



# wwPDB X-ray Structure Validation Summary Report

Sep 14, 2020 – 01:14 AM BST

PDB ID : 6FQB  
Title : MurT/GatD peptidoglycan amidotransferase complex from *Streptococcus pneumoniae* R6  
Authors : Morlot, C.; Contreras-Martel, C.; Leisico, F.; Straume, D.; Peters, K.; Hegnar, O.A.; Simon, N.; Villard, A.M.; Breukink, E.; Gravier-Pelletier, C.; Le Corre, L.; Vollmer, W.; Pietrancosta, N.; Havarstein, L.S.; Zapun, A.  
Deposited on : 2018-02-13  
Resolution : 3.00 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.14.4.dev1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.14.4.dev1

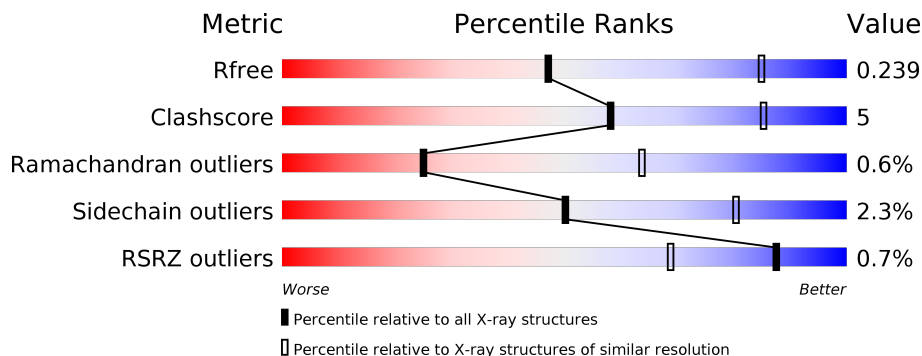
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 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))
$R_{free}$	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 respectively. 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	465	 71% 10% 18%
1	B	465	 72% 8% 19%
1	C	465	 71% 9% 19%
1	D	465	 74% 8% 18%
2	E	260	 87% 8% 5%
2	F	260	 86% 9% 5%

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Mol	Chain	Length	Quality of chain
2	G	260	
2	H	260	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GLN	F	301	-	-	-	X
3	GLN	G	301	-	-	-	X

