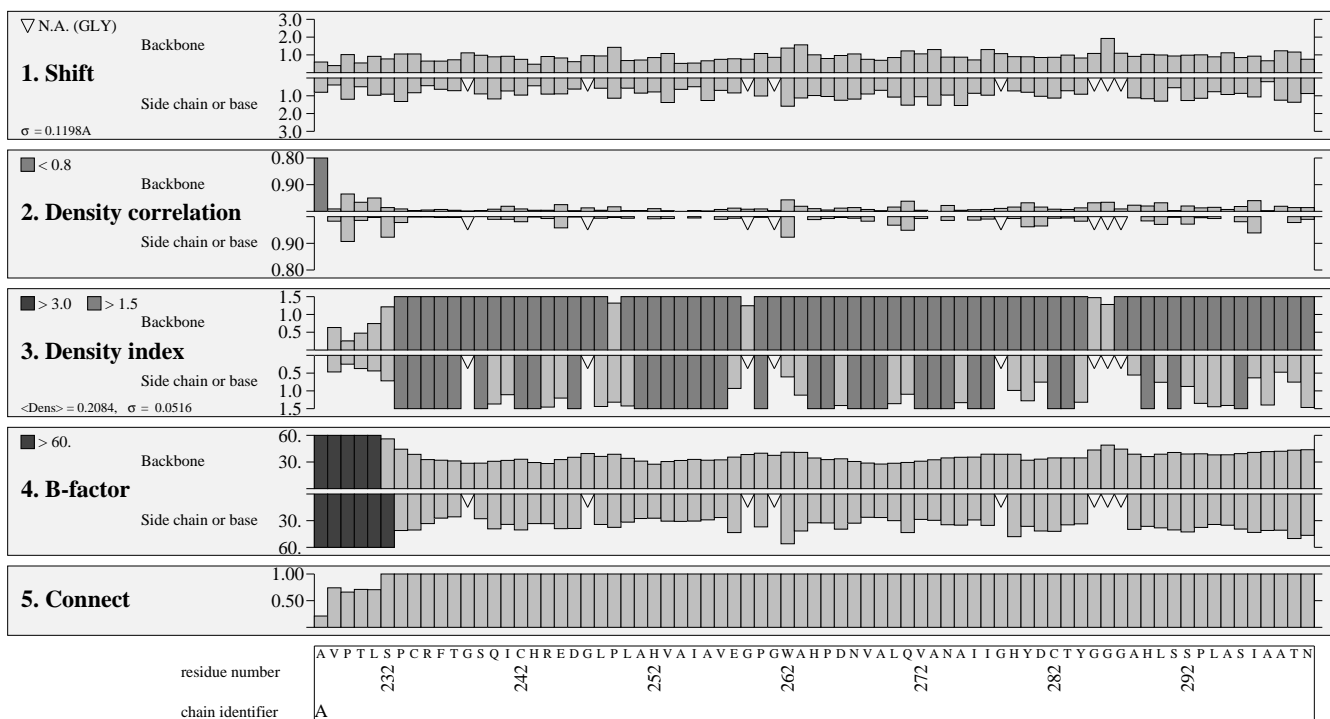
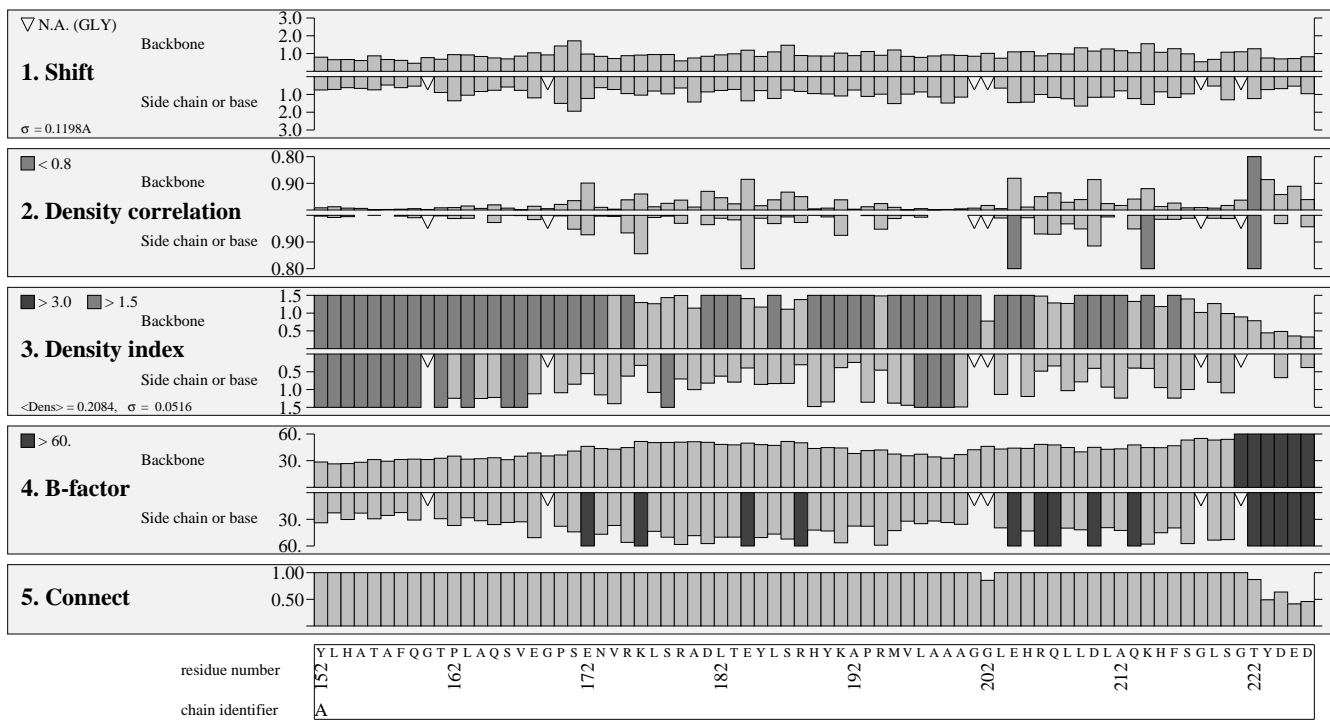
### Local estimation



# Structure Factor Check

## 1PPJ

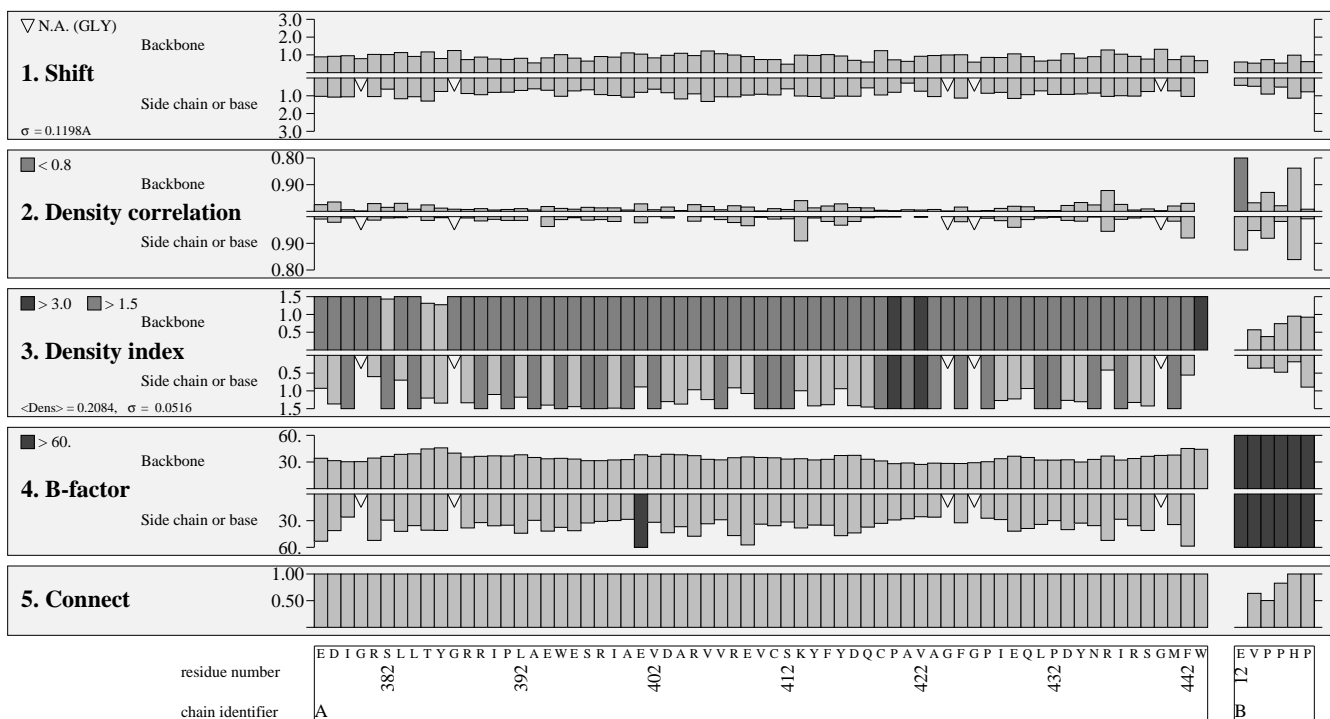
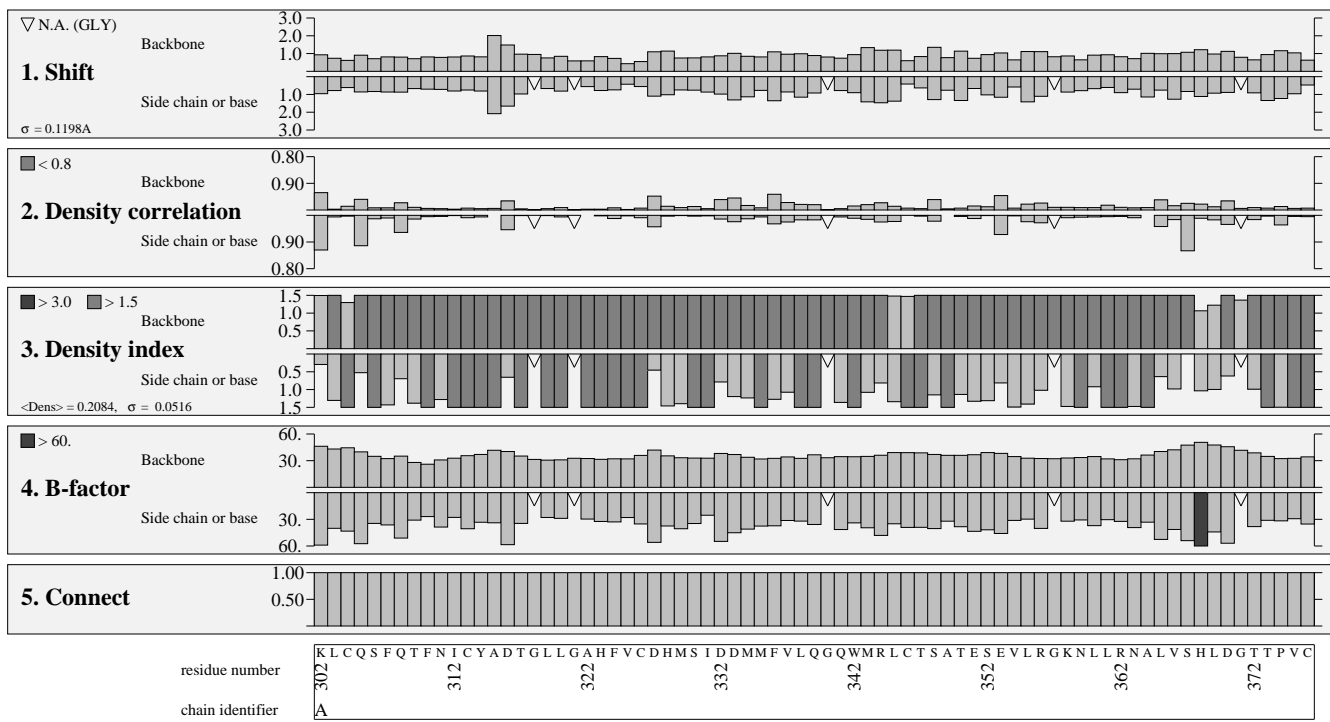
### Local estimation (2)



# Structure Factor Check

## 1PPJ

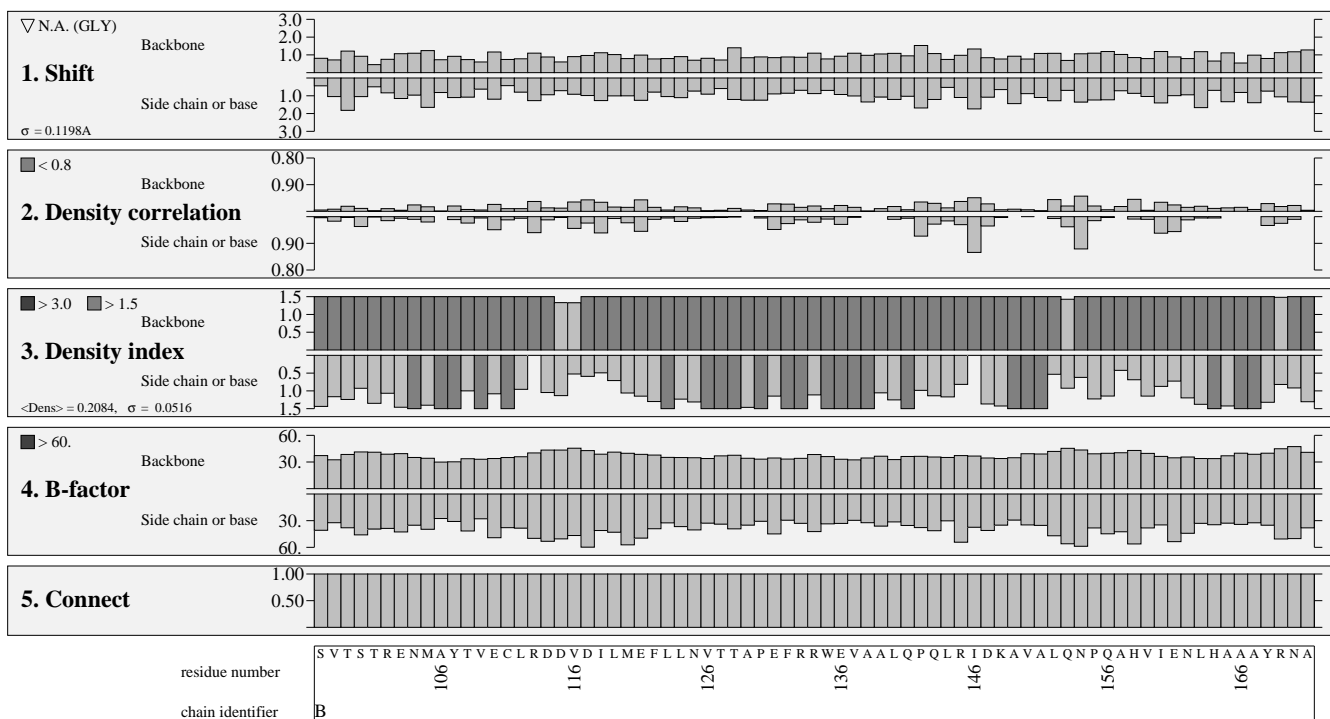
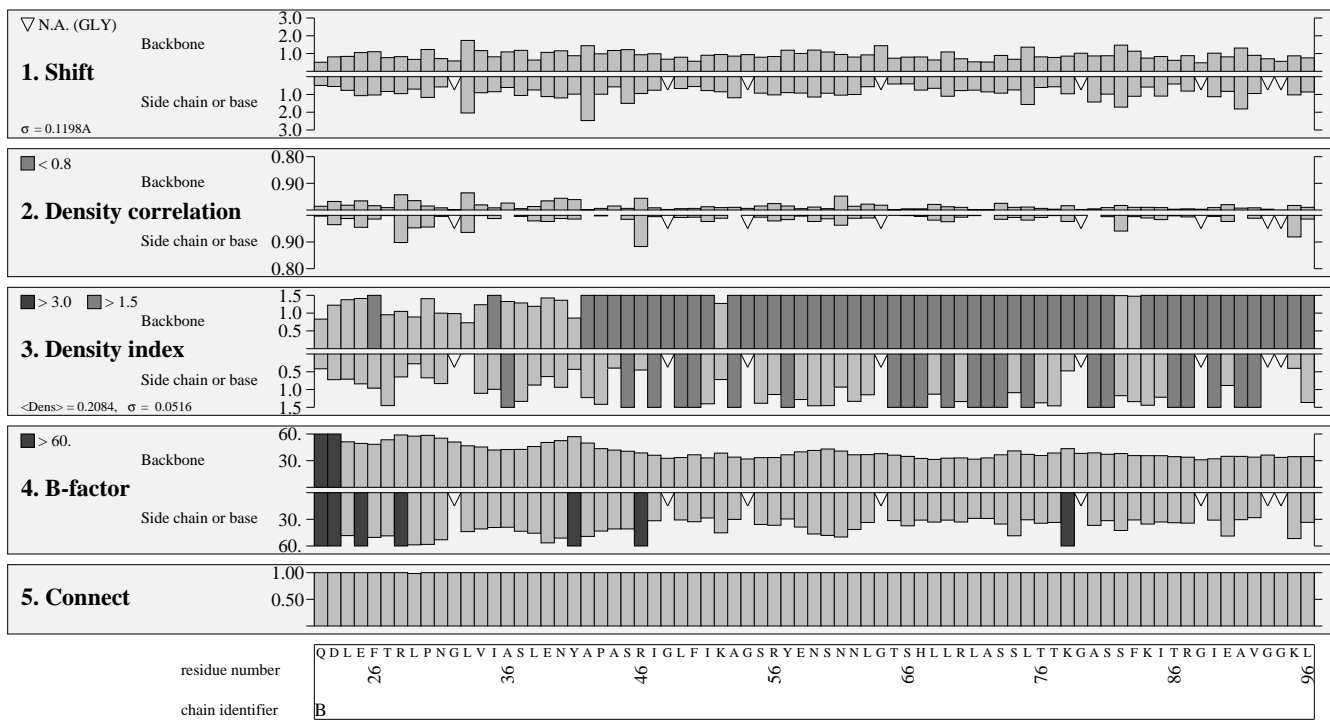
### Local estimation (3)



# Structure Factor Check

## 1PPJ

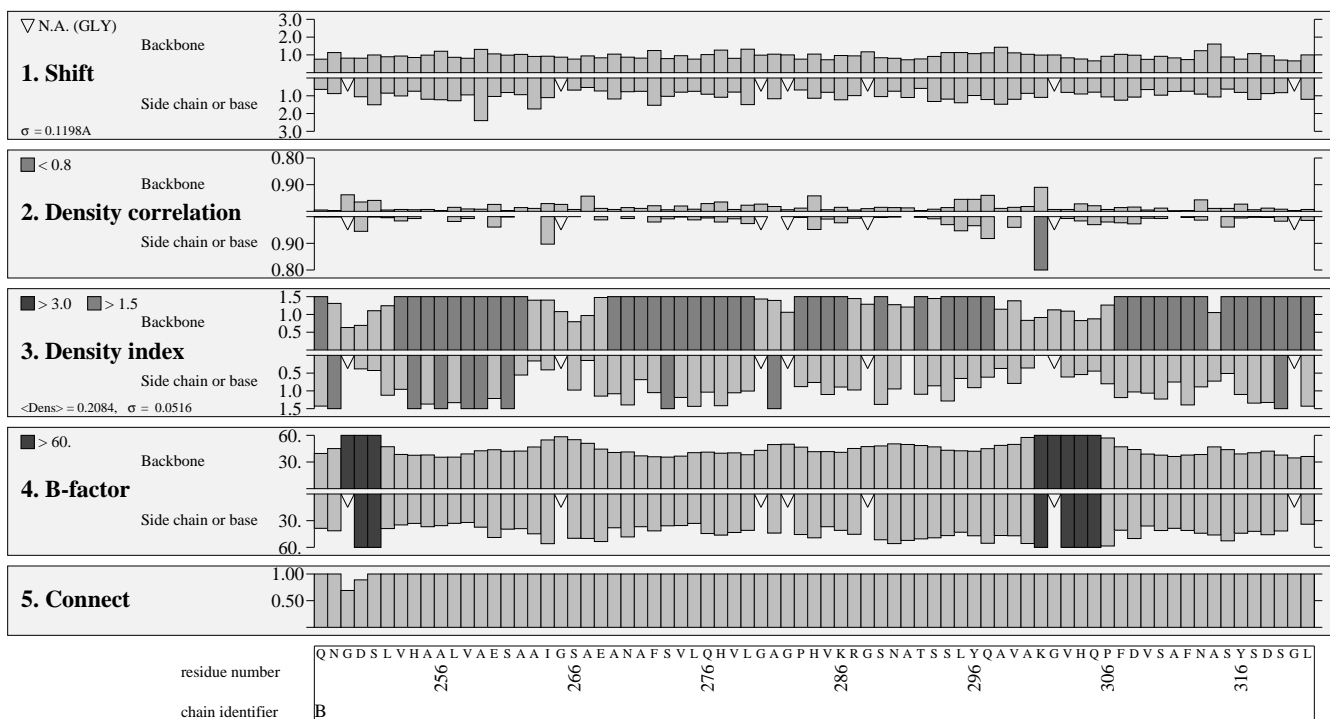
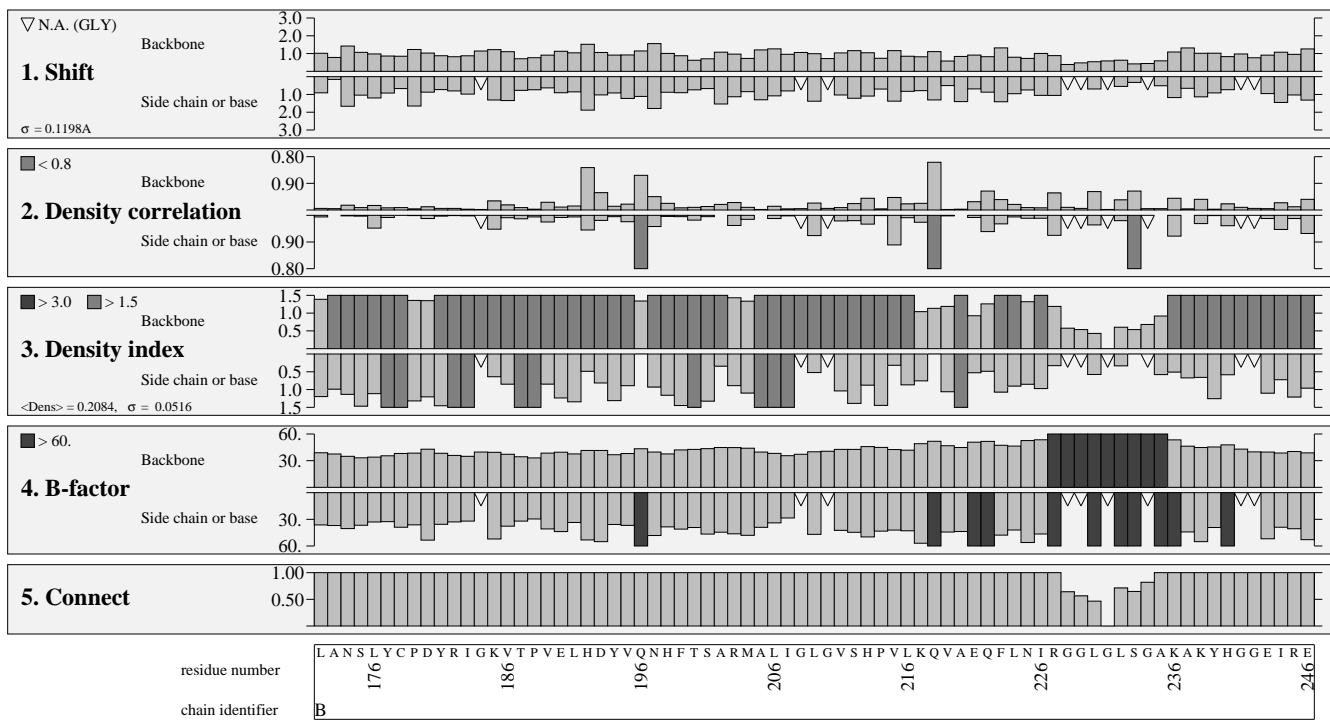
### Local estimation (4)



