



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 24, 2024 – 02:52 PM EDT

PDB ID : 6T9C
Title : Crystal structure of the complex between PPARgamma LBD and the ligand NV1346 (3a)
Authors : Pochetti, G.; Montanari, R.; Capelli, D.
Deposited on : 2019-10-27
Resolution : 1.95 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 ⓘ 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 ⓘ](#)) 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
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)	:	2.37.1

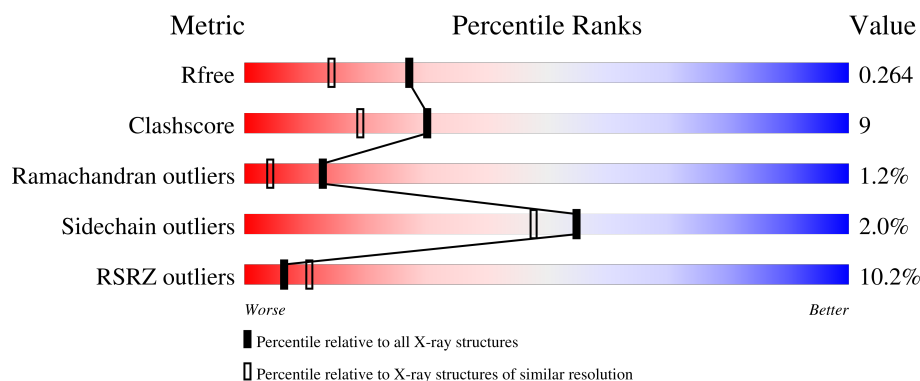
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 $\leq 5\%$. 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	304	<div> <div>5%</div> <div>66%</div> <div>15%</div> <div>17%</div> </div>
1	B	304	<div> <div>12%</div> <div>68%</div> <div>12%</div> <div>18%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4184 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 Peroxisome proliferator-activated receptor gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	0	0
			2004	1294	327	373	10			
1	B	248	Total	C	N	O	S	0	0	0
			1980	1280	320	370	10			

There are 42 discrepancies between the modelled and reference sequences:

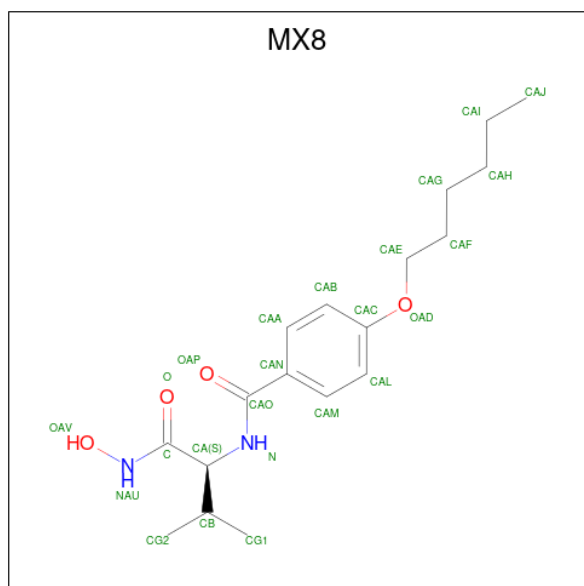
Chain	Residue	Modelled	Actual	Comment	Reference
A	174	MET	-	initiating methionine	UNP P37231
A	175	GLY	-	expression tag	UNP P37231
A	176	SER	-	expression tag	UNP P37231
A	177	SER	-	expression tag	UNP P37231
A	178	HIS	-	expression tag	UNP P37231
A	179	HIS	-	expression tag	UNP P37231
A	180	HIS	-	expression tag	UNP P37231
A	181	HIS	-	expression tag	UNP P37231
A	182	HIS	-	expression tag	UNP P37231
A	183	HIS	-	expression tag	UNP P37231
A	184	SER	-	expression tag	UNP P37231
A	185	SER	-	expression tag	UNP P37231
A	186	GLY	-	expression tag	UNP P37231
A	187	LEU	-	expression tag	UNP P37231
A	188	VAL	-	expression tag	UNP P37231
A	189	PRO	-	expression tag	UNP P37231
A	190	ARG	-	expression tag	UNP P37231
A	191	GLY	-	expression tag	UNP P37231
A	192	SER	-	expression tag	UNP P37231
A	193	HIS	-	expression tag	UNP P37231
A	194	MET	-	expression tag	UNP P37231
B	174	MET	-	initiating methionine	UNP P37231
B	175	GLY	-	expression tag	UNP P37231
B	176	SER	-	expression tag	UNP P37231
B	177	SER	-	expression tag	UNP P37231

