



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:50 AM UTC

PDB ID : 9F7X / pdb_00009f7x
Title : Human PPARgamma ligand binding domain in complex with co-activator 1alpha peptide and bisphenol B (BPB)
Authors : Useini, A.; Strater, N.
Deposited on : 2024-05-05
Resolution : 1.63 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 : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

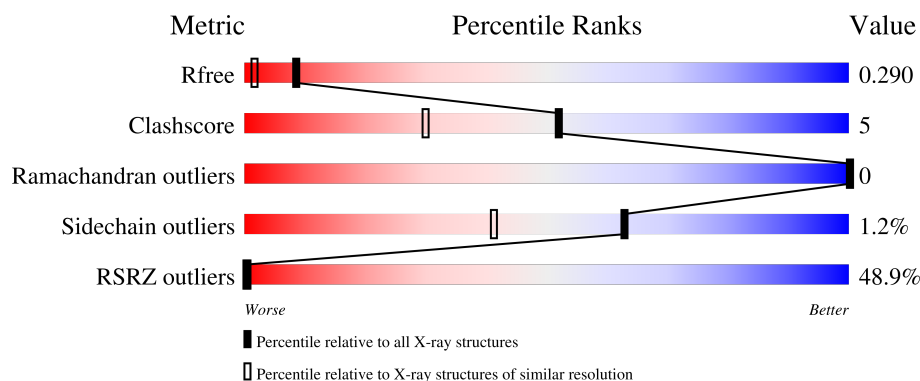
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.63 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}	180053	1141 (1.64-1.64)
Clashscore	190562	1171 (1.64-1.64)
Ramachandran outliers	187476	1151 (1.64-1.64)
Sidechain outliers	187428	1150 (1.64-1.64)
RSRZ outliers	180081	1141 (1.64-1.64)

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	283	45% 81% 12% 6%
2	B	19	37% 53% 5% 42%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4683 atoms, of which 2323 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	265	Total	C	H	N	O	S	0	4	0
			4340	1381	2200	347	401	11			

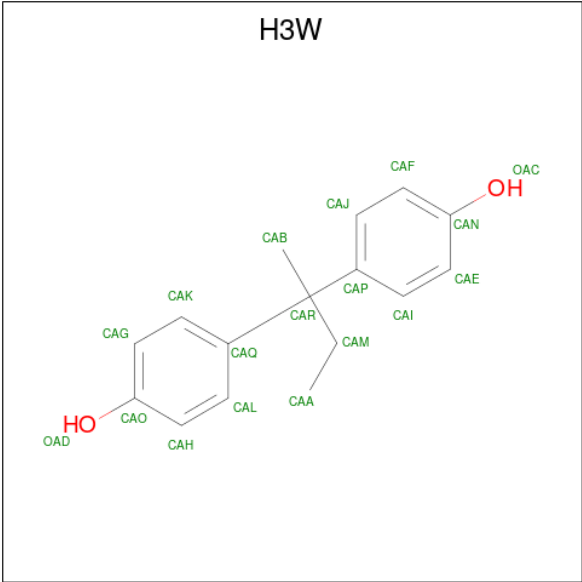
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	195	MET	-	initiating methionine	UNP P37231
A	196	ARG	-	expression tag	UNP P37231
A	197	GLY	-	expression tag	UNP P37231
A	198	SER	-	expression tag	UNP P37231
A	199	HIS	-	expression tag	UNP P37231
A	200	HIS	-	expression tag	UNP P37231
A	201	HIS	-	expression tag	UNP P37231
A	202	HIS	-	expression tag	UNP P37231
A	203	HIS	-	expression tag	UNP P37231
A	204	HIS	-	expression tag	UNP P37231
A	205	GLY	-	expression tag	UNP P37231

- Molecule 2 is a protein called Peroxisome proliferator-activated receptor gamma coactivator 1-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	11	Total	C	H	N	O	0	0	0
			188	58	105	13	12			

- Molecule 3 is bisphenol-B (CCD ID: H3W) (formula: C₁₆H₁₈O₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	H	O	0	1
			36	16	18	2		

