



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 15, 2023 – 08:23 PM EDT

PDB ID : 8EQZ
Title : Crystal structure of pregnane X receptor ligand binding domain complexed with T0901317 analog T0-C6
Authors : Huber, A.D.; Poudel, S.; Seetharaman, J.; Miller, D.J.; Lin, W.; Li, Y.; Chen, T.
Deposited on : 2022-10-11
Resolution : 2.37 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

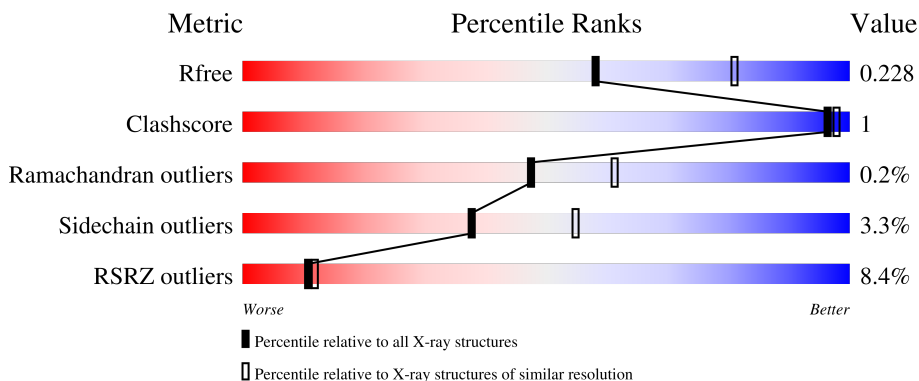
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.37 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	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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	355	 6% 79% 18%
1	B	355	 8% 76% 6% 18%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4753 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 Nuclear receptor subfamily 1 group I member 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	292	2326	1493	399	415	19	0	1	0
1	B	290	2295	1478	390	408	19	0	1	0

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	119	MET	-	initiating methionine	UNP O75469
A	120	LYS	-	expression tag	UNP O75469
A	121	LYS	-	expression tag	UNP O75469
A	122	GLY	-	expression tag	UNP O75469
A	123	HIS	-	expression tag	UNP O75469
A	124	HIS	-	expression tag	UNP O75469
A	125	HIS	-	expression tag	UNP O75469
A	126	HIS	-	expression tag	UNP O75469
A	127	HIS	-	expression tag	UNP O75469
A	128	HIS	-	expression tag	UNP O75469
A	129	GLY	-	expression tag	UNP O75469
A	432C	SER	-	expression tag	UNP O75469
A	432D	GLY	-	expression tag	UNP O75469
A	432E	GLY	-	expression tag	UNP O75469
A	432F	SER	-	expression tag	UNP O75469
A	432G	GLY	-	expression tag	UNP O75469
A	432H	GLY	-	expression tag	UNP O75469
A	432I	SER	-	expression tag	UNP O75469
A	432J	SER	-	expression tag	UNP O75469
A	432K	HIS	-	expression tag	UNP O75469
A	432L	SER	-	expression tag	UNP O75469
A	444	SER	-	expression tag	UNP O75469
A	445	LEU	-	expression tag	UNP O75469
A	446	THR	-	expression tag	UNP O75469
A	447	GLU	-	expression tag	UNP O75469

