



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 10:42 am BST

PDB ID : 3VN2
Title : Crystal Structure of PPARgamma complexed with Telmisartan
Authors : Amano, Y.
Deposited on : 2011-12-21
Resolution : 2.18 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 following versions of software and data (see [references ⓘ](#)) 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

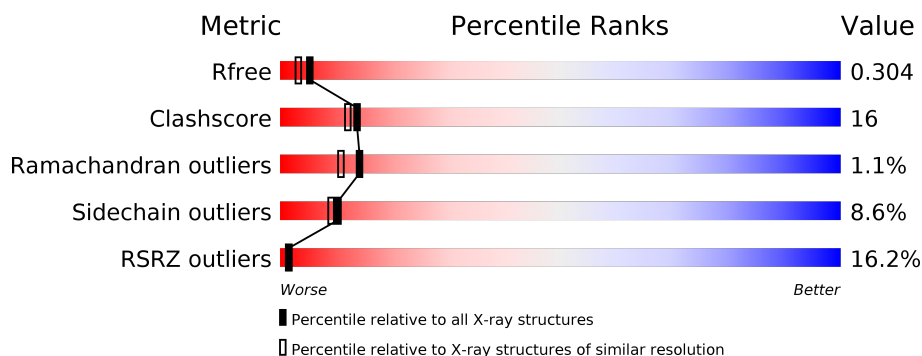
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 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	6864 (2.20-2.16)
Clashscore	141614	7689 (2.20-2.16)
Ramachandran outliers	138981	7564 (2.20-2.16)
Sidechain outliers	138945	7564 (2.20-2.16)
RSRZ outliers	127900	6738 (2.20-2.16)

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 $\leq 5\%$. 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	285	<div> <div>14%</div> <div> <div></div> <div>72%</div> <div>15%</div> <div>5%</div> <div>8%</div> </div> </div>
2	C	16	<div> <div>19%</div> <div> <div></div> <div>50%</div> <div>19%</div> <div>31%</div> </div> </div>

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	TLS	A	501	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2278 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
			Total	C	N	O	S			
1	A	261	2091	1348	340	393	10	0	0	0

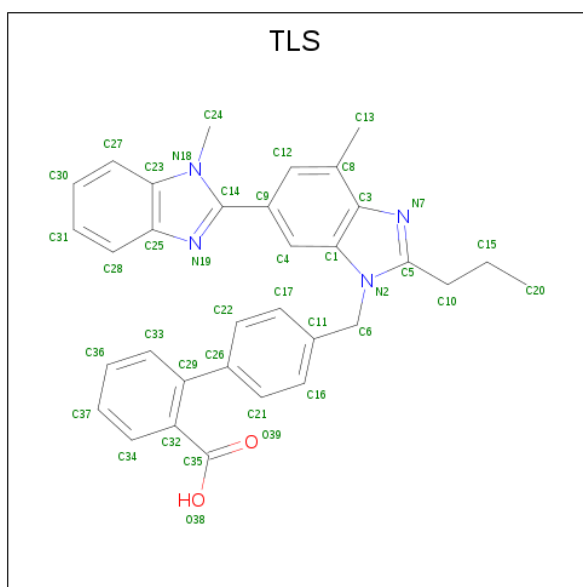
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	193	GLY	-	EXPRESSION TAG	UNP P37231
A	194	SER	-	EXPRESSION TAG	UNP P37231
A	195	HIS	-	EXPRESSION TAG	UNP P37231
A	196	MET	-	EXPRESSION TAG	UNP P37231

- Molecule 2 is a protein called Nuclear receptor coactivator 1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	11	101	64	23	14	0	0	0

- Molecule 3 is 4'-[(1,7'-dimethyl-2'-propyl-1H,3'H-2,5'-bibenzimidazol-3'-yl)methyl]biphenyl-2-carboxylic acid (three-letter code: TLS) (formula: C₃₃H₃₀N₄O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			39	33	4	2		