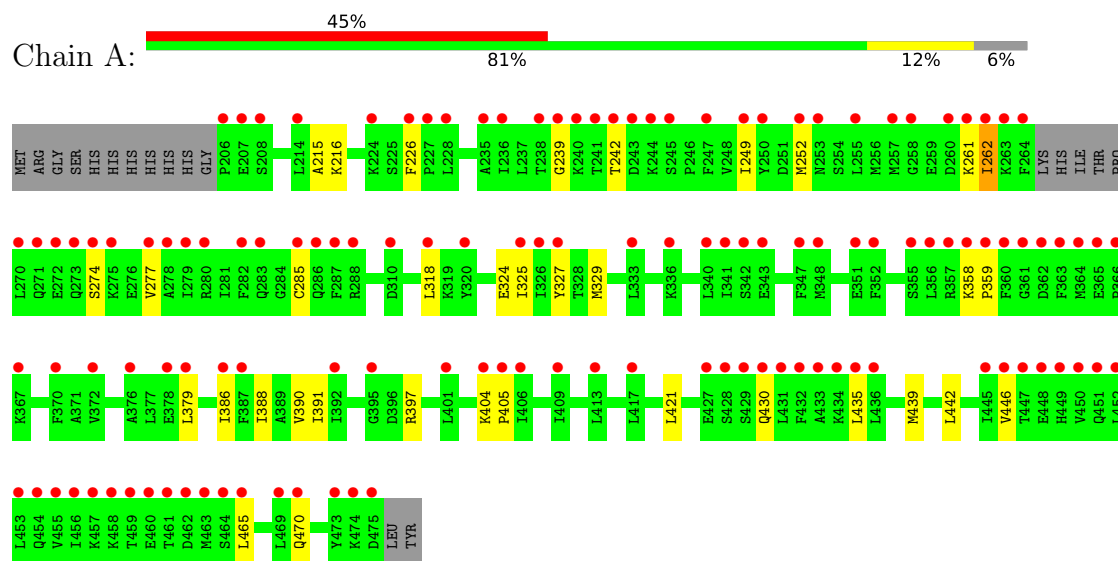
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	112	Total	O	0	4
			116	116		
4	B	3	Total	O	0	0
			3	3		

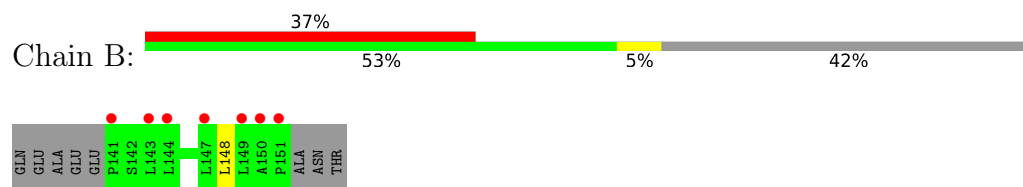
3 Residue-property plots [i](#)

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



- Molecule 2: Peroxisome proliferator-activated receptor gamma coactivator 1-alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	40.36Å 54.62Å 66.72Å 90.00° 93.60° 90.00°	Depositor
Resolution (Å)	42.23 – 1.63 42.23 – 1.63	Depositor EDS
% Data completeness (in resolution range)	40.1 (42.23-1.63) 36.0 (42.23-1.63)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.14 (at 1.63Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.249 , 0.290 0.249 , 0.290	Depositor DCC
R_{free} test set	2075 reflections (5.74%)	wwPDB-VP
Wilson B-factor (Å ²)	14.9	Xtriage
Anisotropy	4.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 35.2	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	0.86	EDS
Total number of atoms	4683	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.13% 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: H3W

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	0.15	0/2190	0.29	0/2948
2	B	0.17	0/84	0.28	0/112
All	All	0.15	0/2274	0.29	0/3060

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	2140	2200	2186	23	2
2	B	83	105	105	1	0
3	A	18	18	0	0	0
4	A	116	0	0	3	0
4	B	3	0	0	0	0
All	All	2360	2323	2291	23	2