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	178	HIS	-	expression tag	UNP P37231
B	179	HIS	-	expression tag	UNP P37231
B	180	HIS	-	expression tag	UNP P37231
B	181	HIS	-	expression tag	UNP P37231
B	182	HIS	-	expression tag	UNP P37231
B	183	HIS	-	expression tag	UNP P37231
B	184	SER	-	expression tag	UNP P37231
B	185	SER	-	expression tag	UNP P37231
B	186	GLY	-	expression tag	UNP P37231
B	187	LEU	-	expression tag	UNP P37231
B	188	VAL	-	expression tag	UNP P37231
B	189	PRO	-	expression tag	UNP P37231
B	190	ARG	-	expression tag	UNP P37231
B	191	GLY	-	expression tag	UNP P37231
B	192	SER	-	expression tag	UNP P37231
B	193	HIS	-	expression tag	UNP P37231
B	194	MET	-	expression tag	UNP P37231

- Molecule 2 is 4-hexoxy- {N}-[(2 {S})-3-methyl-1-(oxidanylamino)-1-oxidanylidene-butane-2-yl]benzamide (three-letter code: MX8) (formula: C₁₈H₂₈N₂O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			24	18	2	4		

- Molecule 3 is water.

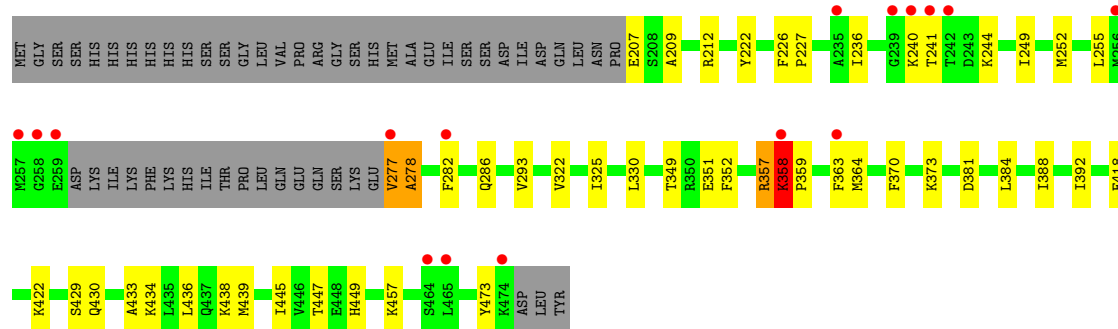
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	96	Total 96	O 96	0	0
3	B	80	Total 80	O 80	0	0

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.

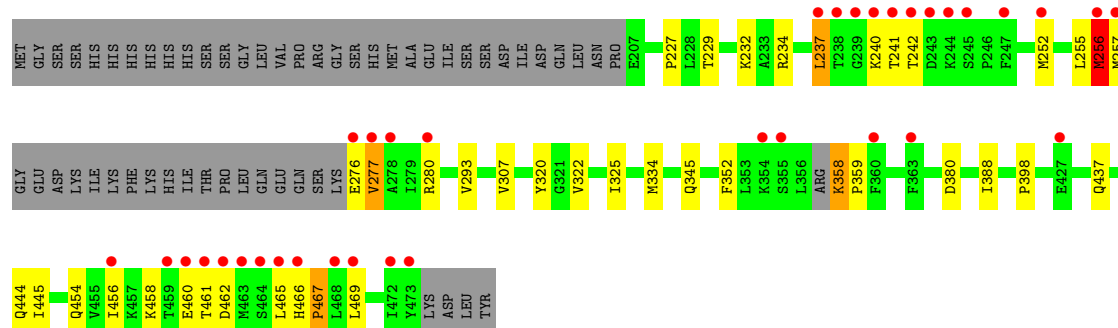
- Molecule 1: Peroxisome proliferator-activated receptor gamma

Chain A: 



- Molecule 1: Peroxisome proliferator-activated receptor gamma

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	93.78Å 60.98Å 119.00Å 90.00° 103.50° 90.00°	Depositor
Resolution (Å)	50.69 – 1.95 57.86 – 1.95	Depositor EDS
% Data completeness (in resolution range)	95.8 (50.69-1.95) 95.9 (57.86-1.95)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 1.95Å)	Xtriage
Refinement program	PHENIX 1.8.4_1496	Depositor
R, R_{free}	0.230 , 0.262 0.234 , 0.264	Depositor DCC
R_{free} test set	2293 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	39.3	Xtriage
Anisotropy	0.377	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4184	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.57% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MX8

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	0/2037	0.58	0/2745
1	B	0.43	0/2014	0.62	0/2718
All	All	0.45	0/4051	0.60	0/5463

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	2004	0	2064	48	0
1	B	1980	0	2036	29	0
2	A	24	0	0	6	0
3	A	96	0	0	8	0
3	B	80	0	0	3	0
All	All	4184	0	4100	75	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 9.

