



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:08 PM UTC

PDB ID : 4KHR / pdb_00004khr
Title : HCV NS5B GT1A C316Y with GSK5852
Authors : Williams, S.P.; Kahler, K.M.; Shotwell, J.B.
Deposited on : 2013-05-01
Resolution : 2.45 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

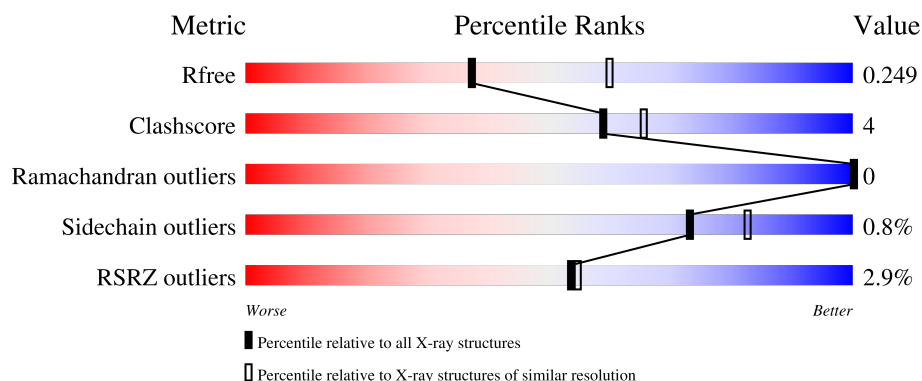
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	579	
1	B	579	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8738 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 NS5B RNA-dependent RNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	562	Total	C	N	O	S	0	0	0
			4291	2708	761	792	30			
1	B	562	Total	C	N	O	S	0	0	0
			4257	2688	746	793	30			

There are 34 discrepancies between the modelled and reference sequences:

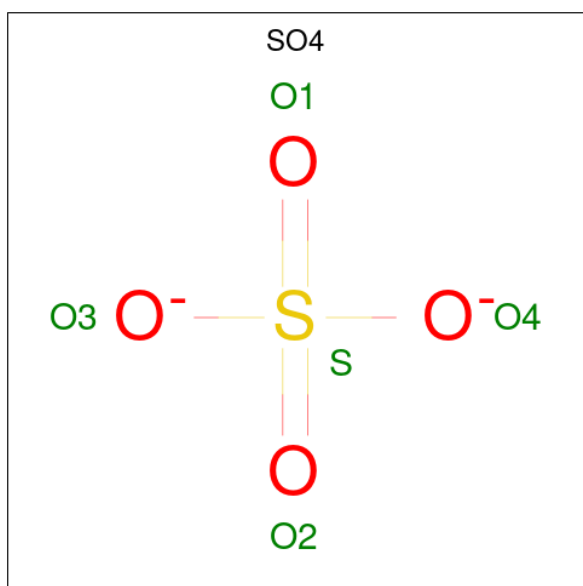
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	expression tag	UNP B1PPP0
A	5	SER	THR	variant	UNP B1PPP0
A	11	VAL	ILE	variant	UNP B1PPP0
A	101	TYR	PHE	engineered mutation	UNP B1PPP0
A	110	SER	CYS	engineered mutation	UNP B1PPP0
A	113	SER	ARG	engineered mutation	UNP B1PPP0
A	114	ARG	LYS	engineered mutation	UNP B1PPP0
A	316	TYR	CYS	engineered mutation	UNP B1PPP0
A	546	ALA	ASP	variant	UNP B1PPP0
A	571	LEU	-	expression tag	UNP B1PPP0
A	572	GLU	-	expression tag	UNP B1PPP0
A	573	HIS	-	expression tag	UNP B1PPP0
A	574	HIS	-	expression tag	UNP B1PPP0
A	575	HIS	-	expression tag	UNP B1PPP0
A	576	HIS	-	expression tag	UNP B1PPP0
A	577	HIS	-	expression tag	UNP B1PPP0
A	578	HIS	-	expression tag	UNP B1PPP0
B	0	MET	-	expression tag	UNP B1PPP0
B	5	SER	THR	variant	UNP B1PPP0
B	11	VAL	ILE	variant	UNP B1PPP0
B	101	TYR	PHE	engineered mutation	UNP B1PPP0
B	110	SER	CYS	engineered mutation	UNP B1PPP0
B	113	SER	ARG	engineered mutation	UNP B1PPP0
B	114	ARG	LYS	engineered mutation	UNP B1PPP0
B	316	TYR	CYS	engineered mutation	UNP B1PPP0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	546	ALA	ASP	variant	UNP B1PPP0
B	571	LEU	-	expression tag	UNP B1PPP0
B	572	GLU	-	expression tag	UNP B1PPP0
B	573	HIS	-	expression tag	UNP B1PPP0
B	574	HIS	-	expression tag	UNP B1PPP0
B	575	HIS	-	expression tag	UNP B1PPP0
B	576	HIS	-	expression tag	UNP B1PPP0
B	577	HIS	-	expression tag	UNP B1PPP0
B	578	HIS	-	expression tag	UNP B1PPP0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



