



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:35 PM GMT

PDB ID : 4YCZ  
Title : Y-COMPLEX HUB (NUP85-NUP120-NUP145C-SEC13 COMPLEX) FROM  
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Deposited on : 2015-02-20  
Resolution : 4.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865



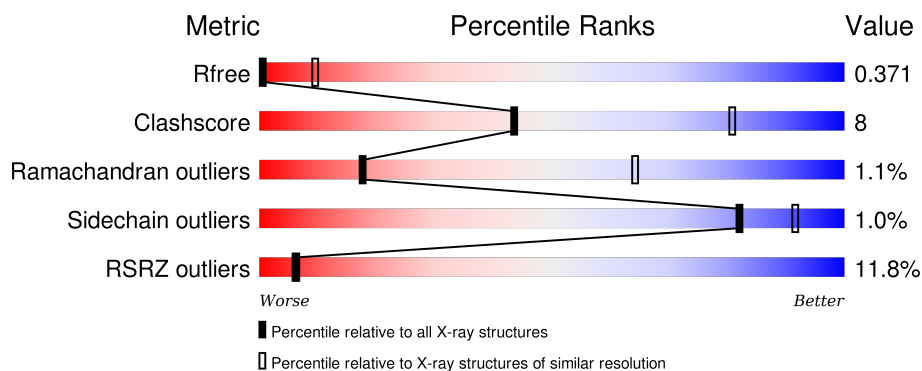
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 4.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	1018 (4.60-3.60)
Clashscore	102246	1117 (4.60-3.60)
Ramachandran outliers	100387	1063 (4.60-3.60)
Sidechain outliers	100360	1049 (4.60-3.60)
RSRZ outliers	91569	1022 (4.60-3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	876	
2	B	933	
3	C	313	



## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10051 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Fusion Protein of Sec13 and Nup145C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	713	Total	C	N	O	S	0	0	0
			4777	3049	843	874	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	expression tag	UNP G2QES5
A	2	PRO	-	expression tag	UNP G2QES5
A	3	GLY	-	expression tag	UNP G2QES5
A	4	SER	-	expression tag	UNP G2QES5

- Molecule 2 is a protein called Nup85.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	590	Total	C	N	O	S	Se	0	0	0
			3962	2596	644	705	5	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	249	GLY	-	expression tag	UNP G2Q7J4
B	250	PRO	-	expression tag	UNP G2Q7J4
B	251	GLY	-	expression tag	UNP G2Q7J4
B	252	SER	-	expression tag	UNP G2Q7J4
B	253	GLU	-	expression tag	UNP G2Q7J4
B	254	PHE	-	expression tag	UNP G2Q7J4
B	255	GLU	-	expression tag	UNP G2Q7J4
B	256	LEU	-	expression tag	UNP G2Q7J4

- Molecule 3 is a protein called Nup120.



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	195	Total	C	N	O	S	0	0	0
			1312	846	220	241	5			

There are 23 discrepancies between the modelled and reference sequences:

