



# wwPDB X-ray Structure Validation Summary Report

Feb 27, 2014 – 05:08 AM GMT

PDB ID : 1RZG  
Title : Crystal structure of Human anti-HIV-1 GP120 reactive antibody 412d  
Authors : Huang, C.C.; Venturi, M.; Majeed, S.; Moore, M.J.; Phogat, S.; Zhang, M.-Y.; Dimitrov, D.S.; Hendrickson, W.A.; Robinson, J.; Sodroski, J.; Wyatt, R.; Choe, H.; Farzan, M.; Kwong, P.D.  
Deposited on : 2003-12-24  
Resolution : 2.00 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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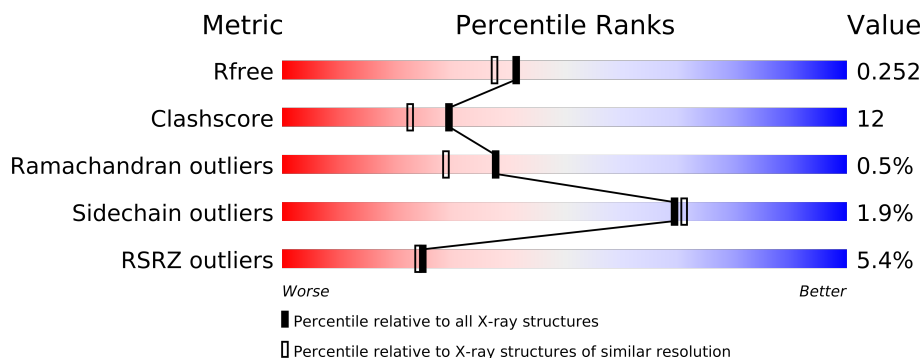
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance





The reported resolution of this entry is 2.00 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))
$R_{free}$	66092	4888 (2.00-2.00)
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (2.00-2.00)
RSRZ outliers	66119	4890 (2.00-2.00)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	231	
1	C	231	
2	B	214	
2	D	214	

## 2 Entry composition i

There are 5 unique types of molecules in this entry. The entry contains 7395 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

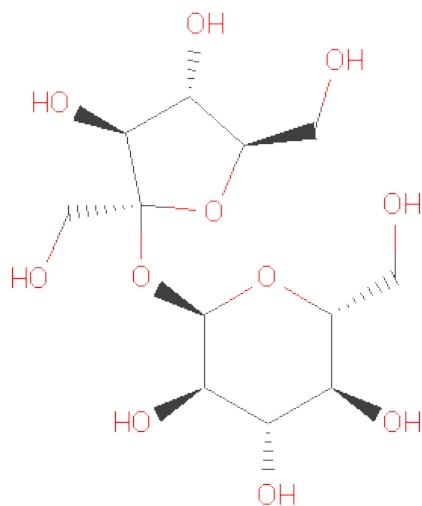
- Molecule 1 is a protein called Fab 412d light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1684	1066	278	332	8			
1	C	214	Total	C	N	O	S	0	0	0
			1617	1029	266	314	8			

- Molecule 2 is a protein called Fab 412d heavy chain.

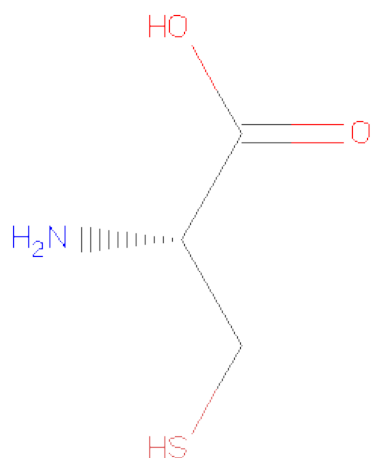
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1642	1024	278	334	6			
2	D	214	Total	C	N	O	S	0	0	0
			1649	1027	279	336	7			

- Molecule 3 is SUGAR (SUCROSE) (three-letter code: SUC) (formula: C<sub>12</sub>H<sub>22</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			23	12	11		
3	A	1	Total	C	O	0	0
			23	12	11		
3	D	1	Total	C	O	0	0
			23	12	11		
3	C	1	Total	C	O	0	0
			23	12	11		
3	A	1	Total	C	O	0	0
			23	12	11		
3	C	1	Total	C	O	0	0
			23	12	11		
3	A	1	Total	C	O	0	0
			23	12	11		

- Molecule 4 is CYSTEINE (three-letter code: CYS, ASP) (formula: C<sub>3</sub>H<sub>7</sub>NO<sub>2</sub>S, C<sub>4</sub>H<sub>7</sub>NO<sub>4</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	D	2	Total	C	N	O	S	0	0
			14	7	2	4	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	176	Total	O	0	0
			176	176		
5	B	193	Total	O	0	0
			193	193		

