

Full wwPDB X-ray Structure Validation Report (i)

Dec 1, 2022 – 12:22 am GMT

mplex with 5-chlorothiophene-2-carboxamide
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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 (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 (1)) were used in the production of this report:

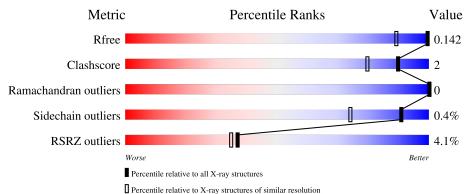
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.31.3
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.12 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	1168 (1.14-1.10)
Clashscore	141614	1205 (1.14-1.10)
Ramachandran outliers	138981	1168 (1.14-1.10)
Sidechain outliers	138945	1165 (1.14-1.10)
RSRZ outliers	127900	1146 (1.14-1.10)

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	Н	259	3% 94% •	•
2	Ι	12	83% 8%	
3	L	28	4% 100%	-



2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 5087 atoms, of which 2272 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 Thrombin heavy chain.

Mol	Chain	Residues		Atoms					ZeroOcc	AltConf	Trace
1	Н	255	Total 4135	C 1356	Н 2023	N 371	O 371	S 14	0	13	1

• Molecule 2 is a protein called Hirudin-2.

Mol	Chain	Residues		Ate	\mathbf{oms}			ZeroOcc	AltConf	Trace
2	Ι	12	Total 92	C 59	N 12	O 20	S 1	0	0	0

• Molecule 3 is a protein called Prothrombin.

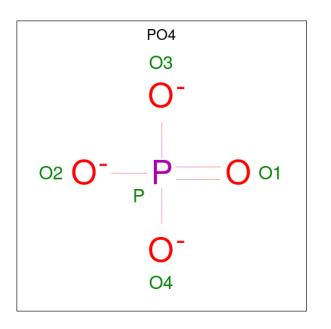
Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
3	L	28	Total 496	C 157	Н 249	N 39	O 50	S 1	0	3	0

• Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	Н	2	Total Na 2 2	0	0

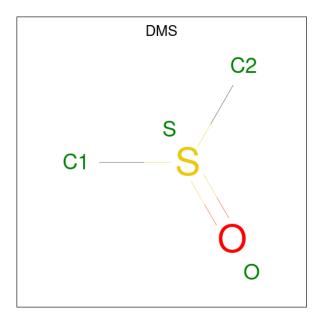
• Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	Н	1	Total 5	0 4	Р 1	0	0

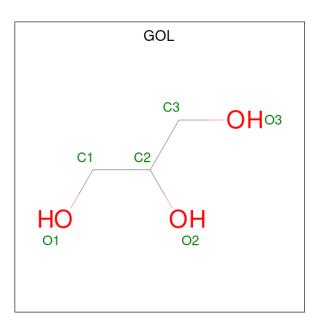
• Molecule 6 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



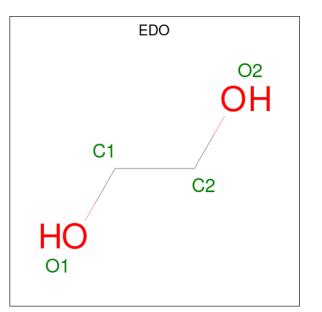
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	Н	1	$\begin{array}{cccc} \text{Total} & \text{C} & \text{O} & \text{S} \\ 8 & 4 & 2 & 2 \end{array}$	0	1
6	Н	1	$\begin{array}{cccc} \text{Total} & \text{C} & \text{O} & \text{S} \\ 8 & 4 & 2 & 2 \end{array}$	0	1

• Molecule 7 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	Н	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
7	Н	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
7	Н	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0