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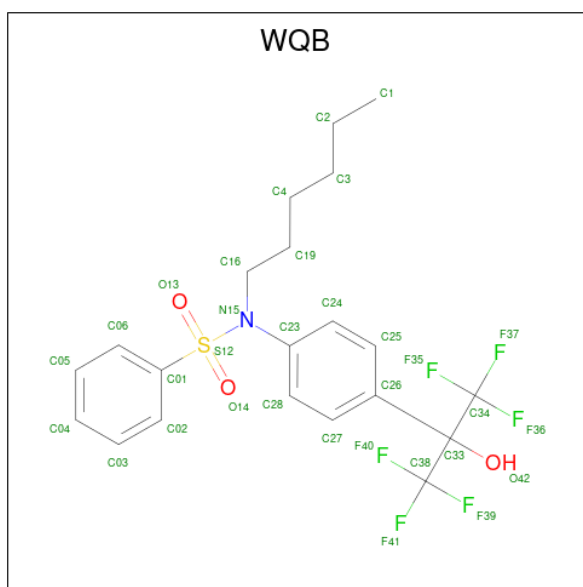
Chain	Residue	Modelled	Actual	Comment	Reference
A	448	ARG	-	expression tag	UNP O75469
A	449	HIS	-	expression tag	UNP O75469
A	450	LYS	-	expression tag	UNP O75469
A	451	ILE	-	expression tag	UNP O75469
A	452	LEU	-	expression tag	UNP O75469
A	453	HIS	-	expression tag	UNP O75469
A	454	ARG	-	expression tag	UNP O75469
A	455	LEU	-	expression tag	UNP O75469
A	456	LEU	-	expression tag	UNP O75469
A	457	GLN	-	expression tag	UNP O75469
A	458	GLU	-	expression tag	UNP O75469
A	459	GLY	-	expression tag	UNP O75469
A	460	SER	-	expression tag	UNP O75469
A	461	PRO	-	expression tag	UNP O75469
A	462	SER	-	expression tag	UNP O75469
A	463	ASP	-	expression tag	UNP O75469
A	464	ILE	-	expression tag	UNP O75469
A	465	THR	-	expression tag	UNP O75469
A	466	THR	-	expression tag	UNP O75469
A	467	LEU	-	expression tag	UNP O75469
A	468	SER	-	expression tag	UNP O75469
A	469	VAL	-	expression tag	UNP O75469
A	470	GLU	-	expression tag	UNP O75469
A	471	PRO	-	expression tag	UNP O75469
A	472	ASP	-	expression tag	UNP O75469
B	119	MET	-	initiating methionine	UNP O75469
B	120	LYS	-	expression tag	UNP O75469
B	121	LYS	-	expression tag	UNP O75469
B	122	GLY	-	expression tag	UNP O75469
B	123	HIS	-	expression tag	UNP O75469
B	124	HIS	-	expression tag	UNP O75469
B	125	HIS	-	expression tag	UNP O75469
B	126	HIS	-	expression tag	UNP O75469
B	127	HIS	-	expression tag	UNP O75469
B	128	HIS	-	expression tag	UNP O75469
B	129	GLY	-	expression tag	UNP O75469
B	431D	SER	-	expression tag	UNP O75469
B	431E	GLY	-	expression tag	UNP O75469
B	431F	GLY	-	expression tag	UNP O75469
B	431G	SER	-	expression tag	UNP O75469
B	431H	GLY	-	expression tag	UNP O75469
B	431I	GLY	-	expression tag	UNP O75469

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Chain	Residue	Modelled	Actual	Comment	Reference
B	431J	SER	-	expression tag	UNP O75469
B	431K	SER	-	expression tag	UNP O75469
B	431L	HIS	-	expression tag	UNP O75469
B	431M	SER	-	expression tag	UNP O75469
B	444	SER	-	expression tag	UNP O75469
B	445	LEU	-	expression tag	UNP O75469
B	446	THR	-	expression tag	UNP O75469
B	447	GLU	-	expression tag	UNP O75469
B	448	ARG	-	expression tag	UNP O75469
B	449	HIS	-	expression tag	UNP O75469
B	450	LYS	-	expression tag	UNP O75469
B	451	ILE	-	expression tag	UNP O75469
B	452	LEU	-	expression tag	UNP O75469
B	453	HIS	-	expression tag	UNP O75469
B	454	ARG	-	expression tag	UNP O75469
B	455	LEU	-	expression tag	UNP O75469
B	456	LEU	-	expression tag	UNP O75469
B	457	GLN	-	expression tag	UNP O75469
B	458	GLU	-	expression tag	UNP O75469
B	459	GLY	-	expression tag	UNP O75469
B	460	SER	-	expression tag	UNP O75469
B	461	PRO	-	expression tag	UNP O75469
B	462	SER	-	expression tag	UNP O75469
B	463	ASP	-	expression tag	UNP O75469
B	464	ILE	-	expression tag	UNP O75469
B	465	THR	-	expression tag	UNP O75469
B	466	THR	-	expression tag	UNP O75469
B	467	LEU	-	expression tag	UNP O75469
B	468	SER	-	expression tag	UNP O75469
B	469	VAL	-	expression tag	UNP O75469
B	470	GLU	-	expression tag	UNP O75469
B	471	PRO	-	expression tag	UNP O75469
B	472	ASP	-	expression tag	UNP O75469