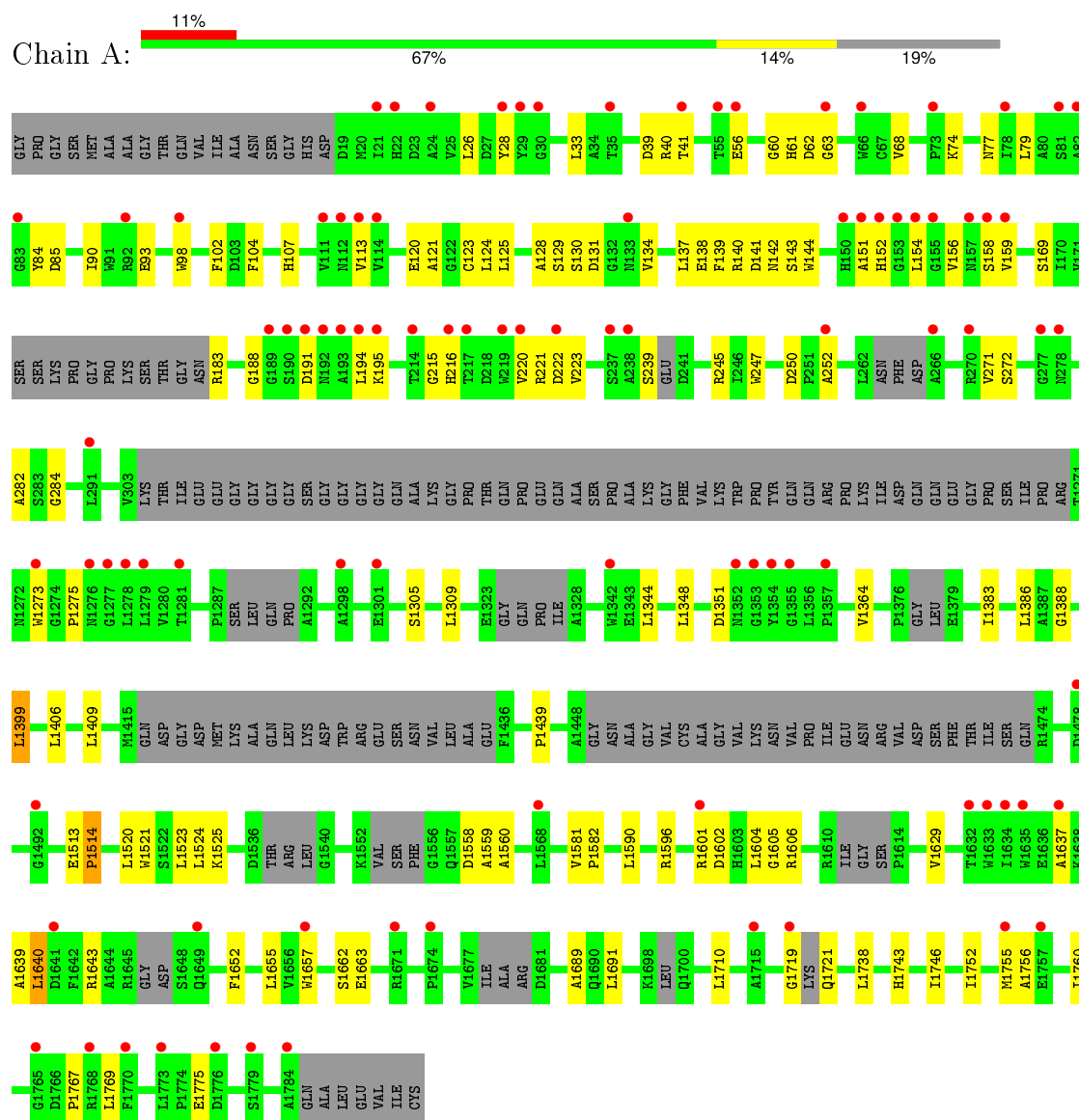
Chain	Residue	Modelled	Actual	Comment	Reference
C	943	GLY	-	expression tag	UNP G2Q2S2
C	944	PRO	-	expression tag	UNP G2Q2S2
C	945	GLY	-	expression tag	UNP G2Q2S2
C	946	SER	-	expression tag	UNP G2Q2S2
C	947	GLU	-	expression tag	UNP G2Q2S2
C	948	PHE	-	expression tag	UNP G2Q2S2
C	949	GLU	-	expression tag	UNP G2Q2S2
C	950	LEU	-	expression tag	UNP G2Q2S2
C	951	MET	-	expression tag	UNP G2Q2S2
C	1242	GLY	-	expression tag	UNP G2Q2S2
C	1243	GLY	-	expression tag	UNP G2Q2S2
C	1244	SER	-	expression tag	UNP G2Q2S2
C	1245	GLY	-	expression tag	UNP G2Q2S2
C	1246	HIS	-	expression tag	UNP G2Q2S2
C	1247	HIS	-	expression tag	UNP G2Q2S2
C	1248	HIS	-	expression tag	UNP G2Q2S2
C	1249	HIS	-	expression tag	UNP G2Q2S2
C	1250	HIS	-	expression tag	UNP G2Q2S2
C	1251	HIS	-	expression tag	UNP G2Q2S2
C	1252	HIS	-	expression tag	UNP G2Q2S2
C	1253	HIS	-	expression tag	UNP G2Q2S2
C	1254	HIS	-	expression tag	UNP G2Q2S2
C	1255	HIS	-	expression tag	UNP G2Q2S2



### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

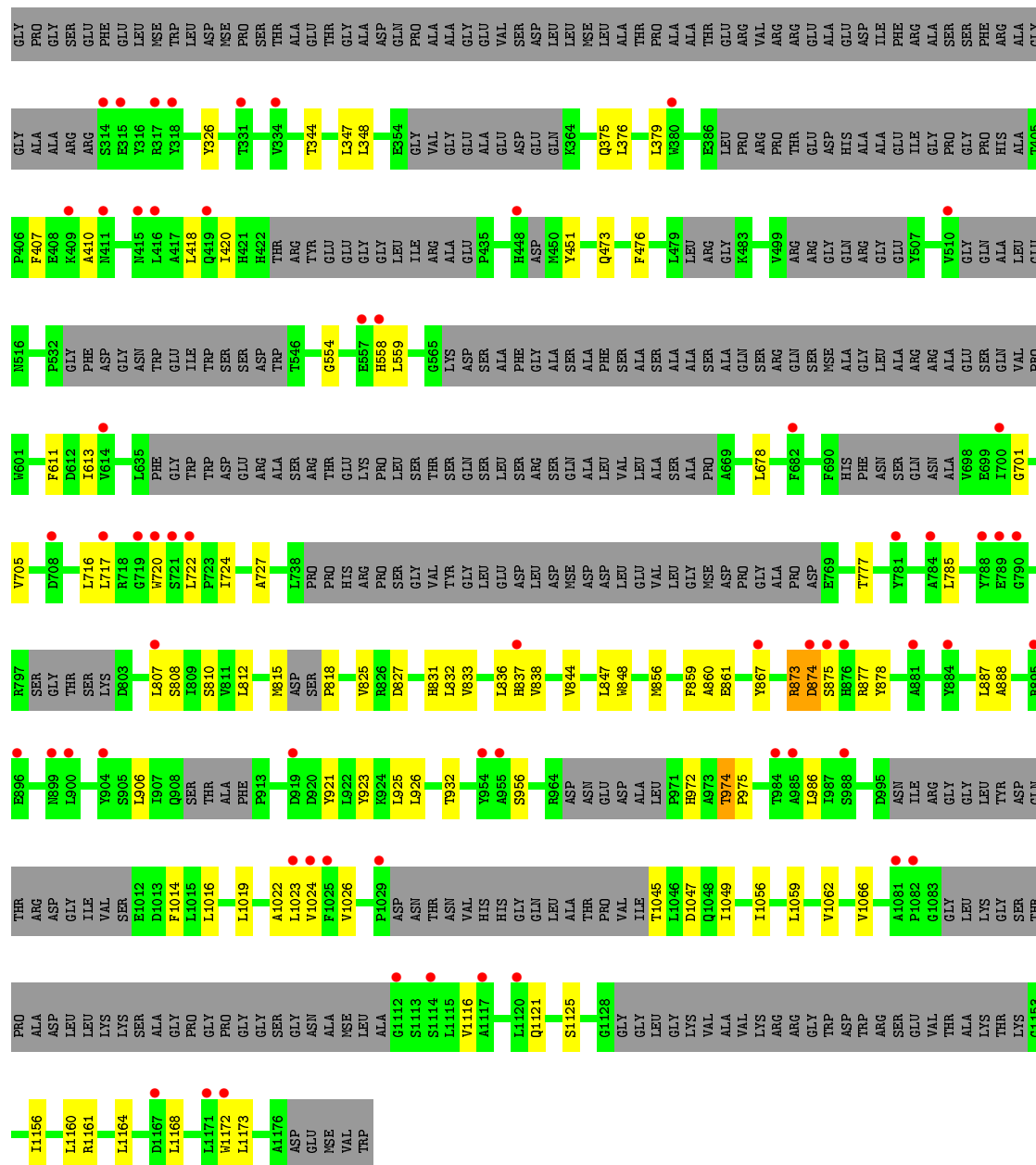
#### • Molecule 1: Fusion Protein of Sec13 and Nup145C



