

Full wwPDB X-ray Structure Validation Report (i)

Sep 14, 2023 – 06:20 AM EDT

PDB ID	:	4MA8
Title	:	Crystal structure of mouse prion protein complexed with Chlorpromazine
Authors	:	Baral, P.K.; Swayampakula, M.; James, M.N.G.
Deposited on		
Resolution	:	2.20 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 (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:

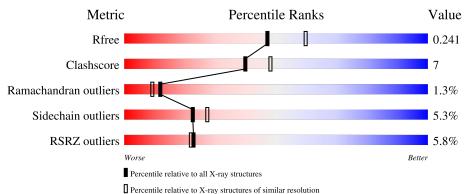
Xtriage (Phenix) EDS buster-report Percentile statistics Refmac CCP4 Ideal geometry (proteins) Ideal geometry (DNA, RNA)	: : : : :	20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove) Engh & Huber (2001) Parkinson et al. (1996)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.35.1

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 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	С	114	11% 69% 23%	•	5%
2	Н	218	4% 85%	12%	•
3	L	213	4% 86%	12%	•



4MA8

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 4649 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 Major prion protein.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	С	108	Total	С	Ν	Ο	\mathbf{S}	0	0	0
1	U	100	890	556	153	172	9	0		

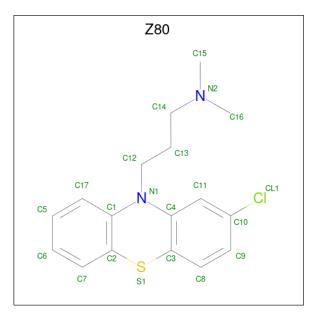
• Molecule 2 is a protein called POM1 heavy chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	Н	218	Total 1642	C 1037	N 265	O 330	S 10	0	0	0

• Molecule 3 is a protein called POM1 light chain.

]	Mol	Chain	Residues		Ate	oms			ZeroOcc	AltConf	Trace
	3	L	213	Total 1652	C 1022	N 280	0 345	${ m S}{ m 5}$	0	0	0

• Molecule 4 is 3-(2-chloro-10H-phenothiazin-10-yl)-N,N-dimethylpropan-1-amine (three-letter code: Z80) (formula: C₁₇H₁₉ClN₂S).





Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
4	С	1	Total 21	C 17		N 2	S 1	0	0

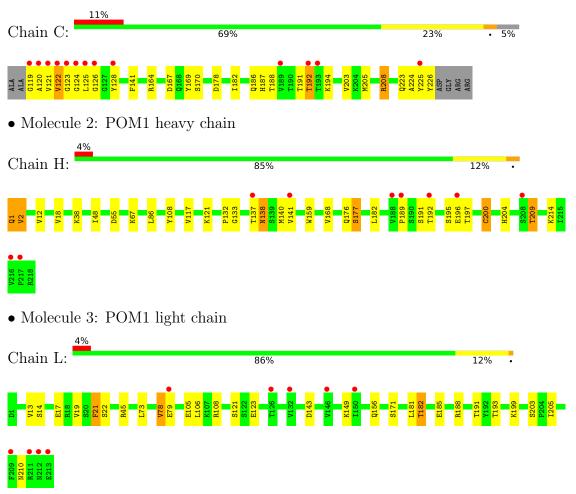
• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	С	90	Total O 90 90	0	0
5	Н	197	Total O 197 197	0	0
5	L	157	Total O 157 157	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: Major prion protein



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	83.26Å 106.88Å 75.59Å	Depositor
a, b, c, α , β , γ	90.00° 95.32° 90.00°	Depositor
Resolution (Å)	34.99 - 2.20	Depositor
	34.97 - 2.20	EDS
% Data completeness	97.2 (34.99-2.20)	Depositor
(in resolution range)	97.2(34.97-2.20)	EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.72 (at 2.20 \text{\AA})$	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.195 , 0.236	Depositor
It, It _{free}	0.198 , 0.241	DCC
R_{free} test set	1634 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	42.9	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.31 , 55.1	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	0.95	EDS
Total number of atoms	4649	wwPDB-VP
Average B, all atoms $(Å^2)$	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.68% 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: $\mathbf{Z80}$

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	Bo	nd lengths	Bond angles		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	С	0.46	0/911	0.70	2/1232~(0.2%)	
2	Н	0.46	0/1688	0.69	0/2306	
3	L	0.51	2/1687~(0.1%)	0.68	3/2291~(0.1%)	
All	All	0.48	2/4286~(0.0%)	0.69	5/5829~(0.1%)	

