



# Full wwPDB X-ray Structure Validation Report ⓘ

Jun 22, 2024 – 07:59 PM EDT

PDB ID : 6BNS

Title : STRUCTURE OF HUMAN PREGNANE X RECEPTOR LIGAND BINDING DOMAIN BOUND TETHERED WITH SRC co-activator peptide and Compound 25a AKA BICYCLIC HEXAFLUOROISOPROPYL 2 ALCOHOL SULFONAMIDES

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Deposited on : 2017-11-17

Resolution : 2.56 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](mailto: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>.

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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

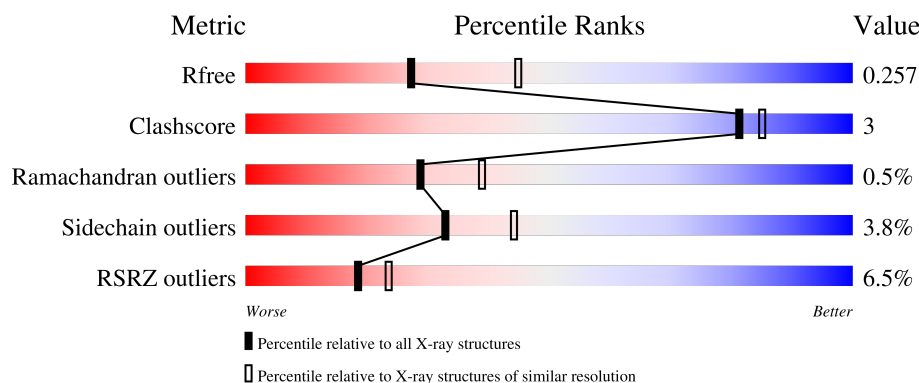
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.56 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	1279 (2.58-2.54)
Clashscore	141614	1327 (2.58-2.54)
Ramachandran outliers	138981	1312 (2.58-2.54)
Sidechain outliers	138945	1312 (2.58-2.54)
RSRZ outliers	127900	1269 (2.58-2.54)

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  $\geq 3$ , 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.

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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

Mol	Chain	Length	Quality of chain
1	A	351	<div><div></div><div>5%</div><div>74%</div><div>8%</div><div>19%</div></div>
1	B	351	<div><div></div><div>6%</div><div>73%</div><div>7%</div><div>19%</div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4583 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, Nuclear receptor coactivator 1 Chimera.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	2	0
			2225	1438	375	393	19			
1	B	283	Total	C	N	O	S	0	0	0
			2212	1430	372	393	17			

There are 26 discrepancies between the modelled and reference sequences:

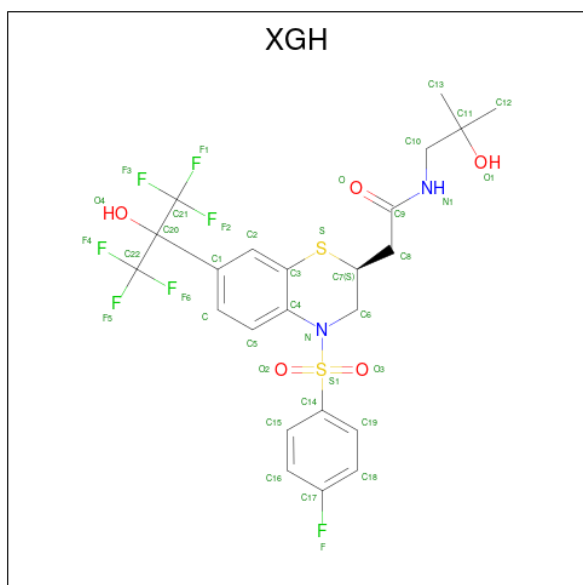
Chain	Residue	Modelled	Actual	Comment	Reference
A	123	HIS	-	expression tag	UNP O75469
A	124	HIS	-	expression tag	UNP O75469
A	125	HIS	-	expression tag	UNP O75469
A	126	HIS	-	expression tag	UNP O75469
A	127	HIS	-	expression tag	UNP O75469
A	128	HIS	-	expression tag	UNP O75469
A	129	GLY	-	expression tag	UNP O75469
A	432C	SER	-	linker	UNP O75469
A	432D	GLY	-	linker	UNP O75469
A	432E	GLY	-	linker	UNP O75469
A	432F	SER	-	linker	UNP O75469
A	432G	GLY	-	linker	UNP O75469
A	432H	GLY	-	linker	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	432C	SER	-	linker	UNP O75469
B	432D	GLY	-	linker	UNP O75469
B	432E	GLY	-	linker	UNP O75469
B	432F	SER	-	linker	UNP O75469