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 19727 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 Mur ligase family protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	383	2989	1906	497	573	13	0	0	0
1	B	378	2952	1886	489	564	13	0	0	0
1	C	375	2937	1876	485	563	13	0	0	0
1	D	380	2977	1900	494	570	13	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	initiating methionine	UNP A0A0B7LND9
A	-16	HIS	-	expression tag	UNP A0A0B7LND9
A	-15	HIS	-	expression tag	UNP A0A0B7LND9
A	-14	HIS	-	expression tag	UNP A0A0B7LND9
A	-13	HIS	-	expression tag	UNP A0A0B7LND9
A	-12	HIS	-	expression tag	UNP A0A0B7LND9
A	-11	HIS	-	expression tag	UNP A0A0B7LND9
A	-10	HIS	-	expression tag	UNP A0A0B7LND9
A	-9	HIS	-	expression tag	UNP A0A0B7LND9
A	-8	GLU	-	expression tag	UNP A0A0B7LND9
A	-7	ASN	-	expression tag	UNP A0A0B7LND9
A	-6	LEU	-	expression tag	UNP A0A0B7LND9
A	-5	TYR	-	expression tag	UNP A0A0B7LND9
A	-4	PHE	-	expression tag	UNP A0A0B7LND9
A	-3	GLN	-	expression tag	UNP A0A0B7LND9
A	-2	GLY	-	expression tag	UNP A0A0B7LND9
A	-1	SER	-	expression tag	UNP A0A0B7LND9
A	0	HIS	-	expression tag	UNP A0A0B7LND9
B	-17	MET	-	initiating methionine	UNP A0A0B7LND9
B	-16	HIS	-	expression tag	UNP A0A0B7LND9
B	-15	HIS	-	expression tag	UNP A0A0B7LND9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP A0A0B7LND9
B	-13	HIS	-	expression tag	UNP A0A0B7LND9
B	-12	HIS	-	expression tag	UNP A0A0B7LND9
B	-11	HIS	-	expression tag	UNP A0A0B7LND9
B	-10	HIS	-	expression tag	UNP A0A0B7LND9
B	-9	HIS	-	expression tag	UNP A0A0B7LND9
B	-8	GLU	-	expression tag	UNP A0A0B7LND9
B	-7	ASN	-	expression tag	UNP A0A0B7LND9
B	-6	LEU	-	expression tag	UNP A0A0B7LND9
B	-5	TYR	-	expression tag	UNP A0A0B7LND9
B	-4	PHE	-	expression tag	UNP A0A0B7LND9
B	-3	GLN	-	expression tag	UNP A0A0B7LND9
B	-2	GLY	-	expression tag	UNP A0A0B7LND9
B	-1	SER	-	expression tag	UNP A0A0B7LND9
B	0	HIS	-	expression tag	UNP A0A0B7LND9
C	-17	MET	-	initiating methionine	UNP A0A0B7LND9
C	-16	HIS	-	expression tag	UNP A0A0B7LND9
C	-15	HIS	-	expression tag	UNP A0A0B7LND9
C	-14	HIS	-	expression tag	UNP A0A0B7LND9
C	-13	HIS	-	expression tag	UNP A0A0B7LND9
C	-12	HIS	-	expression tag	UNP A0A0B7LND9
C	-11	HIS	-	expression tag	UNP A0A0B7LND9
C	-10	HIS	-	expression tag	UNP A0A0B7LND9
C	-9	HIS	-	expression tag	UNP A0A0B7LND9
C	-8	GLU	-	expression tag	UNP A0A0B7LND9
C	-7	ASN	-	expression tag	UNP A0A0B7LND9
C	-6	LEU	-	expression tag	UNP A0A0B7LND9
C	-5	TYR	-	expression tag	UNP A0A0B7LND9
C	-4	PHE	-	expression tag	UNP A0A0B7LND9
C	-3	GLN	-	expression tag	UNP A0A0B7LND9
C	-2	GLY	-	expression tag	UNP A0A0B7LND9
C	-1	SER	-	expression tag	UNP A0A0B7LND9
C	0	HIS	-	expression tag	UNP A0A0B7LND9
D	-17	MET	-	initiating methionine	UNP A0A0B7LND9
D	-16	HIS	-	expression tag	UNP A0A0B7LND9
D	-15	HIS	-	expression tag	UNP A0A0B7LND9
D	-14	HIS	-	expression tag	UNP A0A0B7LND9
D	-13	HIS	-	expression tag	UNP A0A0B7LND9
D	-12	HIS	-	expression tag	UNP A0A0B7LND9
D	-11	HIS	-	expression tag	UNP A0A0B7LND9
D	-10	HIS	-	expression tag	UNP A0A0B7LND9
D	-9	HIS	-	expression tag	UNP A0A0B7LND9

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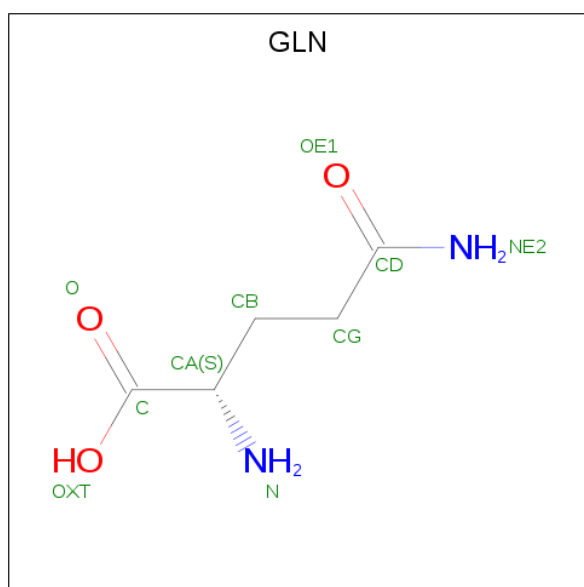
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	GLU	-	expression tag	UNP A0A0B7LND9
D	-7	ASN	-	expression tag	UNP A0A0B7LND9
D	-6	LEU	-	expression tag	UNP A0A0B7LND9
D	-5	TYR	-	expression tag	UNP A0A0B7LND9
D	-4	PHE	-	expression tag	UNP A0A0B7LND9
D	-3	GLN	-	expression tag	UNP A0A0B7LND9
D	-2	GLY	-	expression tag	UNP A0A0B7LND9
D	-1	SER	-	expression tag	UNP A0A0B7LND9
D	0	HIS	-	expression tag	UNP A0A0B7LND9

