wwPDB X-ray Structure Validation Summary Report (i)

Jun 22, 2024 – 11:27 PM EDT

PDB ID	:	6H80
Title	:	Dengue-RdRp3-inhibitor complex co-crystallisation
Authors	:	Talapatra, S.K.; Kozielski, F.
Deposited on	:	2018-07-31
Resolution	:	2.30 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*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (i)) were used in the production of this report:

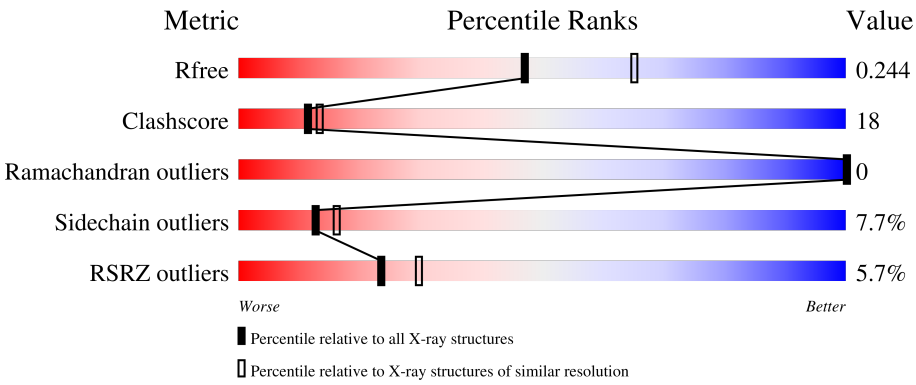
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

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

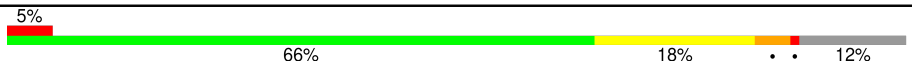
The reported resolution of this entry is 2.30 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	635	

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	ZN	A	1003	-	-	X	-

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4747 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.

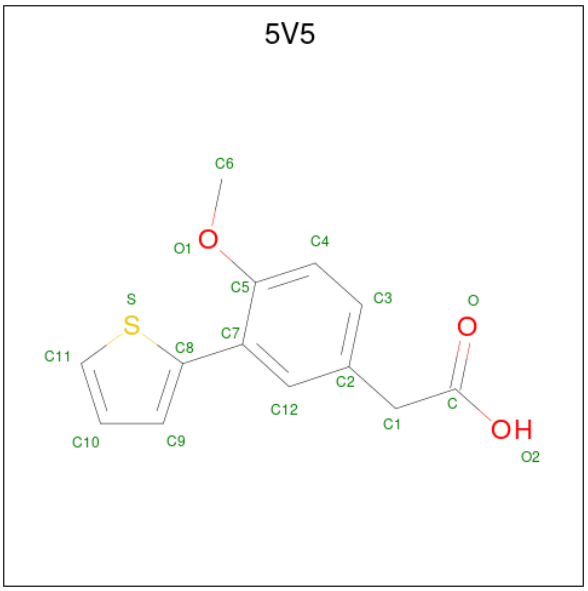
- Molecule 1 is a protein called Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	558	4529	2865	814	819	31	0	3	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	266	GLY	-	expression tag	UNP Q6YMS4
A	267	SER	-	expression tag	UNP Q6YMS4
A	268	HIS	-	expression tag	UNP Q6YMS4
A	269	MET	-	expression tag	UNP Q6YMS4
A	270	LEU	-	expression tag	UNP Q6YMS4
A	271	ASP	-	expression tag	UNP Q6YMS4
A	366	LEU	MET	variant	UNP Q6YMS4
A	372	VAL	ALA	variant	UNP Q6YMS4
A	480	VAL	ALA	variant	UNP Q6YMS4
A	603	VAL	LEU	variant	UNP Q6YMS4

- Molecule 2 is 2-(4-methoxy-3-thiophen-2-yl-phenyl)ethanoic acid (three-letter code: 5V5) (formula: $C_{13}H_{12}O_3S$).