All (75) 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:358:LYS:HB3	1:A:359:PRO:CD	1.68	1.21
1:A:358:LYS:HB3	1:A:359:PRO:HD3	1.17	1.11
1:A:359:PRO:HD2	3:A:604:HOH:O	1.67	0.95
1:B:358:LYS:HB3	1:B:359:PRO:HD2	1.57	0.86
1:A:358:LYS:HA	1:A:358:LYS:HE2	1.58	0.85
1:A:358:LYS:HA	1:A:358:LYS:CE	2.06	0.85
1:B:325:ILE:HD12	1:B:388:ILE:HG23	1.60	0.82
1:A:359:PRO:CD	3:A:604:HOH:O	2.26	0.82
1:B:293:VAL:HG22	1:B:322:VAL:HG21	1.60	0.82
1:A:241:THR:HG21	1:A:244:LYS:HG3	1.65	0.79
1:A:358:LYS:CB	1:A:359:PRO:CD	2.51	0.79
1:A:207:GLU:HG3	1:A:209:ALA:H	1.51	0.76
1:A:363:PHE:HE1	1:A:449:HIS:HE1	1.37	0.71
1:B:227:PRO:O	1:B:232:LYS:NZ	2.20	0.71
1:A:418:GLU:O	1:A:422:LYS:HG3	1.93	0.69
1:A:439:MET:SD	3:A:685:HOH:O	2.51	0.69
1:A:252:MET:SD	1:A:277:VAL:HG11	2.35	0.66
1:A:447:THR:OG1	1:B:444:GLN:NE2	2.30	0.64
1:B:358:LYS:HB3	1:B:359:PRO:CD	2.29	0.62
1:A:430:GLN:HG3	1:A:433:ALA:HB3	1.82	0.62
1:B:241:THR:HG22	1:B:242:THR:H	1.66	0.61
1:A:373:LYS:HE2	1:A:438:LYS:HE3	1.83	0.60
1:A:278:ALA:HB2	3:A:682:HOH:O	2.02	0.59
1:A:384:LEU:O	1:A:388:ILE:HG12	2.05	0.57
1:B:229:THR:H	1:B:232:LYS:HE2	1.70	0.56
1:A:241:THR:HG21	1:A:244:LYS:CG	2.37	0.53
1:B:234:ARG:NH2	1:B:334:MET:O	2.33	0.53
1:B:465:LEU:O	1:B:467:PRO:HD3	2.08	0.53
1:A:436:LEU:HA	1:A:439:MET:HE2	1.91	0.52
1:B:320:TYR:CZ	1:B:398:PRO:HG2	2.44	0.52
1:B:276:GLU:OE1	1:B:277:VAL:N	2.43	0.52
1:A:429:SER:O	1:A:434:LYS:NZ	2.44	0.51
1:A:358:LYS:CB	3:A:604:HOH:O	2.59	0.50
1:A:439:MET:HE1	1:B:437:GLN:HG2	1.94	0.49
1:A:358:LYS:HB3	3:A:604:HOH:O	2.12	0.48
1:A:370:PHE:HB2	1:A:445:ILE:HD11	1.95	0.48
1:B:256:MET:O	1:B:257:MET:HG3	2.12	0.48
1:A:363:PHE:CD2	1:A:364:MET:HG2	2.48	0.48
1:A:363:PHE:HE1	1:A:449:HIS:CE1	2.24	0.47
1:B:460:GLU:HA	1:B:460:GLU:OE1	2.14	0.47
1:A:249:ILE:HD12	1:A:255:LEU:HA	1.97	0.47
1:A:293:VAL:HG22	1:A:322:VAL:HG11	1.95	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:255:LEU:HD23	1:B:277:VAL:HG12	1.96	0.47
1:A:286:GLN:HA	2:A:501:MX8:CG1	2.45	0.47
1:A:330:LEU:HD22	2:A:501:MX8:CAL	2.45	0.47
1:B:466:HIS:HB2	1:B:469:LEU:HD11	1.97	0.47
1:A:282:PHE:HE2	1:A:286:GLN:HE21	1.64	0.46
1:B:240:LYS:HG3	1:B:241:THR:N	2.31	0.46
1:B:456:ILE:C	1:B:458:LYS:H	2.19	0.46
1:B:307:VAL:HG22	3:B:525:HOH:O	2.16	0.45
1:B:242:THR:O	1:B:242:THR:HG22	2.17	0.44
1:B:380:ASP:HB2	3:B:546:HOH:O	2.15	0.44
1:A:212:ARG:HA	1:A:212:ARG:HD2	1.81	0.44
1:A:349:THR:HG22	1:A:352:PHE:H	1.81	0.44
1:A:473:TYR:CE2	2:A:501:MX8:OAV	2.71	0.44
1:B:454:GLN:O	1:B:458:LYS:HD3	2.17	0.44
1:A:357:ARG:HG3	3:A:604:HOH:O	2.17	0.44
1:A:236:ILE:HG23	1:A:244:LYS:O	2.18	0.43
1:B:276:GLU:HB3	1:B:280:ARG:HB3	2.00	0.43
1:B:237:LEU:HA	1:B:237:LEU:HD23	1.79	0.43
1:A:457:LYS:HE3	1:A:457:LYS:HB2	1.82	0.43
1:A:286:GLN:HG2	2:A:501:MX8:CG1	2.49	0.43
1:B:293:VAL:HG22	1:B:322:VAL:CG2	2.42	0.42
1:A:222:TYR:CE2	1:A:381:ASP:HB3	2.55	0.42
1:A:473:TYR:OH	2:A:501:MX8:OAV	2.36	0.42
1:A:226:PHE:HA	1:A:227:PRO:HD3	1.84	0.41
1:A:358:LYS:HB3	1:A:359:PRO:HD2	1.84	0.41
1:A:325:ILE:HD11	1:A:392:ILE:HG13	2.02	0.41
1:A:473:TYR:HE2	2:A:501:MX8:OAV	2.03	0.41
1:B:252:MET:SD	1:B:277:VAL:HG11	2.61	0.41
1:A:359:PRO:HD3	3:A:604:HOH:O	2.10	0.41
1:A:255:LEU:HD23	1:A:277:VAL:CG1	2.51	0.41
1:A:349:THR:HG22	1:A:351:GLU:N	2.35	0.41
1:B:255:LEU:HD22	1:B:352:PHE:HZ	1.86	0.41
1:B:445:ILE:HD11	3:B:547:HOH:O	2.21	0.40