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 (23) 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:215:ALA:O	4:A:671[B]:HOH:O	2.08	0.72
1:A:324:GLU:OE1	4:A:601:HOH:O	2.18	0.57
1:A:325:ILE:HD11	1:A:391:ILE:HB	1.89	0.53
1:A:252:MET:HE1	1:A:277:VAL:HG21	1.91	0.53
1:A:215:ALA:HB1	1:A:386:ILE:HD11	1.93	0.51
1:A:329[B]:MET:SD	1:A:388:ILE:HD11	2.52	0.49
1:A:226:PHE:CD2	1:A:329[A]:MET:HE1	2.47	0.49
1:A:390:VAL:HG11	1:A:439:MET:HE1	1.95	0.49
1:A:216:LYS:NZ	4:A:613:HOH:O	2.45	0.49
1:A:325:ILE:HD12	1:A:388:ILE:HG23	1.96	0.48
1:A:215:ALA:CB	1:A:386:ILE:HD11	2.44	0.48
1:A:318:LEU:HD11	2:B:148:LEU:HD21	1.97	0.45
1:A:442:LEU:O	1:A:446:VAL:HG23	2.18	0.44
1:A:226:PHE:CG	1:A:329[A]:MET:HE1	2.53	0.43
1:A:327[B]:TYR:CE2	1:A:446:VAL:HG22	2.53	0.43
1:A:465:LEU:HD23	1:A:470:GLN:HG2	2.00	0.43
1:A:249:ILE:CD1	1:A:262:ILE:HD11	2.48	0.43
1:A:261:LYS:O	1:A:262:ILE:C	2.61	0.43
1:A:249:ILE:HD11	1:A:262:ILE:HD11	2.01	0.41
1:A:421:LEU:HD11	1:A:435:LEU:HD12	2.02	0.41
1:A:379:LEU:HD11	1:A:435:LEU:HD21	2.03	0.41
1:A:358:LYS:N	1:A:359:PRO:CD	2.84	0.40
1:A:404:LYS:N	1:A:405:PRO:HD2	2.37	0.40

All (2) 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:239:GLY:O	1:A:274:SER:OG[2_545]	2.06	0.14
1:A:397:ARG:O	1:A:430:GLN:NE2[2_656]	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	265/283 (94%)	256 (97%)	9 (3%)	0	100	100
2	B	9/19 (47%)	9 (100%)	0	0	100	100
All	All	274/302 (91%)	265 (97%)	9 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	241/254 (95%)	238 (99%)	3 (1%)	63	41
2	B	10/16 (62%)	10 (100%)	0	100	100
All	All	251/270 (93%)	248 (99%)	3 (1%)	63	41

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	242	THR
1	A	262	ILE
1	A	285	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 oligosaccharides 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	H3W	A	501[B]	-	19,19,19	0.15	0	25,27,27	0.37	0

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	H3W	A	501[B]	-	-	7/15/15/15	0/2/2/2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

