Full wwPDB X-ray Structure Validation Report (i)

Jun 7, 2020 – 02:55 am BST

PDB ID	:	6HTY
Title	:	PXR in complex with P2X4 inhibitor compound 25
Authors	:	Hillig, R.C.; Puetter, V.; Werner, S.; Mesch, S.; Laux-Biehlmann, A.; Braeuer, N.; Dahloef, H.; Klint, J.; ter Laak, A.; Pook, E.; Neagoe, I.; Nubbemeyer, R.; Schulz, S.
Deposited on	:	2018-10-05
Resolution	:	2.22 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 (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

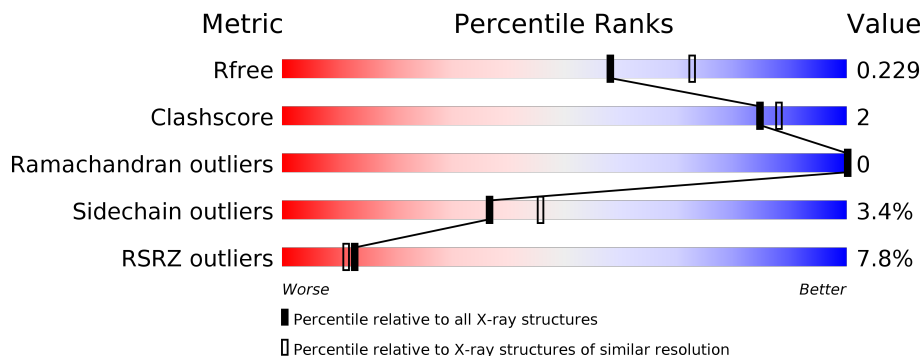|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.22 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	Percentile Ranks	Value
Rfree		0.229
Clashscore		2
Ramachandran outliers		0
Sidechain outliers		3.4%
RSRZ outliers		7.8%

Worse — *Better*

■ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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 <=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	344	8% / 80% green, 7% yellow, 13% grey
1	B	344	5% / 81% green, 6% orange, · , 12% grey

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5181 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	298	Total 2478	C 1585	N 430	O 443	S 20	0	10	0
1	B	302	Total 2500	C 1605	N 430	O 444	S 21	0	8	0

There are 32 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	LYS	cloning artifact	UNP O75469
A	435	GLY	-	linker	UNP O75469
A	436	GLY	-	linker	UNP O75469
A	437	SER	-	linker	UNP O75469
A	438	GLY	-	linker	UNP O75469
A	439	GLY	-	linker	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

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Chain	Residue	Modelled	Actual	Comment	Reference
B	127	HIS	-	expression tag	UNP O75469
B	128	HIS	-	expression tag	UNP O75469
B	129	GLY	LYS	cloning artifact	UNP O75469
B	435	GLY	-	linker	UNP O75469
B	436	GLY	-	linker	UNP O75469
B	437	SER	-	linker	UNP O75469
B	438	GLY	-	linker	UNP O75469
B	439	GLY	-	linker	UNP O75469

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).
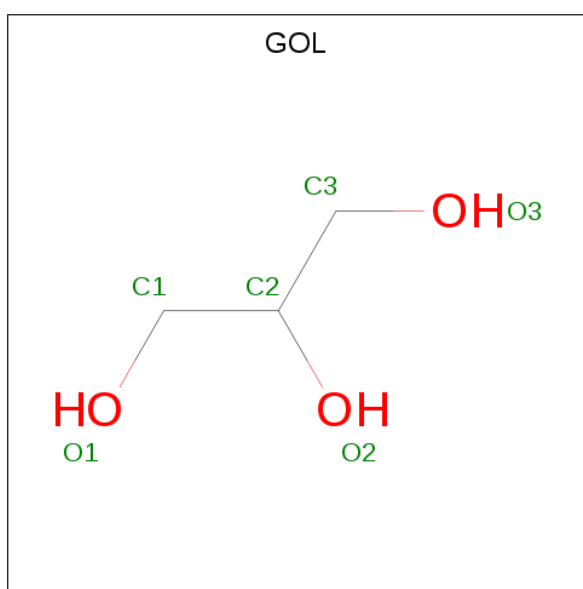
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total C O			0	0
			6	3	3		

- Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).

