Full wwPDB X-ray Structure Validation Report (i)

May 16, 2020 – 07:12 am BST

PDB ID	:	5NQE
Title	:	Human PARP14 (ARTD8), catalytic fragment in complex with an N-aryl piperazine inhibitor
Authors	:	Karlberg, T.; Thorsell, A.G.; Schuler, H.
Deposited on	:	2017-04-20
Resolution	:	2.71 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 following versions of software and data (see references (i)) were used in the production of this report:

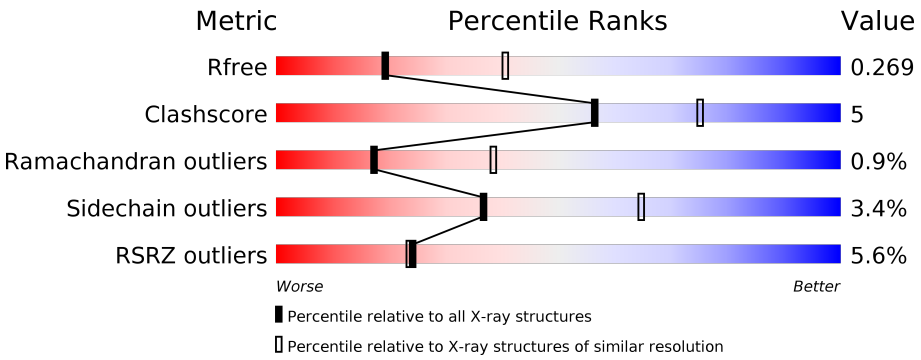
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.71 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	3359 (2.74-2.70)
Clashscore	141614	3686 (2.74-2.70)
Ramachandran outliers	138981	3622 (2.74-2.70)
Sidechain outliers	138945	3623 (2.74-2.70)
RSRZ outliers	127900	3276 (2.74-2.70)

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 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	193	3% 81% 11% • 7%
1	B	193	7% 76% 16% • 7%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3005 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.

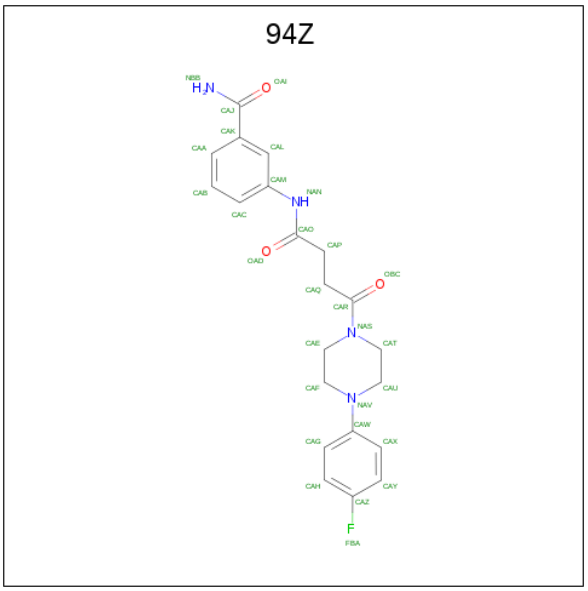
- Molecule 1 is a protein called Poly [ADP-ribose] polymerase 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	180	1465	925	260	275	5	0	0	0
1	B	180	1465	925	260	275	5	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1609	SER	-	expression tag	UNP Q460N5
A	1610	MET	-	expression tag	UNP Q460N5
B	1609	SER	-	expression tag	UNP Q460N5
B	1610	MET	-	expression tag	UNP Q460N5

- Molecule 2 is 3-[[4-[4-(4-fluorophenyl)piperazin-1-yl]-4-oxidanylidene-butanoyl]amino]benzamide (three-letter code: 94Z) (formula: $C_{21}H_{23}FN_4O_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
2	A	1	29	21	1	4	3	0	0
			Total	C	F	N	O		
2	B	1	29	21	1	4	3	0	0

- Molecule 3 is water.