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Chain	Residue	Modelled	Actual	Comment	Reference
B	432G	GLY	-	linker	UNP O75469
B	432H	GLY	-	linker	UNP O75469

- Molecule 2 is 2-[(2S)-4-[(4-fluorophenyl)sulfonyl]-7-(1,1,1,3,3,3-hexafluoro-2-hydroxypropyl)-3,4-dihydro-2H-1,4-benzothiazin-2-yl]-N-(2-hydroxy-2-methylpropyl)acetamide (three-letter code: XGH) (formula: C<sub>23</sub>H<sub>23</sub>F<sub>7</sub>N<sub>2</sub>O<sub>5</sub>S<sub>2</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			39	23	7	2	5	2		
2	B	1	Total	C	F	N	O	S	0	0
			38	23	6	2	5	2		

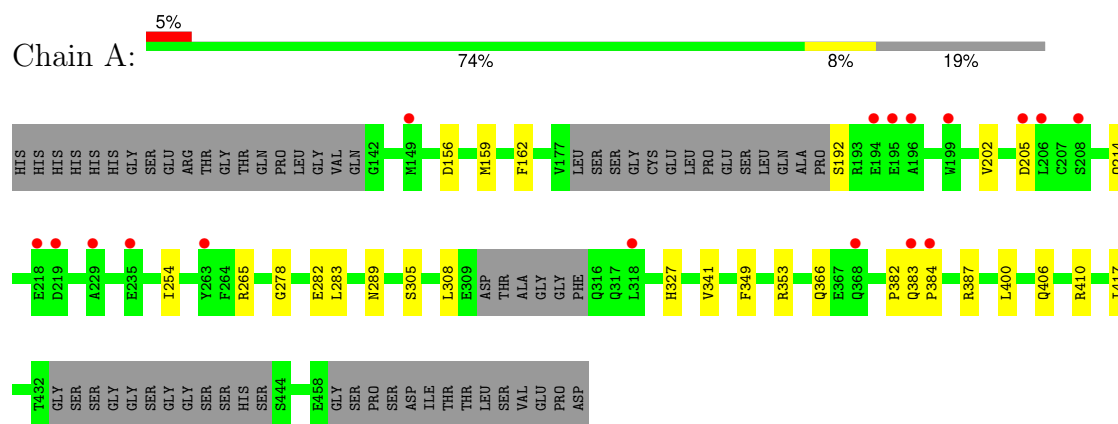
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	38	Total	O	0	0
			38	38		
3	B	31	Total	O	0	0
			31	31		