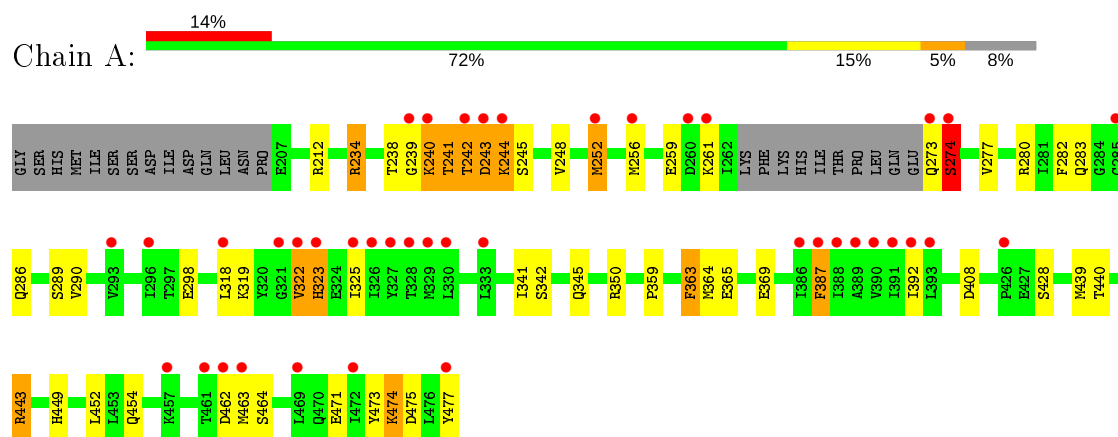
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	47	Total	O	0	0
			47	47		

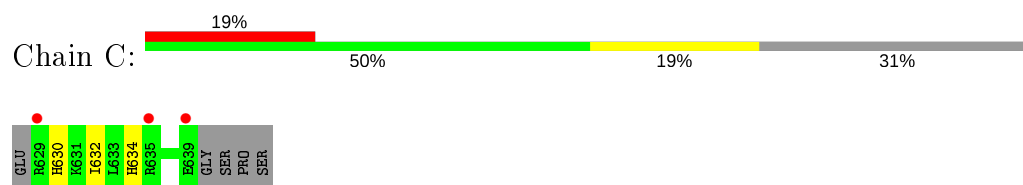
3 Residue-property plots [i](#)

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: Peroxisome proliferator-activated receptor gamma



- Molecule 2: Nuclear receptor coactivator 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	132.85Å 53.50Å 53.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	26.93 – 2.18 26.93 – 2.18	Depositor EDS
% Data completeness (in resolution range)	95.5 (26.93-2.18) 95.5 (26.93-2.18)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.67 (at 2.18Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.250 , 0.309 0.249 , 0.304	Depositor DCC
R_{free} test set	1014 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	0.058	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 59.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.027 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2278	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.64% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	1.07	2/2125 (0.1%)	0.92	3/2861 (0.1%)
2	C	0.79	0/102	0.79	0/134
All	All	1.06	2/2227 (0.1%)	0.92	3/2995 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	298	GLU	CB-CG	5.96	1.63	1.52
1	A	387	PHE	CE1-CZ	5.18	1.47	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	408	ASP	CB-CG-OD1	5.95	123.65	118.30
1	A	322	VAL	CG1-CB-CG2	5.32	119.41	110.90
1	A	443	ARG	NE-CZ-NH1	5.25	122.92	120.30

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	2091	0	2148	60	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	101	0	110	3	0
3	A	39	0	29	28	0
4	A	47	0	0	0	0
All	All	2278	0	2287	72	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 16.