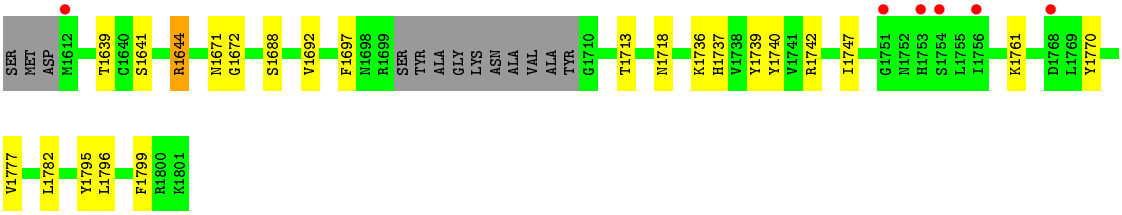
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	7	7	7	0	0
			Total	O		
3	B	10	10	10	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

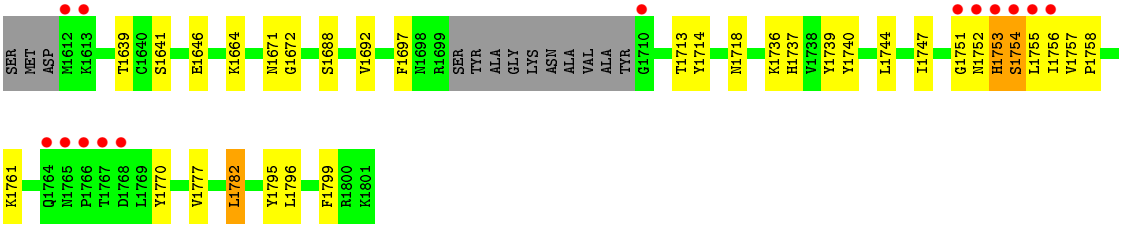
- Molecule 1: Poly [ADP-ribose] polymerase 14

Chain A:



- Molecule 1: Poly [ADP-ribose] polymerase 14

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	83.43Å 90.36Å 80.07Å 90.00° 116.42° 90.00°	Depositor
Resolution (Å)	45.18 – 2.71 45.18 – 2.71	Depositor EDS
% Data completeness (in resolution range)	99.4 (45.18-2.71) 99.3 (45.18-2.71)	Depositor EDS
R_{merge}	0.29	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.32 (at 2.73Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.227 , 0.258 0.236 , 0.269	Depositor DCC
R_{free} test set	724 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	37.0	Xtriage
Anisotropy	0.459	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 40.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	3005	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.83% 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: 94Z

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	0.48	0/1506	0.70	0/2045
1	B	0.49	0/1506	0.74	2/2045 (0.1%)
All	All	0.48	0/3012	0.72	2/4090 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	1754	SER	N-CA-CB	-9.98	95.53	110.50
1	B	1753	HIS	N-CA-C	5.27	125.22	111.00

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	1465	0	1392	12	0
1	B	1465	0	1392	17	0
2	A	29	0	0	0	0
2	B	29	0	0	4	0
3	A	7	0	0	0	0
3	B	10	0	0	0	0
All	All	3005	0	2784	29	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 5.