- Molecule 2 is N-[4-(1,1,1,3,3,3-hexafluoro-2-hydroxypropan-2-yl)phenyl]-N-hexylbenzenesulfonamide (three-letter code: WQB) (formula: C₂₁H₂₃F₆NO₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	F	N	O			S
2	A	1	Total	C	F	N	O	S	0	0
			32	21	6	1	3	1		
2	B	1	Total	C	F	N	O	S	0	0
			32	21	6	1	3	1		

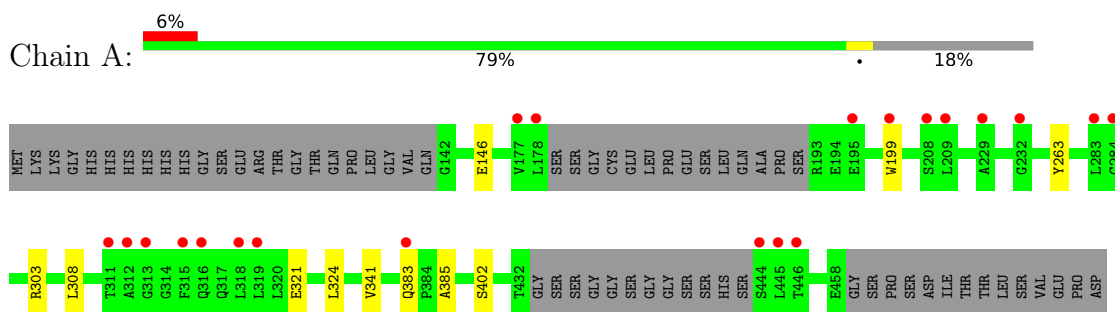
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	42	Total O 42 42	0	0
3	B	26	Total O 26 26	0	0

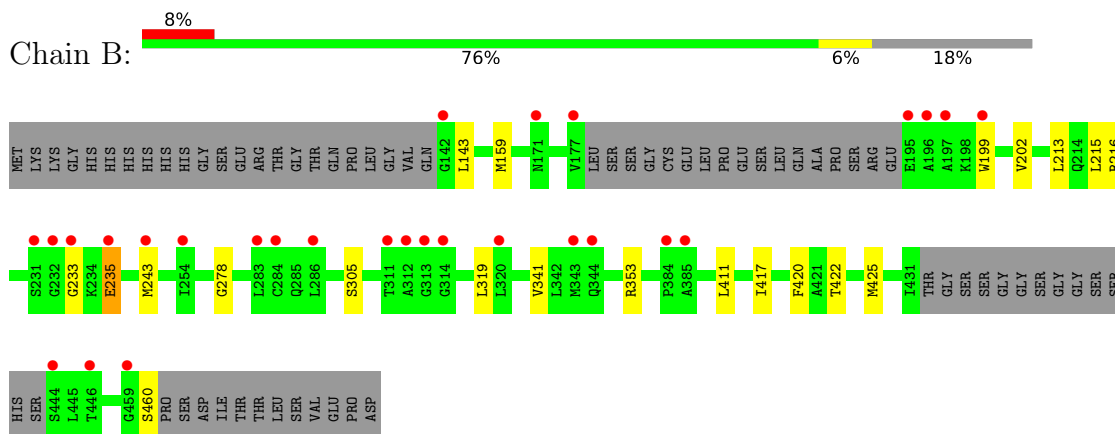
3 Residue-property plots [i](#)