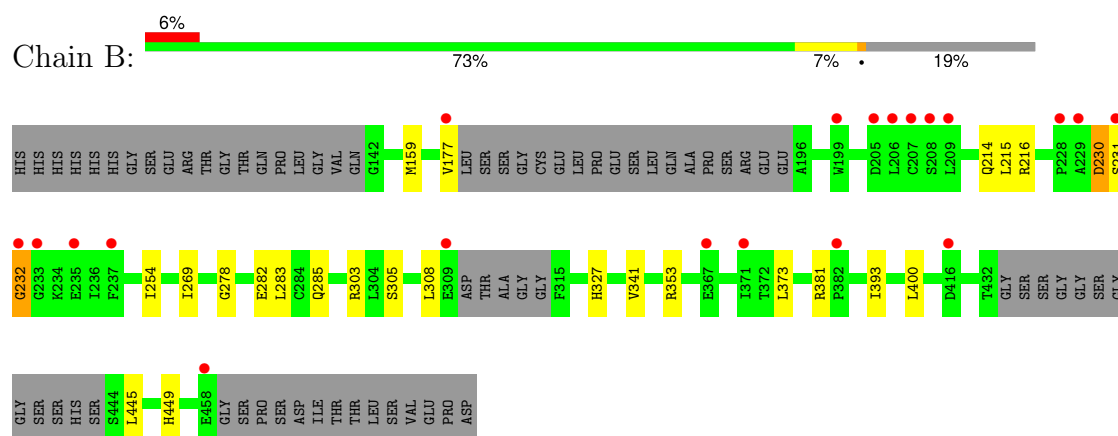
### 3 Residue-property plots

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, Nuclear receptor coactivator 1 Chimera



- Molecule 1: Nuclear receptor subfamily 1 group I member 2, Nuclear receptor coactivator 1 Chimera



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	84.37Å 89.23Å 105.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.54 – 2.56 45.54 – 2.56	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.54-2.56) 99.9 (45.54-2.56)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.77 (at 2.54Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, $R_{free}$	0.203 , 0.246 0.213 , 0.257	Depositor DCC
$R_{free}$ test set	1339 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	48.8	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 51.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4583	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: XGH

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	0.50	0/2277	0.64	0/3080
1	B	0.51	0/2261	0.65	0/3060
All	All	0.51	0/4538	0.65	0/6140

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	2225	0	2120	11	0
1	B	2212	0	2126	12	0
2	A	39	0	0	0	0
2	B	38	0	0	0	0
3	A	38	0	0	2	0
3	B	31	0	0	0	0
All	All	4583	0	4246	23	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 3.

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:289:ASN:HD22	1:A:327:HIS:HD1	1.40	0.68
1:A:282:GLU:HG2	1:A:400:LEU:HG	1.78	0.65
1:B:278:GLY:HA3	1:B:353:ARG:HD2	1.81	0.63
1:B:285:GLN:NE2	1:B:327:HIS:HE2	1.98	0.61
1:A:202:VAL:HG11	1:A:417:ILE:HD11	1.83	0.60
1:A:384:PRO:HG2	3:A:627:HOH:O	2.02	0.58
1:A:384:PRO:CG	3:A:627:HOH:O	2.60	0.50
1:A:254:ILE:HG12	1:A:283:LEU:HB3	1.94	0.49
1:B:282:GLU:HG2	1:B:400:LEU:HG	1.94	0.49
1:B:285:GLN:HE21	1:B:327:HIS:HE2	1.61	0.49
1:B:254:ILE:HD12	1:B:283:LEU:HB3	1.95	0.49
1:A:349:PHE:O	1:A:366:GLN:HB2	2.13	0.47
1:B:214:GLN:HB3	1:B:305:SER:HB2	1.96	0.47
1:A:278:GLY:HA3	1:A:353:ARG:HD2	1.95	0.47
1:A:383:GLN:HA	1:A:384:PRO:HA	1.65	0.46
1:B:445:LEU:O	1:B:449:HIS:CD2	2.68	0.46
1:B:445:LEU:O	1:B:449:HIS:HD2	1.99	0.45
1:A:214:GLN:HB3	1:A:305:SER:HB2	1.97	0.45
1:B:214:GLN:HE21	1:B:216:ARG:HH11	1.66	0.44
1:A:205:ASP:HB3	1:A:410:ARG:HG2	1.99	0.43
1:B:231:SER:HA	1:B:232:GLY:HA3	1.77	0.43
1:B:230:ASP:CG	1:B:231:SER:H	2.22	0.42
1:B:373:LEU:HD21	1:B:393:ILE:HG21	2.02	0.41

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	280/351 (80%)	270 (96%)	9 (3%)	1 (0%)	34	45
1	B	275/351 (78%)	265 (96%)	8 (3%)	2 (1%)	22	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	555/702 (79%)	535 (96%)	17 (3%)	3 (0%)	29	39

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	382	PRO
1	B	230	ASP
1	B	232	GLY

