



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 08:54 PM GMT

PDB ID : 3V6C
Title : Crystal Structure of USP2 in complex with mutated ubiquitin
Authors : Neculai, M.; Ernst, A.; Sidhu, S.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Weigelt, J.; Dhe-Paganon, S.; Structural Genomics Consortium (SGC)
Deposited on : 2011-12-19
Resolution : 1.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

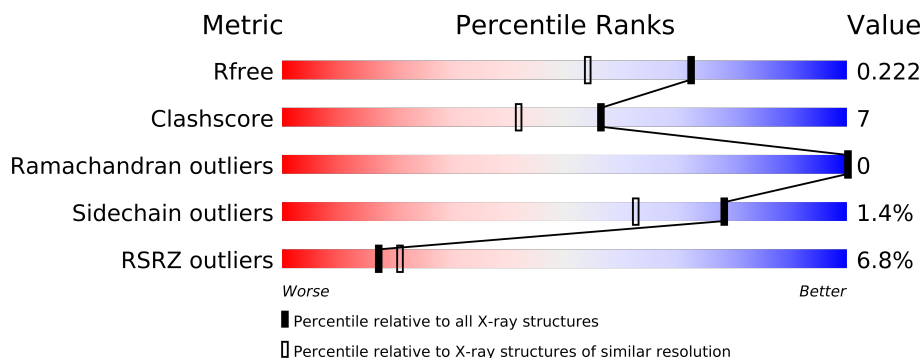
The following versions of software and data (see [references](#)) were used in the production of this report:

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 1.70 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	2456 (1.70-1.70)
Clashscore	79885	2929 (1.70-1.70)
Ramachandran outliers	78287	2878 (1.70-1.70)
Sidechain outliers	78261	2878 (1.70-1.70)
RSRZ outliers	66119	2456 (1.70-1.70)

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 ≥ 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	367	
2	B	91	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
4	GOL	A	702	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 3818 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 Ubiquitin carboxyl-terminal hydrolase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	29	0
			2821	1783	502	514	22			

There are 19 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	239	MET	-	EXPRESSION TAG	UNP O75604
A	240	GLY	-	EXPRESSION TAG	UNP O75604
A	241	SER	-	EXPRESSION TAG	UNP O75604
A	242	SER	-	EXPRESSION TAG	UNP O75604
A	243	HIS	-	EXPRESSION TAG	UNP O75604
A	244	HIS	-	EXPRESSION TAG	UNP O75604
A	245	HIS	-	EXPRESSION TAG	UNP O75604
A	246	HIS	-	EXPRESSION TAG	UNP O75604
A	247	HIS	-	EXPRESSION TAG	UNP O75604
A	248	HIS	-	EXPRESSION TAG	UNP O75604
A	249	SER	-	EXPRESSION TAG	UNP O75604
A	250	SER	-	EXPRESSION TAG	UNP O75604
A	251	GLY	-	EXPRESSION TAG	UNP O75604
A	252	LEU	-	EXPRESSION TAG	UNP O75604
A	253	VAL	-	EXPRESSION TAG	UNP O75604
A	254	PRO	-	EXPRESSION TAG	UNP O75604
A	255	ARG	-	EXPRESSION TAG	UNP O75604
A	256	GLY	-	EXPRESSION TAG	UNP O75604
A	257	SER	-	EXPRESSION TAG	UNP O75604

- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	81	Total	C	N	O	S	0	9	0
			697	439	125	131	2			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	MET	-	EXPRESSION TAG	UNP P0CG48
B	-15	ALA	-	EXPRESSION TAG	UNP P0CG48
B	-14	HIS	-	EXPRESSION TAG	UNP P0CG48
B	-13	HIS	-	EXPRESSION TAG	UNP P0CG48
B	-12	HIS	-	EXPRESSION TAG	UNP P0CG48
B	-11	HIS	-	EXPRESSION TAG	UNP P0CG48
B	-10	HIS	-	EXPRESSION TAG	UNP P0CG48
B	-9	HIS	-	EXPRESSION TAG	UNP P0CG48
B	-8	SER	-	EXPRESSION TAG	UNP P0CG48
B	-7	SER	-	EXPRESSION TAG	UNP P0CG48
B	-6	GLY	-	EXPRESSION TAG	UNP P0CG48
B	-5	LEU	-	EXPRESSION TAG	UNP P0CG48
B	-4	VAL	-	EXPRESSION TAG	UNP P0CG48
B	-3	PRO	-	EXPRESSION TAG	UNP P0CG48
B	0	SER	GLY	engineered mutation	UNP P0CG48
B	6	ASN	LYS	engineered mutation	UNP P0CG48
B	11	THR	LYS	engineered mutation	UNP P0CG48
B	12	HIS	THR	engineered mutation	UNP P0CG48