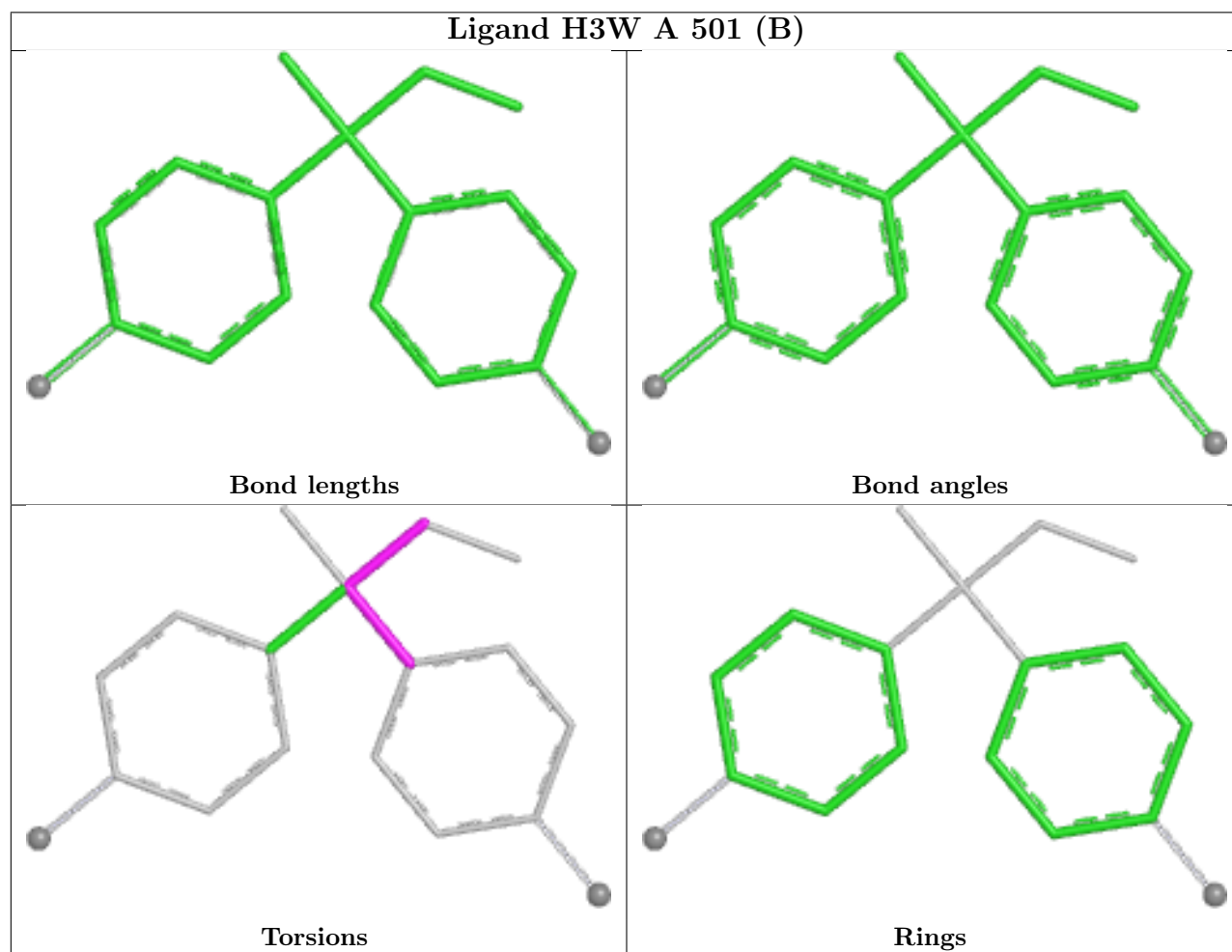
All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501[B]	H3W	CAA-CAM-CAR-CAP
3	A	501[B]	H3W	CAK-CAQ-CAR-CAM
3	A	501[B]	H3W	CAL-CAQ-CAR-CAM
3	A	501[B]	H3W	CAA-CAM-CAR-CAQ
3	A	501[B]	H3W	CAL-CAQ-CAR-CAP
3	A	501[B]	H3W	CAK-CAQ-CAR-CAP
3	A	501[B]	H3W	CAK-CAQ-CAR-CAB

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 ⓘ

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	265/283 (93%)	2.34	128 (48%) 0 0	7, 24, 72, 103	3 (1%)
2	B	11/19 (57%)	3.35	7 (63%) 0 0	13, 22, 64, 80	0
All	All	276/302 (91%)	2.38	135 (48%) 0 0	7, 24, 74, 103	3 (1%)