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: Nuclear receptor subfamily 1 group I member 2



- Molecule 1: Nuclear receptor subfamily 1 group I member 2



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	85.37Å 89.00Å 105.56Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.57 – 2.37 29.57 – 2.37	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.57-2.37) 94.8 (29.57-2.37)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.32 (at 2.36Å)	Xtrriage
Refinement program	PHENIX 1.19.2_4158	Depositor
R, R_{free}	0.204 , 0.228 0.202 , 0.228	Depositor DCC
R_{free} test set	1657 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	47.8	Xtrriage
Anisotropy	0.042	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 45.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.006 for k,h,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4753	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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: WQB

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	0.45	0/2376	0.57	0/3207
1	B	0.44	0/2345	0.60	0/3166
All	All	0.44	0/4721	0.59	0/6373

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 [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	2326	0	2291	3	0
1	B	2295	0	2257	6	0
2	A	32	0	0	0	0
2	B	32	0	0	0	0
3	A	42	0	0	0	0
3	B	26	0	0	0	0
All	All	4753	0	4548	9	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 1.

The worst 5 of 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:B:202:VAL:HG11	1:B:417:ILE:HD11	1.95	0.49
1:B:422:THR:OG1	1:B:425:MET:HG3	2.15	0.47
1:B:233:GLY:C	1:B:235:GLU:H	2.19	0.46
1:A:308:LEU:HD21	1:A:324:LEU:HD21	1.99	0.44
1:B:278:GLY:HA3	1:B:353:ARG:HD2	2.01	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	A	287/355 (81%)	275 (96%)	11 (4%)	1 (0%)	41	53
1	B	285/355 (80%)	275 (96%)	10 (4%)	0	100	100
All	All	572/710 (81%)	550 (96%)	21 (4%)	1 (0%)	47	61

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	385	ALA

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	248/313 (79%)	243 (98%)	5 (2%)	55	72
1	B	243/313 (78%)	232 (96%)	11 (4%)	27	41
All	All	491/626 (78%)	475 (97%)	16 (3%)	38	55

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	341	VAL
1	B	319	LEU
1	B	215	LEU
1	B	305	SER
1	B	213	LEU

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

Mol	Chain	Res	Type
1	A	317	GLN
1	B	214	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](#)

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	WQB	B	501	-	33,33,33	3.02	10 (30%)	50,50,50	2.06	17 (34%)
2	WQB	A	501	-	33,33,33	3.03	11 (33%)	50,50,50	1.98	12 (24%)

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	WQB	B	501	-	-	6/46/46/46	0/2/2/2
2	WQB	A	501	-	-	12/46/46/46	0/2/2/2

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	WQB	C16-N15	9.91	1.56	1.48
2	A	501	WQB	C16-N15	9.07	1.55	1.48
2	A	501	WQB	S12-N15	7.40	1.75	1.65
2	B	501	WQB	C23-N15	6.82	1.54	1.44
2	A	501	WQB	C01-S12	6.72	1.85	1.76

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	WQB	O14-S12-O13	-6.95	108.26	119.52
2	B	501	WQB	O14-S12-O13	-6.27	109.36	119.52
2	B	501	WQB	O13-S12-N15	4.85	112.45	106.71
2	A	501	WQB	O13-S12-N15	4.65	112.21	106.71
2	B	501	WQB	C38-C33-C34	-4.03	105.23	110.28

There are no chirality outliers.