### 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	223/310 (72%)	214 (96%)	9 (4%)	31	42
1	B	226/310 (73%)	218 (96%)	8 (4%)	36	48
All	All	449/620 (72%)	432 (96%)	17 (4%)	33	44

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	156	ASP
1	A	159	MET
1	A	162	PHE
1	A	192	SER
1	A	265	ARG
1	A	308	LEU
1	A	341	VAL
1	A	387	ARG
1	A	406	GLN
1	B	159	MET
1	B	177	VAL
1	B	215	LEU
1	B	269	ILE
1	B	303	ARG
1	B	308	LEU

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Mol	Chain	Res	Type
1	B	341	VAL
1	B	381	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	214	GLN
1	A	272	GLN
1	A	285	GLN
1	A	449	HIS
1	B	214	GLN
1	B	224	ASN
1	B	272	GLN
1	B	285	GLN
1	B	449	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 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	XGH	B	501	-	37,40,41	1.02	3 (8%)	51,63,66	0.74	3 (5%)
2	XGH	A	501	-	39,41,41	0.80	1 (2%)	59,66,66	0.73	2 (3%)

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	XGH	B	501	-	-	1/41/55/58	0/3/3/3
2	XGH	A	501	-	-	1/46/58/58	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	XGH	C6-N	4.08	1.53	1.48
2	A	501	XGH	C6-N	4.02	1.53	1.48
2	B	501	XGH	C10-C11	2.71	1.57	1.52
2	B	501	XGH	C22-C20	2.56	1.56	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	501	XGH	C4-N-S1	2.51	126.88	120.26
2	B	501	XGH	C10-N1-C9	2.36	126.34	123.23
2	A	501	XGH	C10-N1-C9	2.18	126.11	123.23
2	B	501	XGH	C12-C11-C10	2.14	115.56	110.11
2	A	501	XGH	C21-C20-C22	2.06	112.72	110.23

There are no chirality outliers.

All (2) torsion outliers are listed below:

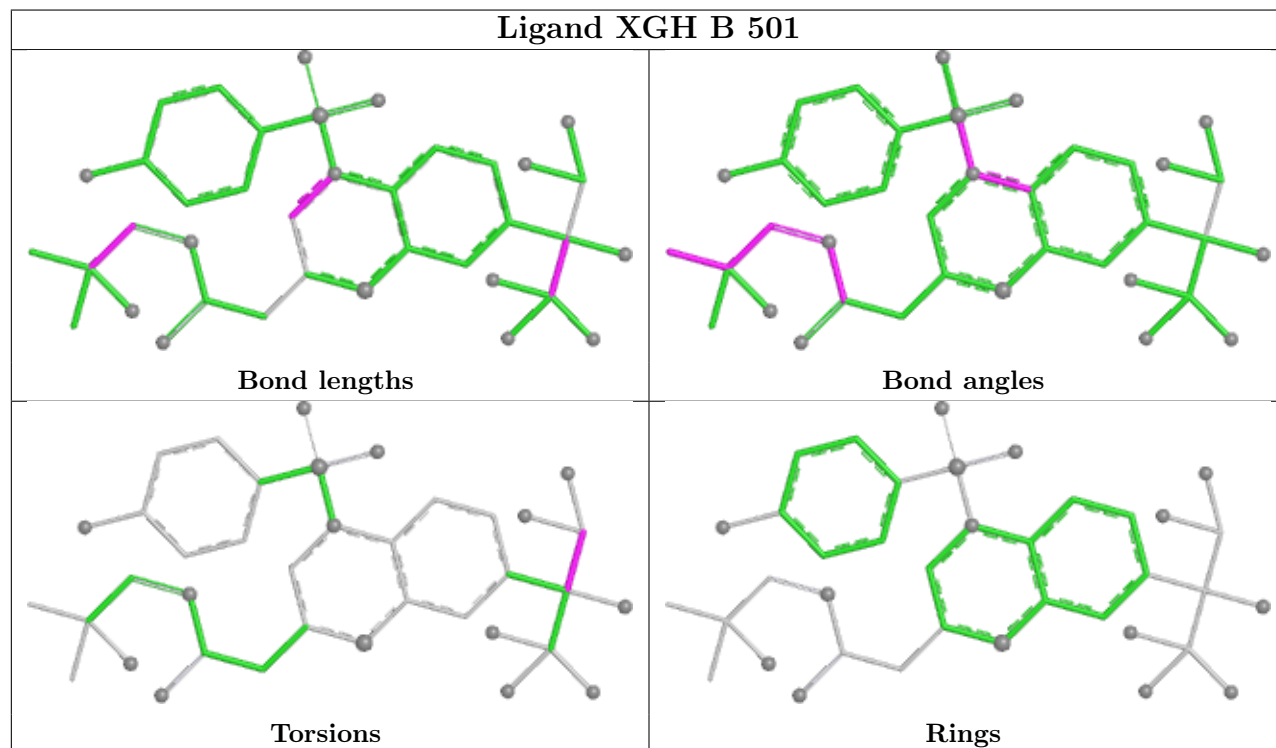
Mol	Chain	Res	Type	Atoms
2	B	501	XGH	C1-C20-C21-F3
2	A	501	XGH	C15-C14-S1-O3