DMS

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 1	S 1	0	0
3	A	1	Total 4	C 2	O 1	S 1	0	0
3	A	1	Total 4	C 2	O 1	S 1	0	0
3	B	1	Total 4	C 2	O 1	S 1	0	0
3	B	1	Total 4	C 2	O 1	S 1	0	0

- Molecule 4 is (2 {R})- {N}-[4-(3-chloranylphenoxy)-3-sulfamoyl-phenyl]-2-phenyl-propana mide (three-letter code: GRH) (formula: $C_{21}H_{19}ClN_2O_4S$).
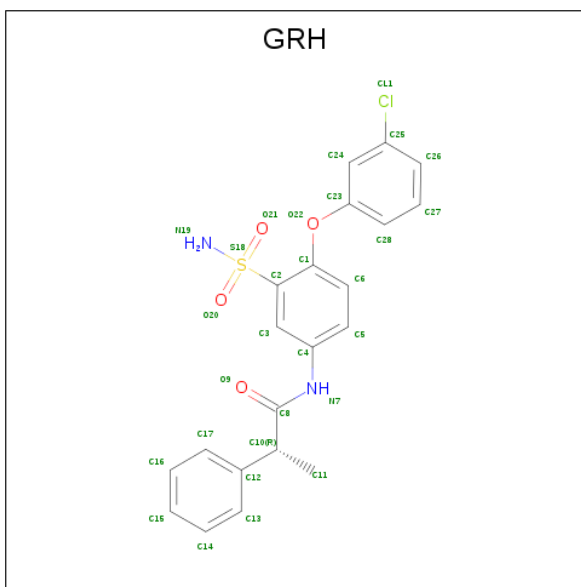
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	B	1	Total	C	Cl	N	O	S	0	0
			29	21	1	2	4	1		

• Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	87	Total	O	0	0
			87	87		
5	B	61	Total	O	0	0
			61	61		

3 Residue-property plots ⓘ

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: Nuclear receptor subfamily 1 group I member 2,Nuclear receptor coactivator 1
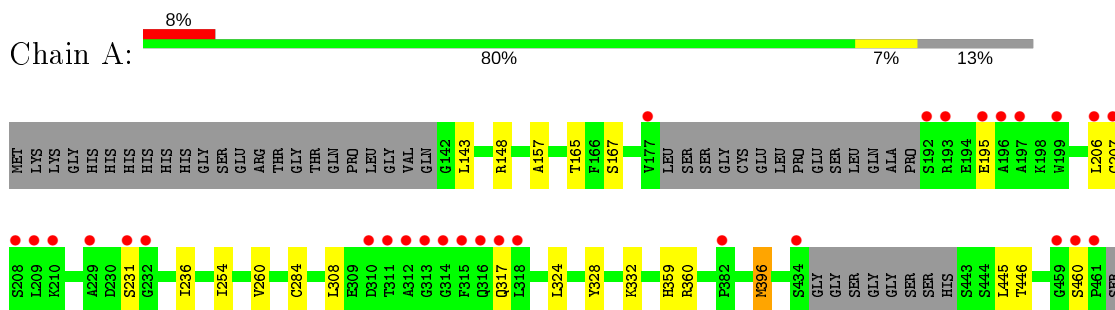
• Molecule 1: Nuclear receptor subfamily 1 group I member 2,Nuclear receptor coactivator 1
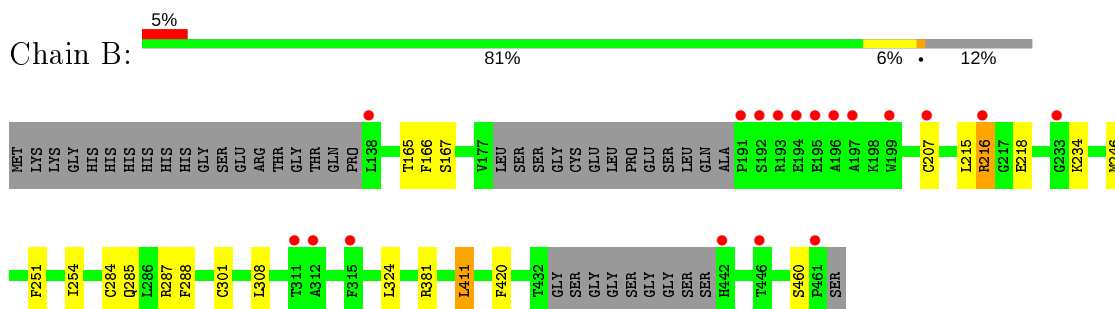
4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	85.42Å 88.62Å 104.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.15 – 2.22 45.15 – 2.22	Depositor EDS
% Data completeness (in resolution range)	99.3 (45.15-2.22) 99.4 (45.15-2.22)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$<I/\sigma(I)>$ [1]	1.43 (at 2.22Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.185 , 0.226 0.190 , 0.229	Depositor DCC
R_{free} test set	1991 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	49.0	Xtriage
Anisotropy	0.285	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 49.1	EDS
L-test for twinning[2]	$<|L|> = 0.47, <L^2> = 0.29$	Xtriage
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5181	wwPDB-VP
Average B, all atoms (Å^2)	70.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.79% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $<|L|>$, $<L^2>$ 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: GOL, DMS, GRH