5 of 18 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	WQB	C24-C23-N15-S12
2	A	501	WQB	C16-N15-S12-C01
2	A	501	WQB	C16-N15-S12-O13

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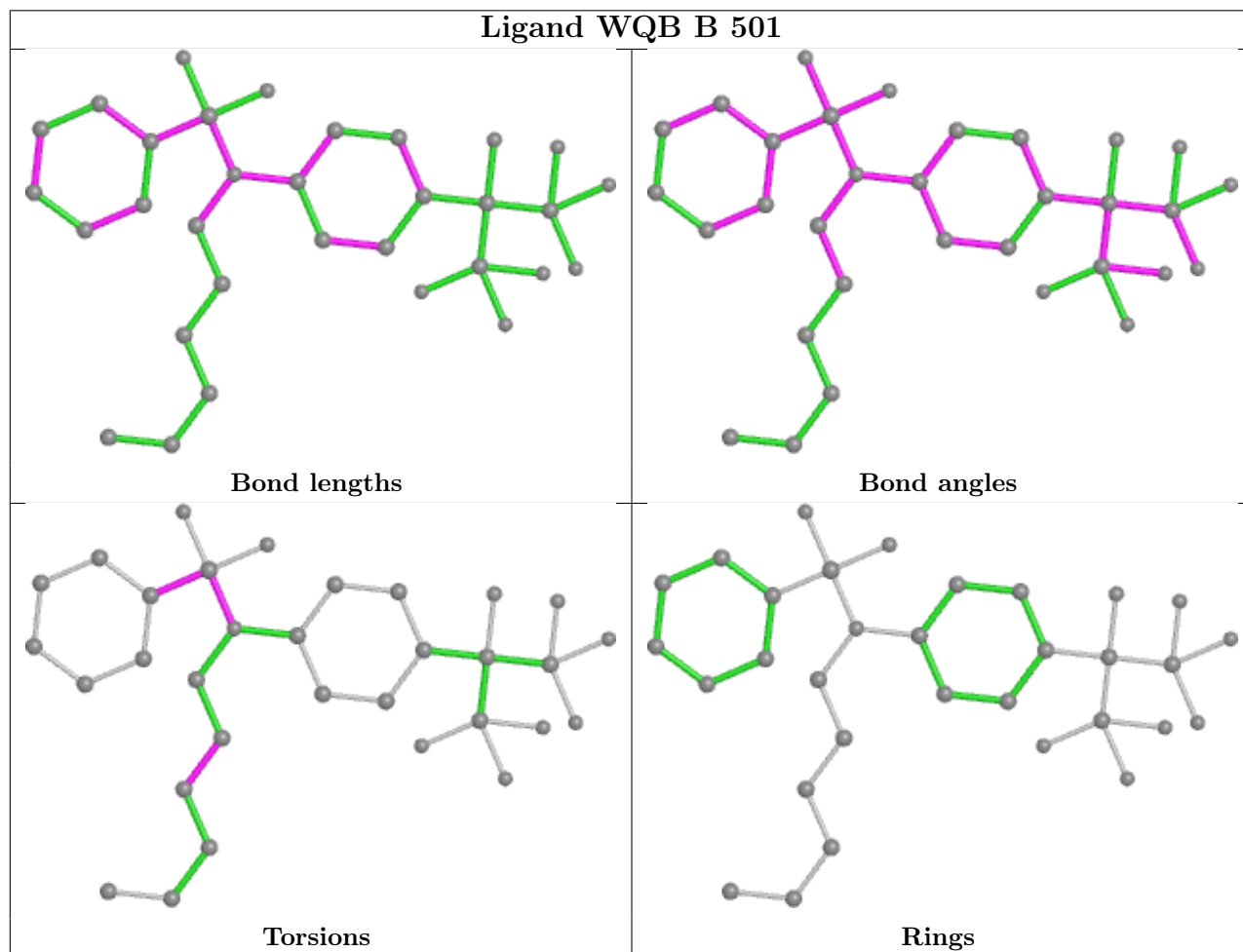