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Cl 1 1	0	0
3	A	1	Total Cl 1 1	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		

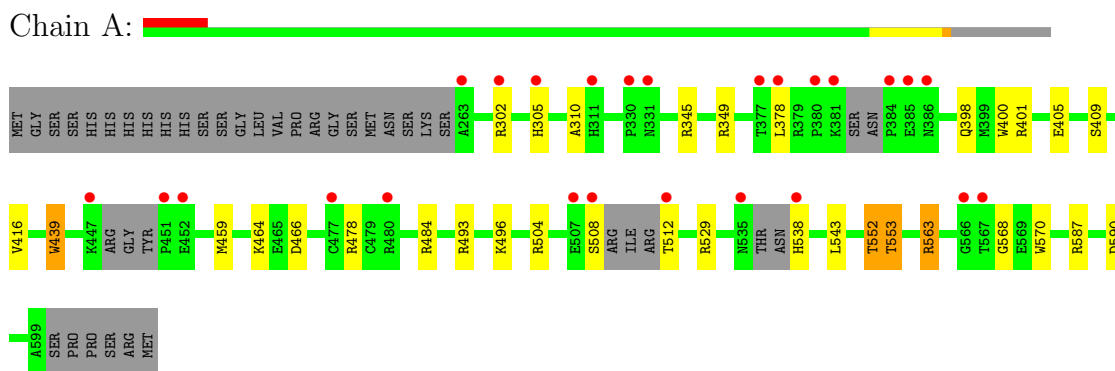
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	227	Total	O	0	1
			228	228		
6	B	63	Total	O	0	0
			63	63		

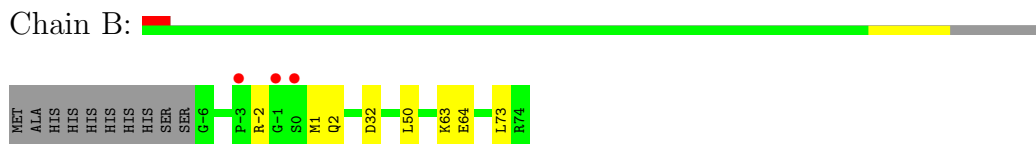
3 Residue-property plots

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: Ubiquitin carboxyl-terminal hydrolase 2



- Molecule 2: Ubiquitin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.73Å 84.08Å 86.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.08 – 1.70 19.77 – 1.71	Depositor EDS
% Data completeness (in resolution range)	97.2 (84.08-1.70) 97.5 (19.77-1.71)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.176 , 0.220 0.176 , 0.222	Depositor DCC
R_{free} test set	2300 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	18.5	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 40.7	EDS
Estimated twinning fraction	0.024 for -h,l,k	Xtriage
L-test for twinning	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 45637 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3818	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: GOL, ZN, CL

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	1.06	4/2950 (0.1%)	1.08	12/3972 (0.3%)
2	B	0.91	0/726	1.11	2/976 (0.2%)
All	All	1.03	4/3676 (0.1%)	1.08	14/4948 (0.3%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	439	TRP	CD2-CE2	5.40	1.47	1.41
1	A	409	SER	CB-OG	5.30	1.49	1.42
1	A	400	TRP	CD2-CE2	5.28	1.47	1.41
1	A	570	TRP	CD2-CE2	5.01	1.47	1.41

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	563[A]	ARG	NE-CZ-NH2	-9.47	115.57	120.30
1	A	563[B]	ARG	NE-CZ-NH2	-9.47	115.57	120.30
1	A	587	ARG	NE-CZ-NH1	-8.94	115.83	120.30
1	A	587	ARG	NE-CZ-NH2	8.02	124.31	120.30
1	A	504	ARG	NE-CZ-NH2	7.89	124.24	120.30
1	A	504	ARG	NE-CZ-NH1	-7.70	116.45	120.30
1	A	349	ARG	NE-CZ-NH2	-6.99	116.81	120.30
1	A	563[A]	ARG	NE-CZ-NH1	6.95	123.78	120.30
1	A	563[B]	ARG	NE-CZ-NH1	6.95	123.78	120.30
2	B	73	LEU	CB-CG-CD1	-6.25	100.38	111.00
1	A	378	LEU	CA-CB-CG	5.89	128.84	115.30
1	A	466	ASP	CB-CG-OD1	5.82	123.54	118.30
2	B	32	ASP	CB-CG-OD1	5.56	123.31	118.30
1	A	378	LEU	CB-CG-CD1	5.17	119.80	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	2821	0	0	21	0
2	B	697	0	0	2	1
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	6	0	0	0	0
5	A	1	0	0	0	0
6	A	228	0	0	10	1
6	B	63	0	0	0	0
All	All	3818	0	0	23	1

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 7.