All (135) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	141	PRO	8.1
1	A	363	PHE	8.0
1	A	452	LEU	7.5
1	A	456	ILE	7.2
1	A	261	LYS	7.2
1	A	287	PHE	7.0
1	A	260	ASP	6.8
1	A	327[A]	TYR	6.6
1	A	270	LEU	6.6
2	B	151	PRO	6.5
1	A	262	ILE	6.4
1	A	429	SER	6.4
1	A	361	GLY	6.1
2	B	150	ALA	6.0
1	A	461	THR	5.8
1	A	454	GLN	5.7
1	A	457	LYS	5.5
1	A	463	MET	5.5
1	A	263	LYS	5.5
1	A	458	LYS	5.4
1	A	428	SER	5.3
1	A	274	SER	5.1
1	A	275	LYS	5.1
1	A	473	TYR	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	273	GLN	5.0
1	A	206	PRO	5.0
1	A	455	VAL	4.9
1	A	358	LYS	4.9
1	A	372	VAL	4.9
1	A	277	VAL	4.9
1	A	351	GLU	4.7
1	A	227	PRO	4.6
1	A	245	SER	4.6
1	A	459	THR	4.5
1	A	445	ILE	4.4
1	A	272	GLU	4.4
1	A	465	LEU	4.4
1	A	430	GLN	4.4
1	A	283	GLN	4.4
1	A	244	LYS	4.3
1	A	451	GLN	4.3
1	A	242	THR	4.2
1	A	282	PHE	4.2
1	A	475	ASP	4.1
1	A	360	PHE	4.0
1	A	366	PRO	4.0
1	A	252	MET	4.0
1	A	264	PHE	4.0
1	A	271	GLN	4.0
1	A	448	GLU	4.0
1	A	462	ASP	3.9
1	A	362	ASP	3.6
1	A	286	GLN	3.6
1	A	450	VAL	3.5
1	A	310	ASP	3.5
1	A	336	LYS	3.5
1	A	347	PHE	3.5
1	A	447	THR	3.5
1	A	446	VAL	3.4
1	A	342	SER	3.4
1	A	279	ILE	3.4
1	A	431	LEU	3.4
1	A	241	THR	3.4
1	A	280	ARG	3.4
1	A	235	ALA	3.3
1	A	432	PHE	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	285	CYS	3.2
1	A	357	ARG	3.2
1	A	359	PRO	3.2
1	A	370	PHE	3.2
1	A	250	TYR	3.1
1	A	367	LYS	3.1
1	A	433	ALA	3.1
1	A	395	GLY	3.1
1	A	434	LYS	3.1
1	A	247	PHE	3.0
1	A	224	LYS	3.0
1	A	243	ASP	3.0
1	A	464	SER	3.0
1	A	255	LEU	2.9
2	B	147	LEU	2.9
1	A	469	LEU	2.9
1	A	340	LEU	2.8
1	A	392	ILE	2.8
1	A	453	LEU	2.8
1	A	236	ILE	2.8
1	A	378	GLU	2.8
1	A	240	LYS	2.7
1	A	239	GLY	2.7
2	B	143	LEU	2.7
1	A	474	LYS	2.7
1	A	436	LEU	2.7
1	A	409	ILE	2.7
1	A	413	LEU	2.6
1	A	435	LEU	2.6
1	A	249	ILE	2.6
1	A	427	GLU	2.6
1	A	228	LEU	2.5
1	A	379	LEU	2.5
1	A	258	GLY	2.5
2	B	149	LEU	2.5
1	A	318	LEU	2.5
1	A	352	PHE	2.5
1	A	387	PHE	2.5
1	A	401	LEU	2.5
1	A	406	ILE	2.5
1	A	257	MET	2.5
1	A	343	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	364	MET	2.4
1	A	253	ASN	2.4
1	A	288	ARG	2.4
1	A	226	PHE	2.4
1	A	348	MET	2.4
1	A	278	ALA	2.3
1	A	356	LEU	2.3
1	A	325	ILE	2.3
1	A	376	ALA	2.3
1	A	326	ILE	2.3
1	A	238	THR	2.2
1	A	208	SER	2.2
1	A	417	LEU	2.2
1	A	365	GLU	2.2
1	A	386	ILE	2.2
1	A	355	SER	2.2
1	A	449	HIS	2.1
2	B	144	LEU	2.1
1	A	405	PRO	2.1
1	A	320	TYR	2.1
1	A	341	ILE	2.1
1	A	470	GLN	2.1
1	A	404	LYS	2.1
1	A	207	GLU	2.0
1	A	460	GLU	2.0
1	A	214	LEU	2.0
1	A	333	LEU	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 oligosaccharides in this entry.