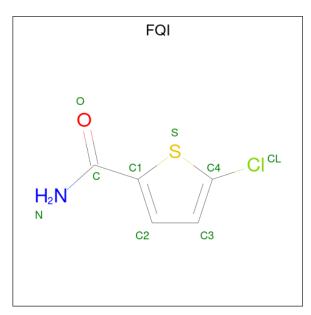
Mol	Chain	Residues	Ato	oms		ZeroOcc	AltConf
8	Н	1	Total 4	$\begin{array}{c} \mathrm{C} \\ \mathrm{2} \end{array}$	O 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	Η	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 4 & 2 & 2 \end{array}$	0	0

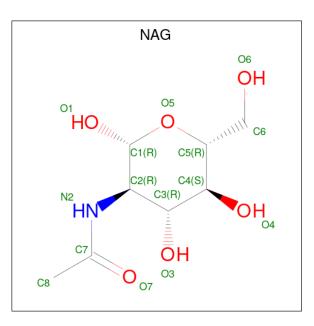
• Molecule 9 is 5-CHLORO-2-THIOPHENECARBOXAMIDE (three-letter code: FQI) (formula: C₅H₄ClNOS).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf			
9	Н	1	Total 9		Cl 1			S 1	0	0

• Molecule 10 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	Н	1	Total C N O 14 8 1 5	0	0

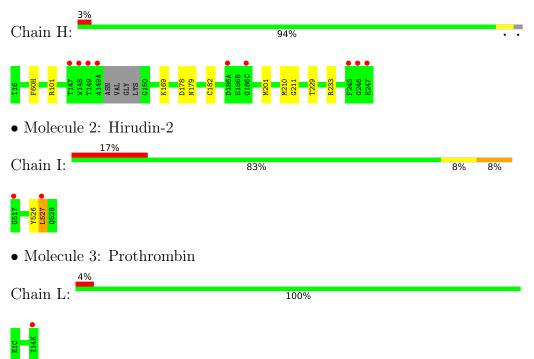
• Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	Н	254	Total O 255 255	0	1
11	Ι	5	$\begin{array}{cc} \text{Total} & \text{O} \\ 5 & 5 \end{array}$	0	0
11	L	32	Total O 32 32	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: Thrombin heavy chain



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	70.11Å 71.36Å 72.10Å	Depositor
a, b, c, α , β , γ	90.00° 100.38° 90.00°	Depositor
Resolution (Å)	35.68 - 1.12	Depositor
Resolution (A)	49.59 - 1.12	EDS
% Data completeness	96.7 (35.68-1.12)	Depositor
(in resolution range)	96.7(49.59-1.12)	EDS
R _{merge}	0.04	Depositor
R _{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.14 (at 1.12 \text{\AA})$	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
D D.	0.125 , 0.141	Depositor
R, R_{free}	0.128 , 0.142	DCC
R_{free} test set	6392 reflections $(5.00%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	12.6	Xtriage
Anisotropy	0.299	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for twinning ²	$ L > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	5087	wwPDB-VP
Average B, all atoms $(Å^2)$	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.49% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: EDO, TYS, DMS, PO4, NAG, FQI, GOL, NA

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		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	Н	0.49	0/2206	0.68	0/2984	
2	Ι	0.32	0/76	1.45	1/101~(1.0%)	
3	L	0.49	0/255	0.68	0/337	
All	All	0.49	0/2537	0.71	1/3422~(0.0%)	

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
2	Ι	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

\mathbf{N}	lol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
	2	Ι	527	LEU	O-C-N	-14.04	100.24	122.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Ι	527	LEU	Mainchain

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



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	Н	2112	2023	2071	9	0
2	Ι	92	0	69	0	0
3	L	247	249	251	0	0
4	Н	2	0	0	0	0
5	Н	5	0	0	0	0
6	Н	16	0	24	0	0
7	Н	18	0	24	3	0
8	Н	8	0	12	2	0
9	Н	9	0	4	0	0
10	Н	14	0	13	0	0
11	Н	255	0	0	1	0
11	Ι	5	0	0	0	0
11	L	32	0	0	0	0
All	All	2815	2272	2468	9	0

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.