All (23) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:464[B]:LYS:CB	1:A:464[B]:LYS:NZ	2.25	0.99
1:A:496:LYS:NZ	6:A:1010:HOH:O	2.01	0.92
1:A:302[B]:ARG:NH2	6:A:1017:HOH:O	2.04	0.91
1:A:590:ASP:OD1	6:A:936:HOH:O	1.96	0.83
1:A:563[A]:ARG:NH2	6:A:918:HOH:O	2.14	0.80
1:A:401[A]:ARG:NH1	1:A:405[A]:GLU:OE2	2.20	0.75
1:A:568:GLY:O	6:A:1015:HOH:O	2.04	0.74
1:A:553[A]:THR:OG1	6:A:916:HOH:O	2.04	0.74
1:A:398:GLN:NE2	1:A:401[B]:ARG:NH2	2.36	0.72
1:A:543:LEU:O	1:A:563[A]:ARG:NH2	2.33	0.61
1:A:552[A]:THR:OG1	6:A:915:HOH:O	2.16	0.60
1:A:508:SER:O	1:A:512:THR:N	2.39	0.55
1:A:484[B]:ARG:NH1	6:A:970:HOH:O	2.40	0.55
1:A:529[B]:ARG:NH2	1:A:538:HIS:N	2.58	0.52
1:A:459[B]:MET:CA	1:A:459[B]:MET:CE	2.91	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:405[B]:GLU:CA	1:A:405[B]:GLU:OE1	2.61	0.48
1:A:493:ARG:NH1	6:A:1009:HOH:O	2.46	0.47
1:A:310:ALA:O	1:A:345:ARG:NH2	2.47	0.46
1:A:416:VAL:CG2	1:A:439:TRP:CE2	2.98	0.46
1:A:305:HIS:N	6:A:967:HOH:O	2.52	0.43
1:A:508:SER:O	1:A:512:THR:CA	2.68	0.42
2:B:2:GLN:NE2	2:B:63[A]:LYS:NZ	2.68	0.41
2:B:63[A]:LYS:NZ	2:B:64:GLU:OE2	2.53	0.41

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	Distance(Å)	Clash(Å)
2:B:-2[B]:ARG:NH1	6:A:904:HOH:O[3_745]	2.04	0.16

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	346/367 (94%)	337 (97%)	9 (3%)	0	100	100
2	B	88/91 (97%)	87 (99%)	1 (1%)	0	100	100
All	All	434/458 (95%)	424 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	323/332 (97%)	318 (98%)	5 (2%)	76	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	82/82 (100%)	78 (95%)	4 (5%)	35	13
All	All	405/414 (98%)	396 (98%)	9 (2%)	78	43

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	478	ARG
1	A	552[A]	THR
1	A	552[B]	THR
1	A	553[A]	THR
1	A	553[B]	THR
2	B	1[A]	MET
2	B	1[B]	MET
2	B	50[A]	LEU
2	B	50[B]	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	$\# Z > 2$
4	GOL	A	702	-	5,5,5	0.68	0	5,5,5	1.06	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
4	GOL	A	702	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

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, 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	327/367 (89%)	0.22	25 (7%) 14 17	10, 19, 44, 65	0
2	B	81/91 (89%)	0.08	3 (3%) 39 44	10, 18, 30, 34	0
All	All	408/458 (89%)	0.19	28 (6%) 17 20	10, 19, 38, 65	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	378	LEU	6.7
1	A	538	HIS	5.1
1	A	535	ASN	3.9
1	A	567	THR	3.8
1	A	384	PRO	3.7
2	B	-1	GLY	3.7
1	A	451	PRO	3.6
1	A	508	SER	3.6
1	A	477[A]	CYS	3.6
1	A	480	ARG	3.5
1	A	263	ALA	3.5
1	A	331	ASN	3.4
1	A	566	GLY	3.4
1	A	507	GLU	3.1
2	B	0	SER	2.9
1	A	305	HIS	2.8
1	A	380	PRO	2.7
1	A	447	LYS	2.7
1	A	512	THR	2.6
2	B	-3	PRO	2.6
1	A	381	LYS	2.6
1	A	302[A]	ARG	2.6
1	A	385	GLU	2.4
1	A	452	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	386	ASN	2.2
1	A	330	PRO	2.2
1	A	377	THR	2.1
1	A	311	HIS	2.0

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 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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
4	GOL	A	702	6/6	0.15	3.93	28,32,34,35	0
3	CL	A	701	1/1	0.03	-2.88	21,21,21,21	0
5	ZN	A	703	1/1	0.02	-3.03	22,22,22,22	0
3	CL	B	101	1/1	0.05	-3.42	26,26,26,26	0

6.5 Other polymers ⓘ

There are no such residues in this entry.