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	Observed(Å)	Ideal(Å)
3	L	79	GLU	CG-CD	7.83	1.63	1.51
3	L	79	GLU	CB-CG	5.45	1.62	1.52

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	С	208	ARG	NE-CZ-NH2	7.88	124.24	120.30
3	L	79	GLU	OE1-CD-OE2	-7.48	114.33	123.30
1	С	208	ARG	NE-CZ-NH1	-7.25	116.67	120.30
3	L	79	GLU	CG-CD-OE1	6.71	131.73	118.30
3	L	79	GLU	CA-CB-CG	6.69	128.11	113.40

All (5) bond angle outliers are listed below:

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	С	890	0	828	30	0
2	Н	1642	0	1578	16	0
3	L	1652	0	1573	14	0
4	С	21	0	19	4	0
5	С	90	0	0	0	0
5	Н	197	0	0	1	0
5	L	157	0	0	2	0
All	All	4649	0	3998	60	0

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 7.

All (60) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	A.t.a	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:C:123:GLY:O	1:C:125:LEU:CD1	1.64	1.41
1:C:124:GLY:CA	1:C:125:LEU:HB2	1.54	1.37
1:C:124:GLY:HA2	1:C:125:LEU:CB	1.53	1.29
1:C:123:GLY:C	1:C:125:LEU:HD12	1.75	1.06
1:C:123:GLY:O	1:C:125:LEU:HD12	0.76	0.93
1:C:123:GLY:O	1:C:125:LEU:CG	2.30	0.79
1:C:128:TYR:CE1	1:C:182:ILE:HD13	2.21	0.76
2:H:137:THR:O	2:H:138:ASN:HB2	1.85	0.75
1:C:208:ARG:HD2	2:H:55:ASP:OD2	1.88	0.72
1:C:122:VAL:HG12	1:C:122:VAL:O	1.96	0.65
1:C:124:GLY:HA2	1:C:125:LEU:HB2	0.73	0.63
1:C:223:GLN:O	1:C:225:TYR:N	2.30	0.63
1:C:188:THR:O	1:C:192:THR:HG23	1.98	0.62
1:C:128:TYR:CD1	1:C:164:ARG:HG2	2.35	0.62
1:C:124:GLY:CA	1:C:125:LEU:CB	2.37	0.59
3:L:21:PHE:CE1	3:L:73:LEU:HD23	2.37	0.58
3:L:45:ARG:NH1	5:L:380:HOH:O	2.36	0.58
2:H:159:TRP:CZ3	2:H:200:CYS:HB3	2.39	0.58
1:C:169:TYR:OH	1:C:178:ASP:OD1	2.19	0.57
2:H:196:GLU:HG2	2:H:197:THR:N	2.20	0.56
2:H:137:THR:O	2:H:138:ASN:CB	2.51	0.55
1:C:186:GLN:HB2	4:C:301:Z80:CL1	2.44	0.54
3:L:191:THR:HG22	3:L:210:ASN:OD1	2.08	0.54
2:H:12:VAL:HG11	2:H:86:LEU:CD1	2.38	0.53
2:H:18:VAL:HG12	2:H:86:LEU:HD11	1.91	0.53
3:L:182:THR:HG23	3:L:185:GLU:HB2	1.92	0.52
2:H:197:THR:HG23	2:H:214:LYS:HE3	1.91	0.52