There are no symmetry-related clashes.

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	247/304 (81%)	237 (96%)	8 (3%)	2 (1%)	19	9
1	B	246/304 (81%)	230 (94%)	12 (5%)	4 (2%)	9	2
All	All	493/608 (81%)	467 (95%)	20 (4%)	6 (1%)	13	4

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	358	LYS
1	B	237	LEU
1	B	256	MET
1	B	358	LYS
1	B	467	PRO
1	A	278	ALA

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	224/273 (82%)	220 (98%)	4 (2%)	59	53
1	B	222/273 (81%)	217 (98%)	5 (2%)	50	42
All	All	446/546 (82%)	437 (98%)	9 (2%)	55	48

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

Mol	Chain	Res	Type
1	A	240	LYS
1	A	277	VAL
1	A	357	ARG
1	A	358	LYS
1	B	256	MET
1	B	277	VAL
1	B	345	GLN
1	B	461	THR
1	B	462	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	444	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	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	MX8	A	501	-	23,24,24	1.26	2 (8%)	28,30,30	1.03	2 (7%)

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	MX8	A	501	-	-	8/25/25/25	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	MX8	CAO-N	3.82	1.43	1.34
2	A	501	MX8	OAD-CAC	2.85	1.44	1.37

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	MX8	CA-N-CAO	-2.34	116.80	121.53
2	A	501	MX8	CB-CA-C	-2.12	106.20	111.38

There are no chirality outliers.