# Structure Factor Check

## 1PPJ

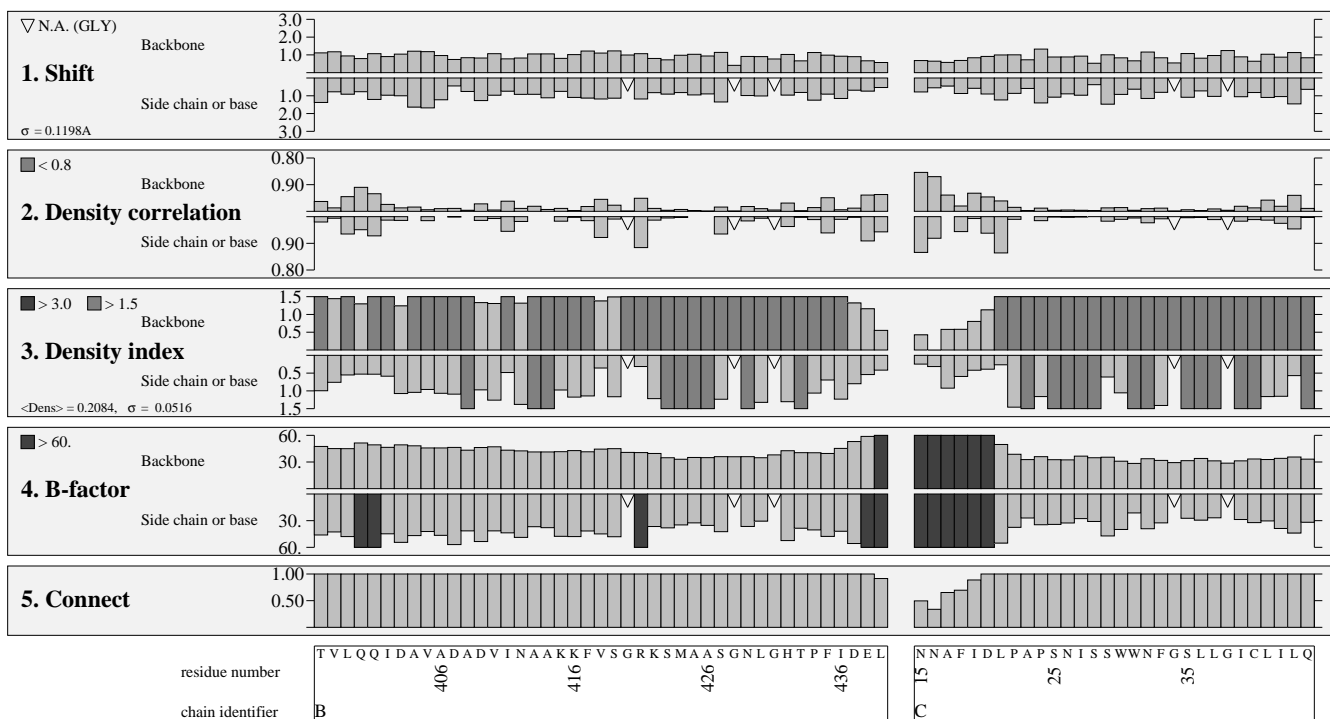
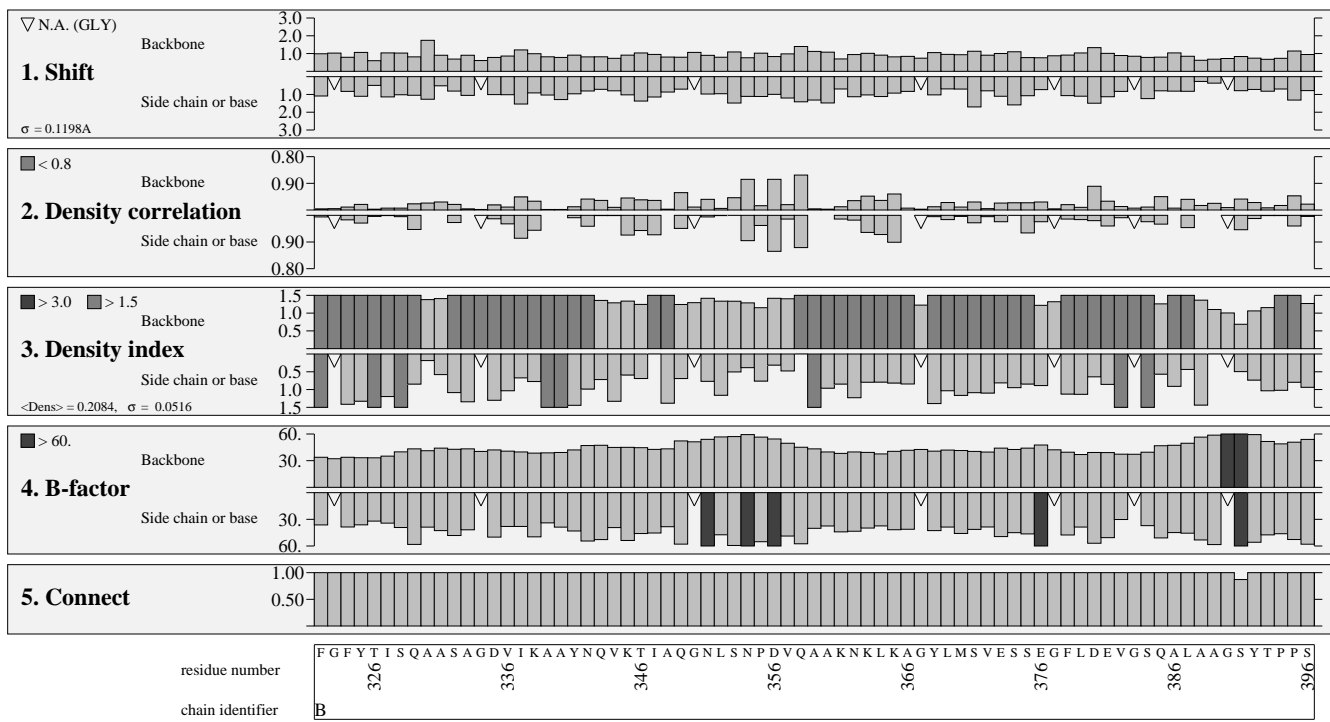
### Local estimation (5)



# Structure Factor Check

## 1PPJ

### Local estimation (6)

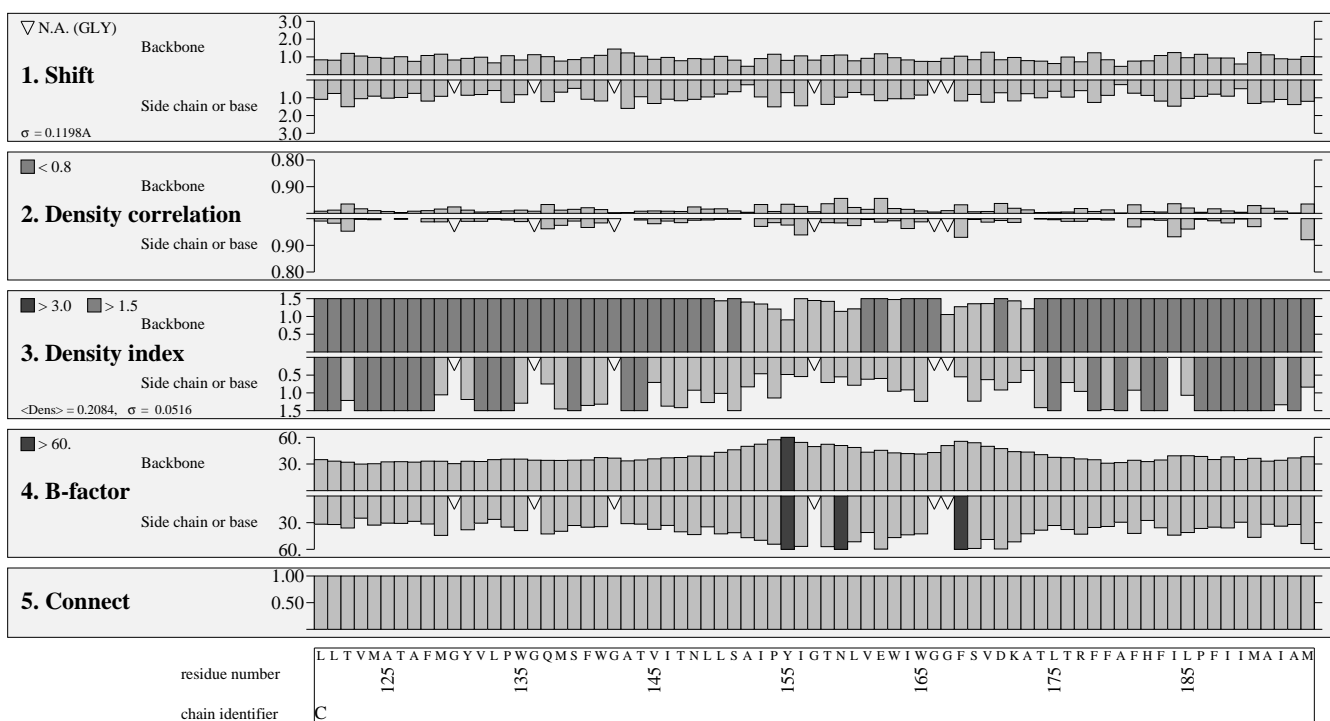
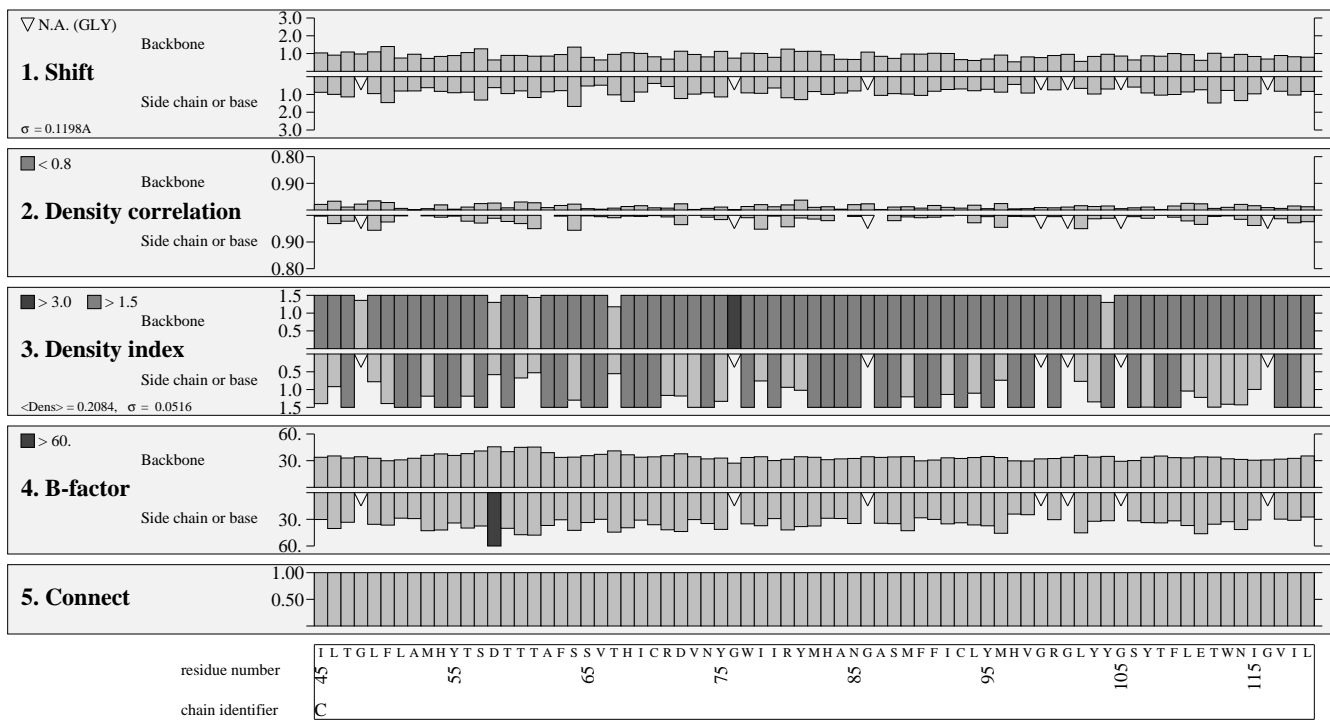




# Structure Factor Check

## 1PPJ

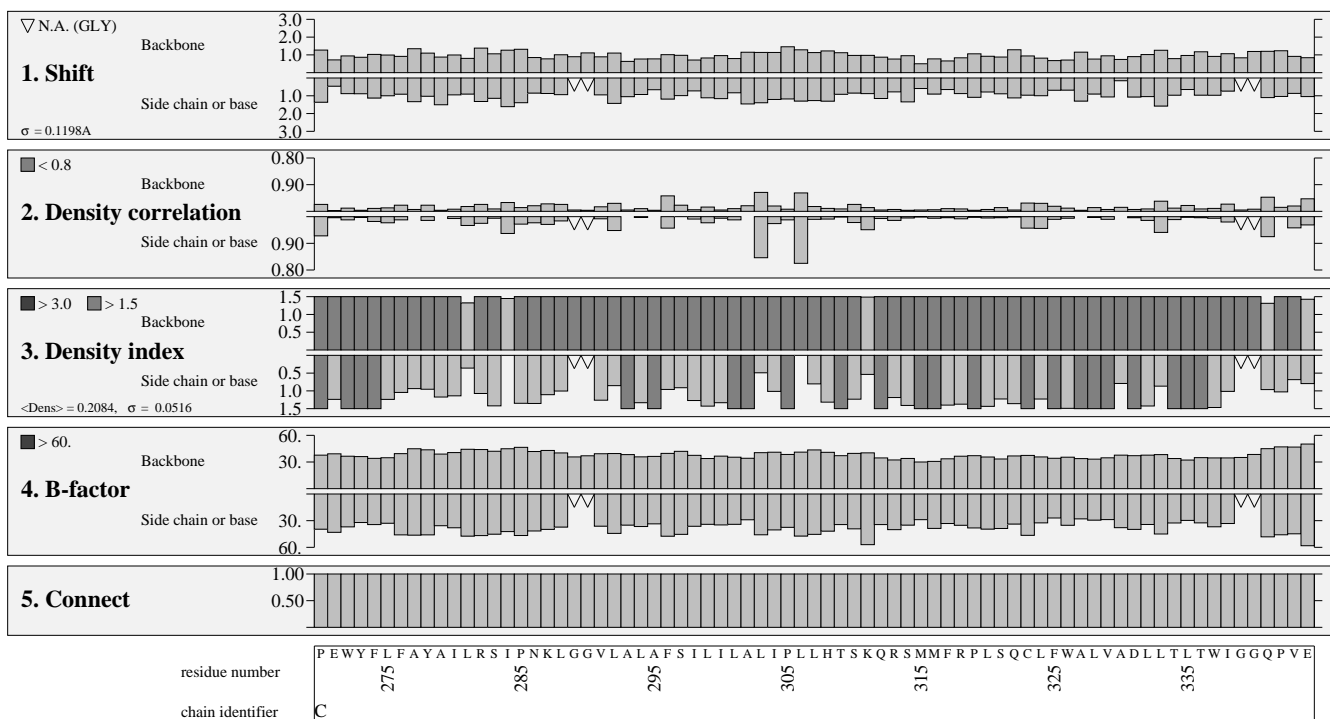
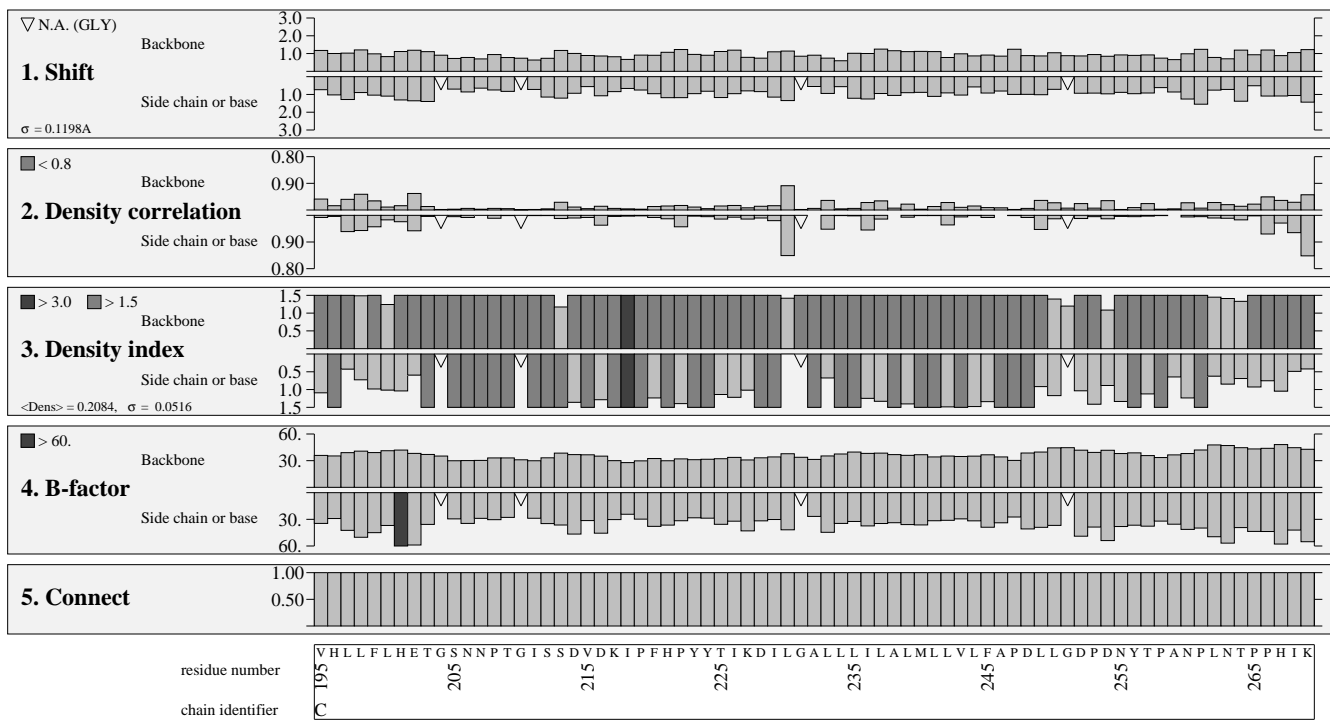
### Local estimation (7)