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Ato 1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:C:187:HIS:O	1:C:191:THR:HG23	2.11	0.51
3:L:182:THR:HG23	3:L:185:GLU:CB	2.40	0.51
4:C:301:Z80:C13	4:C:301:Z80:H5	2.41	0.51
1:C:128:TYR:CE1	1:C:164:ARG:HG2	2.46	0.51
2:H:38:LYS:HB2	2:H:48:ILE:HD11	1.94	0.50
1:C:119:GLY:O	1:C:120:ALA:HB3	2.12	0.50
2:H:189:PRO:O	2:H:191:SER:O	2.30	0.49
1:C:125:LEU:HD21	4:C:301:Z80:C8	2.42	0.49
1:C:125:LEU:HD22	1:C:128:TYR:HB2	1.94	0.48
1:C:125:LEU:HD23	1:C:126:GLY:HA3	1.95	0.47
1:C:121:VAL:HG23	1:C:122:VAL:N	2.29	0.47
1:C:128:TYR:CE1	1:C:182:ILE:CD1	2.94	0.47
3:L:108:ARG:HD2	3:L:171:SER:O	2.15	0.46
1:C:128:TYR:CE1	1:C:164:ARG:CG	2.99	0.46
3:L:13:VAL:HG11	3:L:19:VAL:HG11	1.99	0.45
3:L:185:GLU:HA	3:L:188:ARG:HD3	1.99	0.45
1:C:125:LEU:HD13	1:C:128:TYR:HB2	1.99	0.44
1:C:141:PHE:CZ	1:C:205:MET:HG2	2.52	0.44
3:L:105:GLU:HG2	3:L:106:LEU:N	2.31	0.44
3:L:205:ILE:HA	5:L:435:HOH:O	2.19	0.43
2:H:67:LYS:NZ	5:H:376:HOH:O	2.39	0.43
3:L:121:SER:HB2	3:L:123:GLU:HG2	2.01	0.43
2:H:2:VAL:HG13	2:H:108:TYR:CZ	2.54	0.42
3:L:14:SER:O	3:L:17:GLU:HB3	2.19	0.42
1:C:167:ASP:OD1	1:C:167:ASP:N	2.52	0.42
1:C:124:GLY:N	1:C:125:LEU:HB2	2.25	0.42
2:H:12:VAL:HG21	2:H:86:LEU:HD12	2.02	0.41
2:H:1:GLN:H3	2:H:1:GLN:CD	2.24	0.41
2:H:204:HIS:HB3	2:H:209:THR:HB	2.03	0.41
1:C:186:GLN:HE21	4:C:301:Z80:C10	2.34	0.40
3:L:78:VAL:O	3:L:78:VAL:CG2	2.69	0.40
2:H:176:GLN:O	2:H:177:SER:CB	2.70	0.40
3:L:149:LYS:HB2	3:L:193:THR:OG1	2.21	0.40

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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	\mathbf{C}	106/114~(93%)	100 (94%)	4 (4%)	2(2%)	8 5
2	Η	216/218~(99%)	208 (96%)	3~(1%)	5(2%)	6 3
3	L	211/213~(99%)	205~(97%)	6 (3%)	0	100 100
All	All	533/545~(98%)	513 (96%)	13 (2%)	7 (1%)	12 9

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	С	224	ALA
1	С	122	VAL
2	Н	133	GLY
2	Н	177	SER
2	Н	138	ASN
2	Н	192	THR
2	Н	132	PRO

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	Perce	ntiles
1	С	97/100~(97%)	92~(95%)	5 (5%)	23	28
2	Н	187/187~(100%)	176~(94%)	11 (6%)	19	23
3	L	191/191 (100%)	182 (95%)	9~(5%)	26	33
All	All	475/478 (99%)	450 (95%)	25~(5%)	22	27



Mol	Chain	Res	Type
1	С	170	SER
1	C C C C C	192	THR
1	С	194	LYS
1	С	203	VAL
1		226	TYR
$\begin{array}{c} 2\\ 2 \end{array}$	Н	1	GLN
	Н	2	VAL
2	Н	117	VAL
2	Н	121	LYS
2	Н	140	MET
2	Н	141	VAL
2	Н	168	VAL
2	Н	182	LEU
$\begin{array}{c} 2\\ 2 \end{array}$	Н	195	SER
	Н	200	CYS
2	Н	209	THR
3	L	21	PHE
3	L	22	SER
3	L	78	VAL
3	L	143	ASP
3	L	156	GLN
3	L	181	LEU
3	L	182	THR
3	L	199	LYS
3	L	203	SER

All (25) residues with a non-rotameric sidechain are listed below:

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	С	160	GLN
1	С	168	GLN
1	С	186	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand 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	Res	Link	Bo	ond leng	ths	B	ond ang	les
VIOI	Type	Ullalli	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	Z80	С	301	-	23,23,23	1.48	4 (17%)	32,32,32	1.38	2 (6%)

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	Z80	С	301	-	-	1/6/18/18	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\operatorname{Observed}(\operatorname{\AA})$	$\mathrm{Ideal}(\mathrm{\AA})$
4	С	301	Z80	C10-CL1	-4.09	1.65	1.74
4	С	301	Z80	C1-N1	-3.22	1.35	1.40
4	С	301	Z80	C2-S1	2.94	1.81	1.76
4	С	301	Z80	C4-N1	-2.93	1.35	1.40

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
4	С	301	Z80	C12-N1-C1	5.05	125.61	119.03
4	С	301	Z80	C12-N1-C4	-2.68	115.54	119.03

There are no chirality outliers.



All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	С	301	Z80	N1-C12-C13-C14

There are no ring outliers.