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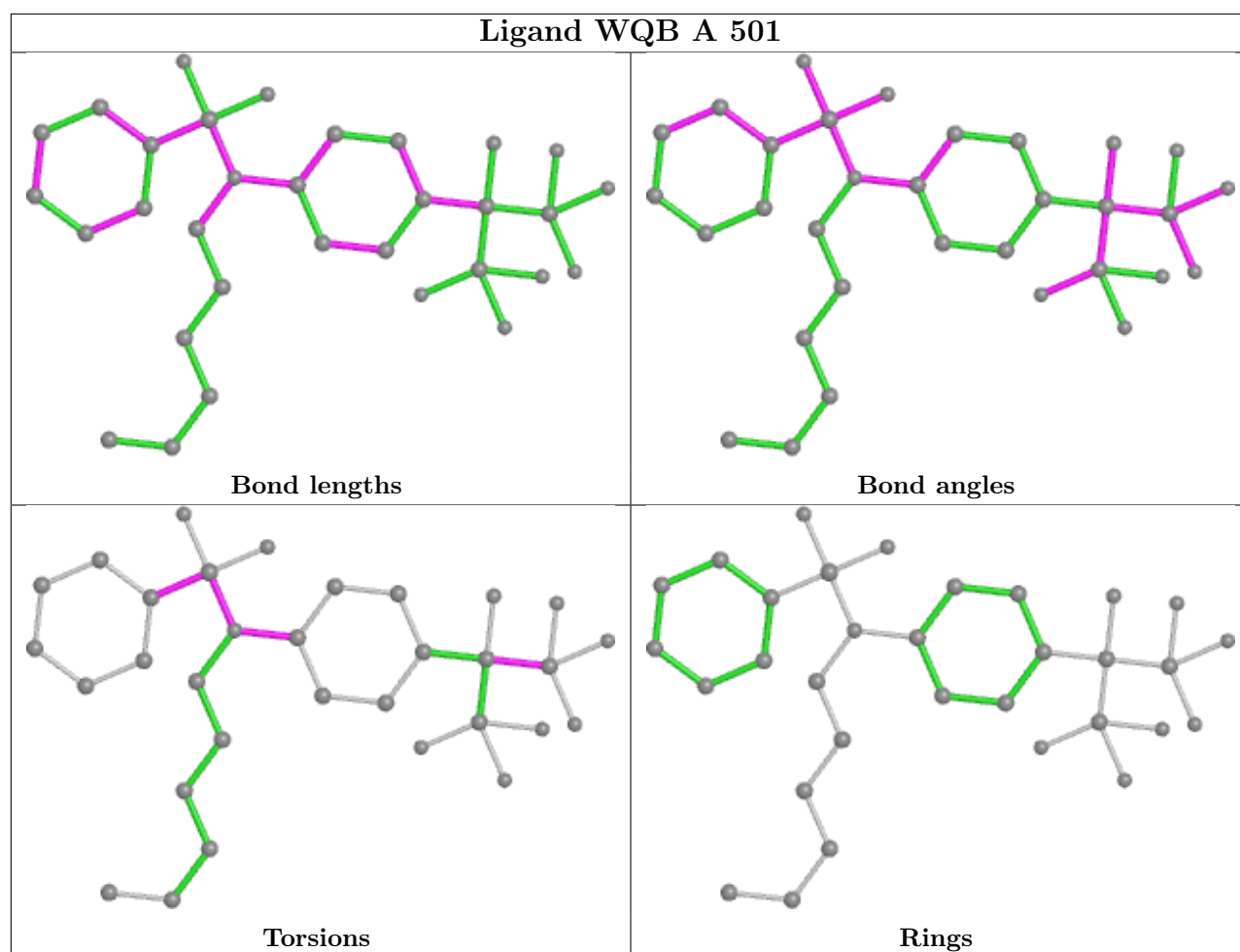
Mol	Chain	Res	Type	Atoms
2	B	501	WQB	C16-C19-C4-C3
2	A	501	WQB	C28-C23-N15-S12