All (72) 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:323:HIS:CD2	3:A:501:TLS:H20	1.60	1.37
1:A:282:PHE:CD1	3:A:501:TLS:C24	2.24	1.21
1:A:244:LYS:O	1:A:244:LYS:HD3	1.47	1.14
1:A:323:HIS:HD2	3:A:501:TLS:C20	1.60	1.14
1:A:282:PHE:CD1	3:A:501:TLS:H24	1.81	1.11
1:A:282:PHE:HD1	3:A:501:TLS:H24	1.12	1.04
1:A:240:LYS:O	1:A:241:THR:HG22	1.58	1.02
1:A:242:THR:HG23	1:A:242:THR:O	1.61	1.00
1:A:342:SER:O	1:A:345:GLN:HG2	1.74	0.87
1:A:282:PHE:CD1	3:A:501:TLS:H24B	2.13	0.82
1:A:242:THR:CG2	1:A:242:THR:O	2.29	0.81
1:A:240:LYS:O	1:A:241:THR:CG2	2.29	0.80
3:A:501:TLS:H12	3:A:501:TLS:C24	2.11	0.79
1:A:323:HIS:CD2	3:A:501:TLS:C20	2.46	0.78
1:A:244:LYS:O	1:A:244:LYS:CD	2.30	0.77
3:A:501:TLS:H4	3:A:501:TLS:C17	2.15	0.76
1:A:323:HIS:HD2	3:A:501:TLS:H20	0.69	0.75
3:A:501:TLS:H21	3:A:501:TLS:C35	2.17	0.74
1:A:474:LYS:HE3	1:A:475:ASP:OD2	1.87	0.73
1:A:273:GLN:O	1:A:274:SER:HB2	1.89	0.72
1:A:364:MET:HG2	3:A:501:TLS:H28	1.73	0.71
3:A:501:TLS:H12	3:A:501:TLS:H24B	1.71	0.71
1:A:244:LYS:C	1:A:244:LYS:HD3	1.87	0.69
1:A:342:SER:O	1:A:345:GLN:CG	2.42	0.68
1:A:244:LYS:HD3	1:A:244:LYS:N	2.10	0.65
1:A:473:TYR:OH	3:A:501:TLS:H20A	1.98	0.64
1:A:364:MET:CG	3:A:501:TLS:H28	2.29	0.63
1:A:243:ASP:N	1:A:243:ASP:OD1	2.30	0.63
1:A:462:ASP:O	1:A:463:MET:C	2.37	0.63
1:A:325:ILE:HD11	1:A:392:ILE:HG13	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:MET:SD	3:A:501:TLS:H33	2.42	0.60
1:A:364:MET:SD	3:A:501:TLS:H22	2.42	0.59
1:A:240:LYS:C	1:A:241:THR:HG22	2.23	0.57
1:A:273:GLN:O	1:A:274:SER:CB	2.53	0.56
1:A:319:LYS:O	1:A:323:HIS:HE1	1.89	0.56
1:A:239:GLY:C	1:A:240:LYS:O	2.42	0.55
1:A:244:LYS:N	1:A:244:LYS:CD	2.69	0.54
1:A:325:ILE:HD11	1:A:392:ILE:CG1	2.36	0.54
1:A:364:MET:HG2	3:A:501:TLS:C28	2.38	0.54
1:A:363:PHE:HE1	1:A:449:HIS:CE1	2.26	0.54
3:A:501:TLS:C35	3:A:501:TLS:C21	2.83	0.53
1:A:244:LYS:C	1:A:244:LYS:CD	2.69	0.52
1:A:282:PHE:CE1	3:A:501:TLS:C24	2.88	0.51
1:A:319:LYS:O	1:A:323:HIS:CE1	2.65	0.50
1:A:240:LYS:O	1:A:241:THR:O	2.30	0.50
1:A:239:GLY:O	1:A:240:LYS:O	2.30	0.50
1:A:350:ARG:NH2	1:A:365:GLU:OE2	2.43	0.50
3:A:501:TLS:C24	3:A:501:TLS:C12	2.85	0.49
3:A:501:TLS:H12	3:A:501:TLS:H24A	1.94	0.49
1:A:286:GLN:O	1:A:290:VAL:HG23	2.12	0.49
3:A:501:TLS:H21	3:A:501:TLS:O39	2.14	0.48
1:A:473:TYR:OH	3:A:501:TLS:C20	2.62	0.48
1:A:241:THR:OG1	1:A:243:ASP:OD1	2.30	0.47
1:A:280:ARG:HH11	1:A:280:ARG:HG3	1.80	0.47
1:A:387:PHE:CE1	1:A:439:MET:HG3	2.50	0.47
1:A:252:MET:HG3	1:A:277:VAL:HG21	1.97	0.47
1:A:256:MET:HA	1:A:259:GLU:OE1	2.14	0.47
3:A:501:TLS:C21	3:A:501:TLS:O39	2.63	0.47
3:A:501:TLS:C11	3:A:501:TLS:H4	2.44	0.46
1:A:341:ILE:O	1:A:342:SER:C	2.54	0.46
1:A:244:LYS:O	1:A:244:LYS:CE	2.65	0.44
1:A:289:SER:HB3	3:A:501:TLS:H10A	1.98	0.44
1:A:244:LYS:H	1:A:244:LYS:CD	2.31	0.44
1:A:212:ARG:HD2	1:A:212:ARG:HA	1.55	0.43
1:A:474:LYS:HG2	1:A:475:ASP:OD2	2.18	0.43
1:A:365:GLU:O	1:A:369:GLU:HG3	2.20	0.42
1:A:359:PRO:HB2	1:A:452:LEU:HD11	2.01	0.42
1:A:471:GLU:OE2	2:C:632:ILE:N	2.37	0.42
1:A:234:ARG:HD2	1:A:234:ARG:HA	1.84	0.41
2:C:630:HIS:O	2:C:634:HIS:HD2	2.03	0.41
1:A:319:LYS:HD2	2:C:630:HIS:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:501:TLS:C4	3:A:501:TLS:C11	2.98	0.41