# Structure Factor Check

## 1PPJ

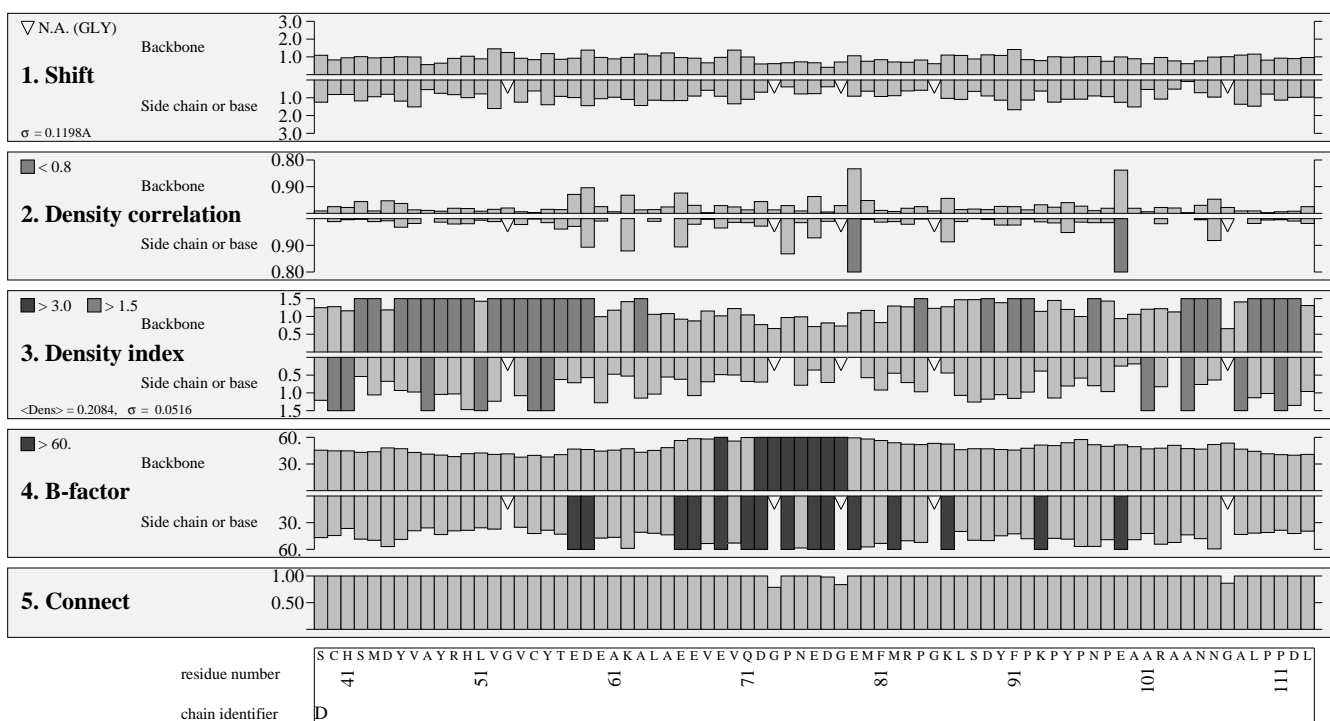
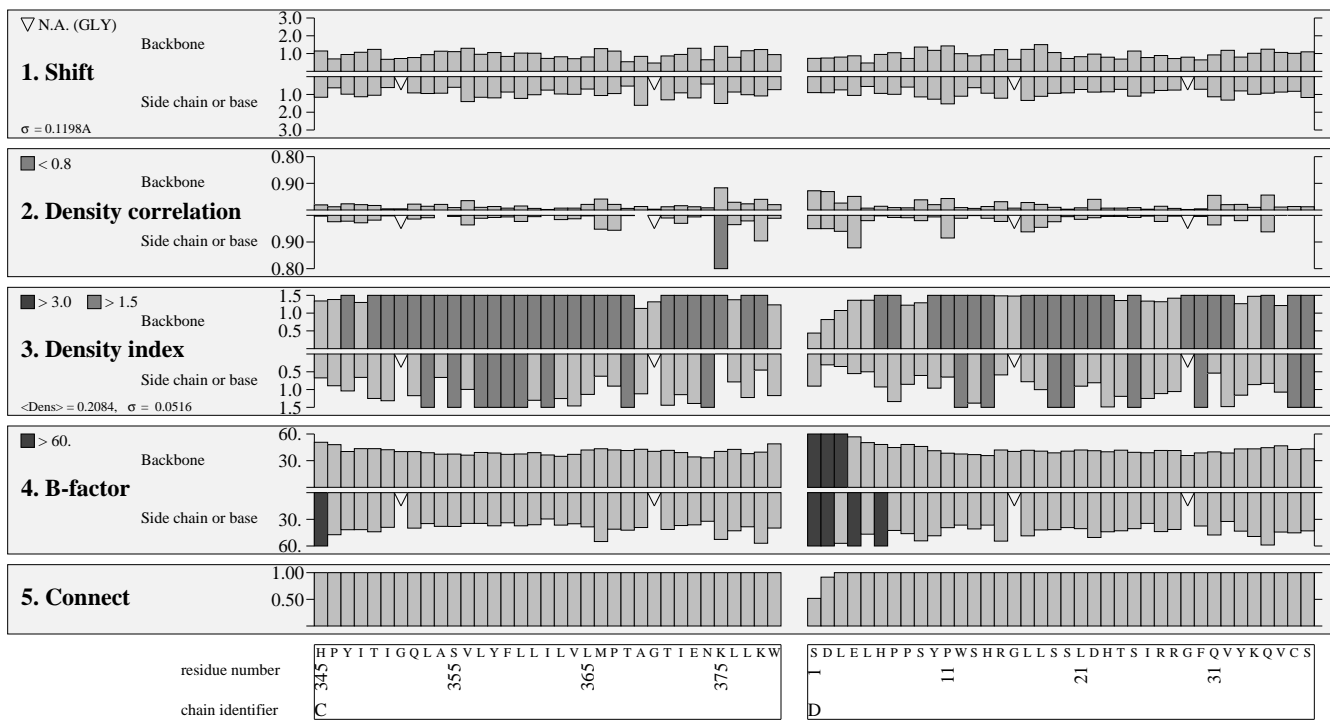
### Local estimation (8)



# Structure Factor Check

## 1PPJ

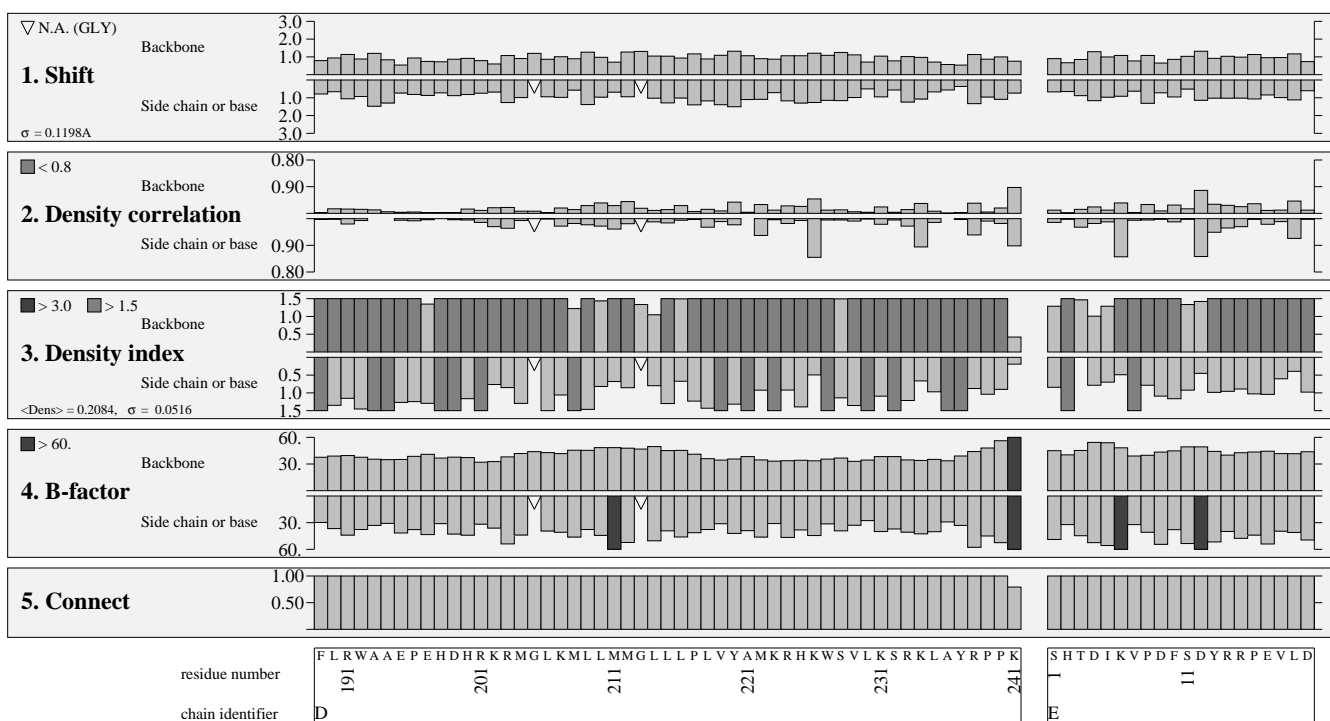
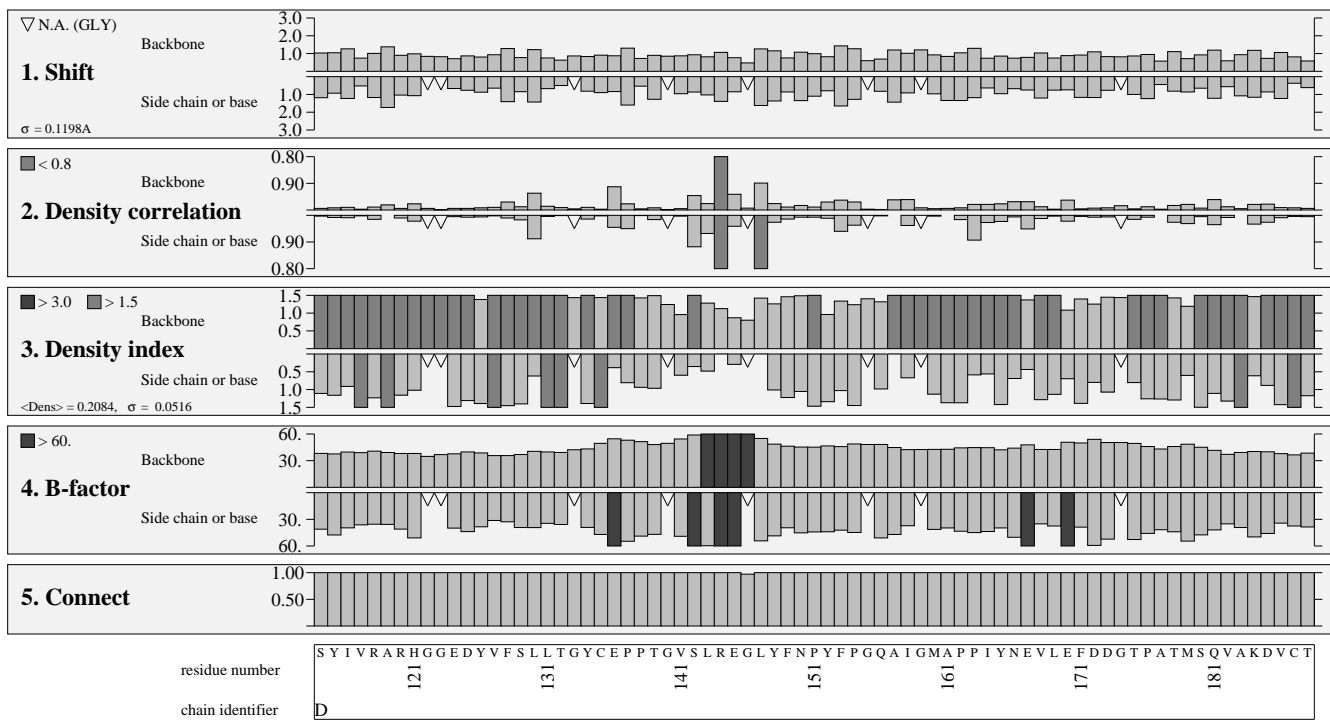
### Local estimation (9)



# Structure Factor Check

## 1PPJ

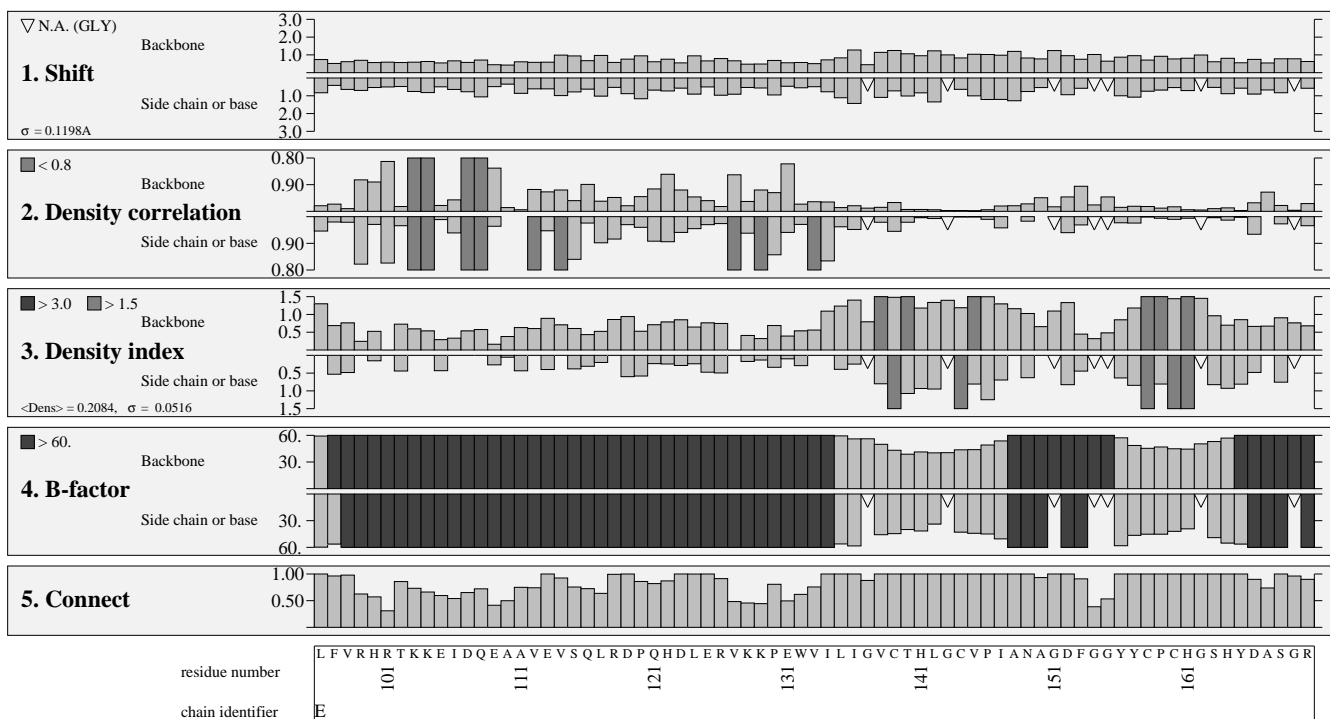
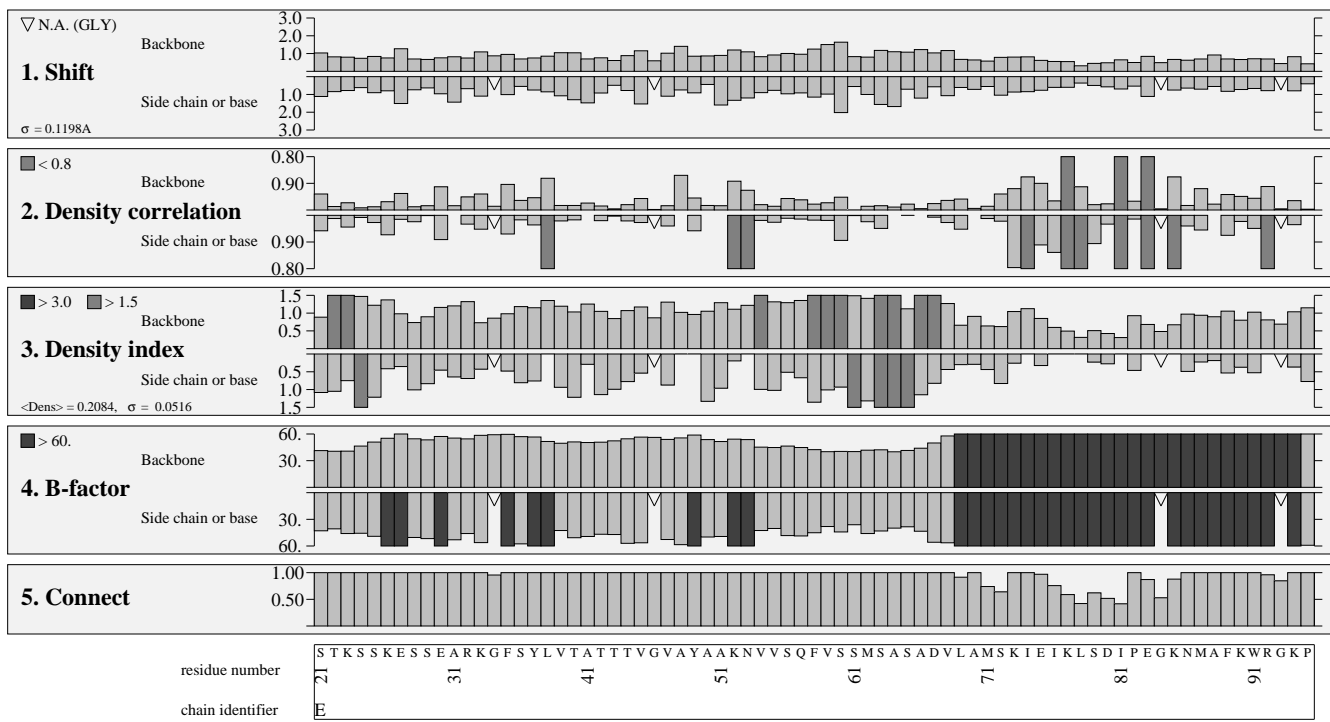
### Local estimation (10)



# Structure Factor Check

## 1PPJ

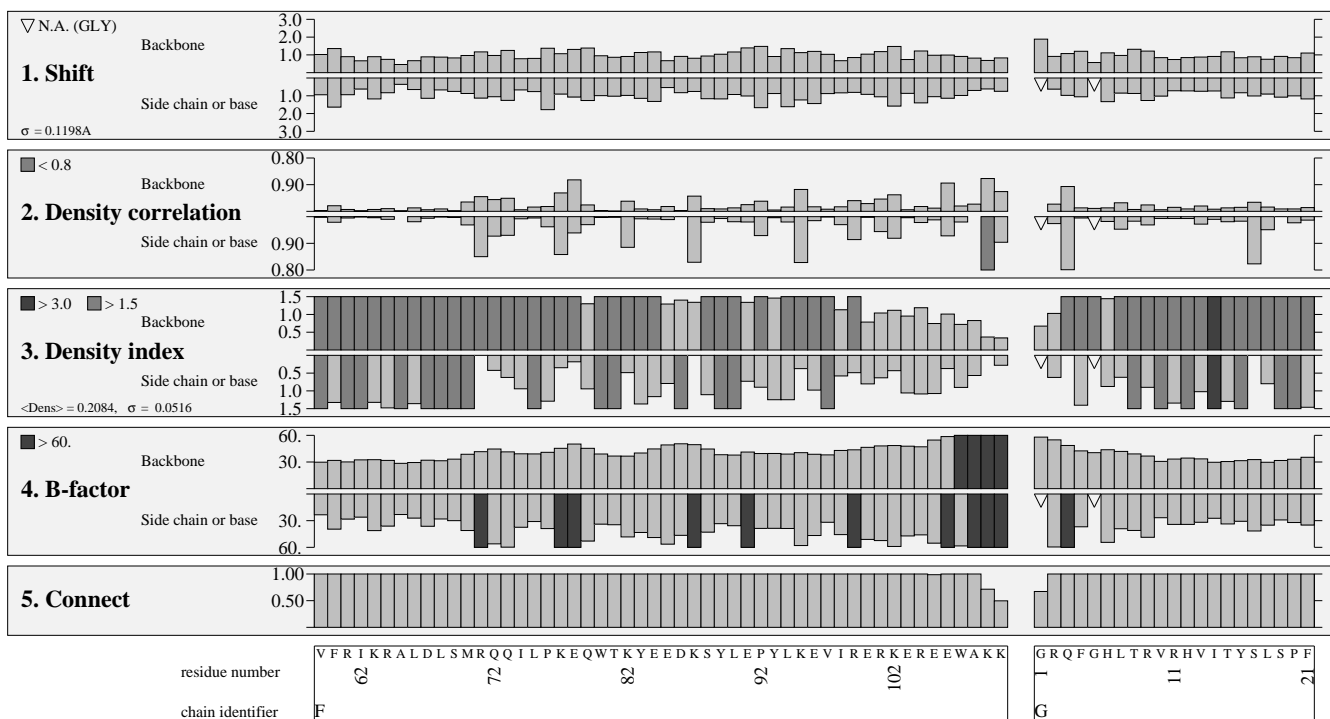
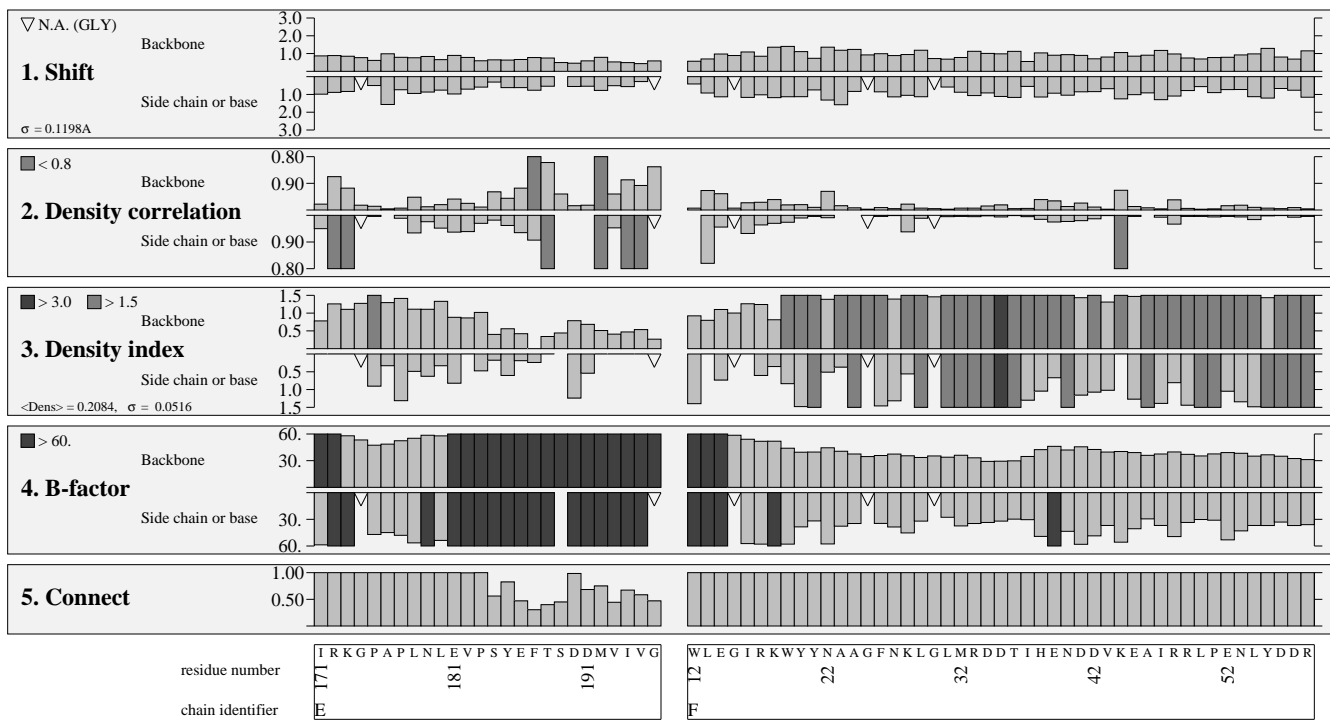
### Local estimation (11)