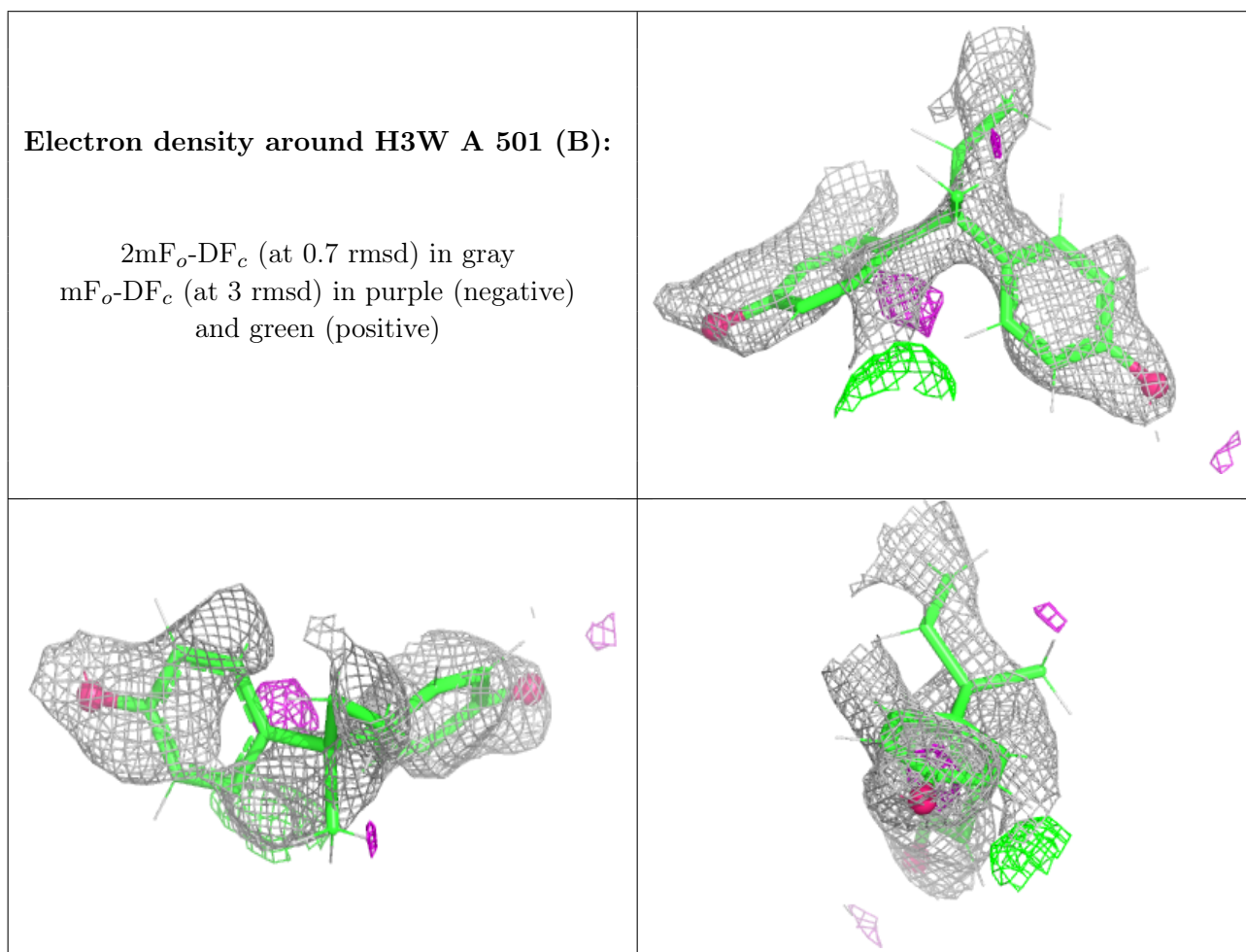
6.4 Ligands [i](#)

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
3	H3W	A	501[B]	18/18	0.66	0.21	30,30,37,38	36

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.