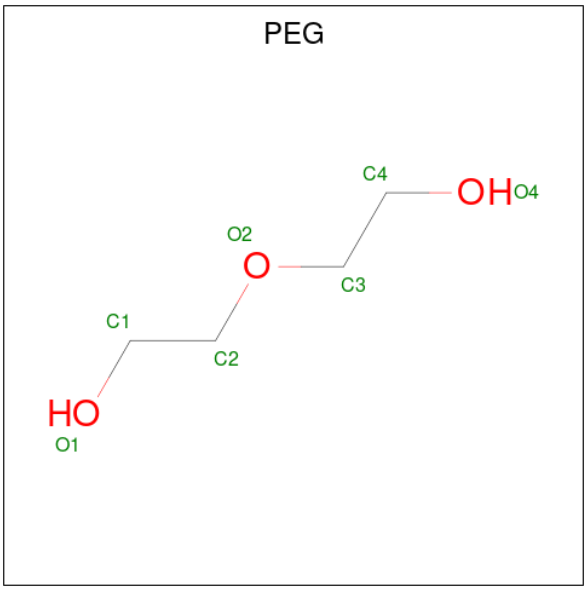


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
2	A	1	17	13	3	1	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	A	2	2	2	0	0

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	7	4	3	0	0
			Total	C	O		
4	A	1	7	4	3	0	0
			Total	C	O		
4	A	1	7	4	3	0	0
			Total	C	O		
4	A	1	7	4	3	0	0
			Total	C	O		
4	A	1	7	4	3	0	0

- Molecule 5 is water.

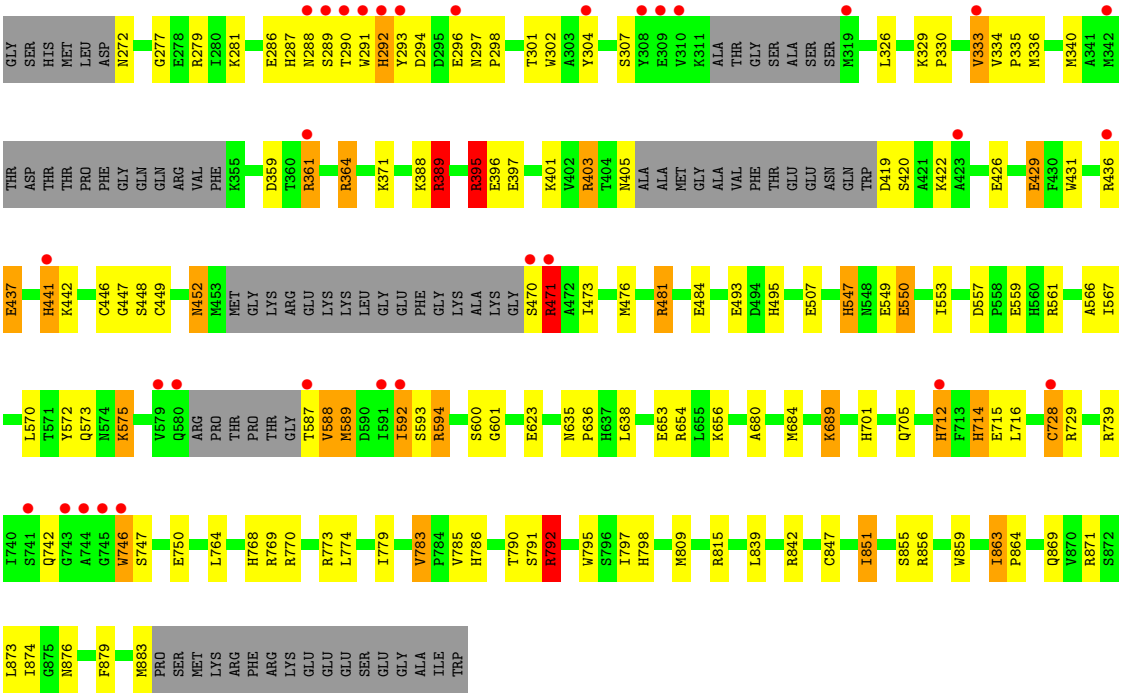
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	164	164	164	0	0

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: Genome polyprotein

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	165.08Å 181.25Å 57.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	52.70 – 2.30 56.74 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (52.70-2.30) 99.9 (56.74-2.30)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.82 (at 2.29Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.191 , 0.236 0.231 , 0.244	Depositor DCC
R_{free} test set	1946 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	48.8	Xtriage
Anisotropy	0.645	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 48.7	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	0.94	EDS
Total number of atoms	4747	wwPDB-VP
Average B, all atoms (Å^2)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.29% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, 5V5, PEG

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	1.18	13/4642 (0.3%)	0.95	18/6293 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	18

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	437	GLU	CD-OE2	-10.67	1.14	1.25
1	A	437	GLU	CD-OE1	-7.80	1.17	1.25
1	A	653	GLU	CD-OE1	-6.31	1.18	1.25
1	A	549	GLU	CD-OE1	-6.18	1.18	1.25
1	A	397	GLU	CD-OE2	-5.71	1.19	1.25

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

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	712	HIS	CA-CB-CG	9.62	129.96	113.60
1	A	441	HIS	CB-CA-C	9.57	129.55	110.40
1	A	728	CYS	CA-CB-SG	9.27	130.68	114.00
1	A	714	HIS	CA-CB-CG	9.20	129.24	113.60
1	A	441	HIS	CA-CB-CG	8.65	128.31	113.60

There are no chirality outliers.