# Structure Factor Check

## 1PPJ

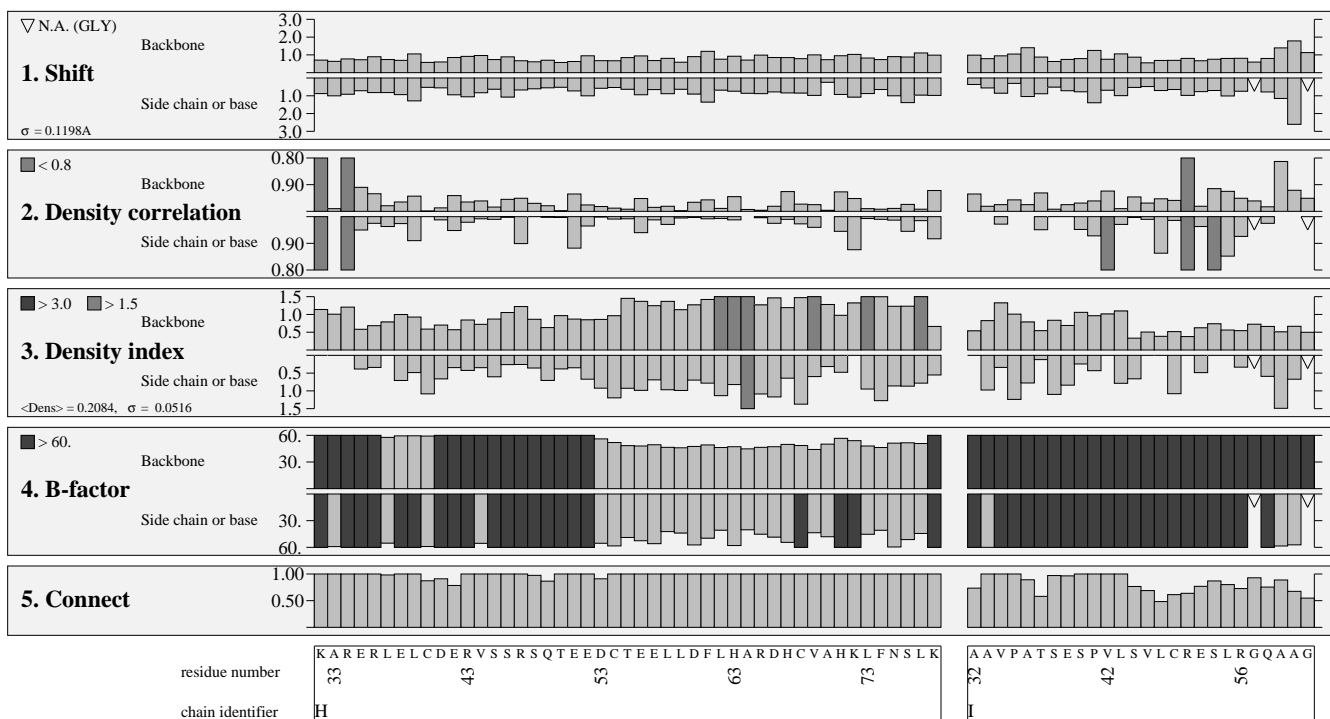
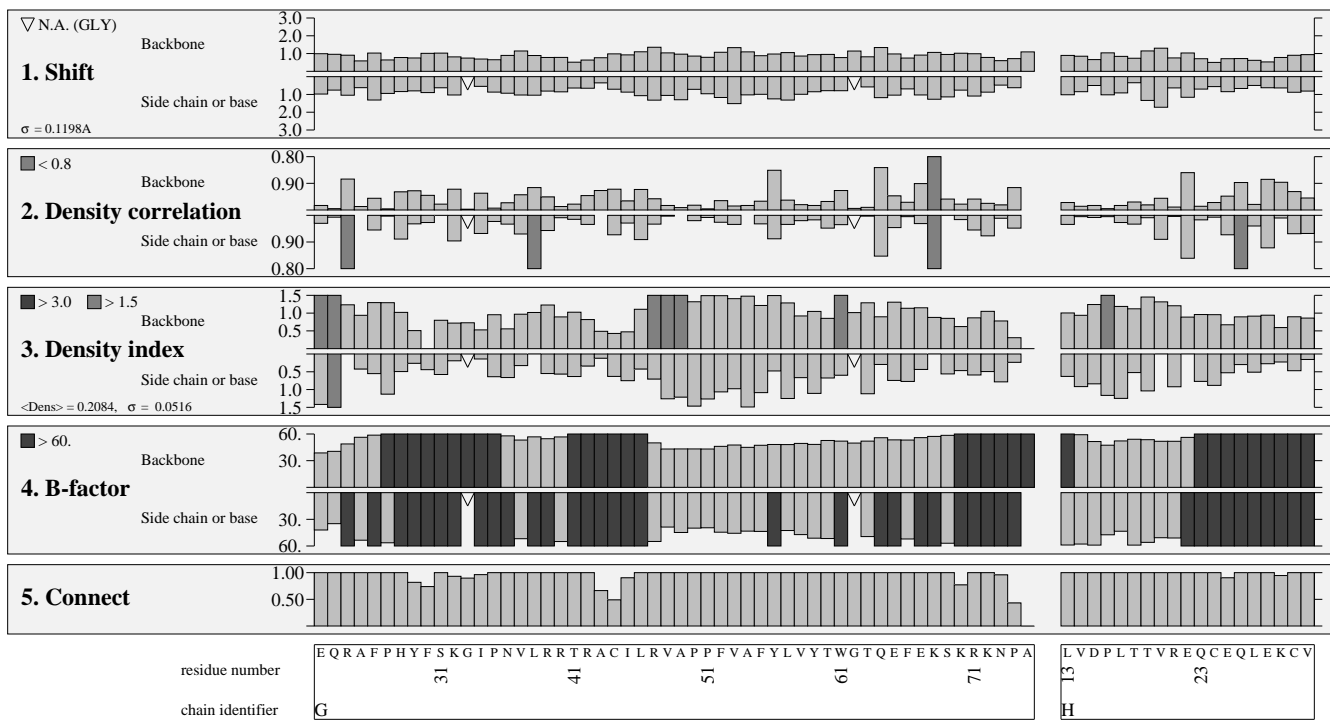
### Local estimation (12)



# Structure Factor Check

## 1PPJ

### Local estimation (13)



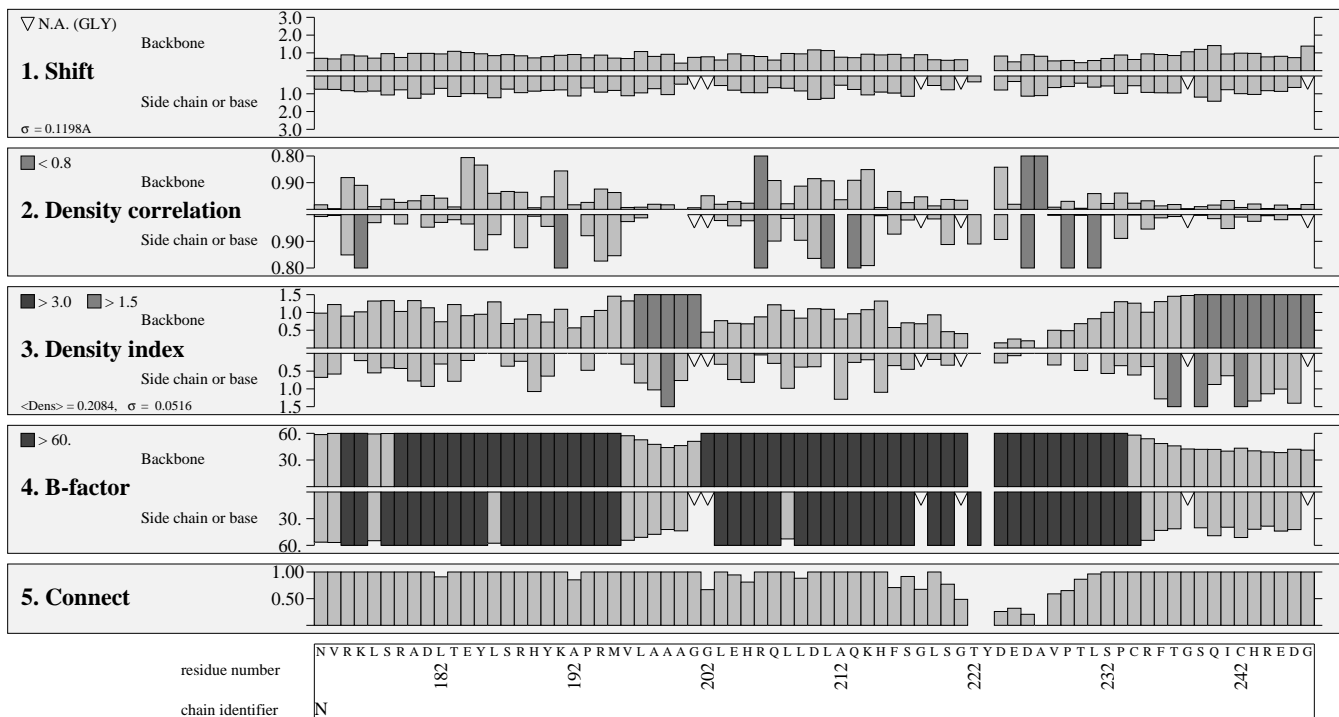
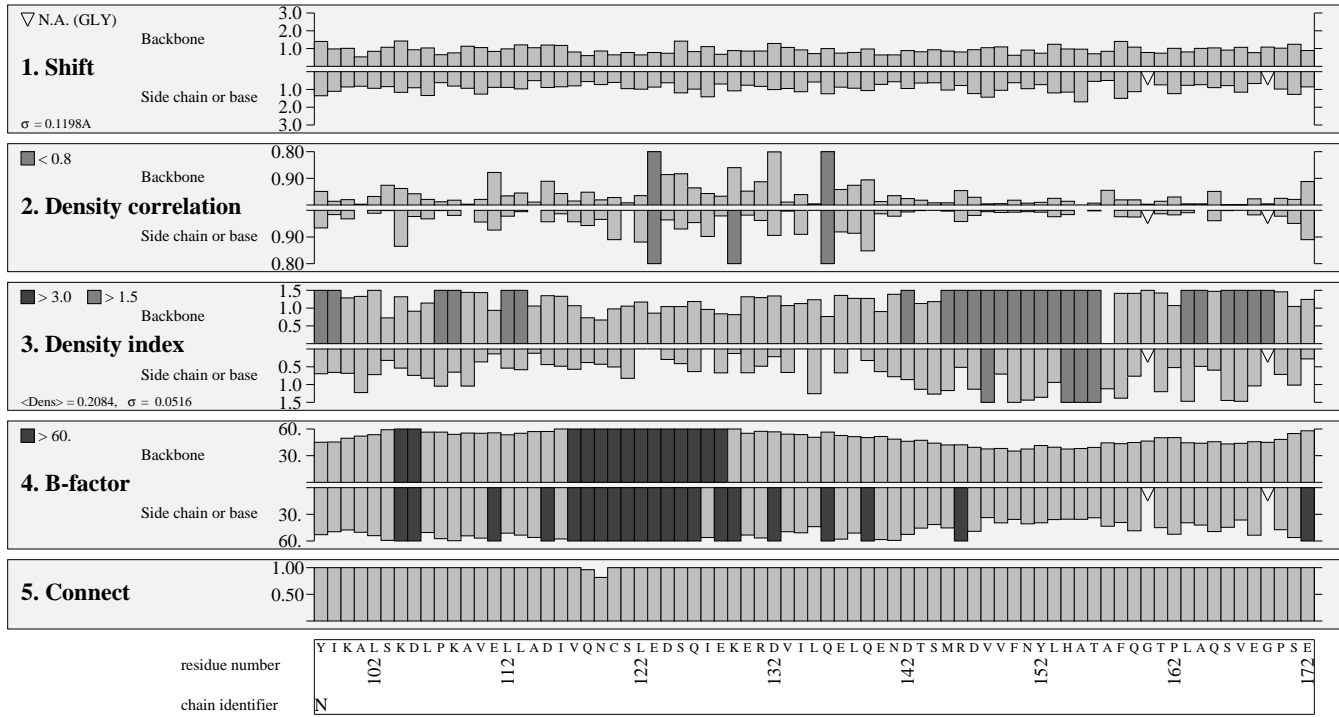




# Structure Factor Check

## 1PPJ

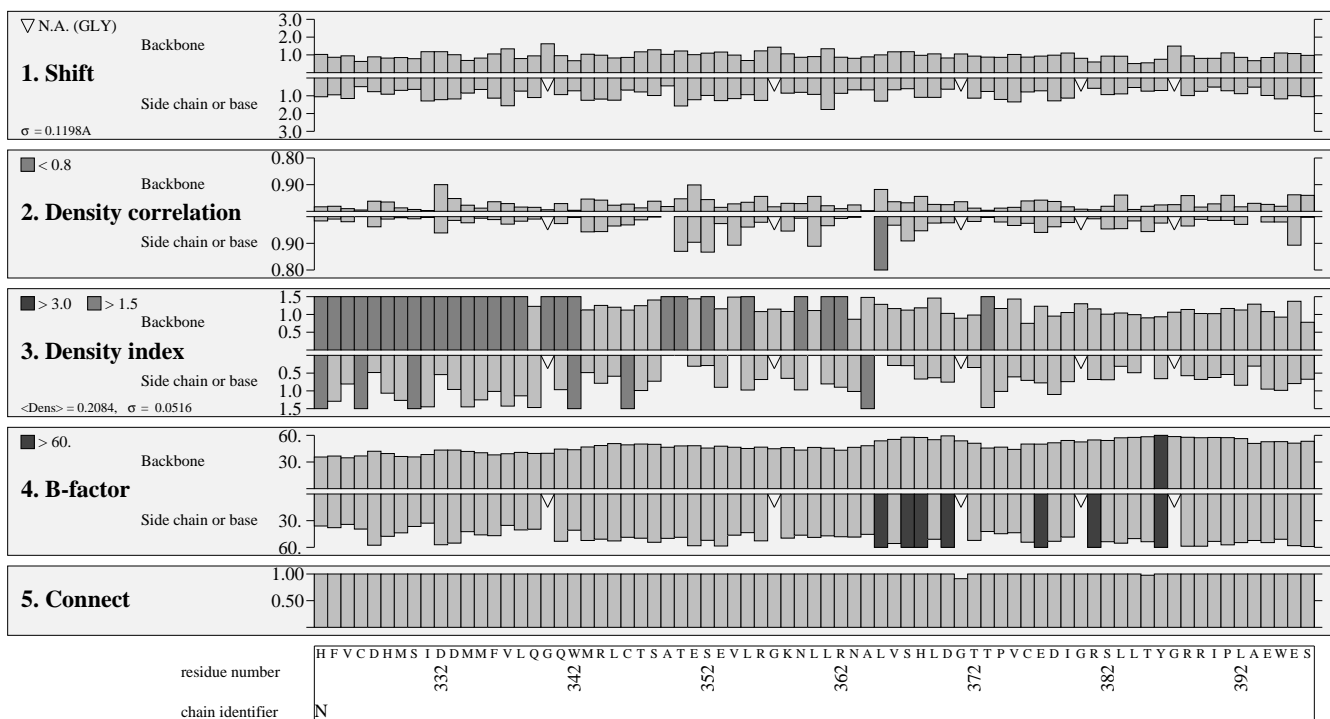
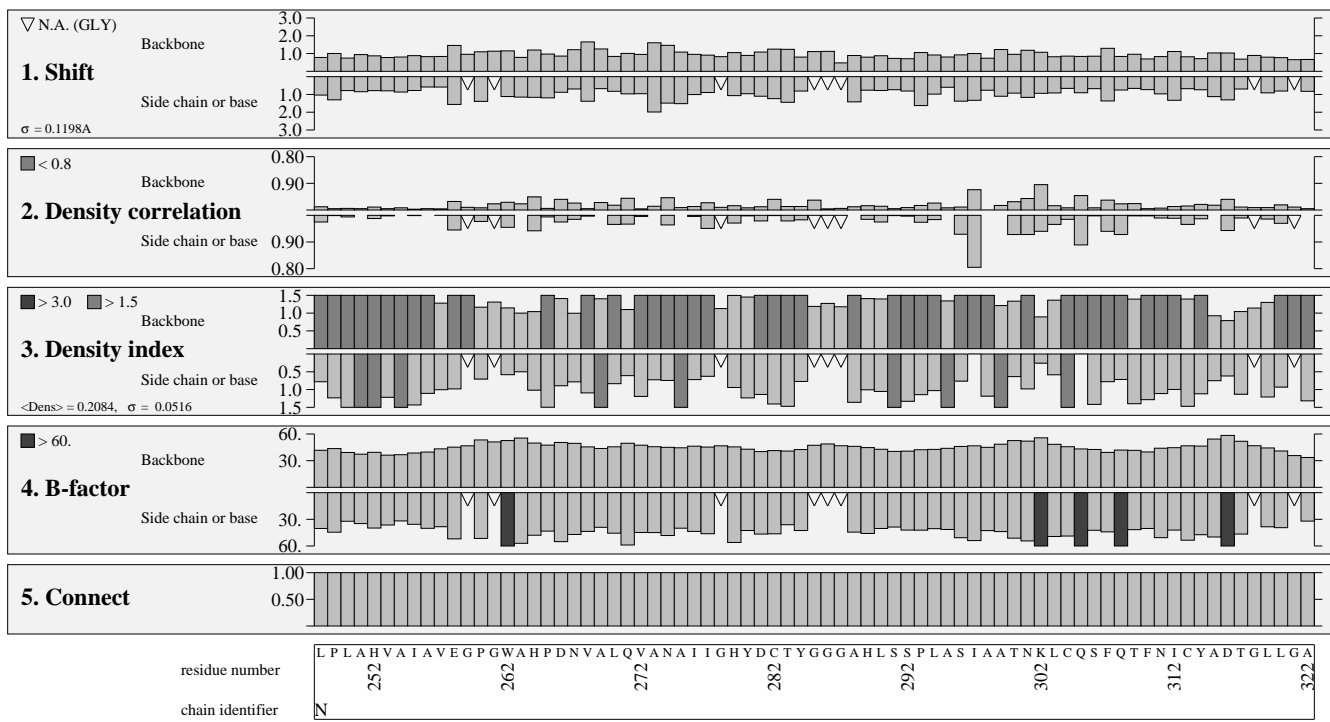
### Local estimation (15)



# Structure Factor Check

## 1PPJ

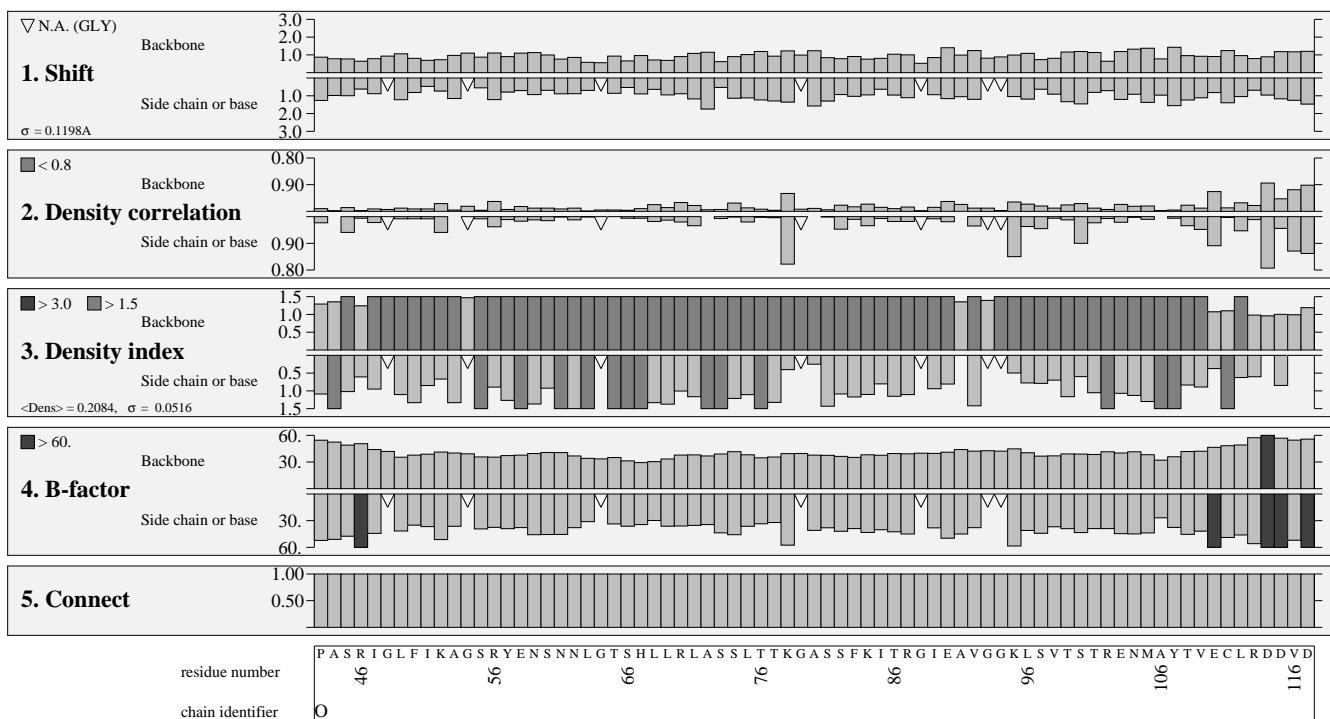
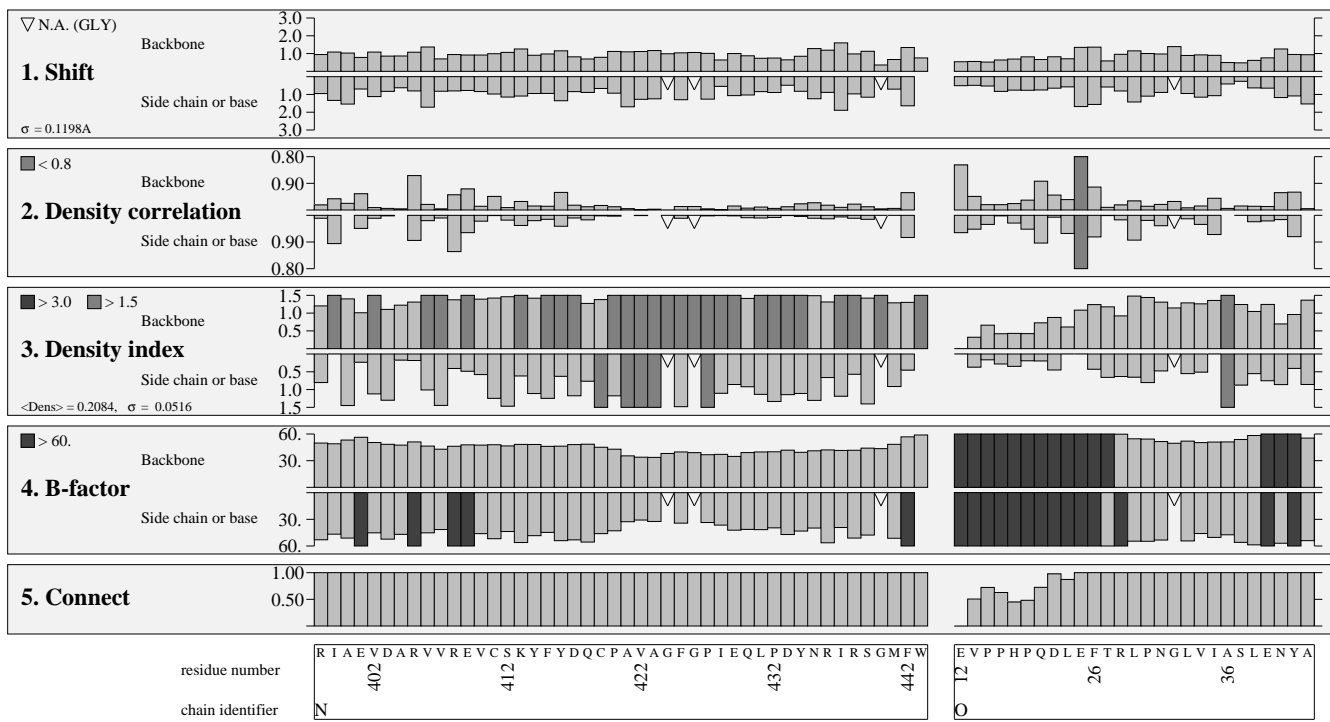
### Local estimation (16)