All (29) 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:1644:ARG:HG3	1:A:1644:ARG:HH21	1.40	0.87
1:B:1751:GLY:O	2:B:1901:94Z:FBA	1.87	0.83
1:B:1664:LYS:HG3	1:B:1744:LEU:HD21	1.78	0.65
1:B:1752:ASN:OD1	1:B:1755:LEU:HG	1.99	0.62
1:B:1697:PHE:HB3	1:B:1713:THR:HG21	1.82	0.61
1:A:1697:PHE:HB3	1:A:1713:THR:HG21	1.84	0.60
1:B:1751:GLY:O	2:B:1901:94Z:CAZ	2.53	0.57
1:B:1736:LYS:HE3	1:B:1799:PHE:CE2	2.39	0.56
1:A:1736:LYS:HE3	1:A:1799:PHE:CE2	2.40	0.55
1:B:1688:SER:O	1:B:1692:VAL:HG23	2.06	0.55
1:B:1757:VAL:HB	1:B:1758:PRO:HD2	1.89	0.54
1:B:1782:LEU:HD11	2:B:1901:94Z:CAG	2.39	0.52
1:B:1664:LYS:CG	1:B:1744:LEU:HD21	2.40	0.50
1:A:1644:ARG:HG3	1:A:1644:ARG:NH2	2.19	0.50
1:B:1671:ASN:OD1	1:B:1747:ILE:HD12	2.12	0.49
1:A:1639:THR:HG21	1:A:1718:ASN:HB3	1.95	0.48
1:A:1644:ARG:CG	1:A:1644:ARG:HH21	2.18	0.48
1:B:1639:THR:HG21	1:B:1718:ASN:HB3	1.96	0.48
1:A:1671:ASN:OD1	1:A:1747:ILE:HD12	2.14	0.47
1:B:1761:LYS:HE3	1:B:1770:TYR:HA	1.97	0.46
1:A:1688:SER:O	1:A:1692:VAL:HG23	2.15	0.46
1:A:1739:TYR:HA	1:A:1795:TYR:O	2.16	0.45
1:B:1739:TYR:HA	1:B:1795:TYR:O	2.16	0.45
1:B:1737:HIS:HB3	1:B:1796:LEU:HD11	2.00	0.43
1:A:1737:HIS:HB3	1:A:1796:LEU:HD11	2.01	0.42
1:A:1761:LYS:HE3	1:A:1770:TYR:HA	2.00	0.42
1:A:1740:TYR:HB3	1:A:1795:TYR:HB2	2.01	0.42
1:B:1740:TYR:HB3	1:B:1795:TYR:HB2	2.02	0.42
1:B:1714:TYR:HB3	2:B:1901:94Z:CAC	2.49	0.42

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	A	176/193 (91%)	173 (98%)	2 (1%)	1 (1%)	25	48
1	B	176/193 (91%)	171 (97%)	3 (2%)	2 (1%)	14	32
All	All	352/386 (91%)	344 (98%)	5 (1%)	3 (1%)	17	38

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1753	HIS
1	A	1672	GLY
1	B	1672	GLY

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	161/170 (95%)	156 (97%)	5 (3%)	40	68
1	B	161/170 (95%)	155 (96%)	6 (4%)	34	61
All	All	322/340 (95%)	311 (97%)	11 (3%)	37	65

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1641	SER
1	A	1644	ARG
1	A	1742	ARG

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Mol	Chain	Res	Type
1	A	1777	VAL
1	A	1782	LEU
1	B	1641	SER
1	B	1646	GLU
1	B	1754	SER
1	B	1756	ILE
1	B	1777	VAL
1	B	1782	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1615	GLN
1	B	1691	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

2 ligands are 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	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	94Z	A	1901	-	31,31,31	3.38	15 (48%)	42,42,42	2.83	18 (42%)
2	94Z	B	1901	-	31,31,31	3.35	15 (48%)	42,42,42	2.86	16 (38%)

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	94Z	A	1901	-	-	1/21/31/31	0/3/3/3
2	94Z	B	1901	-	-	8/21/31/31	0/3/3/3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1901	94Z	CAK-CAJ	-11.81	1.32	1.50
2	A	1901	94Z	CAK-CAJ	-11.13	1.33	1.50
2	B	1901	94Z	FBA-CAZ	-6.43	1.20	1.36
2	A	1901	94Z	FBA-CAZ	-6.22	1.21	1.36
2	A	1901	94Z	CAM-NAN	-5.89	1.29	1.41
2	A	1901	94Z	CAP-CAO	-5.72	1.40	1.51
2	B	1901	94Z	CAP-CAO	-5.21	1.41	1.51
2	A	1901	94Z	OAI-CAJ	-5.02	1.14	1.24
2	B	1901	94Z	OAI-CAJ	-4.91	1.14	1.24
2	B	1901	94Z	CAM-NAN	-4.89	1.31	1.41
2	B	1901	94Z	CAC-CAM	4.12	1.46	1.39
2	A	1901	94Z	CAQ-CAR	-3.90	1.43	1.51
2	A	1901	94Z	CAO-NAN	-3.89	1.27	1.35
2	B	1901	94Z	CAQ-CAR	-3.56	1.43	1.51
2	A	1901	94Z	CAF-NAV	3.20	1.51	1.46
2	A	1901	94Z	CAP-CAQ	-2.63	1.43	1.52
2	A	1901	94Z	CAL-CAM	-2.59	1.35	1.39
2	A	1901	94Z	OAD-CAO	-2.54	1.18	1.23
2	B	1901	94Z	CAL-CAK	-2.52	1.35	1.39
2	B	1901	94Z	CAL-CAM	-2.50	1.35	1.39
2	A	1901	94Z	CAL-CAK	-2.46	1.35	1.39
2	B	1901	94Z	OAD-CAO	-2.42	1.18	1.23
2	B	1901	94Z	CAO-NAN	-2.38	1.30	1.35
2	B	1901	94Z	CAP-CAQ	-2.36	1.44	1.52
2	A	1901	94Z	CAH-CAZ	2.24	1.41	1.37
2	B	1901	94Z	CAF-NAV	2.19	1.50	1.46
2	B	1901	94Z	CAH-CAZ	2.16	1.41	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1901	94Z	CAC-CAM	2.13	1.42	1.39
2	A	1901	94Z	CAU-NAV	2.12	1.50	1.46
2	B	1901	94Z	CAY-CAZ	2.06	1.41	1.37