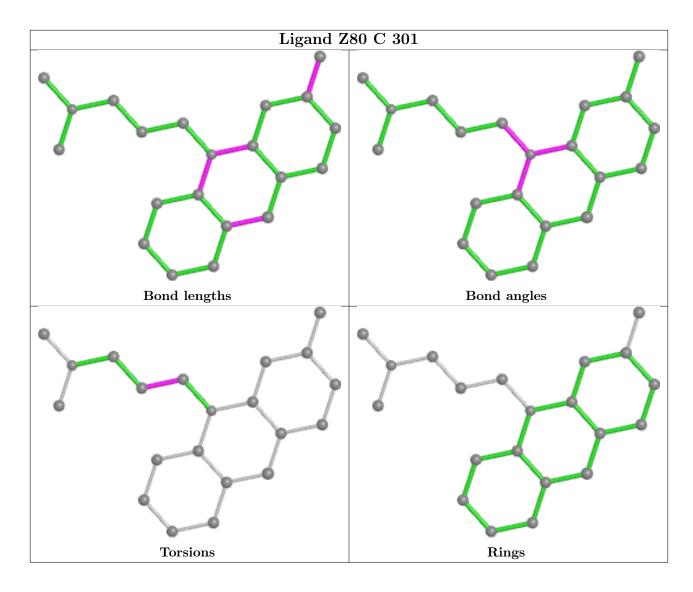
1 monomer is involved in 4 short contacts:

\mathbf{Mol}	Chain	Res	Type	Clashes	Symm-Clashes
4	С	301	Z80	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.







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	<RSRZ $>$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	С	108/114~(94%)	0.58	13 (12%) 4 3	30, 52, 90, 121	7 (6%)
2	Н	218/218~(100%)	0.16	9 (4%) 37 35	29, 52, 93, 126	0
3	L	213/213~(100%)	0.16	9 (4%) 36 34	30, 61, 125, 156	0
All	All	539/545~(98%)	0.25	31 (5%) 23 22	29, 55, 107, 156	7 (1%)

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	С	122	VAL	11.9
1	С	125	LEU	10.3
1	С	124	GLY	8.6
1	С	119	GLY	5.4
1	С	123	GLY	4.5
1	С	121	VAL	4.3
3	L	150	ILE	3.9
2	Н	188	VAL	3.8
3	L	213	GLU	3.5
2	Н	141	VAL	3.4
3	L	212	ASN	3.2
2	Н	196	GLU	3.1
1	С	128	TYR	2.9
1	С	126	GLY	2.9
2	Н	217	PRO	2.7
2	Н	137	THR	2.6
2	Н	189	PRO	2.5
1	С	120	ALA	2.5
3	L	126	THR	2.5
1	С	189	VAL	2.4
1	С	193	THR	2.4
2	Н	208	SER	2.4
3	L	211	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	С	225	TYR	2.3
3	L	146	VAL	2.2
3	L	79	GLU	2.1
1	С	192	THR	2.1
2	Н	216	VAL	2.1
3	L	132	VAL	2.1
2	Н	192	THR	2.0
3	L	209	PHE	2.0

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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.

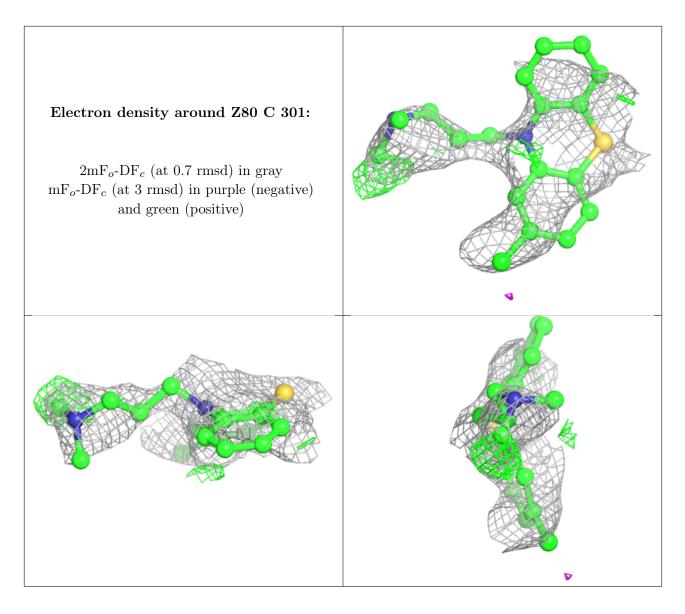
6.4 Ligands (i)

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, 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	$\mathbf{B} ext{-factors}(\mathbf{A}^2)$	Q < 0.9
4	Z80	С	301	21/21	0.70	0.38	$97,\!114,\!120,\!125$	21

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers (i)

There are no such residues in this entry.