# Structure Factor Check

## 1PPJ

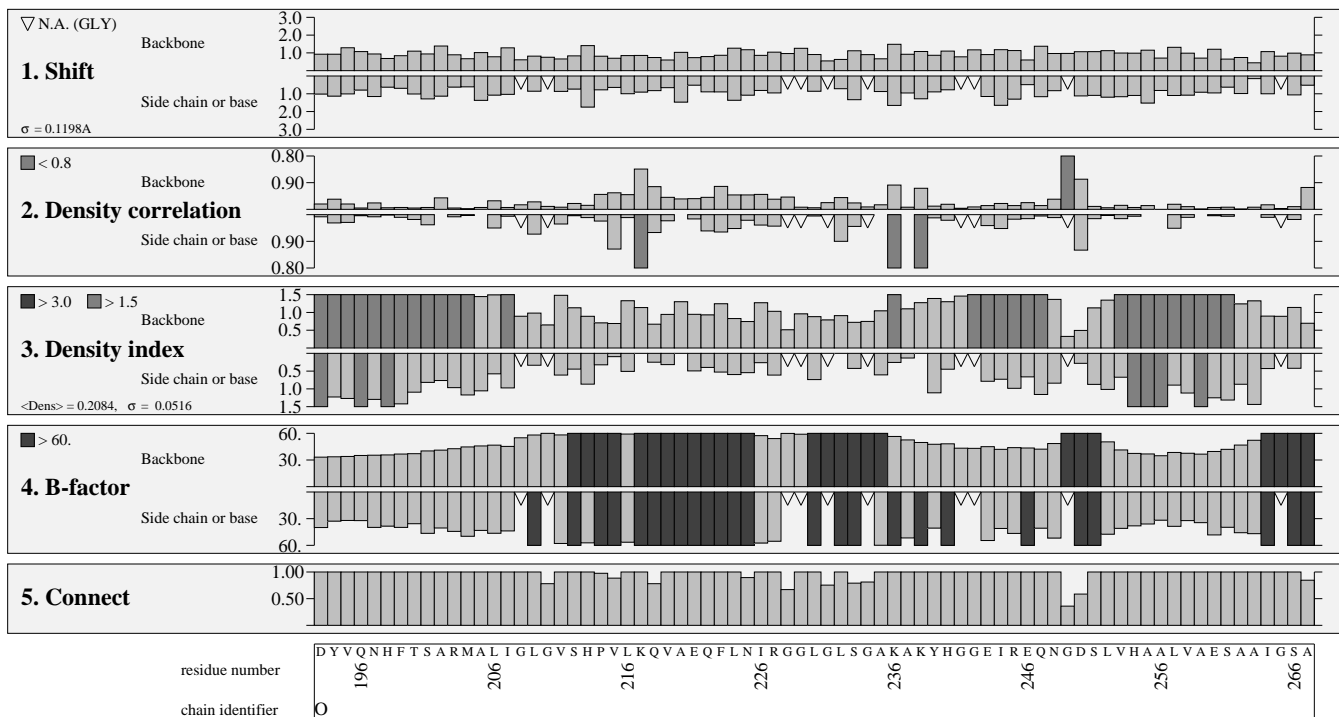
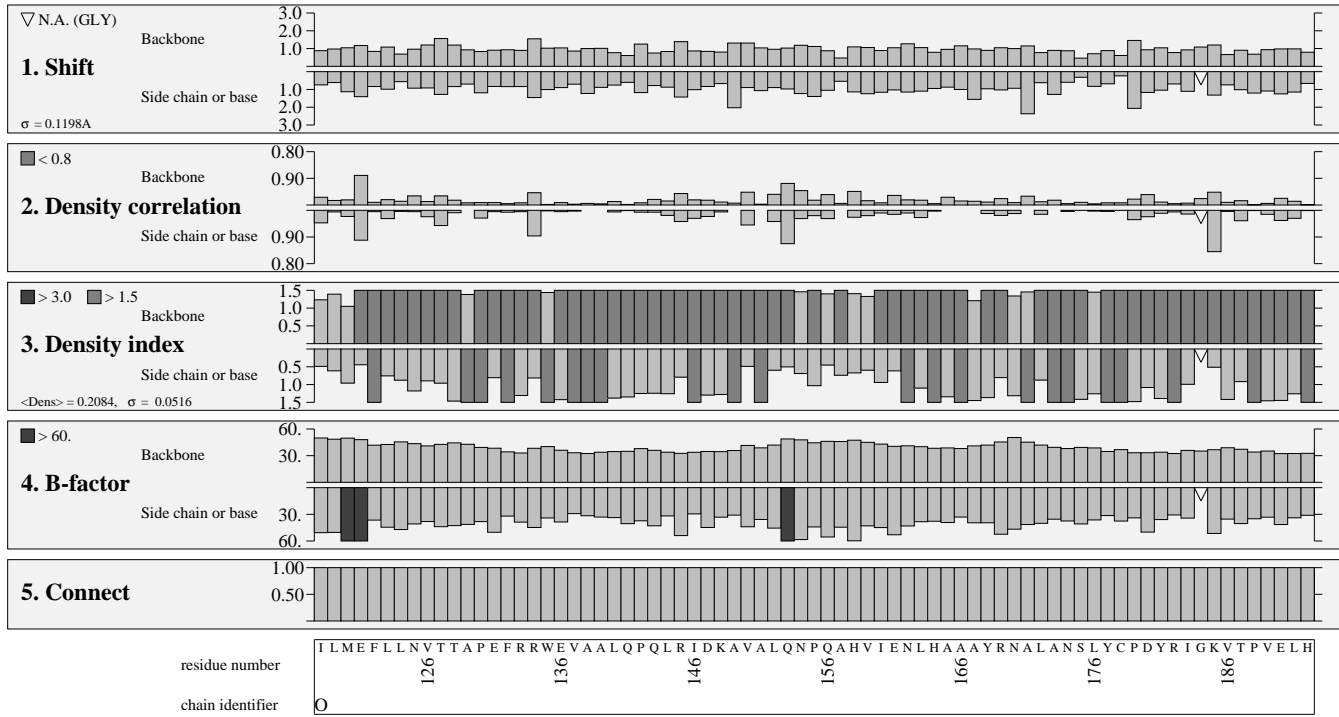
### Local estimation (17)



# Structure Factor Check

## 1PPJ

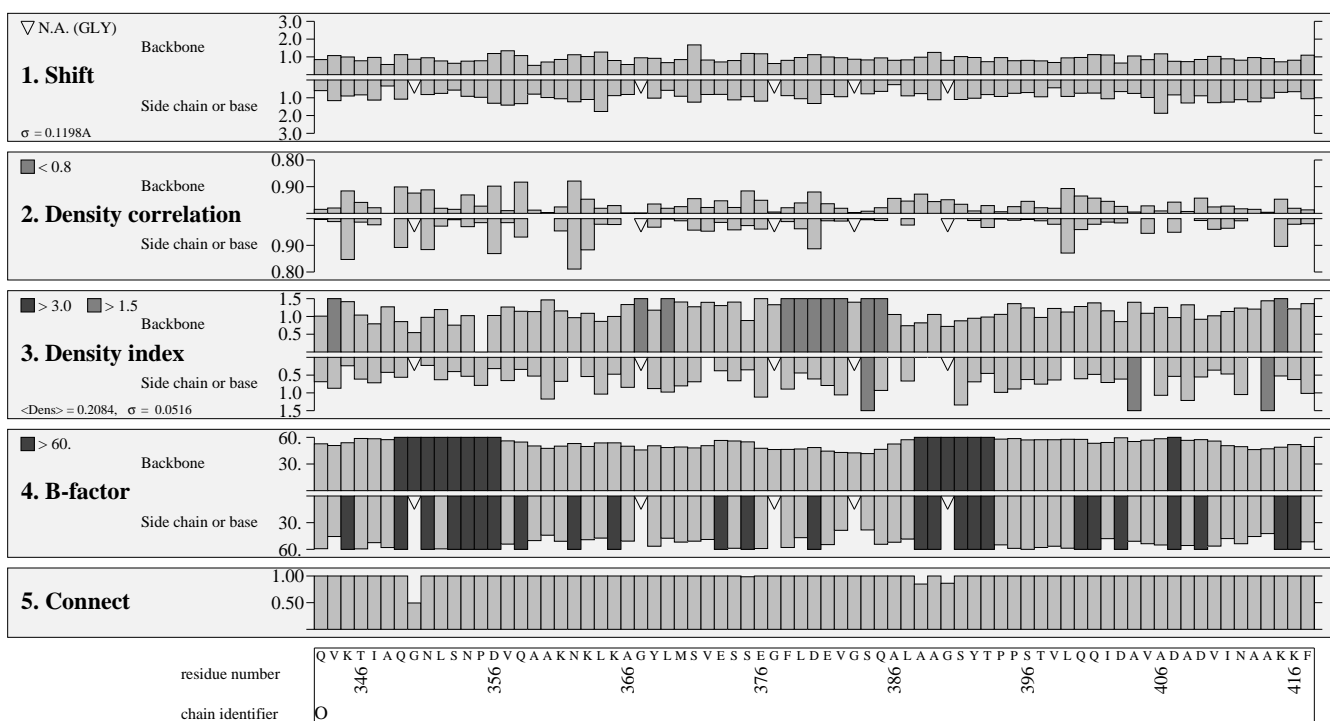
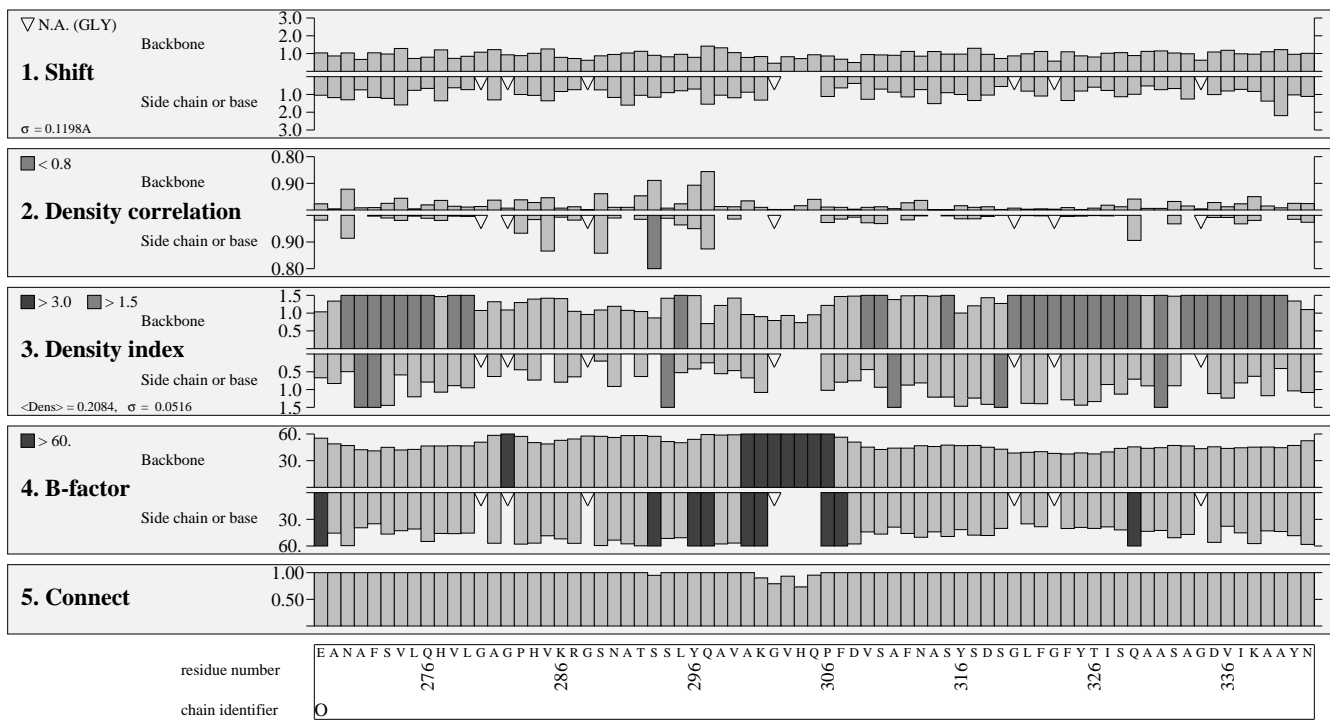
### Local estimation (18)



# Structure Factor Check

## 1PPJ

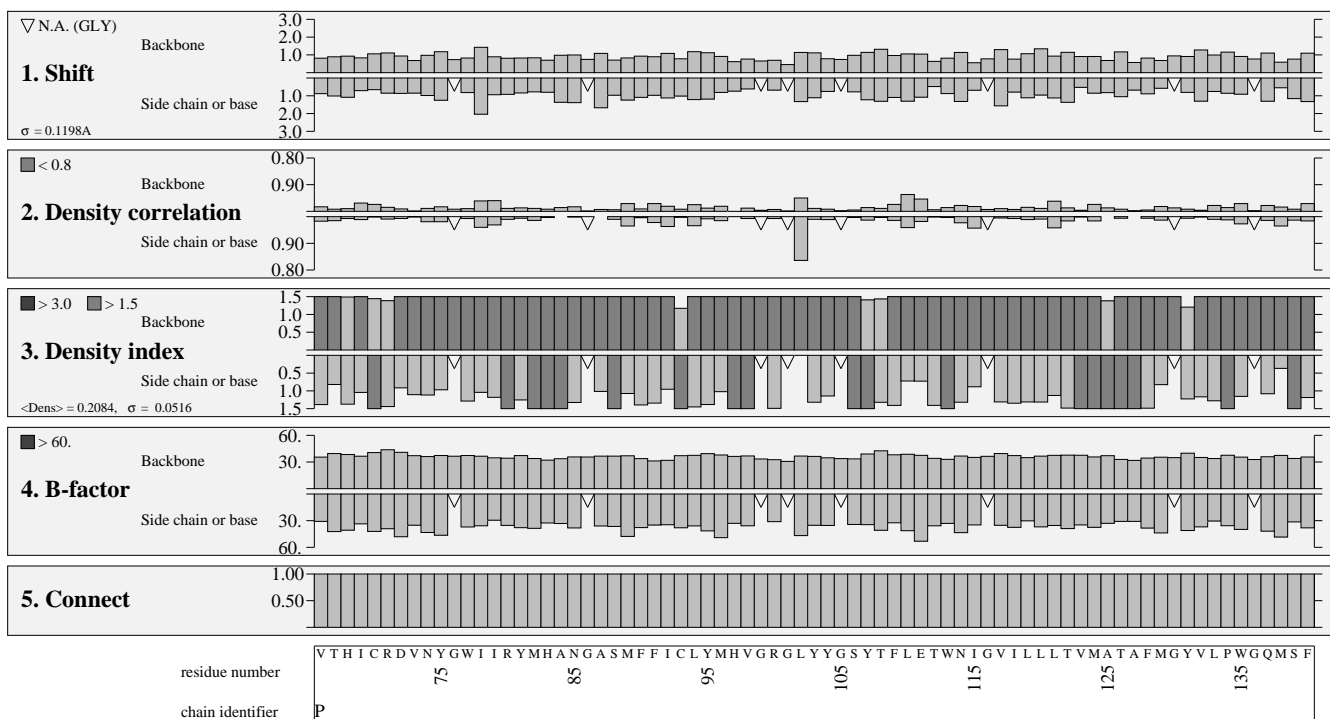
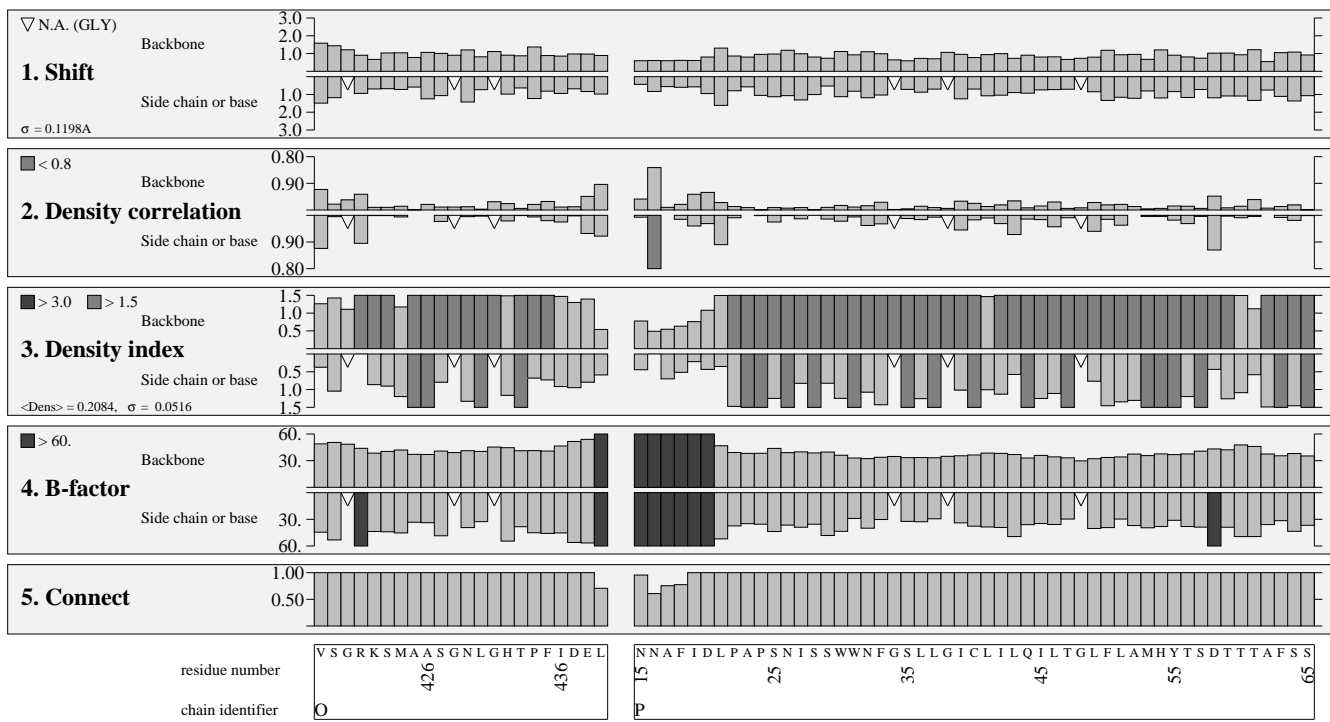
### Local estimation (19)



# Structure Factor Check

## 1PPJ

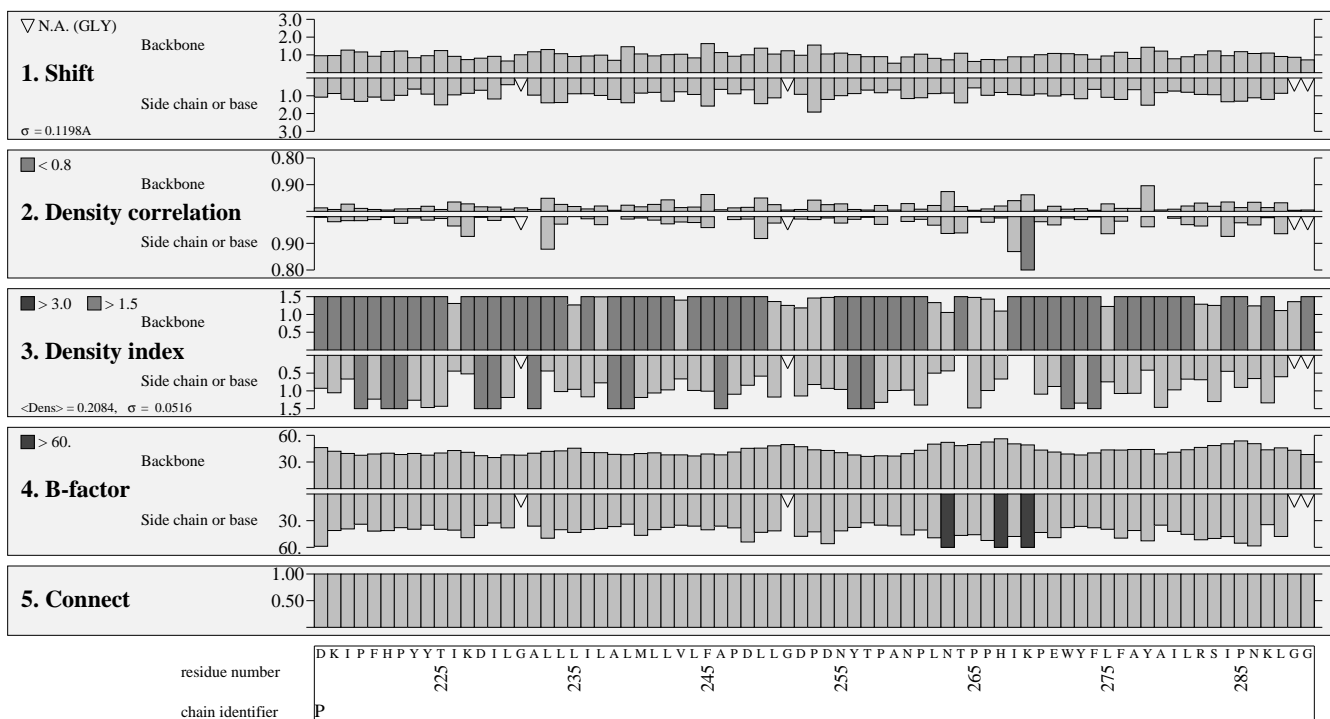
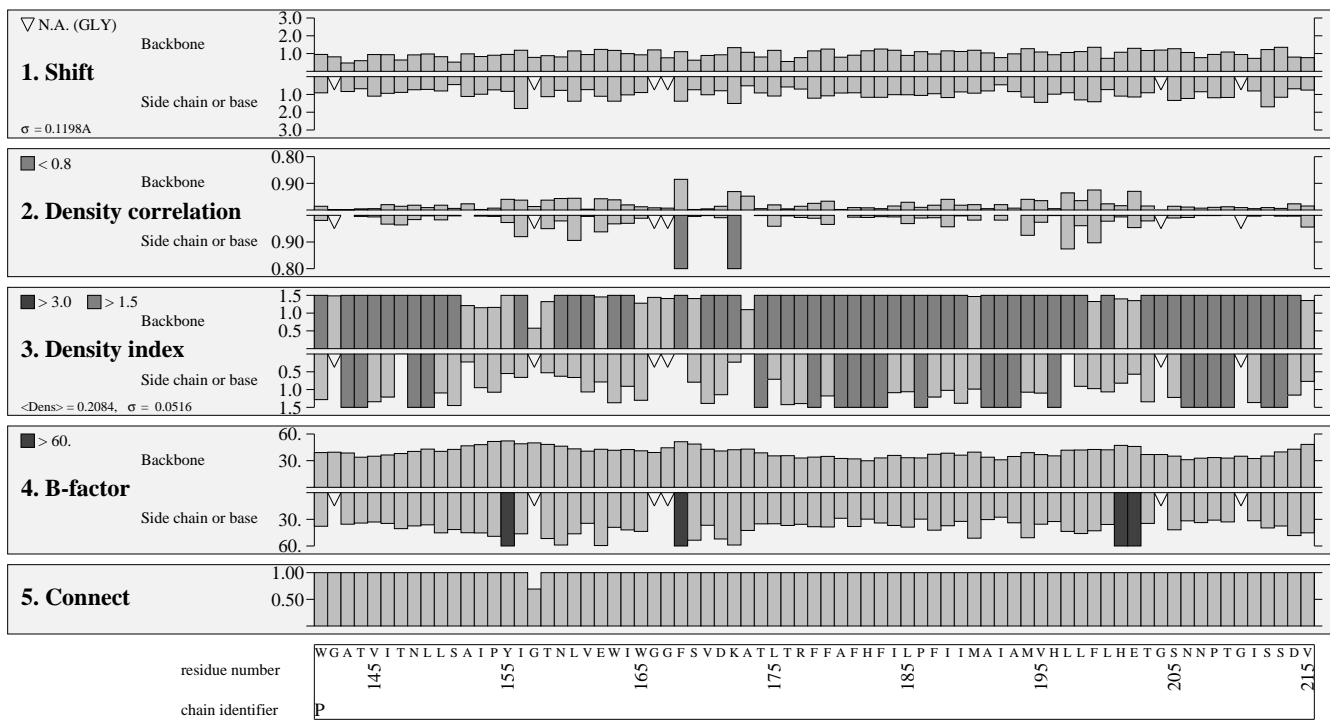
### Local estimation (20)