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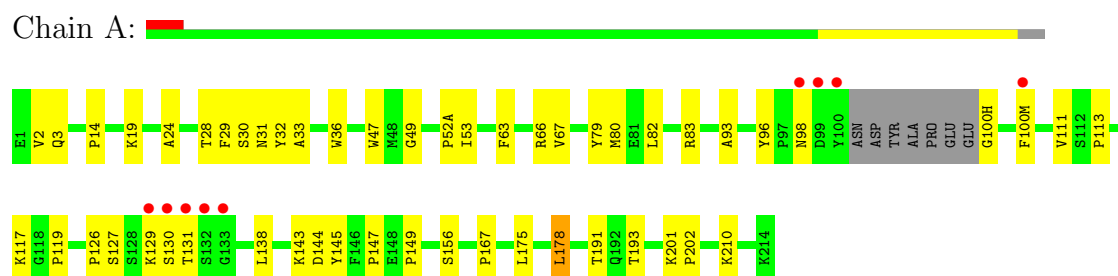
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	103	Total 103	O 103	0	0
5	D	156	Total 156	O 156	0	0

### 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: Fab 412d light chain





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.09Å 89.31Å 85.86Å 90.00° 110.31° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 29.15 – 1.88	Depositor EDS
% Data completeness (in resolution range)	94.1 (20.00-2.00) 86.2 (29.15-1.88)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.06 (at 1.88Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.201 , 0.251 0.202 , 0.252	Depositor DCC
$R_{free}$ test set	5758 reflections (10.14%)	DCC
Wilson B-factor (Å <sup>2</sup> )	26.0	Xtriage
Anisotropy	0.370	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 52.4	EDS
Estimated twinning fraction	0.033 for h,-k,-h-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 66703 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7395	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.70% of the height of the origin peak. No significant pseudotranslation is detected.*

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



## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SUC, TYS

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	0.34	0/1711	0.67	1/2331 (0.0%)
1	C	0.31	0/1643	0.62	0/2242
2	B	0.33	0/1677	0.65	0/2273
2	D	0.32	0/1684	0.64	1/2281 (0.0%)
All	All	0.33	0/6715	0.65	2/9127 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	33	ALA	N-CA-C	-5.16	97.06	111.00
2	D	114	SER	N-CA-C	-5.02	97.44	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1684	0	1639	47	0
1	C	1617	0	1571	60	0
2	B	1642	0	1596	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1649	0	1600	34	0
3	A	92	0	88	1	0
3	C	46	0	44	2	0
3	D	23	0	22	0	0
4	D	14	0	7	1	0
5	A	176	0	0	4	0
5	B	193	0	0	2	0
5	C	103	0	0	3	0
5	D	156	0	0	2	0
All	All	7395	0	6567	163	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 12.

The worst 5 of 163 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:129:LYS:HE2	2:B:208:SER:H	1.16	1.03
1:A:126:PRO:HG3	1:A:138:LEU:HB3	1.41	0.97
1:A:119:PRO:HB3	1:A:145:TYR:HB3	1.59	0.84
1:C:126:PRO:HG3	1:C:138:LEU:HB3	1.59	0.84
1:C:195:ILE:HG12	1:C:210:LYS:HG2	1.60	0.83

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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	220/231 (95%)	211 (96%)	9 (4%)	0	100	100
1	C	208/231 (90%)	180 (86%)	26 (12%)	2 (1%)	22	12
2	B	211/214 (99%)	202 (96%)	9 (4%)	0	100	100
2	D	212/214 (99%)	203 (96%)	7 (3%)	2 (1%)	25	14
All	All	851/890 (96%)	796 (94%)	51 (6%)	4 (0%)	38	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	25	SER
1	C	100(I)	MET
2	D	213	GLU
2	D	2	ILE

### 5.3.2 Protein sidechains ⓘ

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	187/193 (97%)	185 (99%)	2 (1%)	84	86
1	C	179/193 (93%)	173 (97%)	6 (3%)	49	45
2	B	188/189 (100%)	188 (100%)	0	100	100
2	D	189/189 (100%)	184 (97%)	5 (3%)	59	58
All	All	743/764 (97%)	730 (98%)	13 (2%)	69	75

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	149	PRO
1	C	202	PRO
2	D	152	ASN
1	C	145	TYR
2	D	147	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	79	GLN
2	B	91	HIS
2	D	91	HIS
2	B	31	ASN
2	D	31	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	TYS	A	100	1	16,16,17	5.04	4 (25%)	20,22,24	1.38	1 (5%)
1	TYS	C	100	1	16,16,17	4.92	4 (25%)	20,22,24	0.72	1 (5%)