All (8) torsion outliers are listed below:

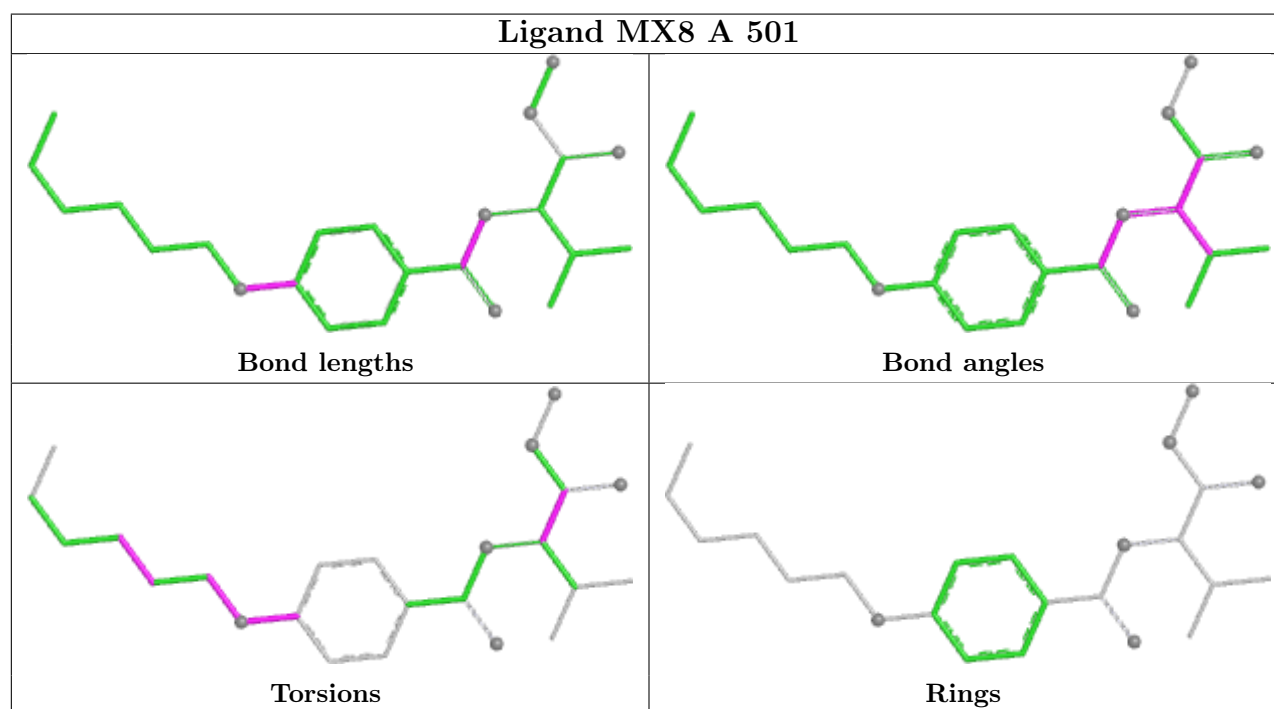
Mol	Chain	Res	Type	Atoms
2	A	501	MX8	CAF-CAE-OAD-CAC
2	A	501	MX8	CAE-CAF-CAG-CAH
2	A	501	MX8	O-C-CA-N
2	A	501	MX8	NAU-C-CA-N
2	A	501	MX8	NAU-C-CA-CB
2	A	501	MX8	O-C-CA-CB
2	A	501	MX8	CAL-CAC-OAD-CAE
2	A	501	MX8	CAB-CAC-OAD-CAE

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	MX8	6	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 than 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

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	251/304 (82%)	0.54	16 (6%) 19 28	30, 44, 62, 93	0
1	B	248/304 (81%)	1.06	35 (14%) 2 4	30, 46, 89, 113	0
All	All	499/608 (82%)	0.79	51 (10%) 6 11	30, 45, 80, 113	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	242	THR	20.0
1	B	465	LEU	15.2
1	B	257	MET	12.3
1	A	259	GLU	10.6
1	B	238	THR	10.5
1	B	276	GLU	9.2
1	B	473	TYR	8.1
1	B	469	LEU	7.4
1	B	243	ASP	7.1
1	A	258	GLY	6.6
1	A	277	VAL	5.8
1	B	459	THR	5.5
1	B	277	VAL	5.4
1	B	256	MET	5.4
1	B	462	ASP	5.3
1	B	461	THR	5.1
1	B	463	MET	5.1
1	B	241	THR	5.0
1	B	363	PHE	4.7
1	B	466	HIS	4.6
1	B	468	LEU	3.9
1	A	363	PHE	3.8
1	A	358	LYS	3.8
1	B	460	GLU	3.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	239	GLY	3.7
1	B	472	ILE	3.7
1	A	241	THR	3.7
1	B	252	MET	3.7
1	A	235	ALA	3.6
1	B	456	ILE	3.5
1	B	464	SER	3.4
1	B	237	LEU	3.2
1	B	247	PHE	3.2
1	B	240	LYS	3.1
1	A	242	THR	3.1
1	A	256	MET	2.8
1	B	244	LYS	2.5
1	A	465	LEU	2.5
1	A	257	MET	2.3
1	A	464	SER	2.3
1	B	245	SER	2.3
1	A	474	LYS	2.3
1	B	278	ALA	2.3
1	A	240	LYS	2.3
1	B	355	SER	2.2
1	A	282	PHE	2.2
1	B	354	LYS	2.1
1	B	360	PHE	2.0
1	B	239	GLY	2.0
1	B	427	GLU	2.0
1	B	280	ARG	2.0