- Molecule 2 is a protein called Cobyric acid synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	E	247	Total 1958	C 1242	N 326	O 385	S 5	0	0	0
2	F	247	Total 1958	C 1242	N 326	O 385	S 5	0	0	0
2	G	247	Total 1958	C 1242	N 326	O 385	S 5	0	0	0
2	H	247	Total 1958	C 1242	N 326	O 385	S 5	0	0	0

- Molecule 3 is GLUTAMINE (three-letter code: GLN) (formula: C<sub>5</sub>H<sub>10</sub>N<sub>2</sub>O<sub>3</sub>).



<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>				<b>ZeroOcc</b>	<b>AltConf</b>
3	E	1	Total 10	C 5	N 2	O 3	0	0
3	F	1	Total 10	C 5	N 2	O 3	0	0
3	G	1	Total 10	C 5	N 2	O 3	0	0
3	H	1	Total 10	C 5	N 2	O 3	0	0







## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	288.43Å 288.43Å 115.10Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 3.00 49.14 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.2 (50.00-3.00) 96.2 (49.14-3.00)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.06	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.16 (at 3.01Å)	Xtrriage
Refinement program	REFMAC 5.8.0189	Depositor
R, $R_{free}$	0.189 , 0.228 0.204 , 0.239	Depositor DCC
$R_{free}$ test set	6854 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	88.4	Xtrriage
Anisotropy	0.049	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 50.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.011 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	19727	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	88.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.59	0/3043	0.78	1/4133 (0.0%)
1	B	0.55	0/3005	0.78	1/4080 (0.0%)
1	C	0.56	0/2990	0.77	1/4061 (0.0%)
1	D	0.58	0/3030	0.77	1/4115 (0.0%)
2	E	0.62	0/2001	0.72	0/2707
2	F	0.56	0/2001	0.72	0/2707
2	G	0.59	0/2001	0.75	0/2707
2	H	0.58	0/2001	0.72	0/2707
All	All	0.58	0/20072	0.76	4/27217 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	CYS	CA-CB-SG	5.26	123.47	114.00
1	D	205	CYS	CA-CB-SG	5.25	123.44	114.00
1	B	205	CYS	CA-CB-SG	5.24	123.44	114.00
1	C	205	CYS	CA-CB-SG	5.13	123.23	114.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	2989	0	2986	48	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	2952	0	2945	28	0
1	C	2937	0	2929	24	0
1	D	2977	0	2973	17	0
2	E	1958	0	1857	22	0
2	F	1958	0	1857	14	1
2	G	1958	0	1857	18	0
2	H	1958	0	1857	24	1
3	E	10	0	7	0	0
3	F	10	0	7	1	0
3	G	10	0	7	0	0
3	H	10	0	7	3	0
All	All	19727	0	19289	189	1

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 5.

The worst 5 of 189 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:116:LEU:O	1:A:116:LEU:HD12	1.70	0.91
2:H:219:ARG:HH11	2:H:219:ARG:HG3	1.34	0.91
1:B:115:SER:OG	1:B:119:ILE:CD1	2.22	0.88
1:B:81:PRO:O	1:B:83:GLY:N	2.07	0.88
1:C:431:GLU:O	1:C:434:GLU:HG2	1.75	0.86

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:116:TYR:OH	2:H:116:TYR:OH[2_555]	2.05	0.15

