Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:08 PM UTC

PDB ID	:	3U25 / pdb_00003u25
Title	:	Crystal structure of P. aeruginoas azurin containing a Tyr-His hydrogen bonded pair
Authors	:	Warren, J.J.; Winkler, J.R.; Gray, H.B.
Deposited on	:	2011-09-30
Resolution	:	1.18 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *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.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

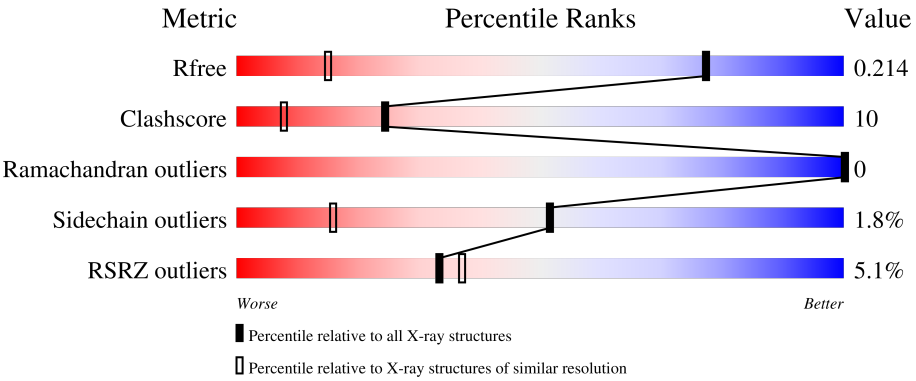
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.18 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}	180053	1789 (1.20-1.16)
Clashscore	190562	1845 (1.20-1.16)
Ramachandran outliers	187476	1789 (1.20-1.16)
Sidechain outliers	187428	1789 (1.20-1.16)
RSRZ outliers	180081	1787 (1.20-1.16)

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 of the lower bar indicate the fraction of residues that contain outliers for >=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 <=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	127	5% 83% 14%
1	B	127	6% 83% 13%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2209 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 Azurin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	127	Total	C	N	O	S	0	4	0
			988	618	165	195	10			
1	B	127	Total	C	N	O	S	0	3	0
			983	615	164	194	10			

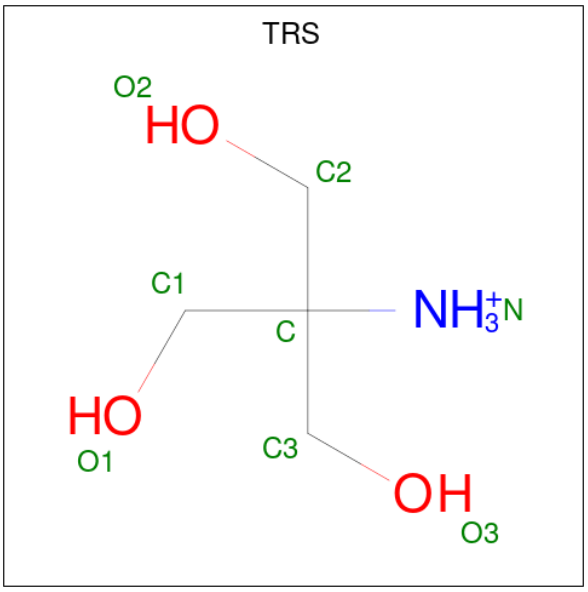
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	HIS	ILE	engineered mutation	UNP P00282
A	48	TYR	TRP	engineered mutation	UNP P00282
A	72	PHE	TYR	engineered mutation	UNP P00282
A	108	PHE	TYR	engineered mutation	UNP P00282
B	20	HIS	ILE	engineered mutation	UNP P00282
B	48	TYR	TRP	engineered mutation	UNP P00282
B	72	PHE	TYR	engineered mutation	UNP P00282
B	108	PHE	TYR	engineered mutation	UNP P00282

- Molecule 2 is COPPER (II) ION (CCD ID: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cu	0	0
			1	1		
2	B	1	Total	Cu	0	0
			1	1		

- Molecule 3 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (CCD ID: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 8 4 1 3	0	0
3	B	1	Total C N O 8 4 1 3	0	0

- Molecule 4 is water.

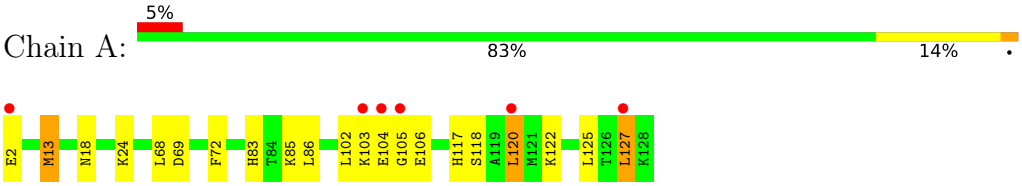
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	114	Total O 114 114	0	0
4	B	106	Total O 106 106	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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.