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.

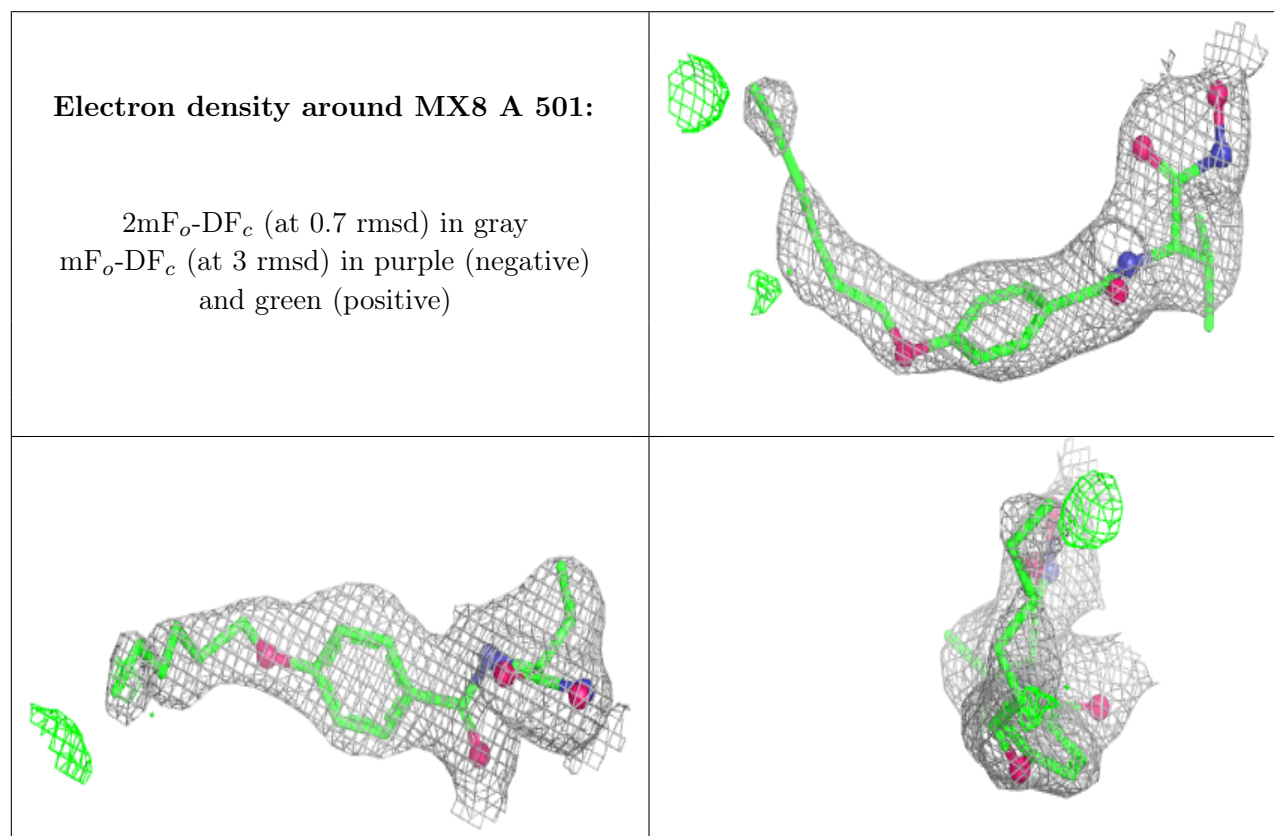
6.4 Ligands [i](#)

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
2	MX8	A	501	24/24	0.90	0.20	55,59,61,64	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.