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:238:THR:O	1:A:274:SER:OG[3_556]	2.15	0.05

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	257/285 (90%)	243 (95%)	11 (4%)	3 (1%)	13	9
2	C	9/16 (56%)	8 (89%)	1 (11%)	0	100	100
All	All	266/301 (88%)	251 (94%)	12 (4%)	3 (1%)	14	11

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	240	LYS
1	A	241	THR
1	A	274	SER

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	234/257 (91%)	213 (91%)	21 (9%)	9	8
2	C	11/15 (73%)	11 (100%)	0	100	100
All	All	245/272 (90%)	224 (91%)	21 (9%)	10	9

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	234	ARG
1	A	242	THR
1	A	243	ASP
1	A	244	LYS
1	A	245	SER
1	A	248	VAL
1	A	252	MET
1	A	261	LYS
1	A	274	SER
1	A	283	GLN
1	A	318	LEU
1	A	322	VAL
1	A	323	HIS
1	A	363	PHE
1	A	428	SER
1	A	440	THR
1	A	443	ARG
1	A	454	GLN
1	A	464	SER
1	A	474	LYS
1	A	477	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	283	GLN
1	A	323	HIS
1	A	437	GLN
1	A	451	GLN
1	A	470	GLN
2	C	630	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	$\# Z > 2$
3	TLS	A	501	-	37,44,44	1.02	2 (5%)	44,64,64	1.90	10 (22%)

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
3	TLS	A	501	-	-	8/15/19/19	0/6/6/6

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	TLS	C8-C3	-2.97	1.37	1.42
3	A	501	TLS	C29-C26	-2.05	1.45	1.49

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	TLS	C9-C4-C1	-5.33	116.17	121.87
3	A	501	TLS	C4-C1-C3	4.93	125.22	120.55
3	A	501	TLS	C9-C14-N19	3.62	128.51	122.71
3	A	501	TLS	C10-C5-N7	3.12	128.69	124.22
3	A	501	TLS	C27-C23-C25	2.65	125.63	121.30
3	A	501	TLS	C9-C12-C8	2.54	125.33	122.34
3	A	501	TLS	C36-C33-C29	2.35	124.30	120.33
3	A	501	TLS	C30-C27-C23	-2.31	115.02	119.44
3	A	501	TLS	C33-C29-C32	-2.22	116.47	118.67
3	A	501	TLS	C22-C17-C11	-2.16	118.05	121.03