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1901	94Z	CAQ-CAR-NAS	9.69	133.14	118.01
2	B	1901	94Z	OBC-CAR-CAQ	-8.52	97.05	121.31
2	B	1901	94Z	CAQ-CAR-NAS	8.08	130.62	118.01
2	A	1901	94Z	OBC-CAR-CAQ	-6.57	102.61	121.31
2	B	1901	94Z	CAP-CAQ-CAR	5.71	132.66	111.92
2	A	1901	94Z	CAP-CAQ-CAR	4.60	128.62	111.92
2	A	1901	94Z	CAU-CAT-NAS	-4.49	100.82	110.44
2	A	1901	94Z	CAL-CAM-NAN	-4.43	105.71	120.18
2	B	1901	94Z	CAL-CAM-NAN	-4.30	106.16	120.18
2	B	1901	94Z	OAI-CAJ-CAK	-4.16	114.66	119.63
2	A	1901	94Z	CAQ-CAP-CAO	4.13	119.80	112.56
2	A	1901	94Z	CAU-NAV-CAF	4.03	120.42	111.52
2	B	1901	94Z	CAQ-CAP-CAO	3.98	119.53	112.56
2	B	1901	94Z	CAU-NAV-CAF	3.95	120.23	111.52
2	B	1901	94Z	CAK-CAJ-NBB	3.58	122.05	117.75
2	A	1901	94Z	CAP-CAO-NAN	-3.46	108.49	114.59
2	B	1901	94Z	CAU-CAT-NAS	-3.42	103.11	110.44
2	A	1901	94Z	CAC-CAM-NAN	3.25	131.32	120.40
2	A	1901	94Z	OAI-CAJ-CAK	-3.24	115.76	119.63
2	B	1901	94Z	CAC-CAM-NAN	3.23	131.25	120.40
2	B	1901	94Z	OAD-CAO-NAN	3.11	129.30	123.63
2	A	1901	94Z	CAK-CAJ-NBB	3.10	121.47	117.75
2	B	1901	94Z	CAF-CAE-NAS	3.04	116.95	110.44
2	A	1901	94Z	OAD-CAO-NAN	3.00	129.09	123.63
2	A	1901	94Z	CAC-CAM-CAL	2.75	122.91	119.65
2	A	1901	94Z	CAY-CAZ-CAH	-2.59	119.38	122.83
2	B	1901	94Z	CAC-CAM-CAL	2.46	122.57	119.65
2	B	1901	94Z	CAY-CAZ-CAH	-2.43	119.60	122.83
2	A	1901	94Z	CAB-CAC-CAM	-2.26	117.02	119.72
2	B	1901	94Z	CAP-CAO-NAN	-2.22	110.69	114.59
2	A	1901	94Z	FBA-CAZ-CAH	2.21	122.30	118.54
2	A	1901	94Z	CAE-NAS-CAR	2.13	129.77	122.81
2	A	1901	94Z	CAY-CAX-CAW	2.01	122.97	120.32
2	B	1901	94Z	FBA-CAZ-CAH	2.00	121.94	118.54