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	0.54	0/2553	0.73	1/3434 (0.0%)
1	B	0.55	0/2573	0.73	1/3461 (0.0%)
All	All	0.55	0/5126	0.73	2/6895 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	396	MET	CG-SD-CE	6.99	111.38	100.20
1	B	216	ARG	NE-CZ-NH1	5.15	122.88	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	2478	0	2494	10	0
1	B	2500	0	2528	12	0
2	A	6	0	8	0	0
3	A	12	0	18	0	0
3	B	8	0	12	0	0
4	B	29	0	0	2	0
5	A	87	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	61	0	0	0	0
All	All	5181	0	5060	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 2.

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:308:LEU:HD11	1:A:324:LEU:HD21	1.70	0.73
1:B:165:THR:HG1	1:B:167:SER:HG	1.49	0.61
4:B:501:GRH:C6	4:B:501:GRH:C24	2.79	0.58
1:A:157:ALA:HB2	1:A:260:VAL:HG22	1.88	0.56
1:A:165:THR:HG1	1:A:167[B]:SER:HG	1.54	0.55
1:A:308:LEU:CD1	1:A:324:LEU:HD21	2.37	0.55
1:B:285:GLN:HE22	4:B:501:GRH:C3	2.19	0.54
1:B:411:LEU:HD12	1:B:411:LEU:O	2.13	0.48
1:B:246[A]:MET:SD	1:B:288:PHE:HZ	2.39	0.46
1:B:207:CYS:O	1:B:207:CYS:SG	2.74	0.45
1:B:308:LEU:HD11	1:B:324:LEU:HD11	1.97	0.45
1:A:254:ILE:CD1	1:A:284[B]:CYS:SG	3.06	0.44
1:A:308:LEU:HD22	1:A:324:LEU:HD11	1.99	0.44
1:B:166:PHE:HE2	1:B:246[B]:MET:SD	2.40	0.44
1:A:206:LEU:HD12	1:A:236:ILE:HD12	2.00	0.43
1:B:166:PHE:CD1	1:B:301:CYS:HB3	2.54	0.43
1:B:254[B]:ILE:HD11	1:B:287:ARG:HD2	2.02	0.42
1:B:251:PHE:CD1	1:B:284[B]:CYS:SG	3.12	0.41
1:B:166:PHE:CE2	1:B:246[B]:MET:CE	3.03	0.41
1:A:157:ALA:CB	1:A:260:VAL:HG22	2.49	0.41
1:B:411:LEU:HD13	1:B:420:PHE:CZ	2.56	0.41
1:A:324:LEU:HD22	1:A:328:TYR:HE2	1.86	0.40
1:A:143:LEU:O	1:A:148:ARG:NH1	2.54	0.40