There are no ring outliers.

No monomer is involved in short contacts.

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 [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	292/355 (82%)	0.39	21 (7%) 15 16	36, 56, 98, 132	0
1	B	290/355 (81%)	0.42	28 (9%) 7 8	33, 60, 96, 121	0
All	All	582/710 (81%)	0.41	49 (8%) 11 12	33, 57, 97, 132	0

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	313	GLY	7.1
1	A	445	LEU	6.5
1	A	446	THR	5.4
1	A	444	SER	5.4
1	B	314	GLY	5.1

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](#)

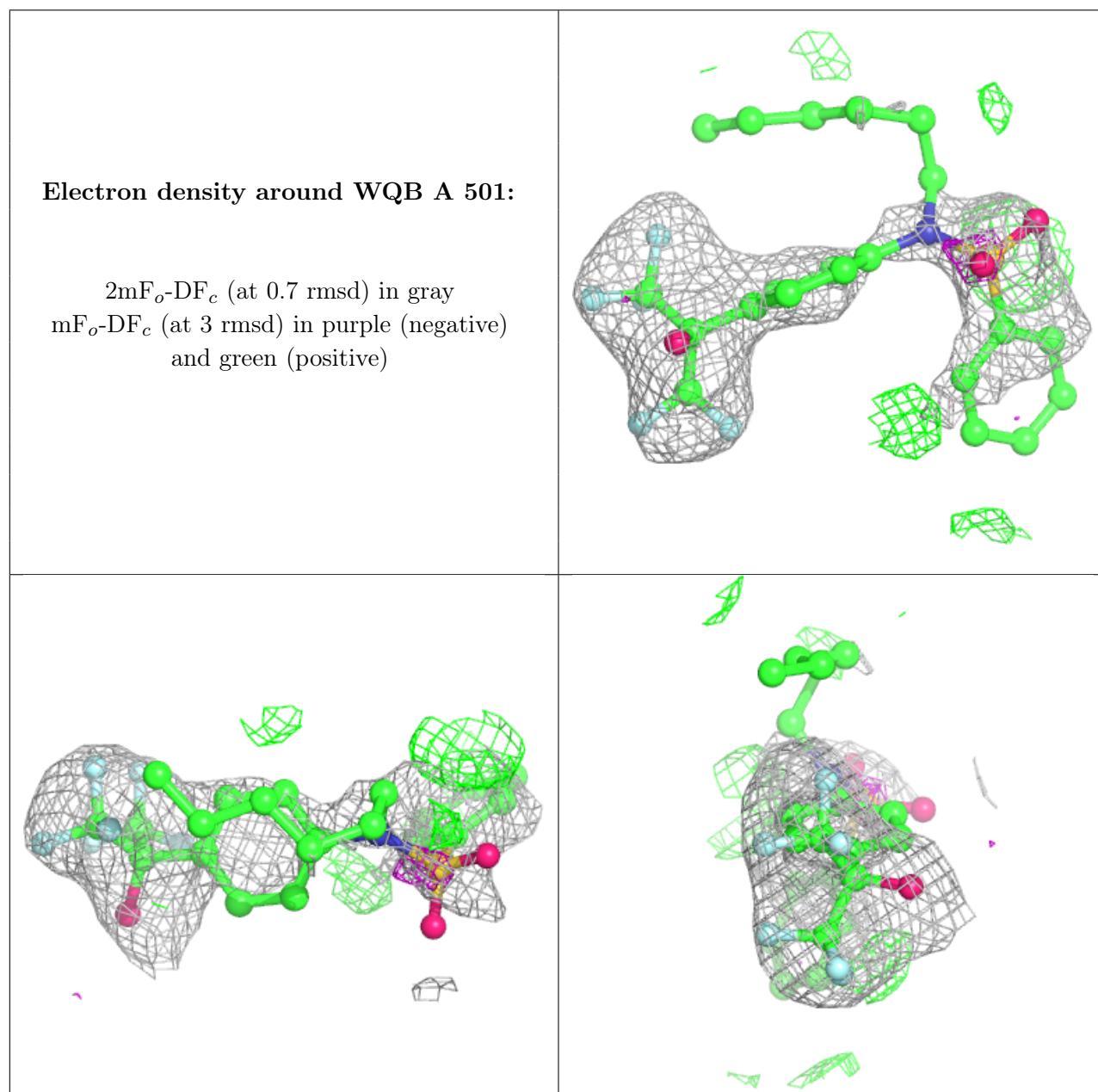
There are no monosaccharides in this entry.