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1901	94Z	CAQ-CAR-NAS-CAE
2	B	1901	94Z	CAQ-CAR-NAS-CAT
2	B	1901	94Z	CAP-CAQ-CAR-NAS
2	B	1901	94Z	OAI-CAJ-CAK-CAA
2	B	1901	94Z	CAO-CAP-CAQ-CAR
2	B	1901	94Z	OAI-CAJ-CAK-CAL
2	B	1901	94Z	NBB-CAJ-CAK-CAA
2	B	1901	94Z	NBB-CAJ-CAK-CAL
2	A	1901	94Z	CAO-CAP-CAQ-CAR

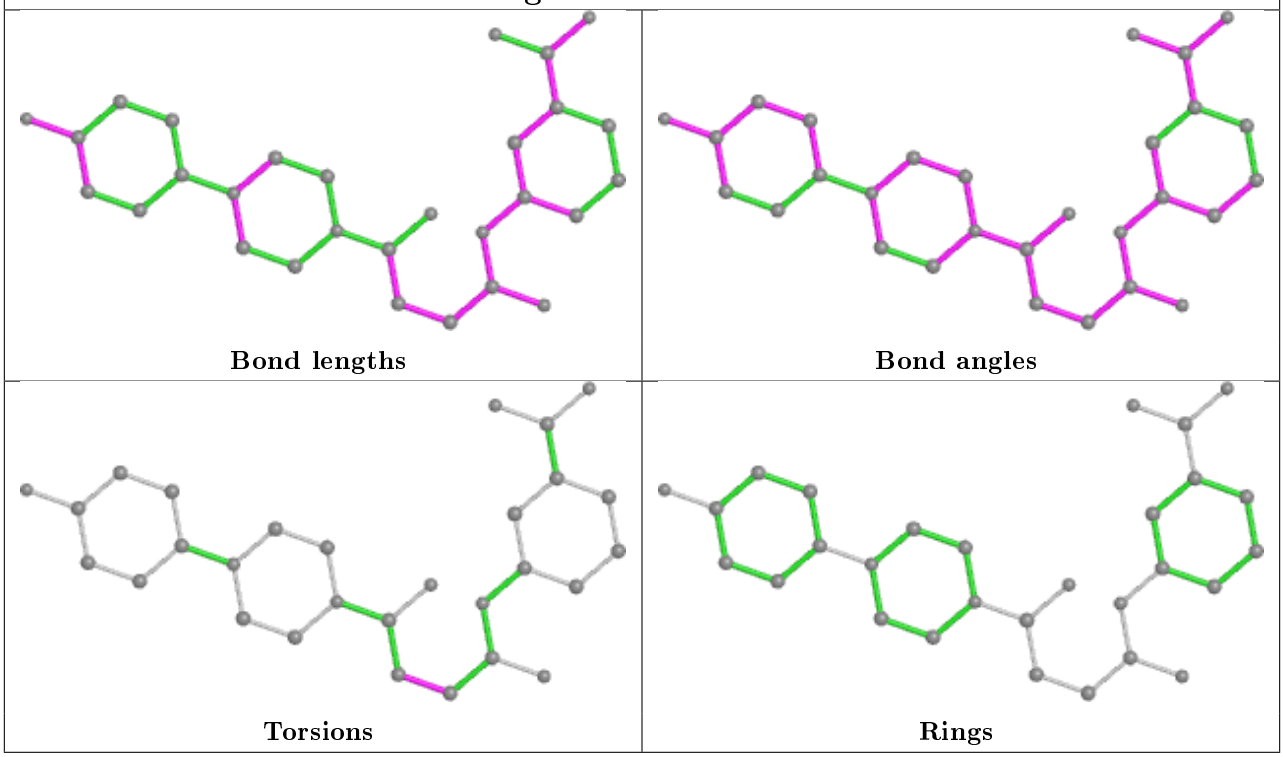
There are no ring outliers.