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	TLS	C11-C6-N2-C5
3	A	501	TLS	C15-C10-C5-N2
3	A	501	TLS	C22-C26-C29-C32
3	A	501	TLS	C21-C26-C29-C32
3	A	501	TLS	C22-C26-C29-C33
3	A	501	TLS	C11-C6-N2-C1
3	A	501	TLS	C5-C10-C15-C20
3	A	501	TLS	C21-C26-C29-C33

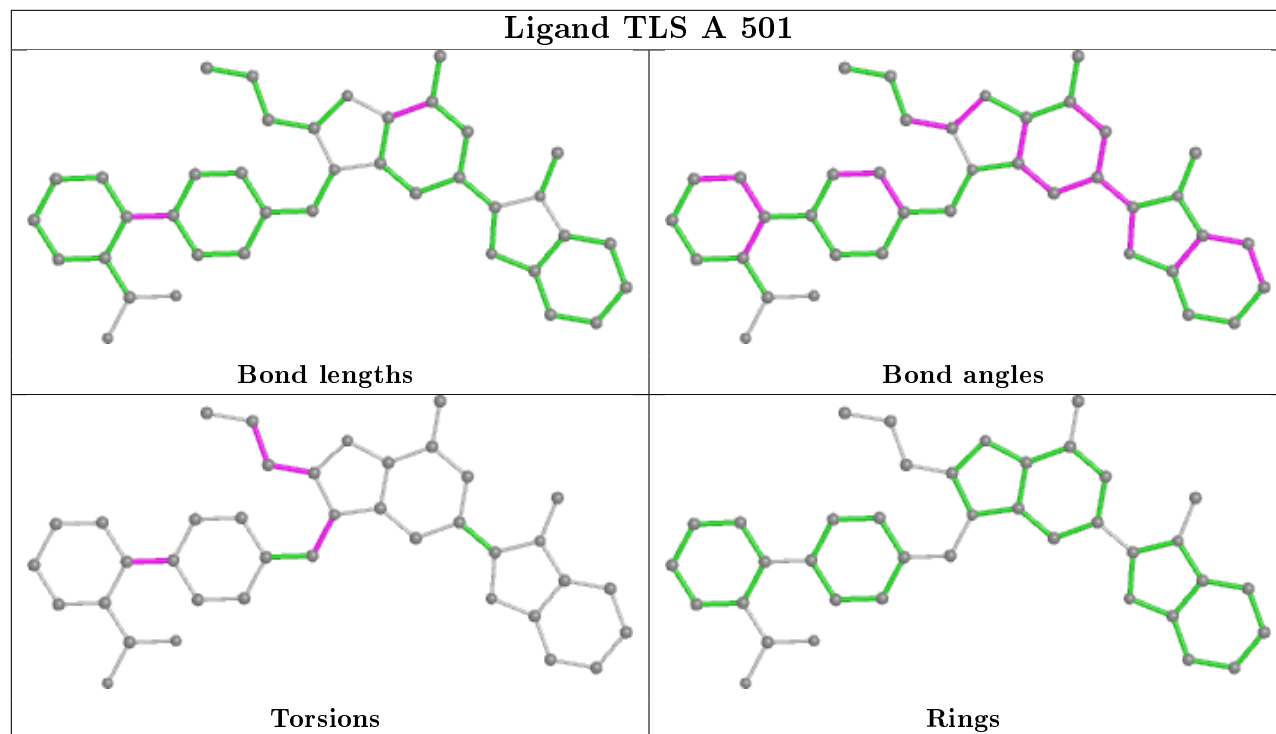
There are no ring outliers.