# Structure Factor Check

## 1PPJ

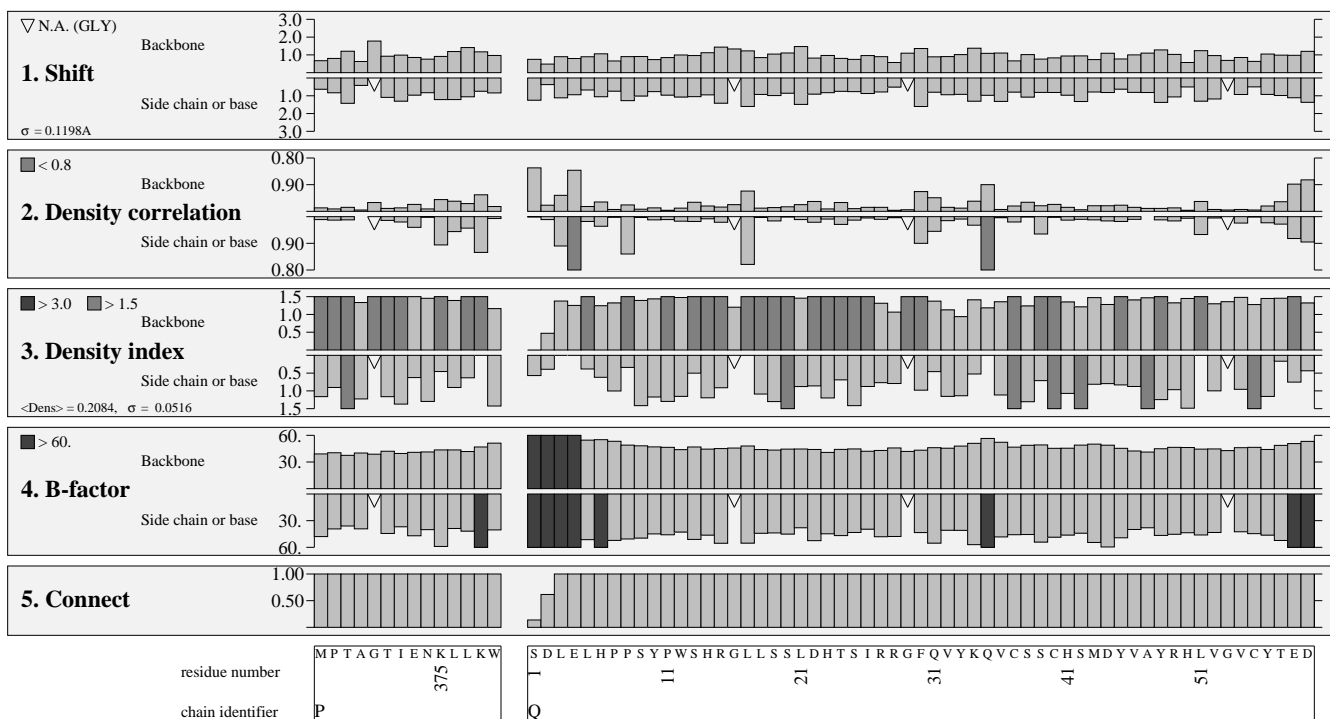
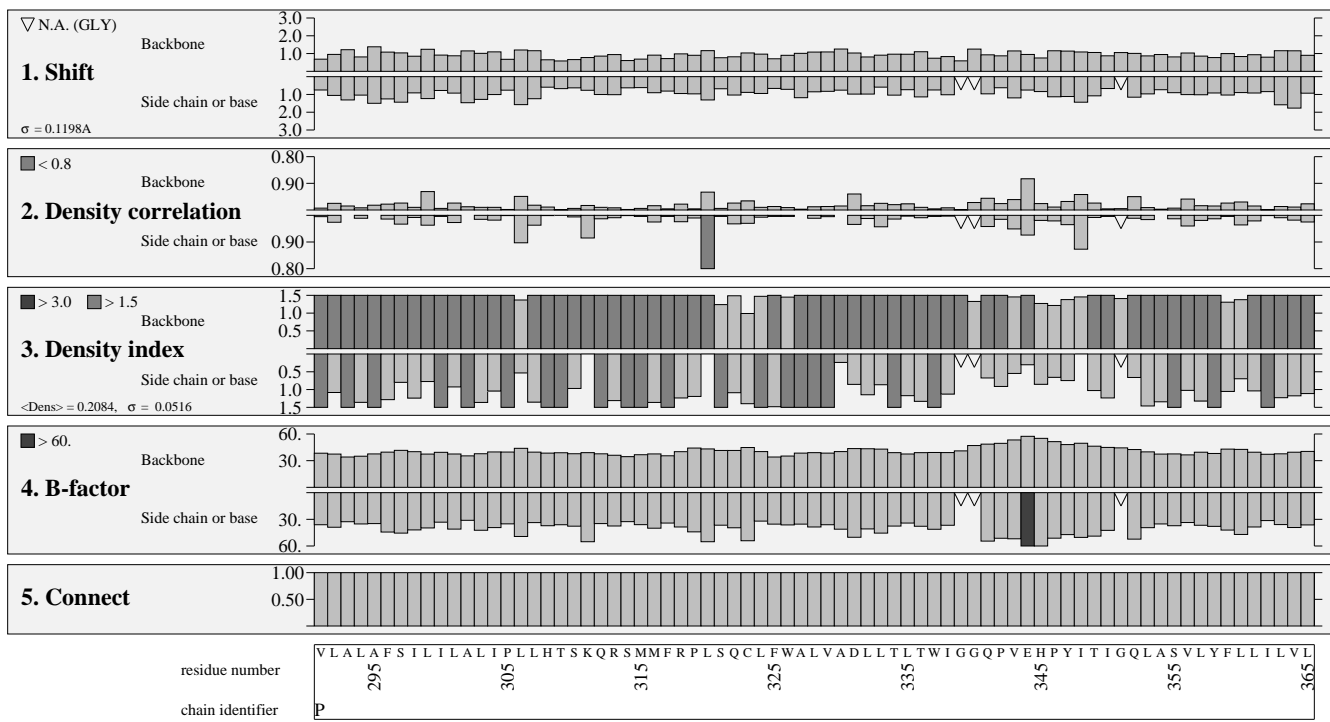
### Local estimation (21)



# Structure Factor Check

## 1PPJ

### Local estimation (22)

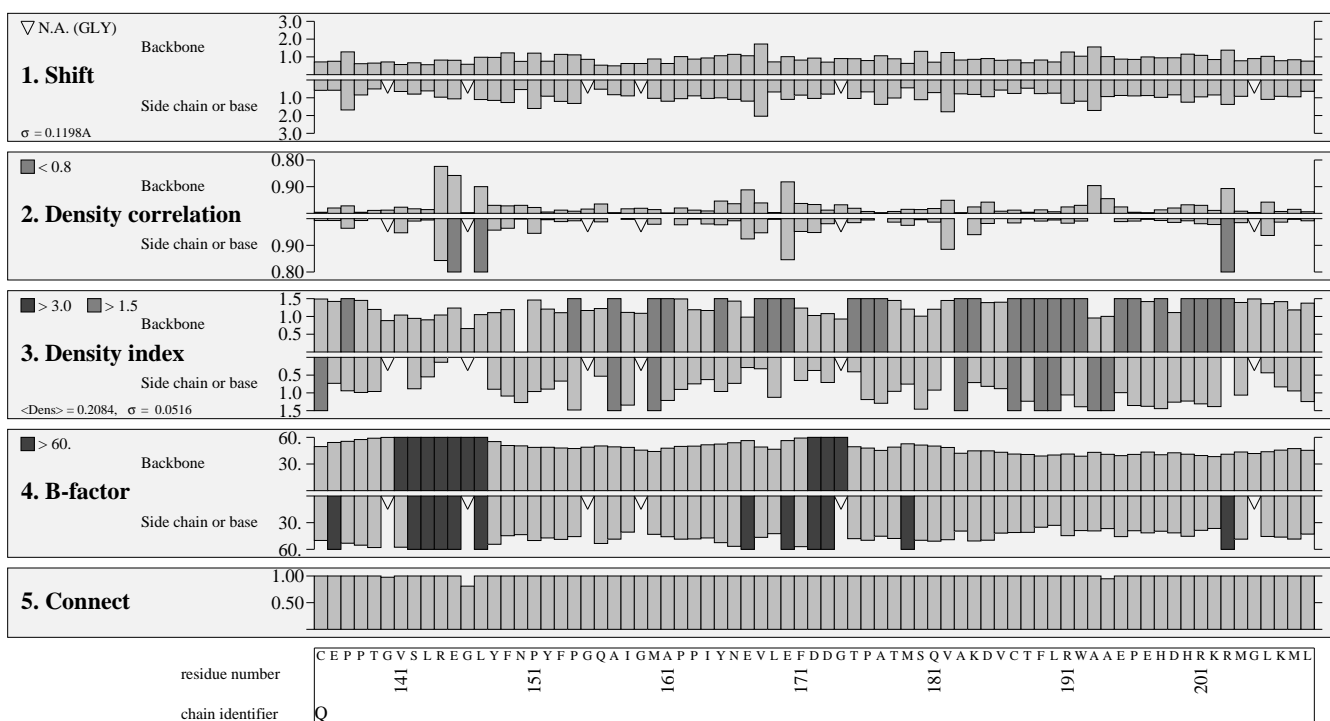
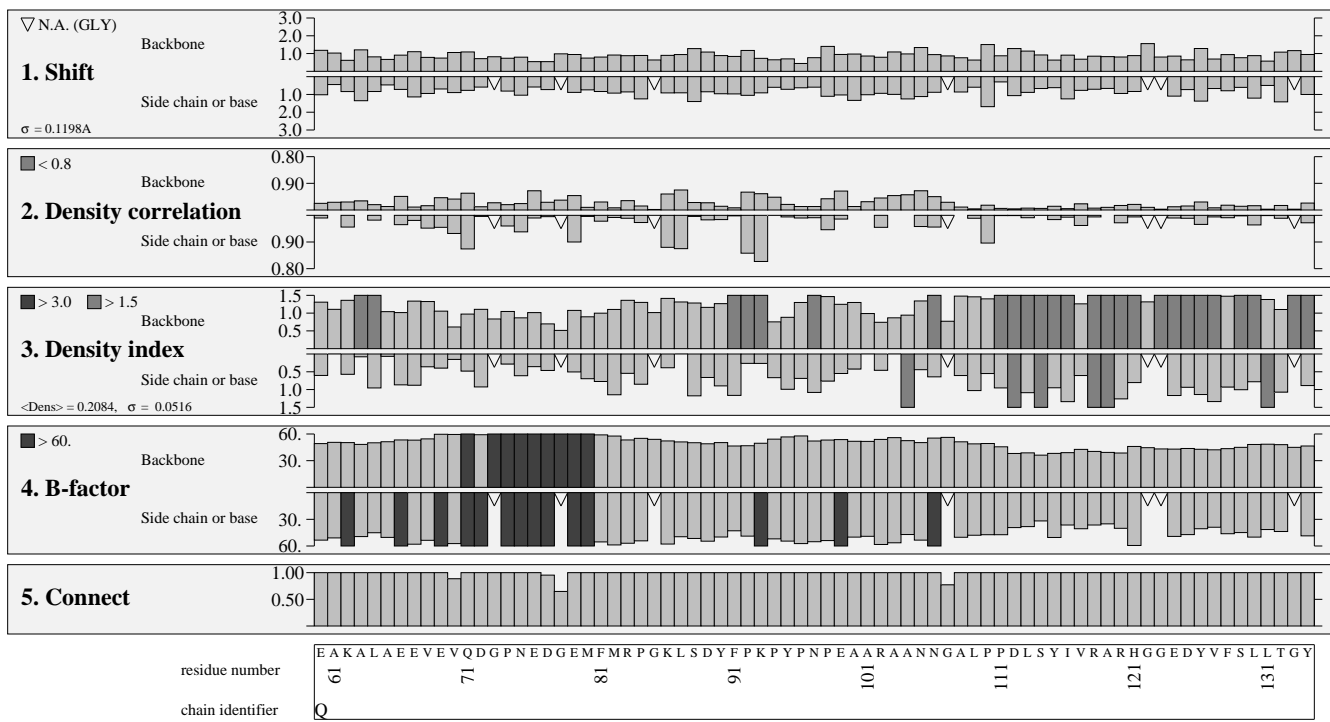




# Structure Factor Check

## 1PPJ

### Local estimation (23)

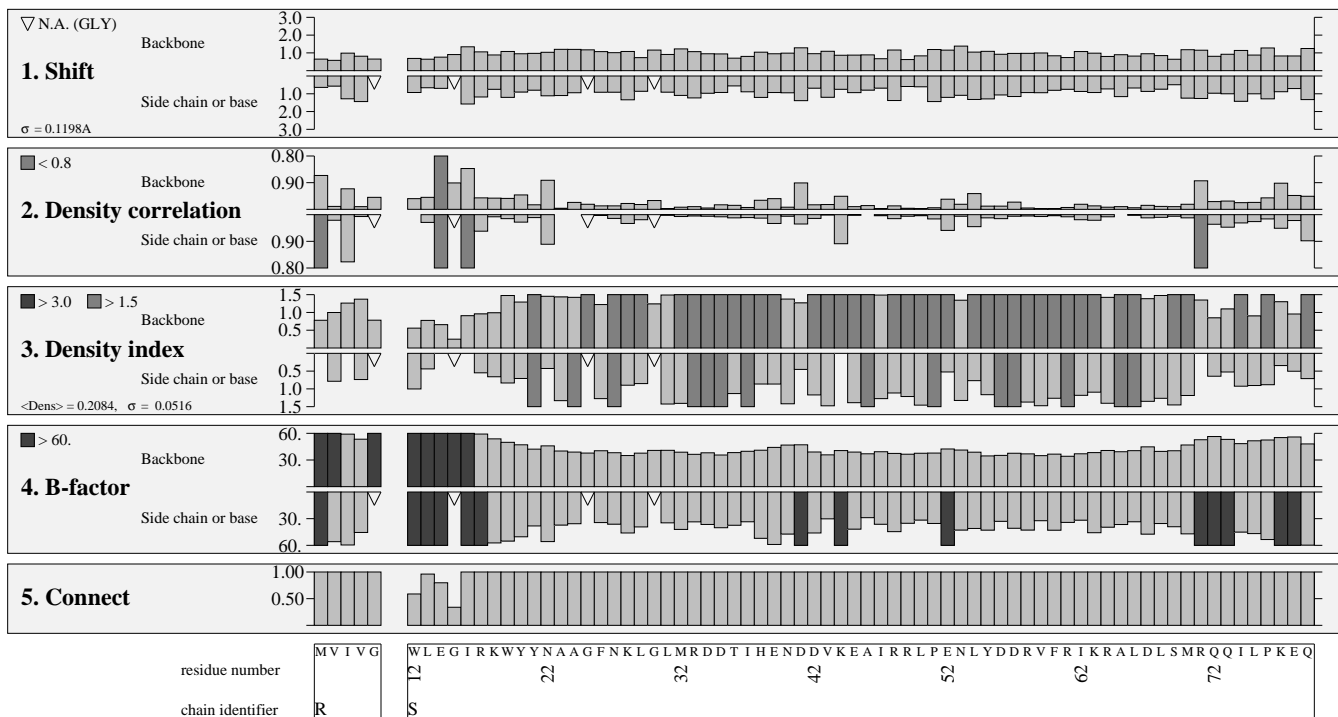
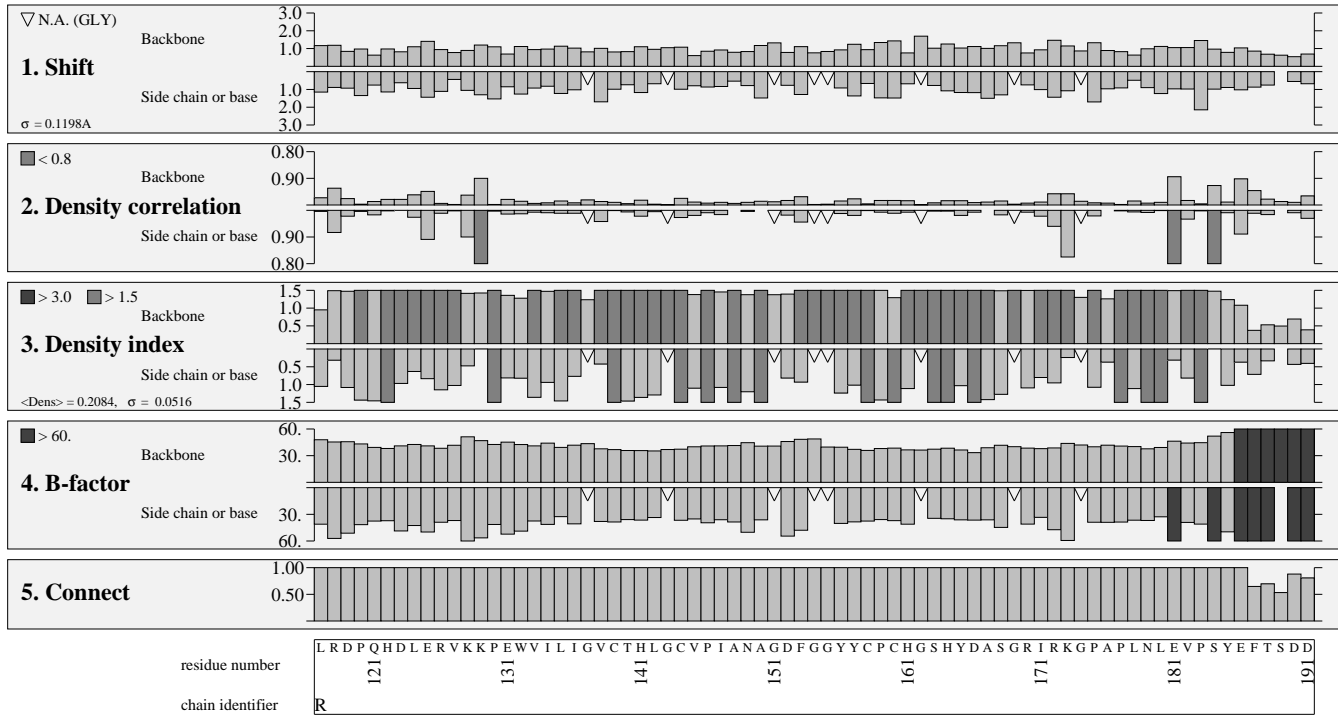