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 2.

All (9) 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:H:169[A]:LYS:CE	8:H:1256:EDO:H11	2.06	0.85
1:H:101:ARG:HE	7:H:1254:GOL:H31	1.64	0.62
1:H:169[A]:LYS:HG3	11:H:2178:HOH:O	2.10	0.52
1:H:178:ASP:O	1:H:233:ARG:HD3	2.14	0.48
1:H:60(H):PHE:CE1	8:H:1255:EDO:H21	2.49	0.47
1:H:101:ARG:HE	7:H:1254:GOL:H11	1.80	0.46
1:H:201:MET:SD	1:H:210:MET:HG3	2.57	0.45
1:H:211:GLY:HA2	1:H:229:THR:O	2.17	0.44
1:H:179:ASN:HD21	7:H:1254:GOL:H11	1.84	0.43

There are no symmetry-related clashes.

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	Η	264/259~(102%)	255~(97%)	9~(3%)	0	100	100	
2	Ι	9/12~(75%)	9 (100%)	0	0	100	100	
3	L	29/28~(104%)	28~(97%)	1 (3%)	0	100	100	
All	All	302/299~(101%)	292 (97%)	10 (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	Rotameric Outliers	
1	Н	224/225~(100%)	223~(100%)	1 (0%)	91 74
2	Ι	6/10~(60%)	6 (100%)	0	100 100
3	L	27/26~(104%)	27~(100%)	0	100 100
All	All	257/261~(98%)	256 (100%)	1 (0%)	91 74

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	Н	182	CYS

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.



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

1 non-standard protein/DNA/RNA residue is 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	Dog	Link Bond lengths			Bond angles			
WIOI	туре	Ullalli	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2
2	TYS	Ι	526	2	$15,\!16,\!17$	1.62	2 (13%)	18,22,24	1.02	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
2	TYS	Ι	526	2	-	0/10/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	Ι	526	TYS	OH-S	-4.32	1.51	1.58
2	Ι	526	TYS	CE1-CD1	2.80	1.43	1.38

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
2	Ι	526	TYS	OH-S-01	-2.59	100.15	107.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.



5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 2 are monoatomic - leaving 12 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	Trune	Chain	Res	Link	Bo	ond leng	ths	B	ond ang	les
IVIOI	Type	Unam	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
10	NAG	Н	1258	1	14,14,15	1.95	5 (35%)	17,19,21	1.02	0
6	DMS	Н	1250[A]	-	3,3,3	0.61	0	3,3,3	0.44	0
7	GOL	Н	1252	-	$5,\!5,\!5$	0.31	0	$5,\!5,\!5$	0.56	0
9	FQI	Н	1257	-	6,9,9	0.46	0	3,12,12	1.15	0
8	EDO	Н	1256	-	3,3,3	0.46	0	2,2,2	0.33	0
6	DMS	Н	1251[B]	-	3,3,3	0.63	0	3,3,3	0.37	0
7	GOL	Н	1254	-	$5,\!5,\!5$	0.37	0	5, 5, 5	0.37	0
6	DMS	Н	1250[B]	-	3,3,3	0.66	0	3,3,3	0.58	0
5	PO4	Н	1249	-	4,4,4	1.12	0	6,6,6	1.69	2 (33%)
8	EDO	Н	1255	-	3,3,3	0.52	0	2,2,2	0.22	0
7	GOL	Н	1253	-	$5,\!5,\!5$	0.33	0	5, 5, 5	0.23	0
6	DMS	Н	1251[A]	-	3,3,3	0.54	0	3,3,3	0.42	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
10	NAG	Н	1258	1	-	2/6/23/26	0/1/1/1
7	GOL	Н	1252	-	-	0/4/4/4	-
9	FQI	Н	1257	-	-	0/0/4/4	0/1/1/1
8	EDO	Н	1256	-	-	0/1/1/1	-
7	GOL	Η	1254	-	-	2/4/4/4	-
8	EDO	Н	1255	-	-	1/1/1/1	-
7	GOL	Н	1253	-	_	2/4/4/4	_