5 of 18 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	361	ARG	Sidechain
1	A	364	ARG	Sidechain
1	A	389	ARG	Sidechain
1	A	395	ARG	Sidechain
1	A	403	ARG	Sidechain

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	4529	0	4355	158	1
2	A	17	0	0	0	0
3	A	2	0	0	2	0
4	A	35	0	50	2	0
5	A	164	0	0	14	0
All	All	4747	0	4405	159	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 18.

The worst 5 of 159 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:712:HIS:HD2	1:A:714:HIS:NE2	1.25	1.30
1:A:764[A]:LEU:HD23	1:A:809:MET:CE	1.64	1.27
1:A:712:HIS:CD2	3:A:1003:ZN:ZN	1.22	1.23
1:A:712:HIS:NE2	1:A:728:CYS:HB3	1.54	1.21
1:A:712:HIS:CD2	1:A:714:HIS:NE2	2.08	1.20

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)
1:A:333:VAL:CG2	1:A:333:VAL:CG2[3_654]	1.82	0.38

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	549/635 (86%)	535 (97%)	14 (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	473/552 (86%)	437 (92%)	36 (8%)	13 16

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	791	SER
1	A	876	ASN
1	A	792	ARG
1	A	855	SER
1	A	446	CYS

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	452	ASN
1	A	712	HIS
1	A	768	HIS

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Mol	Chain	Res	Type
1	A	862	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)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	$\#\|Z\| > 2$
2	5V5	A	1001	-	18,18,18	2.02	4 (22%)	19,24,24	2.75	2 (10%)
4	PEG	A	1005	-	6,6,6	0.47	0	5,5,5	0.68	0
4	PEG	A	1006	-	6,6,6	0.50	0	5,5,5	0.55	0
4	PEG	A	1007	-	6,6,6	0.60	0	5,5,5	0.34	0
4	PEG	A	1008	-	6,6,6	0.69	0	5,5,5	0.80	0
4	PEG	A	1004	-	6,6,6	0.48	0	5,5,5	0.53	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
2	5V5	A	1001	-	-	0/9/10/10	0/2/2/2
4	PEG	A	1005	-	-	1/4/4/4	-
4	PEG	A	1006	-	-	3/4/4/4	-
4	PEG	A	1007	-	-	2/4/4/4	-
4	PEG	A	1008	-	-	4/4/4/4	-
4	PEG	A	1004	-	-	3/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1001	5V5	C7-C8	5.82	1.53	1.48
2	A	1001	5V5	C8-S	-3.42	1.69	1.72
2	A	1001	5V5	O1-C5	3.28	1.42	1.37
2	A	1001	5V5	C10-C11	2.18	1.41	1.34

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1001	5V5	C10-C11-S	-10.94	104.10	112.98
2	A	1001	5V5	C2-C1-C	-2.17	107.55	113.71

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1004	PEG	O2-C3-C4-O4
4	A	1008	PEG	O2-C3-C4-O4
4	A	1004	PEG	O1-C1-C2-O2
4	A	1006	PEG	O1-C1-C2-O2
4	A	1008	PEG	C1-C2-O2-C3

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1007	PEG	2	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, 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	558/635 (87%)	0.27	32 (5%) 23 30	41, 57, 101, 122	0

The worst 5 of 32 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	441	HIS	8.8
1	A	470	SER	6.3
1	A	319	MET	5.3
1	A	292	HIS	5.2
1	A	592	ILE	5.1

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, 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
4	PEG	A	1008	7/7	0.57	0.27	64,66,74,76	0
4	PEG	A	1007	7/7	0.79	0.36	75,79,80,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	PEG	A	1005	7/7	0.84	0.16	66,78,79,80	0
4	PEG	A	1004	7/7	0.85	0.20	63,71,75,78	0
4	PEG	A	1006	7/7	0.85	0.15	60,64,72,75	0
3	ZN	A	1003	1/1	0.95	0.04	58,58,58,58	0
2	5V5	A	1001	17/17	0.96	0.15	43,51,65,69	0
3	ZN	A	1002	1/1	0.96	0.13	65,65,65,65	0

6.5 Other polymers (i)

There are no such residues in this entry.