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	302/344 (88%)	292 (97%)	10 (3%)	0	100	100
1	B	304/344 (88%)	294 (97%)	10 (3%)	0	100	100
All	All	606/688 (88%)	586 (97%)	20 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	276/302 (91%)	264 (96%)	12 (4%)	29	35
1	B	278/302 (92%)	271 (98%)	7 (2%)	47	58
All	All	554/604 (92%)	535 (97%)	19 (3%)	37	46

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	195	GLU
1	A	207	CYS
1	A	231	SER
1	A	317	GLN
1	A	332	LYS
1	A	359[A]	HIS
1	A	359[B]	HIS
1	A	360	ARG

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Mol	Chain	Res	Type
1	A	396	MET
1	A	445	LEU
1	A	446	THR
1	A	460	SER
1	B	215	LEU
1	B	216	ARG
1	B	218	GLU
1	B	234	LYS
1	B	381	ARG
1	B	411	LEU
1	B	460	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	316	GLN
1	A	386	HIS
1	B	406	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

7 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

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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	DMS	B	503	-	3,3,3	0.57	0	3,3,3	0.50	0
3	DMS	A	503	-	3,3,3	0.52	0	3,3,3	0.56	0
3	DMS	B	502	-	3,3,3	0.54	0	3,3,3	0.55	0
3	DMS	A	504	-	3,3,3	0.53	0	3,3,3	0.55	0
2	GOL	A	501	-	5,5,5	0.45	0	5,5,5	0.42	0
4	GRH	B	501	-	31,31,31	1.56	4 (12%)	42,44,44	1.67	7 (16%)
3	DMS	A	502	-	3,3,3	0.54	0	3,3,3	0.38	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
2	GOL	A	501	-	-	2/4/4/4	-
4	GRH	B	501	-	-	8/22/22/22	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	501	GRH	C4-N7	-5.00	1.31	1.41
4	B	501	GRH	O20-S18	3.94	1.51	1.43
4	B	501	GRH	O21-S18	3.37	1.50	1.43
4	B	501	GRH	C2-S18	-2.70	1.74	1.77

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	501	GRH	O21-S18-O20	-5.12	110.35	118.76
4	B	501	GRH	C1-O22-C23	-4.30	107.26	118.00
4	B	501	GRH	C26-C25-CL1	3.68	125.10	119.35
4	B	501	GRH	O22-C1-C2	3.26	121.93	118.07
4	B	501	GRH	C24-C25-CL1	-3.12	115.25	119.15
4	B	501	GRH	C23-C24-C25	2.76	121.37	118.14
4	B	501	GRH	O20-S18-C2	2.10	110.37	107.29

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	GOL	O1-C1-C2-C3
4	B	501	GRH	C1-C2-S18-O20
4	B	501	GRH	C1-C2-S18-O21
4	B	501	GRH	C1-C2-S18-N19
4	B	501	GRH	C3-C2-S18-O20
4	B	501	GRH	C3-C2-S18-N19
4	B	501	GRH	C12-C10-C8-N7
4	B	501	GRH	C12-C10-C8-O9
4	B	501	GRH	C3-C2-S18-O21
2	A	501	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	501	GRH	2	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 then 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.