All (5) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$Observed(\text{\AA})$	Ideal(Å)
10	Н	1258	NAG	C7-N2	4.14	1.48	1.34
10	Н	1258	NAG	C4-C3	-3.20	1.44	1.52
10	Н	1258	NAG	O5-C5	3.04	1.49	1.43
10	Н	1258	NAG	C3-C2	-2.31	1.47	1.52
10	Н	1258	NAG	C6-C5	-2.01	1.45	1.51

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
5	Н	1249	PO4	04-P-01	-2.85	100.46	110.89
5	Н	1249	PO4	O3-P-O2	2.45	115.84	107.97

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
7	Н	1254	GOL	C1-C2-C3-O3
7	Н	1254	GOL	O2-C2-C3-O3
7	Н	1253	GOL	C1-C2-C3-O3
7	Н	1253	GOL	O2-C2-C3-O3
10	Н	1258	NAG	O5-C5-C6-O6
10	Н	1258	NAG	C4-C5-C6-O6
8	Н	1255	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	Н	1256	EDO	1	0
7	Н	1254	GOL	3	0
8	Н	1255	EDO	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^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q<0.9
1	Н	255/259~(98%)	-0.01	9 (3%) 44 43	9, 16, 35, 58	0
2	Ι	11/12~(91%)	1.07	2(18%) 1 2	28, 33, 47, 48	0
3	L	28/28~(100%)	-0.08	1 (3%) 42 41	11, 14, 28, 36	0
All	All	294/299~(98%)	0.02	12 (4%) 37 35	9, 16, 38, 58	0

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Н	149	THR	9.5
1	Н	149(A)	ALA	6.8
1	Н	148	TRP	6.8
2	Ι	517	GLY	5.5
1	Н	147	THR	3.7
1	Н	246	GLY	3.0
2	Ι	527	LEU	2.7
1	Н	247	GLU	2.7
1	Н	186(A)	ASP	2.3
1	Н	245	PHE	2.1
1	Н	186(C)	GLY	2.1
3	L	14(K)	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (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^{th} 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
2	TYS	Ι	526	16/17	0.98	0.08	22,27,32,32	0



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^{th} 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
10	NAG	Н	1258	14/15	0.79	0.17	37,42,44,46	0
7	GOL	Н	1254	6/6	0.81	0.14	49,51,51,52	0
8	EDO	Н	1255	4/4	0.84	0.19	38,42,45,46	0
7	GOL	Н	1252	6/6	0.91	0.14	21,30,33,33	6
7	GOL	Н	1253	6/6	0.92	0.11	22,30,33,34	6
8	EDO	Н	1256	4/4	0.94	0.17	$23,\!27,\!29,\!30$	0
5	PO4	Н	1249	5/5	0.96	0.09	$17,\!17,\!19,\!19$	5
6	DMS	Н	1251[A]	4/4	0.97	0.09	$19,\!21,\!23,\!23$	4
6	DMS	Н	1251[B]	4/4	0.97	0.09	28,28,29,29	4
6	DMS	Н	1250[A]	4/4	0.99	0.09	$12,\!14,\!16,\!17$	4
6	DMS	Н	1250[B]	4/4	0.99	0.09	$35,\!36,\!36,\!36$	4
4	NA	Н	1248	1/1	1.00	0.08	$12,\!12,\!12,\!12$	0
9	FQI	Н	1257	9/9	1.00	0.07	$13,\!14,\!17,\!18$	0
4	NA	Н	1247	1/1	1.00	0.07	$14,\!14,\!14,\!14$	0

6.5 Other polymers (i)

There are no such residues in this entry.