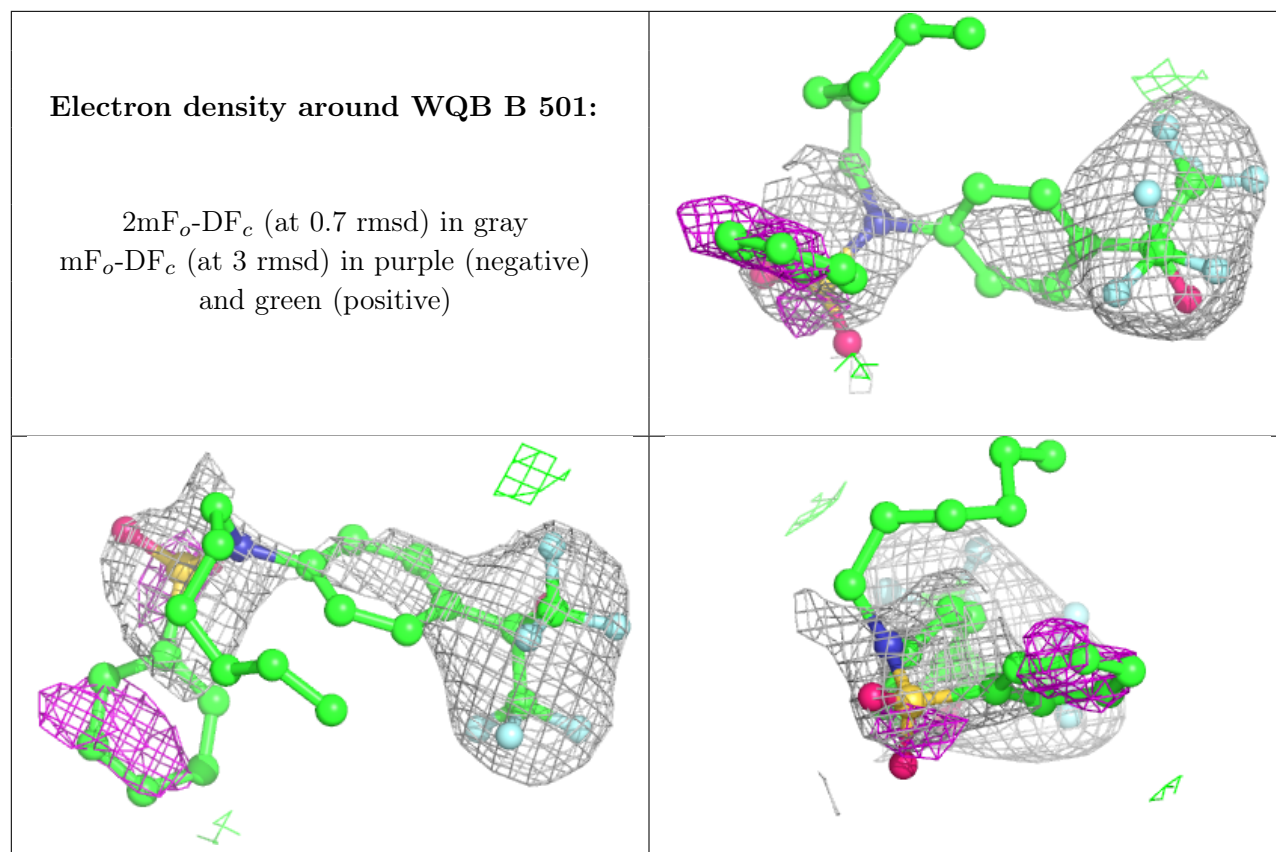
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
2	WQB	A	501	32/32	0.85	0.25	75,90,109,145	0
2	WQB	B	501	32/32	0.90	0.23	82,98,112,128	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 [i](#)

There are no such residues in this entry.