## 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	377/465 (81%)	342 (91%)	32 (8%)	3 (1%)	19	57
1	B	370/465 (80%)	334 (90%)	33 (9%)	3 (1%)	19	57
1	C	367/465 (79%)	332 (90%)	32 (9%)	3 (1%)	19	57
1	D	372/465 (80%)	338 (91%)	32 (9%)	2 (0%)	29	68
2	E	245/260 (94%)	230 (94%)	15 (6%)	0	100	100
2	F	245/260 (94%)	228 (93%)	16 (6%)	1 (0%)	34	72
2	G	245/260 (94%)	229 (94%)	16 (6%)	0	100	100
2	H	245/260 (94%)	230 (94%)	13 (5%)	2 (1%)	19	57
All	All	2466/2900 (85%)	2263 (92%)	189 (8%)	14 (1%)	25	64

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	58	HIS
1	B	89	GLY
2	F	58	HIS
1	A	120	CYS
1	D	373	PRO

### 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	323/395 (82%)	313 (97%)	10 (3%)	40	75
1	B	318/395 (80%)	310 (98%)	8 (2%)	47	79
1	C	319/395 (81%)	309 (97%)	10 (3%)	40	75
1	D	323/395 (82%)	313 (97%)	10 (3%)	40	75
2	E	207/219 (94%)	206 (100%)	1 (0%)	88	96
2	F	207/219 (94%)	204 (99%)	3 (1%)	67	88
2	G	207/219 (94%)	204 (99%)	3 (1%)	67	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	H	207/219 (94%)	204 (99%)	3 (1%)	67 88
All	All	2111/2456 (86%)	2063 (98%)	48 (2%)	50 80

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	196	HIS
1	C	304	ARG
1	D	411	THR
1	C	43	SER
1	C	205	CYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
2	E	25	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	GLN	G	301	-	5,9,9	0.98	1 (20%)	5,11,11	0.25	0
3	GLN	H	301	-	5,9,9	0.82	0	5,11,11	0.18	0
3	GLN	E	301	-	5,9,9	0.74	0	5,11,11	0.44	0
3	GLN	F	301	-	5,9,9	0.94	1 (20%)	5,11,11	0.19	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GLN	G	301	-	-	2/5/9/9	-
3	GLN	H	301	-	-	2/5/9/9	-
3	GLN	E	301	-	-	2/5/9/9	-
3	GLN	F	301	-	-	2/5/9/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	301	GLN	CA-N	2.10	1.51	1.47
3	F	301	GLN	CA-N	2.05	1.51	1.47

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	301	GLN	NE2-CD-CG-CB
3	F	301	GLN	OE1-CD-CG-CB
3	F	301	GLN	NE2-CD-CG-CB
3	E	301	GLN	OE1-CD-CG-CB
3	G	301	GLN	OE1-CD-CG-CB

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	H	301	GLN	3	0
3	F	301	GLN	1	0

## 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	383/465 (82%)	-0.23	5 (1%) 77 51	30, 83, 130, 162	0
1	B	378/465 (81%)	-0.23	4 (1%) 80 56	66, 94, 132, 161	0
1	C	375/465 (80%)	-0.22	4 (1%) 80 56	30, 90, 134, 165	0
1	D	380/465 (81%)	-0.25	3 (0%) 86 65	58, 89, 131, 162	0
2	E	247/260 (95%)	-0.39	0 100 100	46, 67, 95, 143	0
2	F	247/260 (95%)	-0.27	1 (0%) 92 79	56, 85, 124, 143	0
2	G	247/260 (95%)	-0.36	0 100 100	51, 78, 122, 146	0
2	H	247/260 (95%)	-0.31	0 100 100	51, 82, 117, 143	0
All	All	2504/2900 (86%)	-0.27	17 (0%) 87 69	30, 85, 127, 165	0

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	439	ARG	4.6
1	C	122	TYR	3.4
1	B	122	TYR	3.0
1	A	439	ARG	3.0
1	A	137	GLN	2.8

### 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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	GLN	F	301	10/10	0.65	0.49	111,140,151,153	0
3	GLN	G	301	10/10	0.68	0.41	102,124,137,140	0
3	GLN	H	301	10/10	0.69	0.39	97,120,132,139	0
3	GLN	E	301	10/10	0.87	0.30	88,105,125,125	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.