# Structure Factor Check

## 1PPJ

### Local estimation (25)

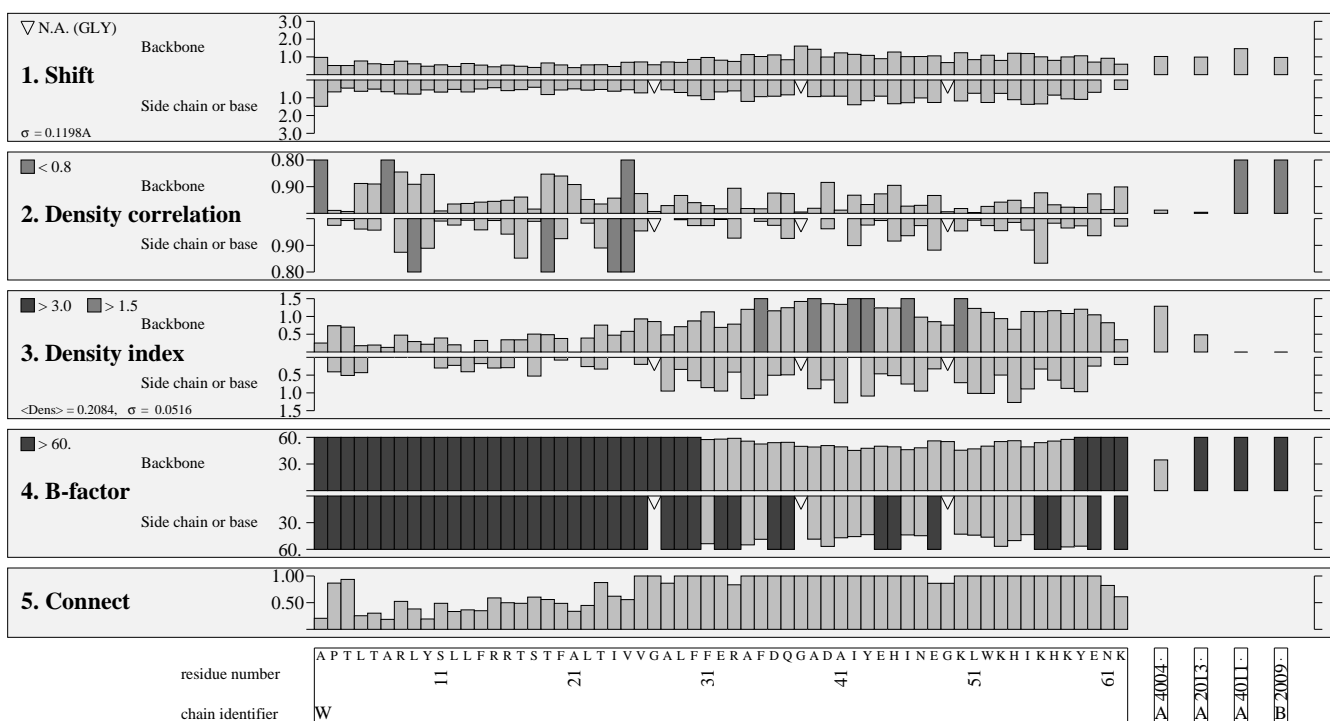
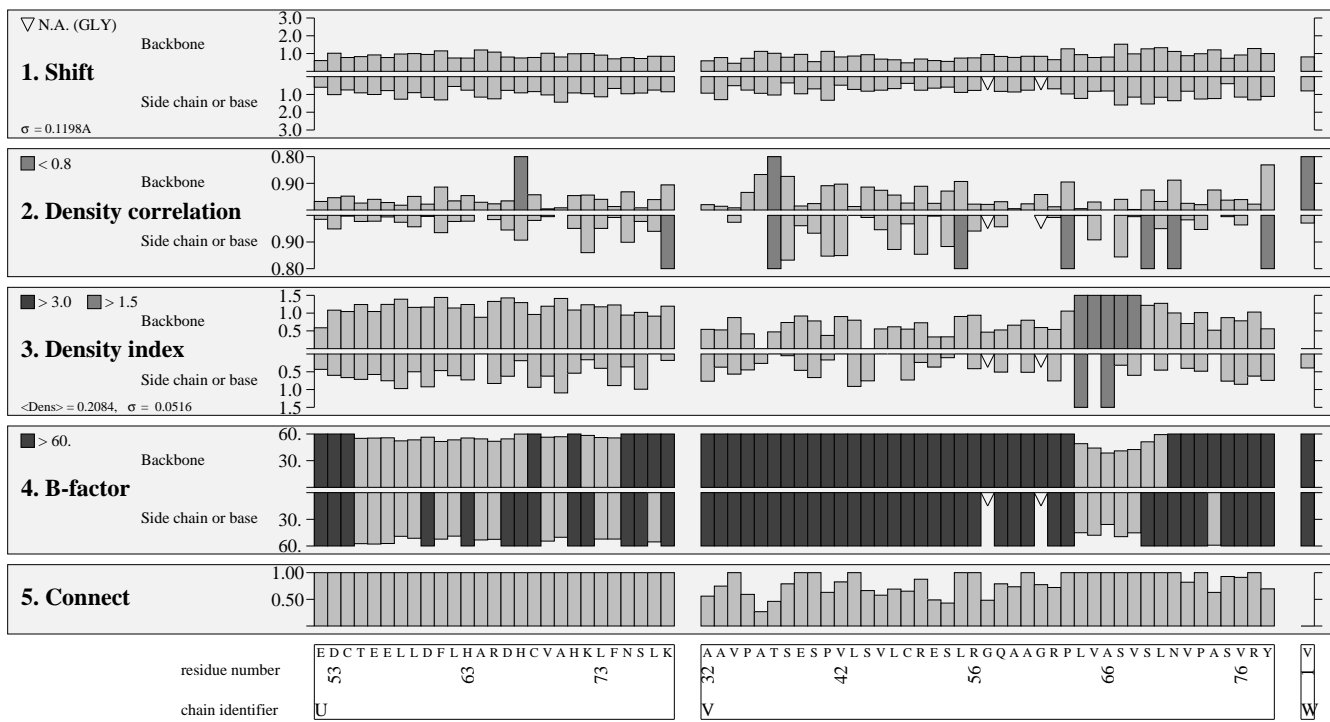




# Structure Factor Check

## 1PPJ

### Local estimation (27)

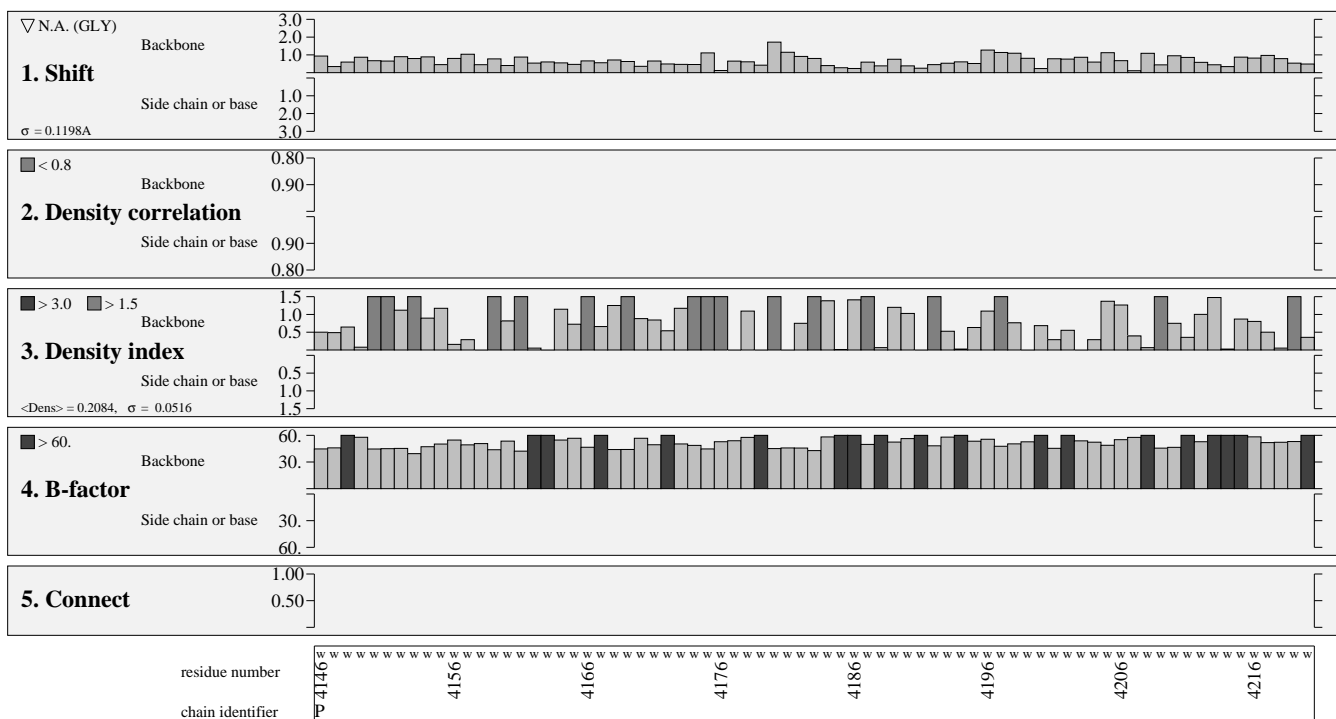
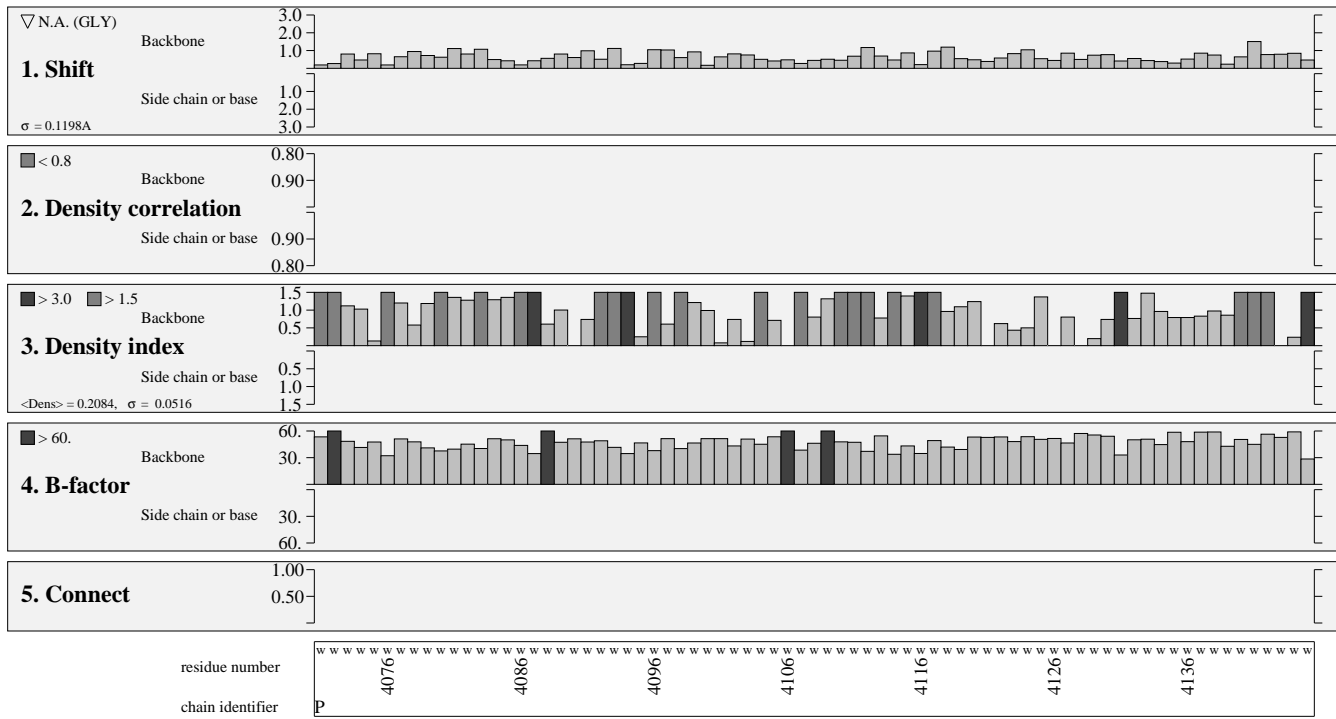




# Structure Factor Check

## 1PPJ

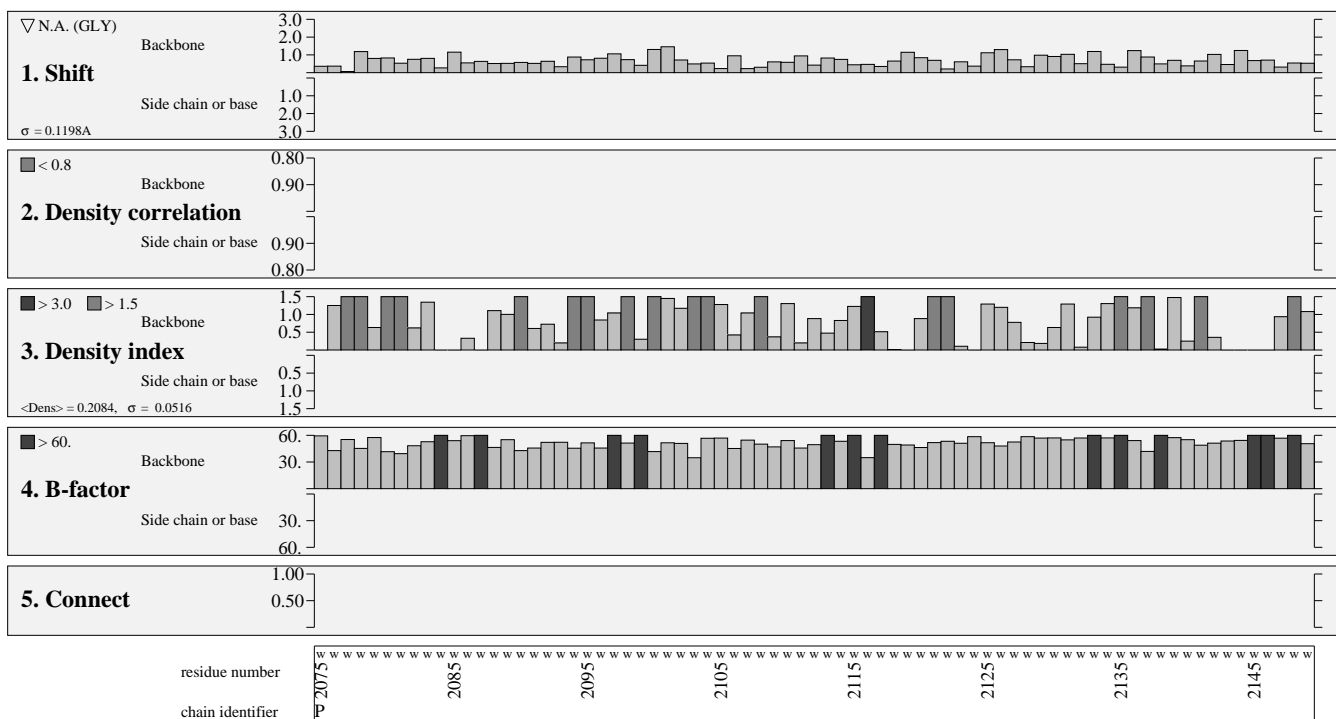
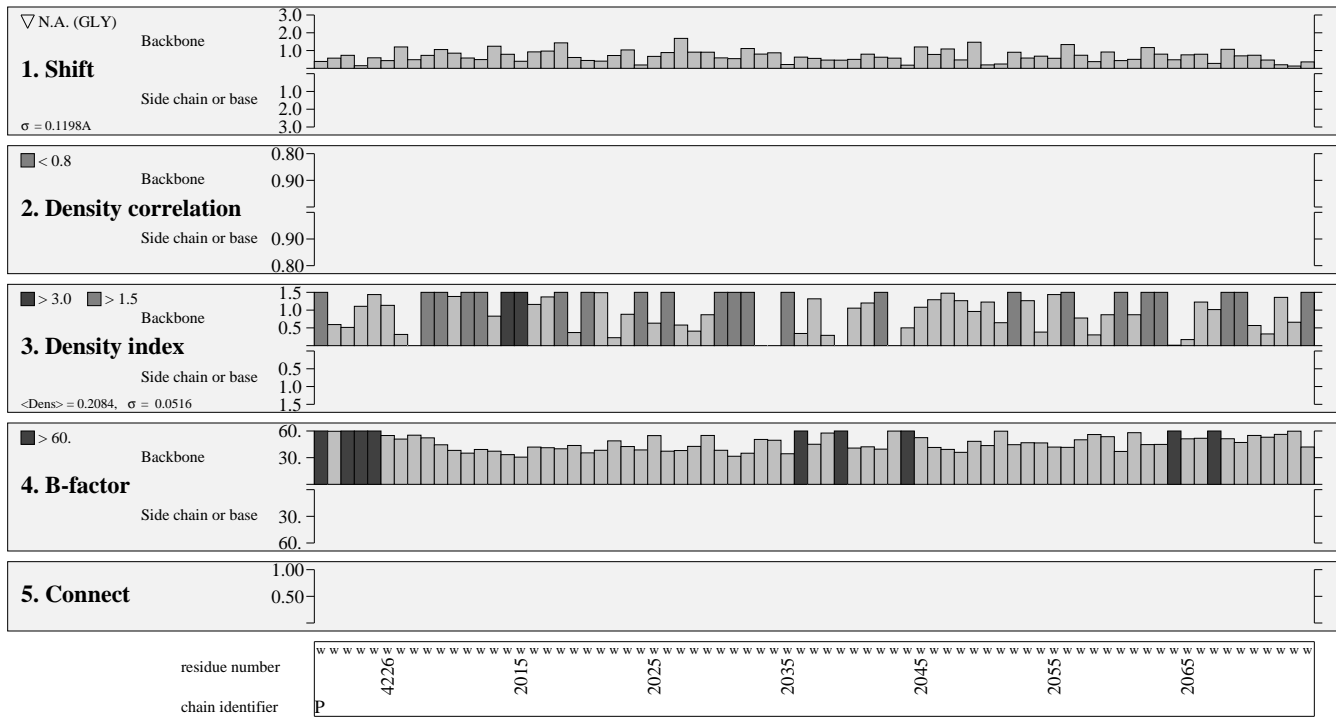
### Local estimation (29)



# Structure Factor Check

## 1PPJ

### Local estimation (30)



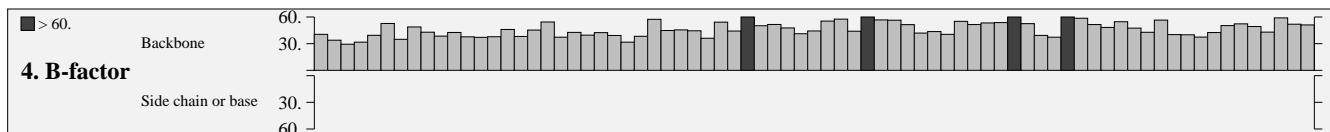
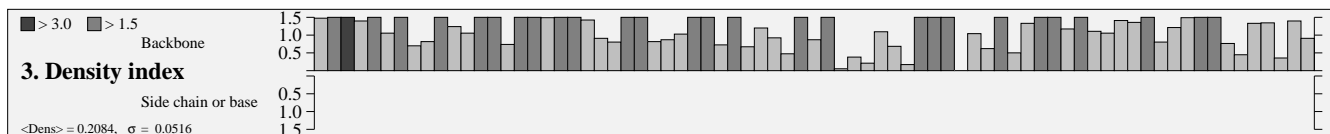
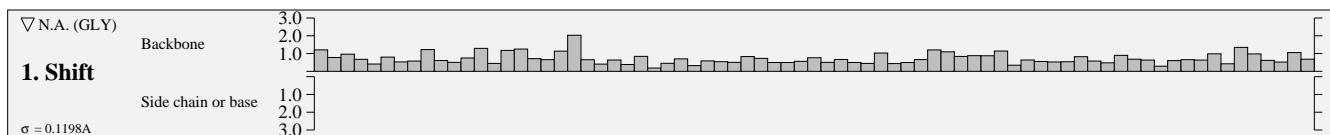




# Structure Factor Check

## 1PPJ

### Local estimation (32)

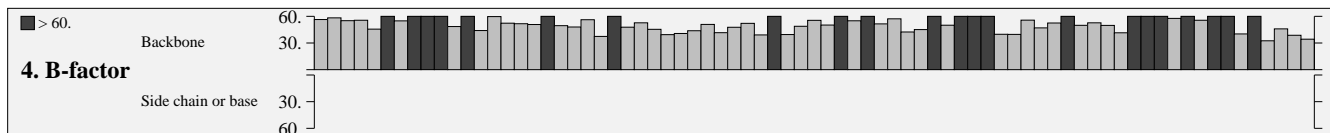
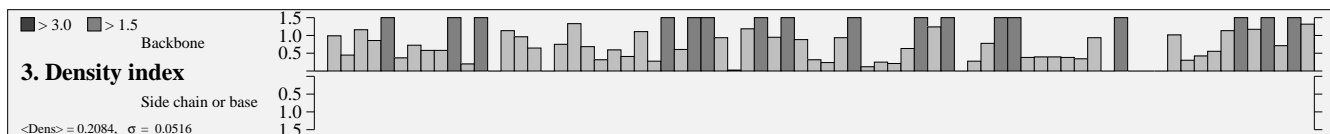
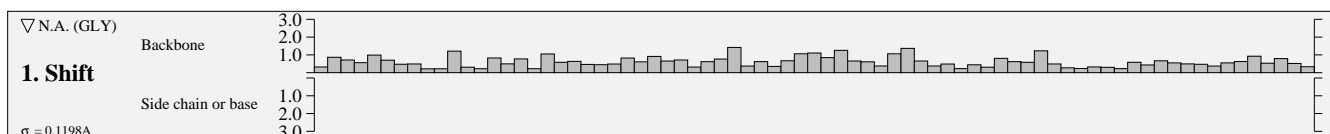