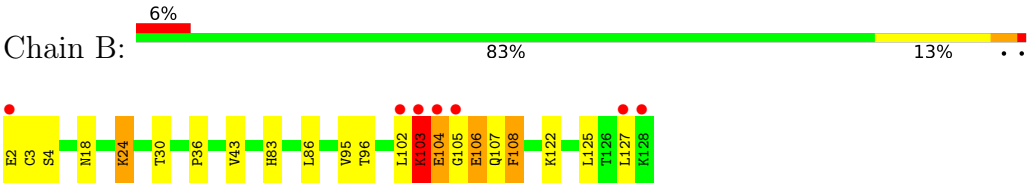
- Molecule 1: Azurin

Chain A:



- Molecule 1: Azurin

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	48.03Å 56.33Å 82.91Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.18 20.00 – 1.18	Depositor EDS
% Data completeness (in resolution range)	94.9 (20.00-1.18) 94.8 (20.00-1.18)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	6.80 (at 1.18Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.195 , 0.217 0.192 , 0.214	Depositor DCC
R_{free} test set	3566 reflections (4.81%)	wwPDB-VP
Wilson B-factor (Å^2)	11.7	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 36.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	2209	wwPDB-VP
Average B, all atoms (Å^2)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.02% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	1.60	6/1017 (0.6%)	1.32	4/1367 (0.3%)
1	B	1.55	8/1009 (0.8%)	1.27	4/1356 (0.3%)
All	All	1.57	14/2026 (0.7%)	1.29	8/2723 (0.3%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	13	MET	SD-CE	-14.68	1.42	1.79
1	B	36	PRO	C-O	6.92	1.30	1.23
1	A	118	SER	N-CA	6.65	1.54	1.46
1	B	104	GLU	CA-C	5.90	1.61	1.52
1	B	105	GLY	N-CA	5.79	1.53	1.45
1	B	122	LYS	C-O	5.75	1.30	1.23
1	B	95	VAL	CA-CB	5.73	1.62	1.54
1	A	120	LEU	CA-C	5.70	1.60	1.52
1	A	120	LEU	C-O	5.43	1.30	1.24
1	A	118	SER	CA-C	-5.41	1.45	1.52
1	B	43	VAL	CA-C	-5.40	1.47	1.52
1	B	86	LEU	C-O	5.10	1.30	1.24
1	A	102	LEU	CA-C	5.07	1.59	1.52
1	B	108	PHE	CA-C	-5.05	1.46	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	106	GLU	N-CA-C	-6.13	100.64	110.14
1	A	120	LEU	CA-C-O	5.70	126.56	120.24
1	A	122	LYS	O-C-N	-5.59	117.44	123.42
1	B	96	THR	CA-C-O	-5.21	115.08	120.70
1	B	103	LYS	CB-CG-CD	5.09	123.00	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	69	ASP	CB-CG-OD1	5.04	129.99	118.40
1	B	104	GLU	N-CA-C	5.03	118.88	112.34
1	A	106	GLU	N-CA-C	5.00	116.98	110.53

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	988	0	970	28	2
1	B	983	0	964	13	2
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	8	0	12	2	2
3	B	8	0	12	1	2
4	A	114	0	0	0	0
4	B	106	0	0	1	0
All	All	2209	0	1958	39	4

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 10.

All (39) 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:B:83:HIS:NE2	3:B:1:TRS:O3	1.80	1.14
1:A:83:HIS:NE2	3:A:129:TRS:O1	1.81	1.11
1:A:24:LYS:HG2	1:A:127:LEU:CD1	1.83	1.06
1:A:24:LYS:HG2	1:A:127:LEU:HD11	1.06	1.04
1:A:24:LYS:CG	1:A:127:LEU:HD11	1.94	0.98
1:A:24:LYS:CG	1:A:127:LEU:CD1	2.48	0.92
1:A:103:LYS:HG3	1:A:105:GLY:H	1.40	0.86
1:B:103:LYS:HB3	4:B:266:HOH:O	1.79	0.83
1:B:104:GLU:HA	1:B:127:LEU:HD12	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:MET:HE2	1:A:120:LEU:HD12	1.77	0.65
1:A:103:LYS:HG3	1:A:105:GLY:N	2.14	0.61
1:A:68[A]:LEU:HD23	1:A:72:PHE:CE2	2.35	0.61
1:A:24:LYS:HG3	1:A:127:LEU:HD13	1.84	0.60
1:A:24:LYS:CG	1:A:127:LEU:HD13	2.32	0.59
1:A:13:MET:CE	1:A:120:LEU:HD12	2.35	0.56
1:A:18[B]:ASN:ND2	1:B:18:ASN:H	2.04	0.55
1:A:127:LEU:HD13	1:A:127:LEU:C	2.30	0.55
1:B:125:LEU:C	1:B:125:LEU:HD23	2.32	0.54
1:A:125:LEU:C	1:A:125:LEU:HD23	2.32	0.54
1:B:24:LYS:HD3	1:B:104:GLU:CD	2.33	0.54
1:A:24:LYS:HG3	1:A:127:LEU:CD1	2.36	0.52
1:A:24:LYS:HZ2	1:A:104:GLU:HG3	1.75	0.51
1:A:83:HIS:CE1	3:A:129:TRS:O1	2.61	0.51
1:A:68[B]:LEU:HD13	1:A:72:PHE:CE2	2.46	0.51
1:A:68[A]:LEU:HD23	1:A:72:PHE:HE2	1.77	0.49
1:A:13:MET:HE3	1:A:117:HIS:CD2	2.48	0.49
1:B:102:LEU:O	1:B:103:LYS:HE3	2.13	0.49
1:A:24:LYS:NZ	1:A:104:GLU:HG3	2.29	0.48
1:B:2[B]:GLU:HG3	1:B:3:CYS:SG	2.53	0.48
1:B:106:GLU:HB3	1:B:108:PHE:CZ	2.49	0.47
1:B:24:LYS:HE3	1:B:24:LYS:HB3	1.87	0.45
1:A:18[A]:ASN:HD21	1:B:18:ASN:HB2	1.82	0.43
1:A:68[B]:LEU:CD1	1:A:86:LEU:CD2	2.97	0.43
1:B:106:GLU:HG3	1:B:107:GLN:O	2.21	0.41
1:B:4:SER:HA	1:B:30:THR:O	2.20	0.41
1:A:127:LEU:CD1	1:A:127:LEU:C	2.94	0.41
1:A:13:MET:HE2	1:A:120:LEU:CD1	2.49	0.41
1:A:68[B]:LEU:HD11	1:A:86:LEU:CD2	2.51	0.40