Ligand GRH B 501

Bond lengths

Bond angles

Torsions

Rings
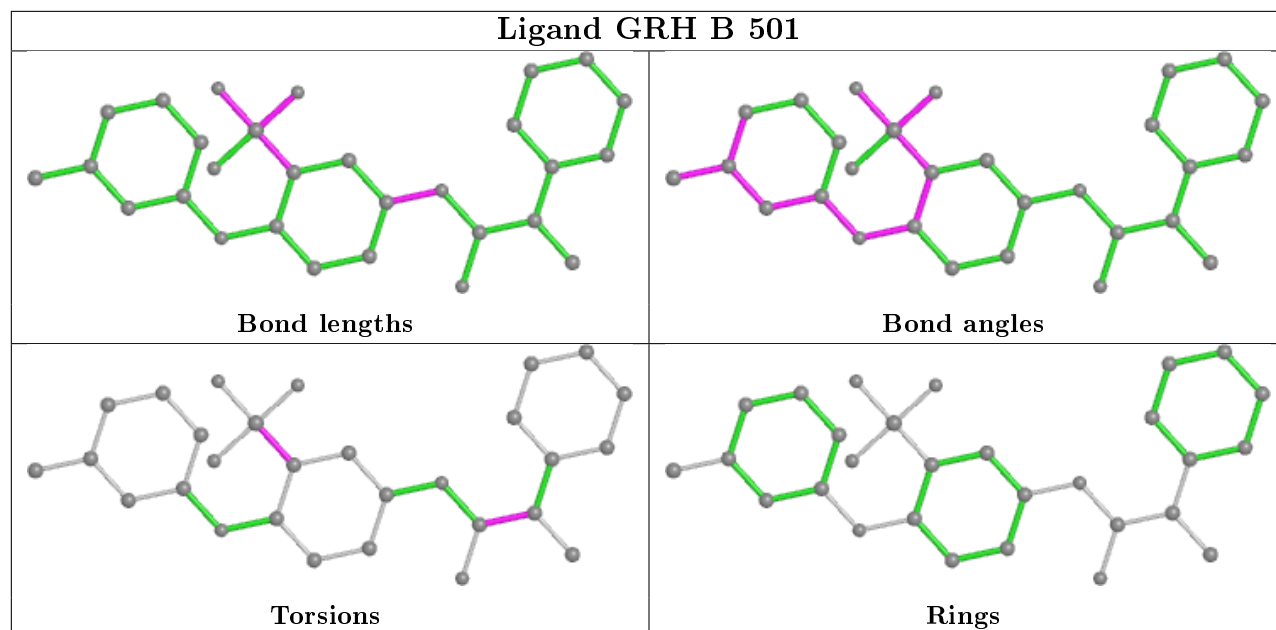
5.7 Other polymers (i)

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	298/344 (86%)	0.28	29 (9%)	7	6	35, 62, 141, 199	0
1	B	302/344 (87%)	0.22	18 (5%)	21	20	36, 61, 138, 191	0
All	All	600/688 (87%)	0.25	47 (7%)	13	11	35, 62, 141, 199	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	312	ALA	11.1
1	A	311	THR	8.1
1	B	312	ALA	7.8
1	B	193	ARG	7.1
1	B	207	CYS	6.1
1	B	192	SER	5.9
1	B	138	LEU	5.7
1	B	194	GLU	5.6
1	B	191	PRO	5.1
1	A	313	GLY	4.9
1	A	177	VAL	4.9
1	A	193	ARG	4.4
1	A	195	GLU	4.2
1	B	311	THR	4.2
1	B	197	ALA	4.1
1	A	314	GLY	3.9
1	A	199	TRP	3.8
1	A	197	ALA	3.7
1	A	232	GLY	3.5
1	A	207	CYS	3.5
1	A	316	GLN	3.3
1	A	209	LEU	3.3
1	A	461	PRO	3.3
1	A	192	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	317	GLN	3.0
1	B	195	GLU	2.9
1	B	315	PHE	2.8
1	B	199	TRP	2.7
1	A	318	LEU	2.7
1	A	196	ALA	2.7
1	A	208	SER	2.6
1	A	229	ALA	2.5
1	B	196	ALA	2.5
1	A	206	LEU	2.5
1	A	315	PHE	2.5
1	A	382	PRO	2.4
1	A	460	SER	2.4
1	A	459	GLY	2.4
1	B	446	THR	2.4
1	B	216	ARG	2.3
1	A	210	LYS	2.3
1	B	442	HIS	2.2
1	A	434	SER	2.2
1	B	233	GLY	2.2
1	A	231	SER	2.2
1	A	310	ASP	2.1
1	B	461	PRO	2.1

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)