residue number

chain identifier

4009 4019 4029 4039 4049 4059 4069

P



residue number

chain identifier

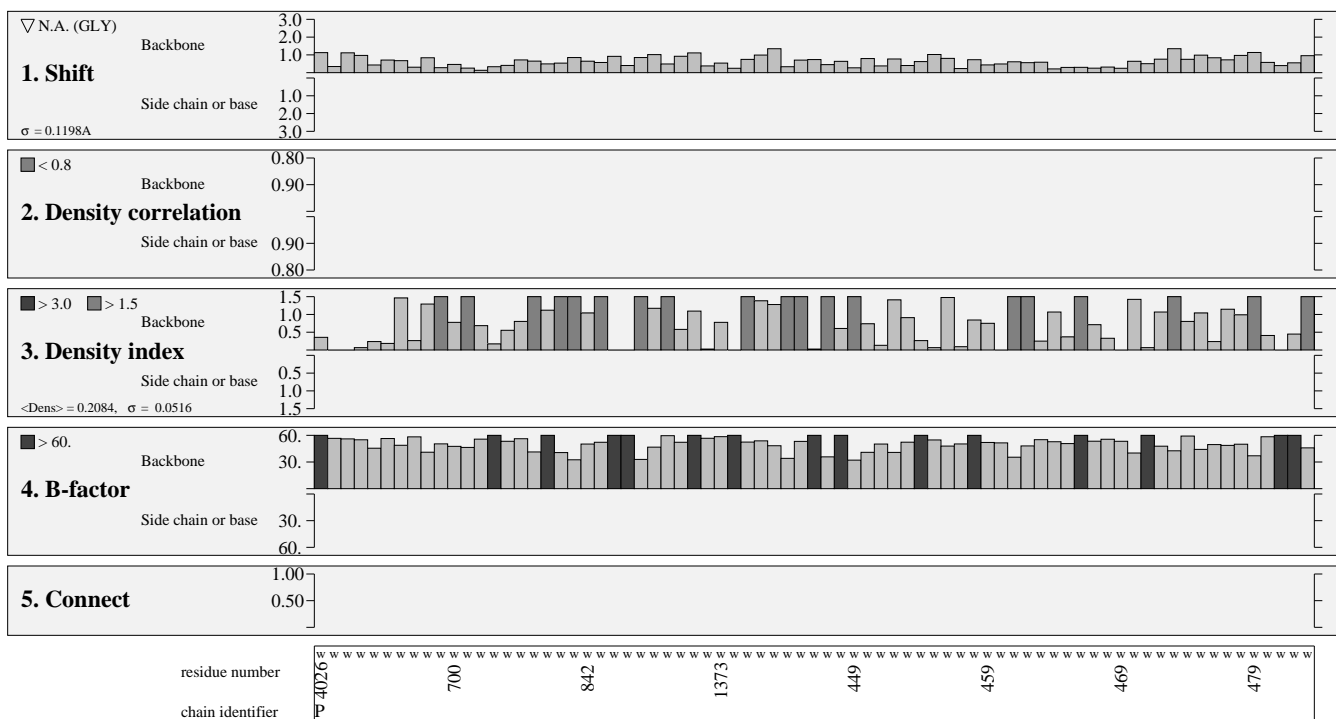
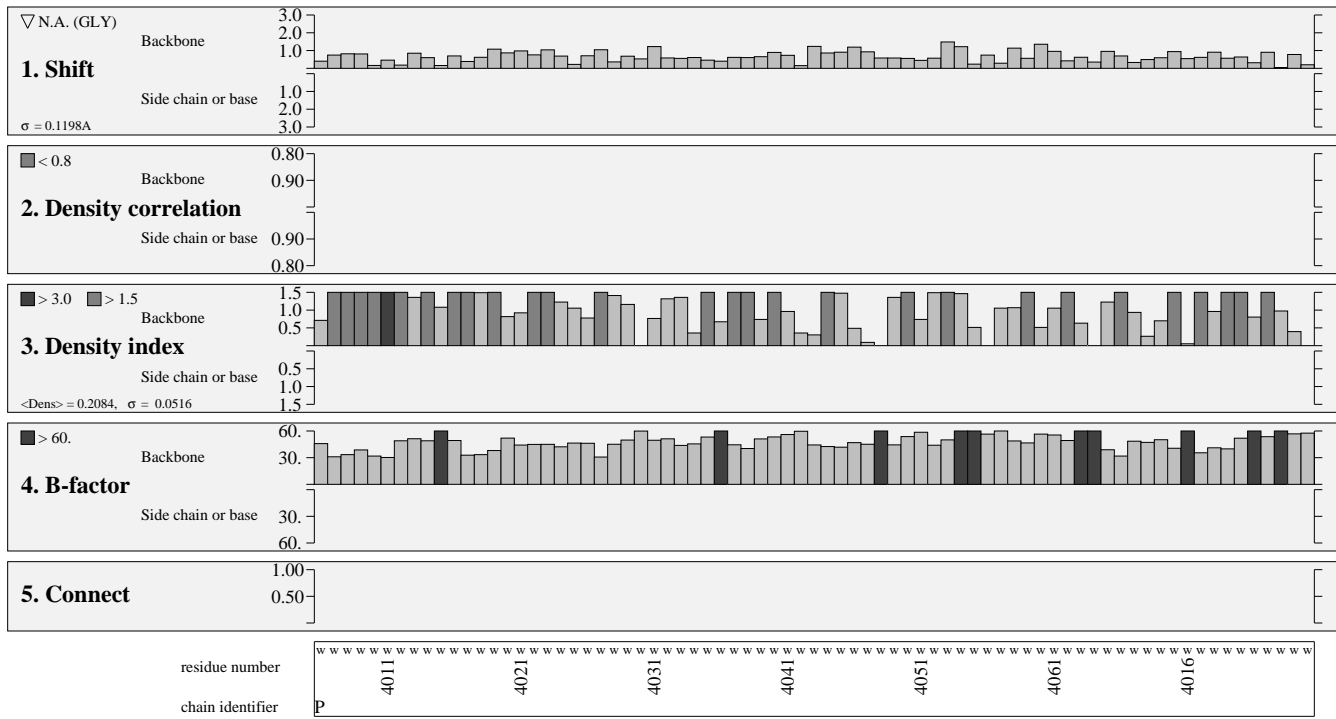
4079 4089 4099 511 521 531 541 551

P

# Structure Factor Check

## 1PPJ

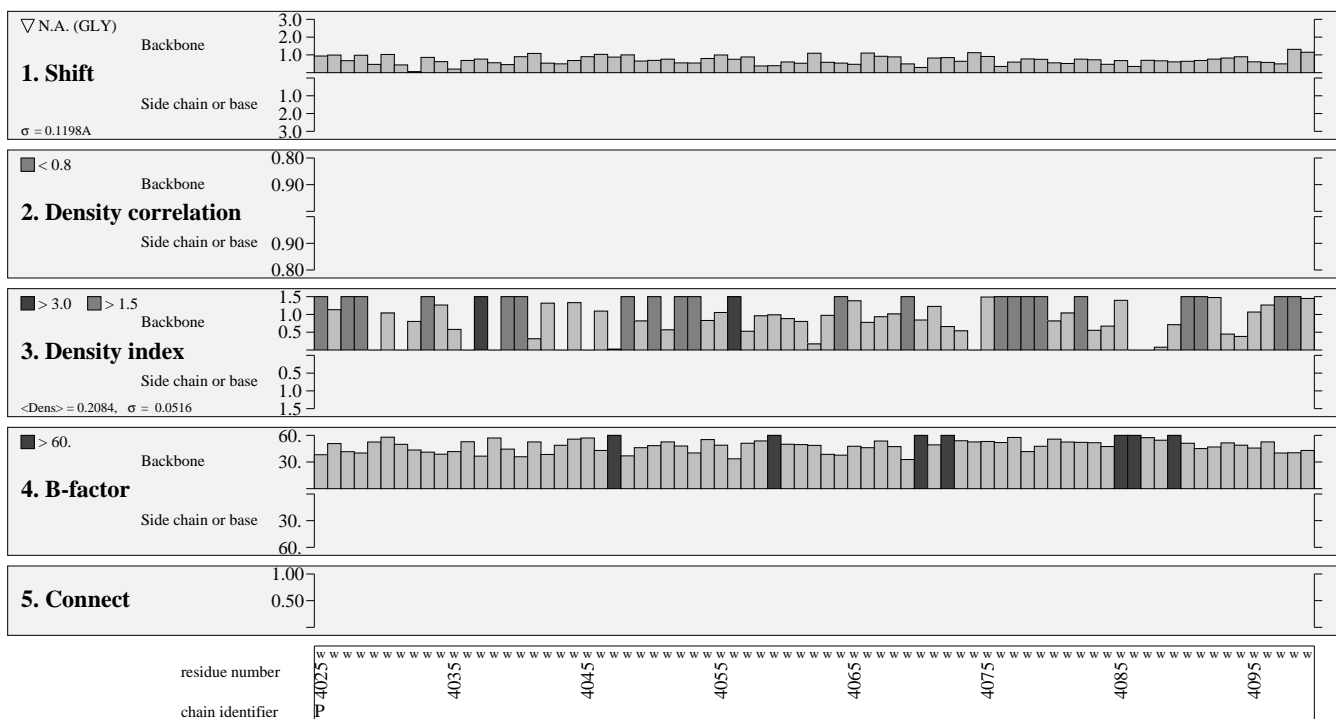
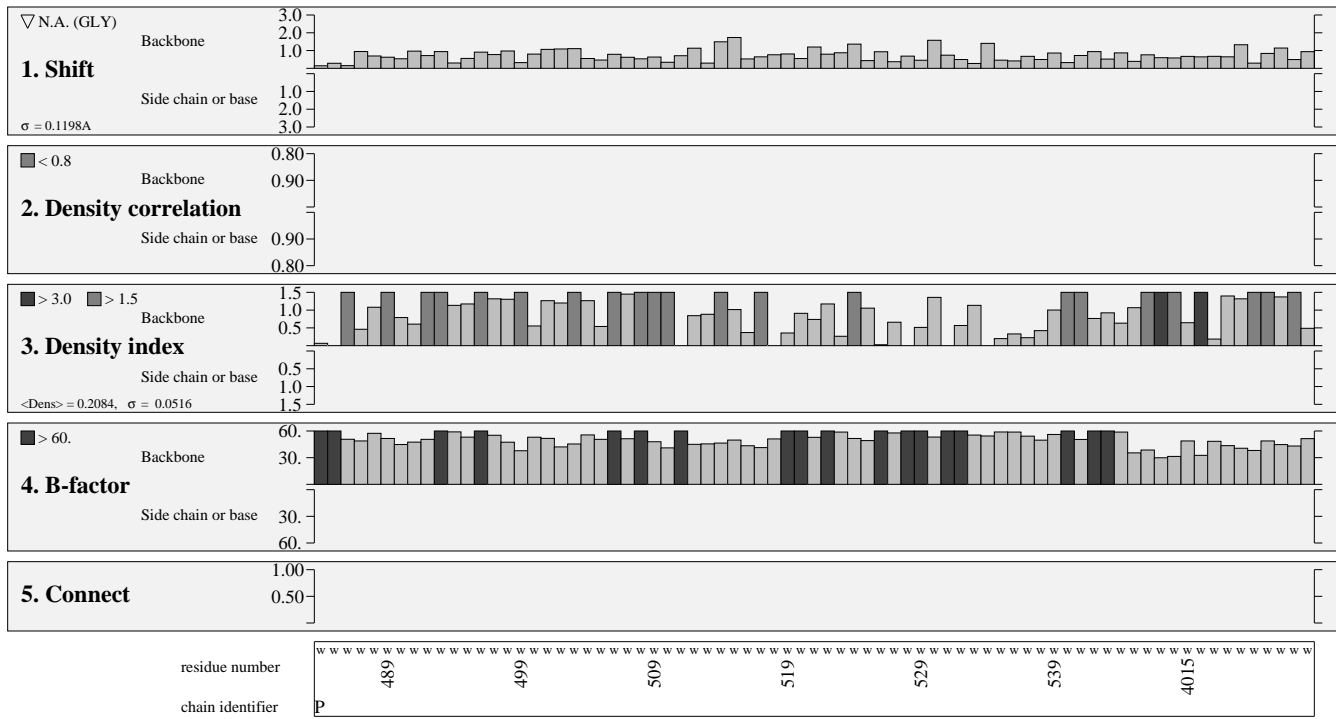
### Local estimation (33)



# Structure Factor Check

## 1PPJ

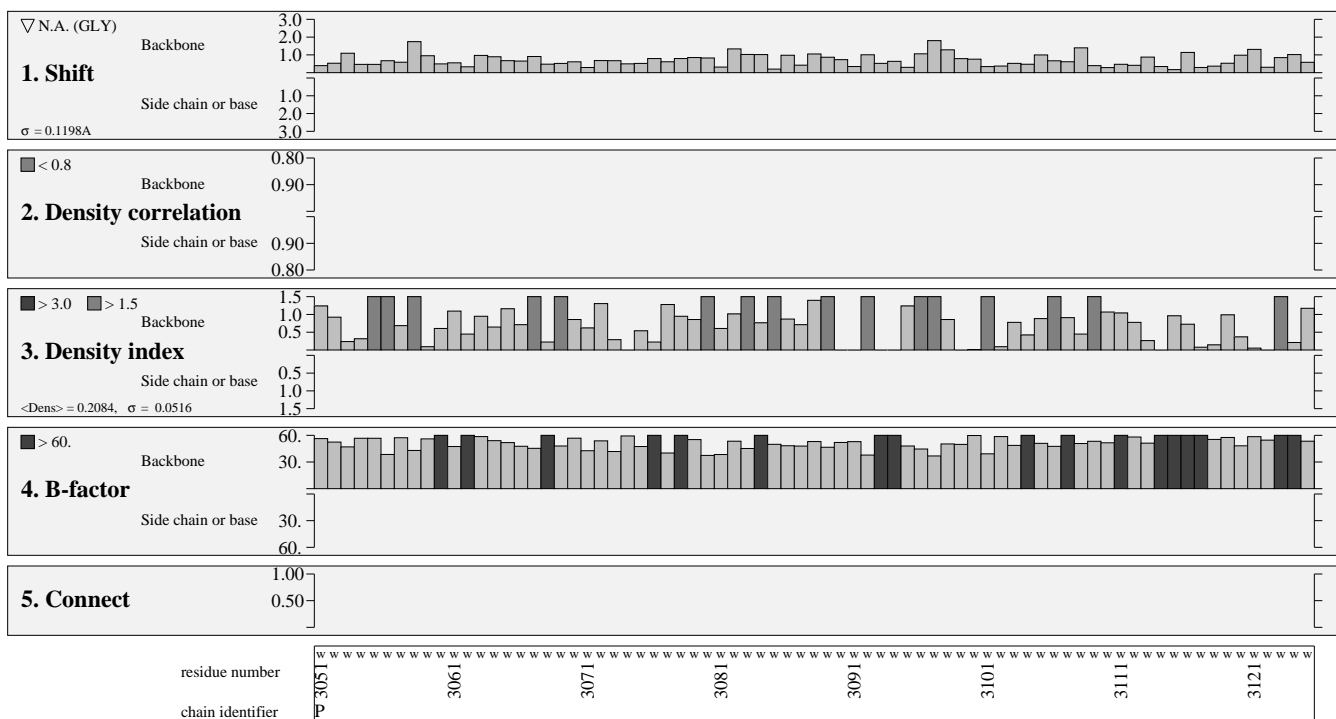
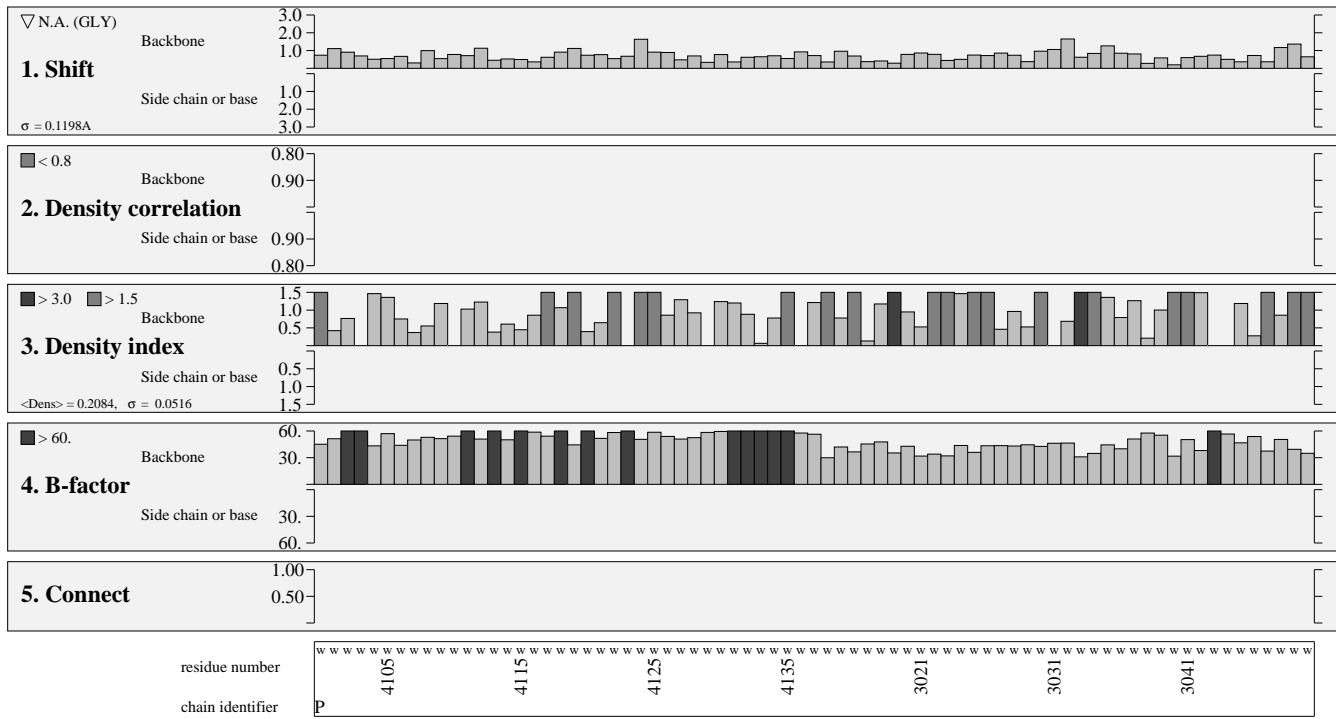
### Local estimation (34)



# Structure Factor Check

## 1PPJ

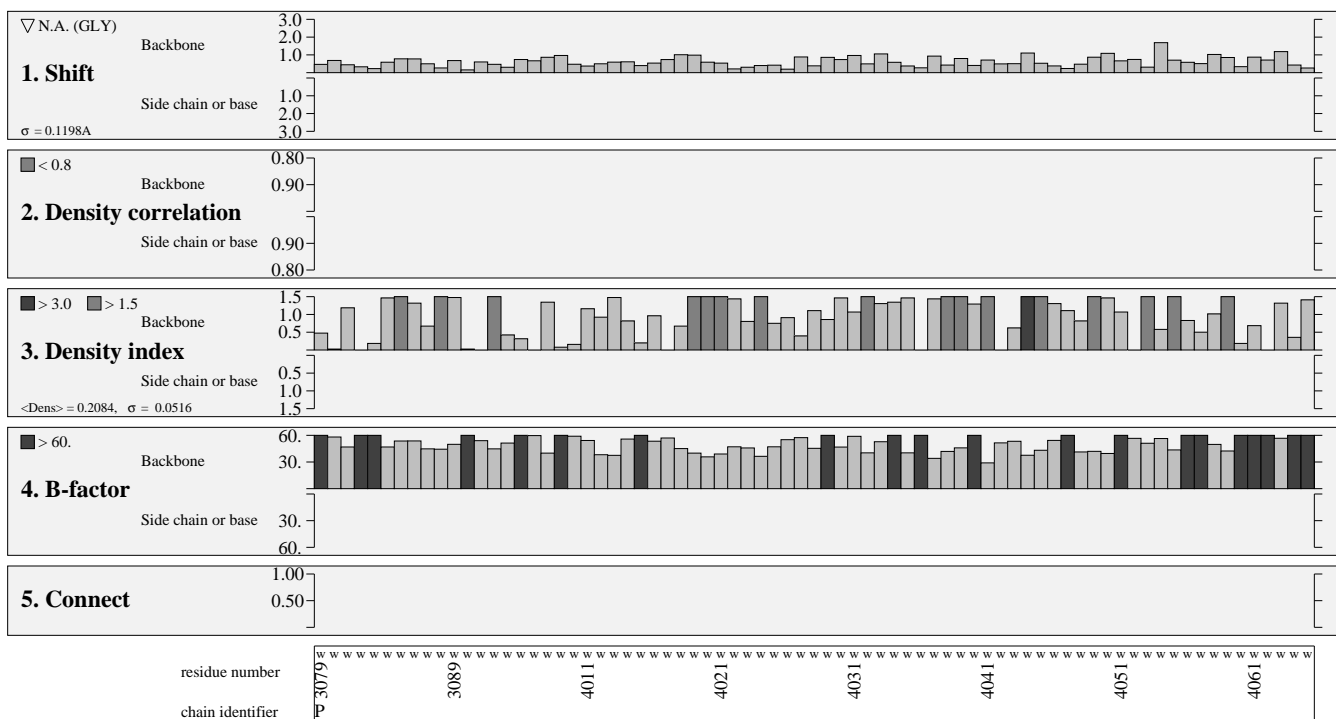
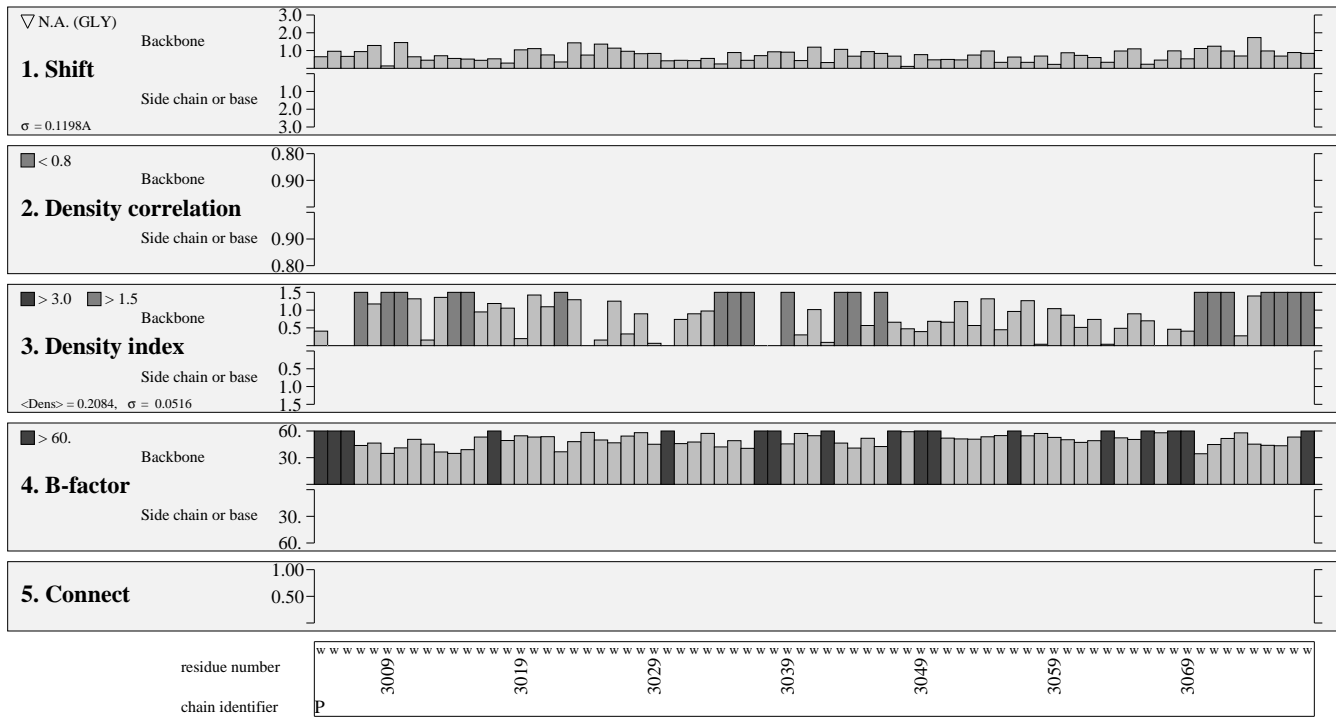
### Local estimation (35)



# Structure Factor Check

## 1PPJ

### Local estimation (36)



# Structure Factor Check

## 1PPJ

### Local estimation (37)