All (4) 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)
1:A:2[B]:GLU:OE1	3:A:129:TRS:O1[4_455]	1.80	0.40
1:B:2[B]:GLU:OE1	3:B:1:TRS:O3[4_554]	1.80	0.40
1:B:2[B]:GLU:OE1	3:B:1:TRS:C3[4_554]	2.05	0.15
1:A:2[B]:GLU:OE1	3:A:129:TRS:C1[4_455]	2.12	0.08

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	128/127 (101%)	124 (97%)	4 (3%)	0	100	100
1	B	127/127 (100%)	123 (97%)	4 (3%)	0	100	100
All	All	255/254 (100%)	247 (97%)	8 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	114/110 (104%)	112 (98%)	2 (2%)	51	16
1	B	113/110 (103%)	111 (98%)	2 (2%)	51	16
All	All	227/220 (103%)	223 (98%)	4 (2%)	51	16

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	LYS
1	A	127	LEU
1	B	24	LYS
1	B	103	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	32	ASN
1	A	38	ASN
1	A	107	GLN
1	B	107	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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	TRS	B	1	-	7,7,7	1.58	1 (14%)	9,9,9	0.61	0
3	TRS	A	129	-	7,7,7	1.76	1 (14%)	9,9,9	0.88	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	TRS	B	1	-	-	3/9/9/9	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TRS	A	129	-	-	3/9/9/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	129	TRS	O1-C1	4.58	1.56	1.42
3	B	1	TRS	O3-C3	3.69	1.54	1.42

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	129	TRS	N-C-C1-O1
3	A	129	TRS	C2-C-C1-O1
3	B	1	TRS	N-C-C3-O3
3	A	129	TRS	C3-C-C1-O1
3	B	1	TRS	C1-C-C3-O3
3	B	1	TRS	C2-C-C3-O3

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1	TRS	1	2
3	A	129	TRS	2	2

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

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, 95th 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^2)	Q<0.9
1	A	127/127 (100%)	0.24	6 (4%)	36	40	6, 10, 19, 33	4 (3%)
1	B	127/127 (100%)	0.30	7 (5%)	30	34	6, 11, 19, 33	3 (2%)
All	All	254/254 (100%)	0.27	13 (5%)	33	37	6, 11, 19, 33	7 (2%)

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	105	GLY	5.9
1	A	120	LEU	3.7
1	A	104	GLU	3.7
1	B	127	LEU	3.5
1	B	102	LEU	3.3
1	A	127	LEU	3.1
1	B	2[A]	GLU	2.9
1	A	103	LYS	2.9
1	B	103	LYS	2.8
1	B	128	LYS	2.8
1	B	104	GLU	2.7
1	A	2[A]	GLU	2.1
1	A	105	GLY	2.1

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

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

6.3 Carbohydrates

There are no oligosaccharides 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. The B-factors column lists the minimum, median, 95th 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^2)	Q<0.9
3	TRS	B	1	8/8	0.92	0.11	5,13,15,15	0
3	TRS	A	129	8/8	0.94	0.10	5,14,16,20	0
2	CU	A	1	1/1	1.00	0.01	8,8,8,8	0
2	CU	B	129	1/1	1.00	0.01	8,8,8,8	0

6.5 Other polymers

There are no such residues in this entry.