1 monomer is involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	501	TLS	28	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	261/285 (91%)	0.80	41 (15%) 2 2	32, 52, 86, 96	0
2	C	11/16 (68%)	1.36	3 (27%) 0 0	59, 69, 86, 89	0
All	All	272/301 (90%)	0.82	44 (16%) 1 1	32, 53, 87, 96	0

All (44) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	463	MET	9.2
1	A	477	TYR	6.5
1	A	322	VAL	6.0
1	A	326	ILE	5.6
1	A	325	ILE	5.3
1	A	274	SER	4.3
2	C	629	ARG	3.8
1	A	392	ILE	3.8
1	A	242	THR	3.8
1	A	462	ASP	3.5
1	A	461	THR	3.5
2	C	639	GLU	3.5
1	A	243	ASP	3.4
1	A	273	GLN	3.4
1	A	391	ILE	3.4
1	A	387	PHE	3.4
1	A	244	LYS	3.4
1	A	328	THR	3.4
1	A	296	ILE	3.4
1	A	327	TYR	3.3
1	A	239	GLY	3.2
1	A	240	LYS	3.2
1	A	318	LEU	3.1
1	A	293	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	390	VAL	2.9
1	A	330	LEU	2.9
1	A	386	ILE	2.9
1	A	388	ILE	2.8
1	A	256	MET	2.8
1	A	261	LYS	2.8
1	A	472	ILE	2.7
1	A	393	LEU	2.6
1	A	321	GLY	2.6
1	A	329	MET	2.5
1	A	389	ALA	2.4
1	A	260	ASP	2.4
1	A	426	PRO	2.3
1	A	323	HIS	2.3
1	A	469	LEU	2.2
1	A	252	MET	2.1
1	A	285	CYS	2.1
1	A	333	LEU	2.1
2	C	635	ARG	2.0
1	A	457	LYS	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 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.

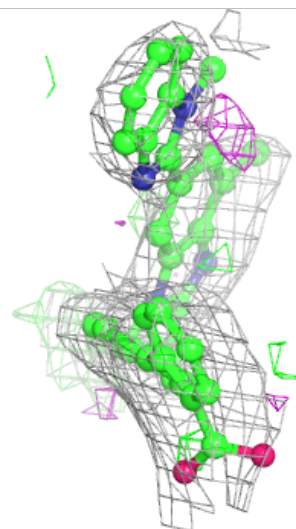
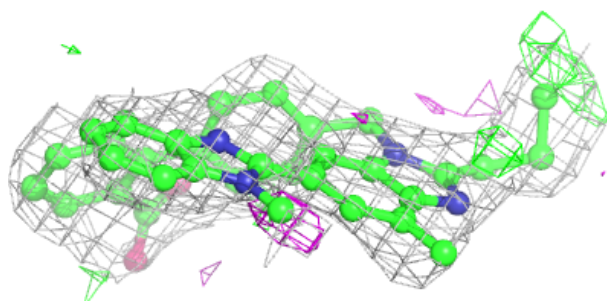
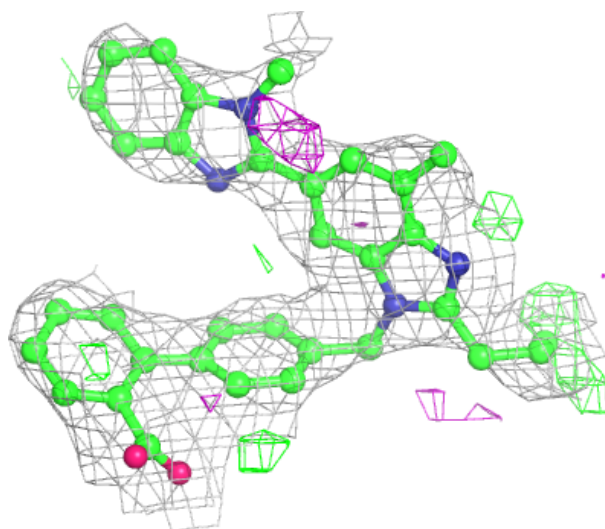
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	TLS	A	501	39/39	0.74	0.37	87,91,99,99	0

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 TLS A 501:

$2mF_o-DF_c$ (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.