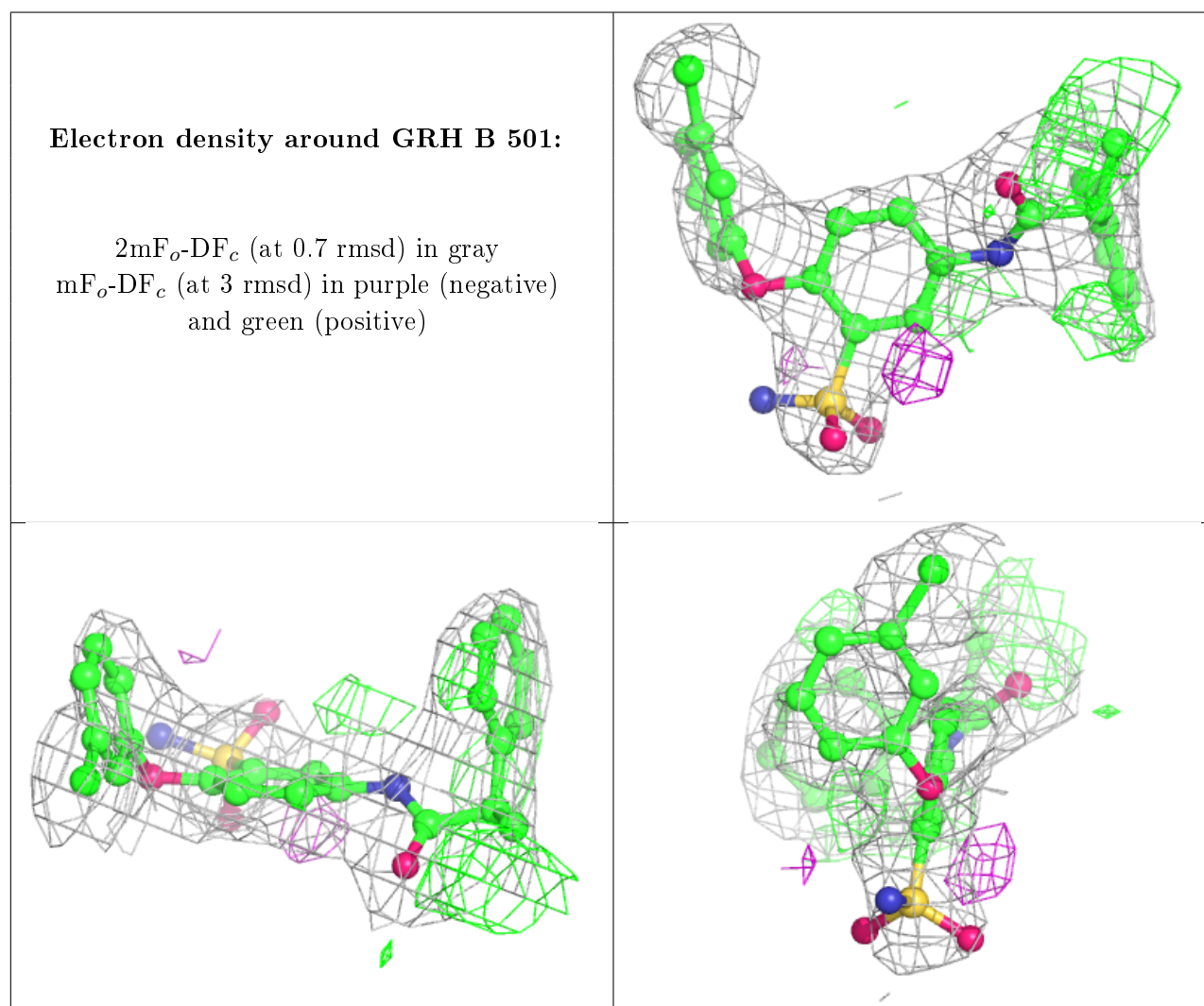There are no carbohydrates in this entry.

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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	GRH	B	501	29/29	0.59	0.24	88,136,161,169	0
2	GOL	A	501	6/6	0.84	0.39	83,96,106,106	0
3	DMS	A	504	4/4	0.86	0.18	99,100,106,132	0
3	DMS	A	503	4/4	0.91	0.30	104,106,114,123	0
3	DMS	B	503	4/4	0.92	0.14	81,93,106,124	0
3	DMS	B	502	4/4	0.95	0.17	66,74,76,83	0
3	DMS	A	502	4/4	0.97	0.15	62,66,71,78	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 GRH B 501:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative) and green (positive)

6.5 Other polymers (i)

There are no such residues in this entry.