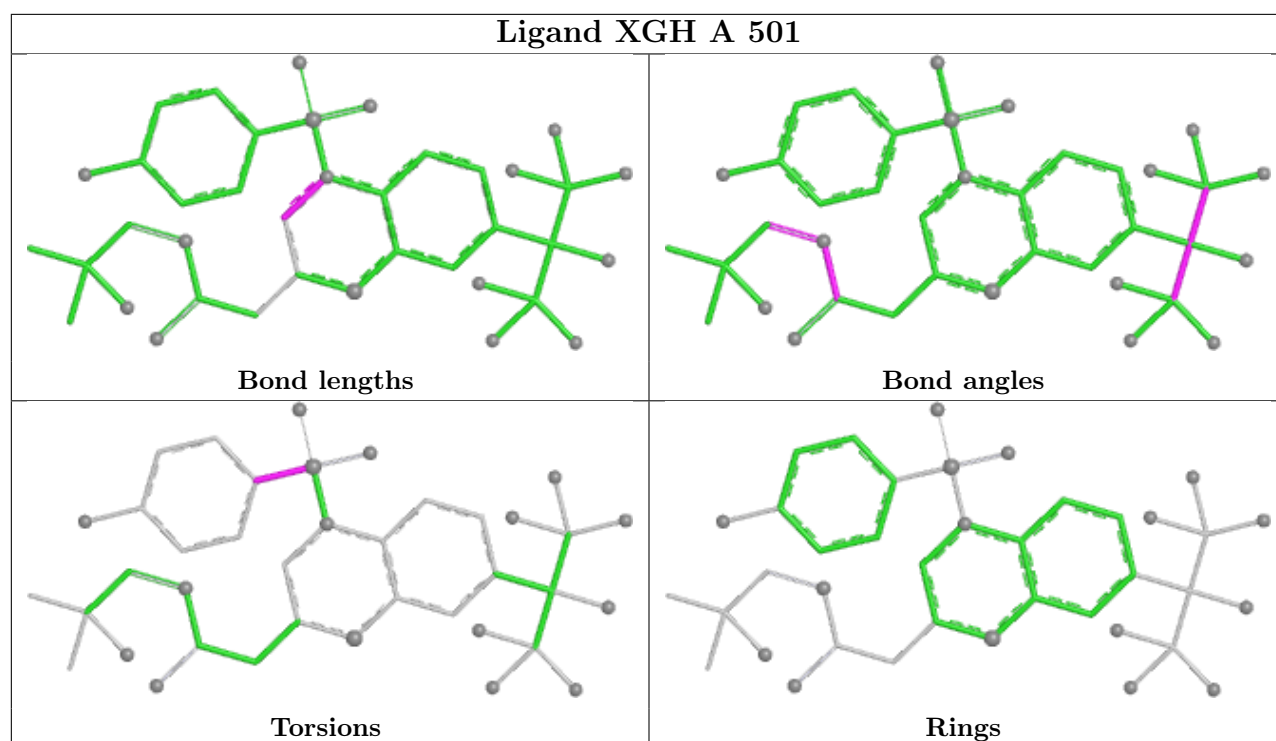
There are no ring outliers.