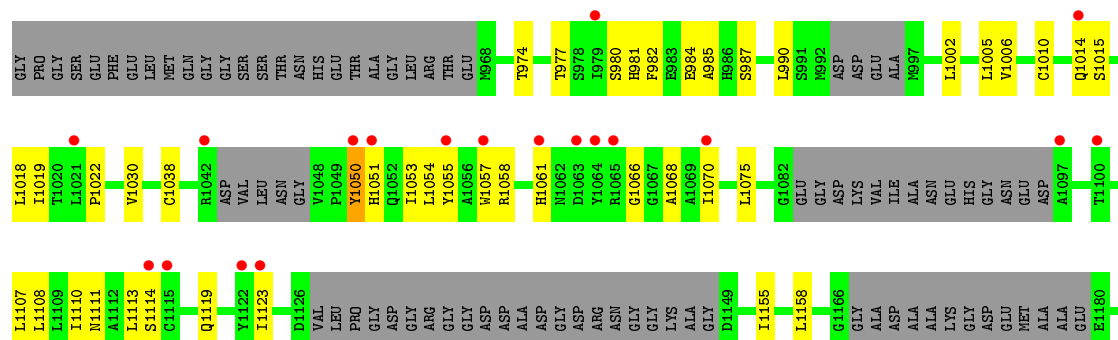
#### • Molecule 2: Nup85



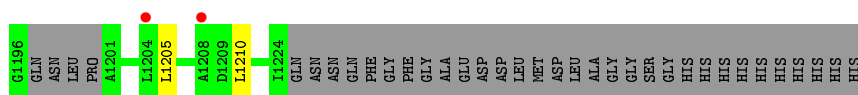




### • Molecule 3: Nup120









## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	104.98Å 212.02Å 170.64Å 90.00° 107.21° 90.00°	Depositor
Resolution (Å)	163.00 – 4.10 163.00 – 4.10	Depositor EDS
% Data completeness (in resolution range)	97.4 (163.00-4.10) 97.5 (163.00-4.10)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.19	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 4.15Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1951)	Depositor
R, $R_{free}$	0.319 , 0.358 0.339 , 0.371	Depositor DCC
$R_{free}$ test set	1975 reflections (7.82%)	DCC
Wilson B-factor (Å <sup>2</sup> )	160.4	Xtriage
Anisotropy	0.460	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 350.2	EDS
Estimated twinning fraction	0.079 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.40$ , $\langle L^2 \rangle = 0.23$	Xtriage
Outliers	0 of 27238 reflections	Xtriage
$F_o, F_c$ correlation	0.85	EDS
Total number of atoms	10051	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	158.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.83% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.20	0/4879	0.36	0/6697
2	B	0.20	0/4014	0.35	0/5488
3	C	0.23	0/1322	0.39	0/1805
All	All	0.20	0/10215	0.36	0/13990

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4777	0	4010	73	0
2	B	3962	0	3566	57	0
3	C	1312	0	1190	32	0
All	All	10051	0	8766	153	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 8.

The worst 5 of 153 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ASP:HB2	1:A:85:ASP:HB3	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1605:GLY:HA2	1:A:1637:ALA:HB1	1.76	0.68
2:B:722:LEU:HD13	2:B:724:ILE:HD12	1.76	0.67
2:B:1023:LEU:HG	2:B:1160:LEU:HD23	1.80	0.64
2:B:1161:ARG:NH1	3:C:1114:SER:OG	2.31	0.64

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	679/876 (78%)	611 (90%)	61 (9%)	7 (1%)	19	65
2	B	548/933 (59%)	507 (92%)	36 (7%)	5 (1%)	21	67
3	C	181/313 (58%)	164 (91%)	14 (8%)	3 (2%)	11	56
All	All	1408/2122 (66%)	1282 (91%)	111 (8%)	15 (1%)	17	64

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	TRP
2	B	878	TYR
1	A	1514	PRO
2	B	837	HIS
2	B	875	SER

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was



analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	356/700 (51%)	354 (99%)	2 (1%)	90	95
2	B	320/725 (44%)	315 (98%)	5 (2%)	70	88
3	C	108/253 (43%)	107 (99%)	1 (1%)	84	92
All	All	784/1678 (47%)	776 (99%)	8 (1%)	82	91

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	777	THR
3	C	1050	TYR
2	B	874	ASP
2	B	678	LEU
2	B	873	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	1014	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.



## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	713/876 (81%)	0.69	93 (13%) 5 5	60, 142, 204, 287	0
2	B	578/933 (61%)	0.51	62 (10%) 8 7	82, 166, 228, 311	0
3	C	195/313 (62%)	0.38	21 (10%) 8 6	85, 178, 243, 270	0
All	All	1486/2122 (70%)	0.58	176 (11%) 6 6	60, 156, 226, 311	0

The worst 5 of 176 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	874	ASP	6.5
2	B	1120	LEU	6.1
2	B	721	SER	5.8
3	C	1050	TYR	5.8
1	A	1354	TYR	5.6

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.