1 monomer is involved in 4 short contacts:

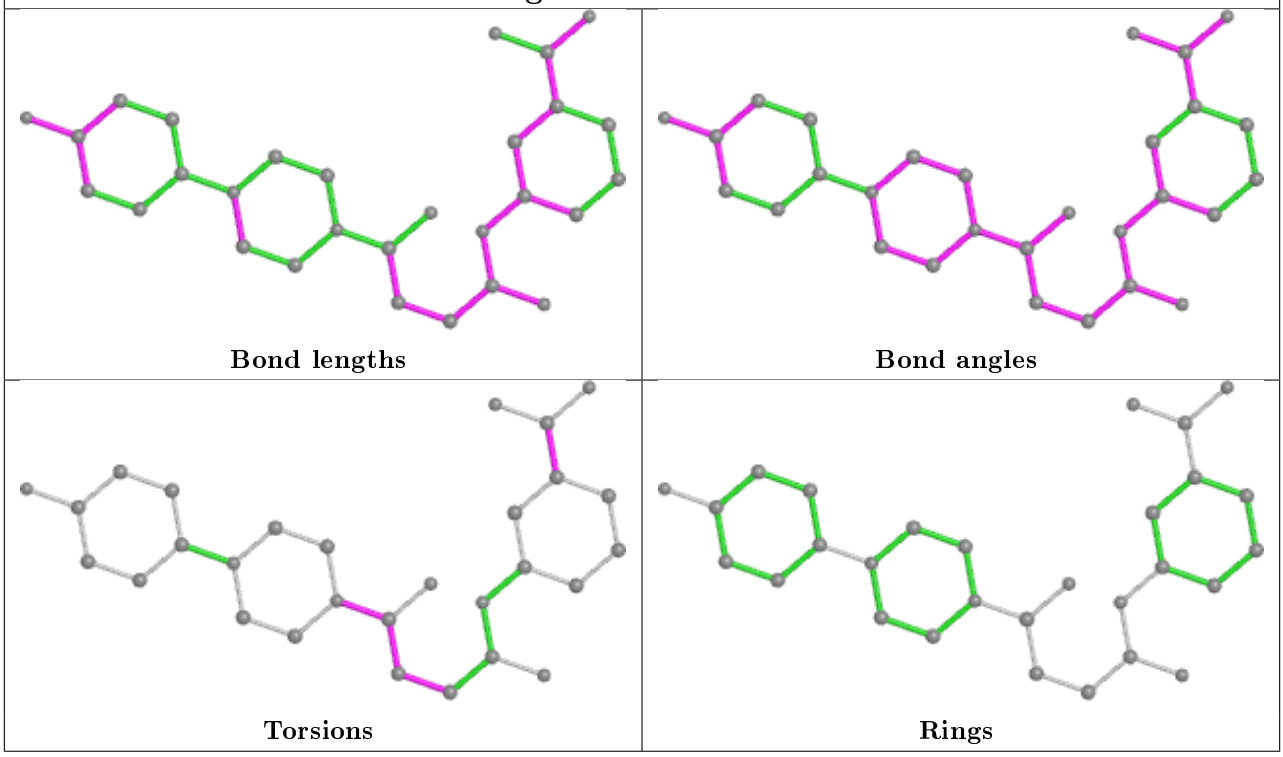
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1901	94Z	4	0

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.

Ligand 94Z A 1901



Ligand 94Z B 1901



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	180/193 (93%)	0.47	6 (3%)	46	47	18, 34, 75, 93	0
1	B	180/193 (93%)	0.61	14 (7%)	13	11	18, 34, 88, 104	0
All	All	360/386 (93%)	0.54	20 (5%)	24	23	18, 34, 82, 104	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1767	THR	6.8
1	B	1768	ASP	5.4
1	B	1751	GLY	4.5
1	B	1756	ILE	4.4
1	B	1612	MET	4.0
1	B	1613	LYS	3.8
1	A	1756	ILE	3.8
1	B	1753	HIS	3.7
1	A	1612	MET	3.4
1	A	1751	GLY	3.3
1	B	1752	ASN	3.2
1	B	1754	SER	3.0
1	B	1755	LEU	2.9
1	B	1766	PRO	2.8
1	A	1768	ASP	2.6
1	B	1710	GLY	2.6
1	B	1765	ASN	2.5
1	B	1764	GLN	2.3
1	A	1753	HIS	2.2
1	A	1754	SER	2.1

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 carbohydrates in this entry.