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

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	286/351 (81%)	0.36	17 (5%) 22 27	32, 53, 86, 107	0
1	B	283/351 (80%)	0.39	20 (7%) 16 20	32, 52, 92, 110	0
All	All	569/702 (81%)	0.37	37 (6%) 18 23	32, 53, 91, 110	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	206	LEU	10.0
1	B	207	CYS	6.4
1	B	205	ASP	5.5
1	B	208	SER	4.2
1	A	199	TRP	4.0
1	B	231	SER	3.5
1	A	205	ASP	3.5
1	A	149	MET	3.5
1	B	232	GLY	3.3
1	A	229	ALA	3.2
1	B	233	GLY	2.9
1	B	177	VAL	2.9
1	B	237	PHE	2.9
1	A	384	PRO	2.8
1	B	209	LEU	2.8
1	A	383	GLN	2.7
1	A	196	ALA	2.7
1	A	235	GLU	2.5
1	B	229	ALA	2.5
1	A	206	LEU	2.4
1	A	318	LEU	2.4
1	A	263	TYR	2.3
1	A	194	GLU	2.3
1	A	219	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	195	GLU	2.3
1	A	208	SER	2.3
1	A	368	GLN	2.2
1	B	416	ASP	2.1
1	B	309	GLU	2.1
1	B	228	PRO	2.1
1	B	458	GLU	2.1
1	B	235	GLU	2.1
1	B	371	ILE	2.1
1	A	218	GLU	2.1
1	B	367	GLU	2.0
1	B	199	TRP	2.0
1	B	382	PRO	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, 95<sup>th</sup> 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.

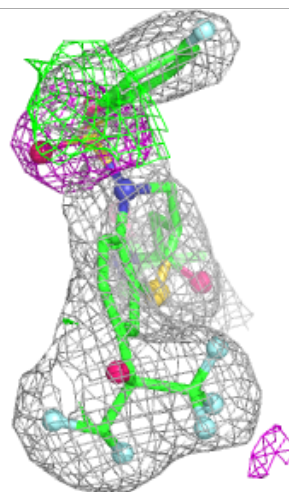
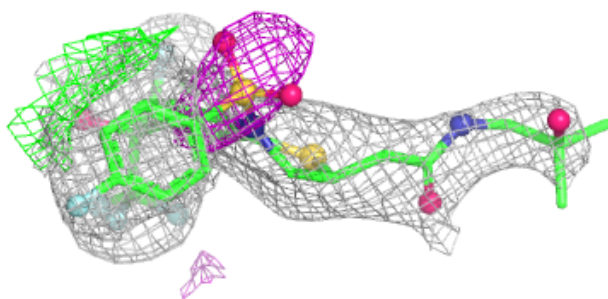
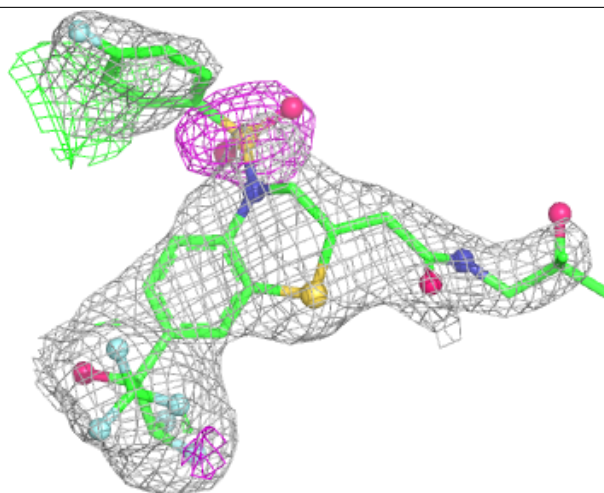
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
2	XGH	B	501	38/39	0.80	0.33	74,87,111,114	0
2	XGH	A	501	39/39	0.84	0.20	72,79,103,106	0