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
1	TYS	A	100	1	-	0/9/11/13	0/1/1/1
1	TYS	C	100	1	-	0/9/11/13	0/1/1/1

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	100	TYS	O-C	17.85	1.23	1.11
1	C	100	TYS	O-C	17.27	1.23	1.11
1	A	100	TYS	OH-S	-8.24	1.48	1.63
1	C	100	TYS	OH-S	-8.18	1.48	1.63
1	C	100	TYS	OH-CZ	-3.61	1.38	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	100	TYS	CZ-OH-S	5.72	127.56	118.98
1	C	100	TYS	CZ-OH-S	2.33	122.48	118.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

9 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	SUC	A	9001	-	24,24,24	0.96	1 (4%)	36,36,36	1.00	3 (8%)
3	SUC	A	9002	-	24,24,24	0.98	1 (4%)	36,36,36	0.98	3 (8%)
3	SUC	A	9005	-	24,24,24	0.99	1 (4%)	36,36,36	0.90	2 (5%)
3	SUC	A	9007	-	24,24,24	1.00	1 (4%)	36,36,36	0.99	2 (5%)
3	SUC	C	9004	-	24,24,24	0.95	1 (4%)	36,36,36	0.95	2 (5%)
3	SUC	C	9006	-	24,24,24	1.03	1 (4%)	36,36,36	0.99	2 (5%)
3	SUC	D	9003	-	24,24,24	0.98	1 (4%)	36,36,36	0.99	2 (5%)
4	CYS	D	9004	2,4	5,5,6	7.86	2 (40%)	3,5,7	2.34	1 (33%)
4	ASP	D	9005	4	7,7,8	7.72	2 (28%)	6,8,10	1.62	1 (16%)

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	SUC	A	9001	-	-	0/12/51/51	0/2/2/2
3	SUC	A	9002	-	-	0/12/51/51	0/2/2/2
3	SUC	A	9005	-	-	0/12/51/51	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SUC	A	9007	-	-	0/12/51/51	0/2/2/2
3	SUC	C	9004	-	-	0/12/51/51	0/2/2/2
3	SUC	C	9006	-	-	0/12/51/51	0/2/2/2
3	SUC	D	9003	-	-	0/12/51/51	0/2/2/2
4	CYS	D	9004	2,4	-	0/2/4/6	0/0/0/0
4	ASP	D	9005	4	-	0/4/6/8	0/0/0/0

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	9005	ASP	O-C	20.22	1.25	1.11
4	D	9004	CYS	O-C	17.40	1.23	1.11
3	C	9006	SUC	C4-C5	2.81	1.59	1.53
3	A	9002	SUC	C4-C5	2.76	1.59	1.53
3	A	9005	SUC	C4-C5	2.75	1.59	1.53

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	9004	CYS	C-CA-N	-4.00	109.83	113.83
4	D	9005	ASP	C-CA-N	-3.56	110.27	113.83
3	D	9003	SUC	C1-O5-C5	2.72	119.02	113.73
3	A	9001	SUC	C1-O5-C5	2.72	119.01	113.73
3	A	9007	SUC	C1-O5-C5	2.65	118.89	113.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	224/231 (96%)	0.03	9 (4%) 36 36	17, 29, 54, 82	0
1	C	214/231 (92%)	0.82	31 (14%) 3 3	22, 45, 67, 88	0
2	B	213/214 (99%)	-0.30	1 (0%) 88 89	16, 27, 42, 65	0
2	D	214/214 (100%)	-0.12	5 (2%) 57 57	22, 32, 49, 87	0
All	All	865/890 (97%)	0.11	46 (5%) 25 25	16, 32, 60, 88	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	98	ASN	7.2
1	A	130	SER	5.2
1	C	99	ASP	5.0
1	A	129	LYS	4.9
1	C	25	SER	4.7

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

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	TYS	A	100	16/17	0.45	-	72,81,89,89	0
1	TYS	C	100	16/17	0.51	-	78,86,95,96	0

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

### 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	SUC	A	9007	23/23	0.22	-	82,84,86,86	0
3	SUC	A	9002	23/23	0.10	-	22,30,33,36	0
4	ASP	D	9005	8/9	0.21	-	86,86,87,87	0
3	SUC	C	9006	23/23	0.22	-	67,71,73,73	0
3	SUC	A	9005	23/23	0.14	-	30,36,40,42	0
3	SUC	D	9003	23/23	0.16	-	42,46,48,49	0
3	SUC	A	9001	23/23	0.09	-	26,28,32,34	0
3	SUC	C	9004	23/23	0.11	-	43,46,48,49	0
4	CYS	D	9004	6/7	0.29	-	87,87,87,89	0

### 6.5 Other polymers ⓘ

There are no such residues in this entry.