6.4 Ligands (i)

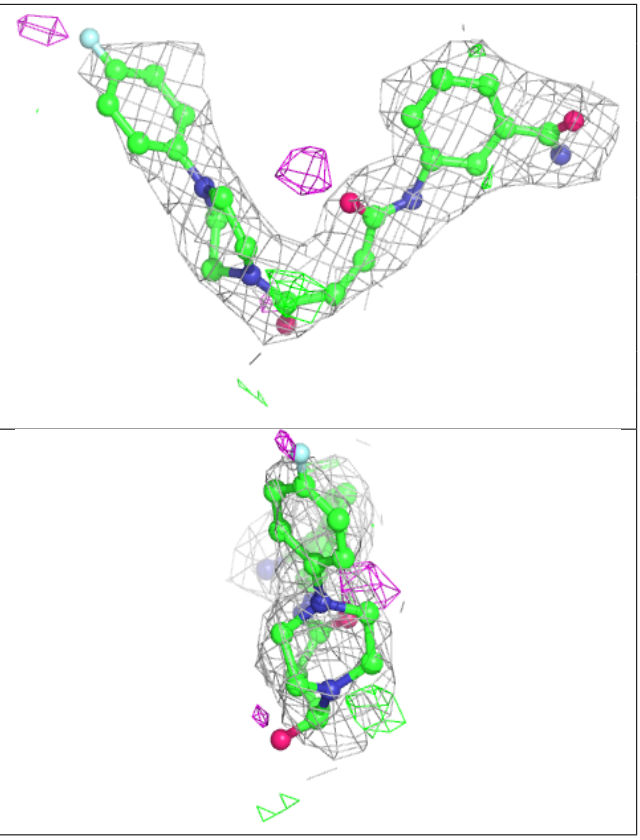
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

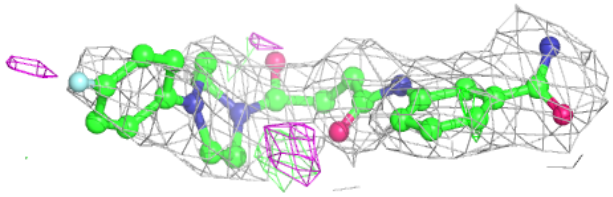
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	94Z	B	1901	29/29	0.86	0.29	25,57,75,77	0
2	94Z	A	1901	29/29	0.91	0.28	24,51,73,74	0

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.

Electron density around 94Z B 1901:

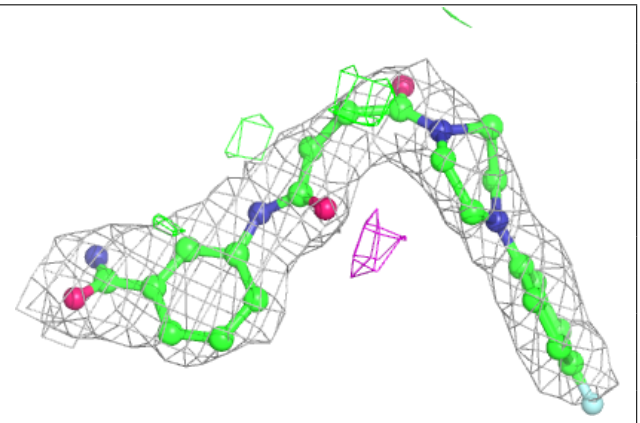
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

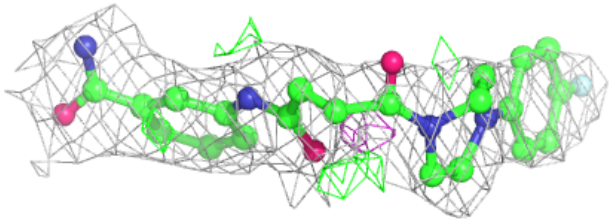


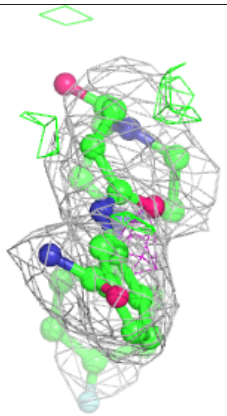


Electron density around 94Z A 1901:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)







6.5 Other polymers (i)

There are no such residues in this entry.