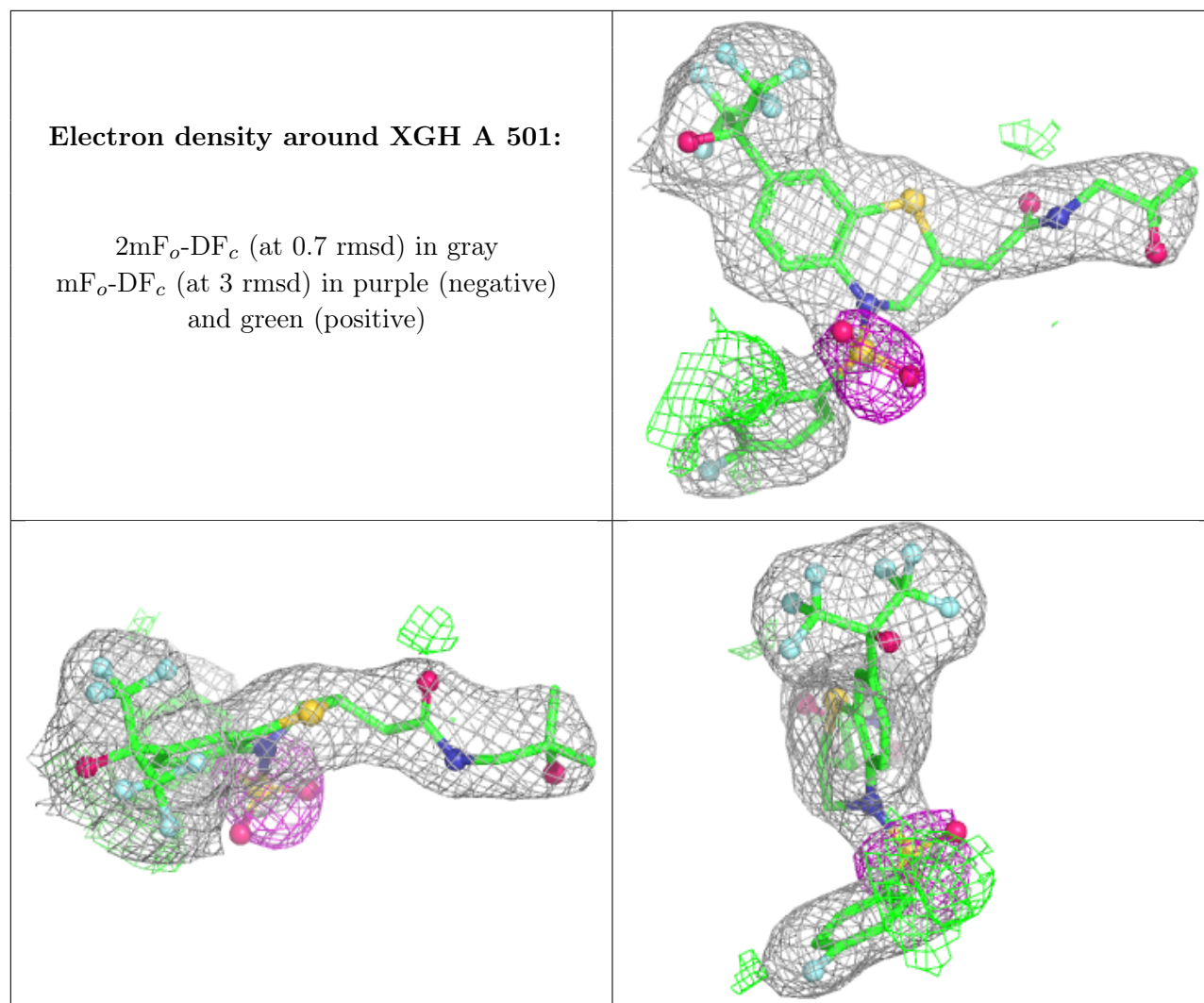
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



**Electron density around XGH B 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 ⓘ

There are no such residues in this entry.