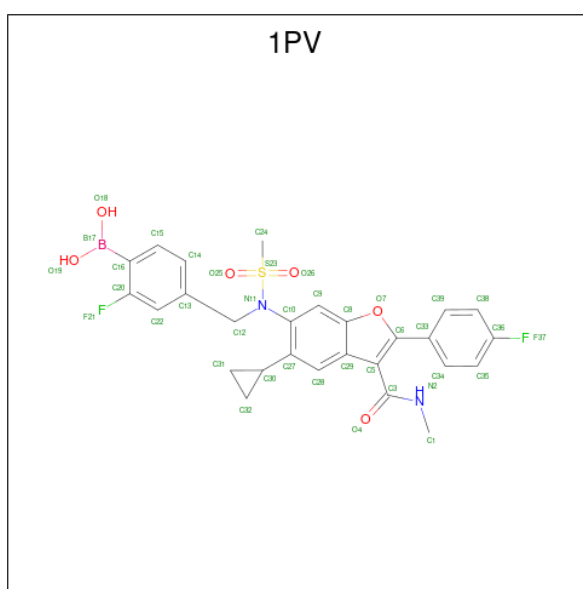
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is [4-({[5-cyclopropyl-2-(4-fluorophenyl)-3-(methylcarbamoyl)-1-benzofuran-6-yl](methylsulfonyl)amino}methyl)-2-fluorophenyl]boronic acid (CCD ID: 1PV) (formula: C₂₇H₂₅BF₂N₂O₆S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
3	A	1	Total	B	C	F	N	O	S	0	0
			39	1	27	2	2	6	1		

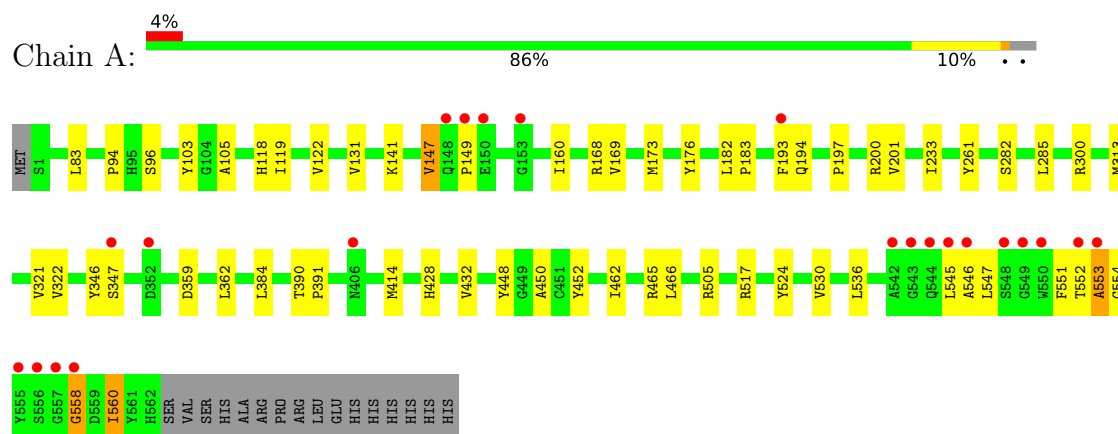
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	51	Total	O	0	0
			51	51		
4	B	50	Total	O	0	0
			50	50		

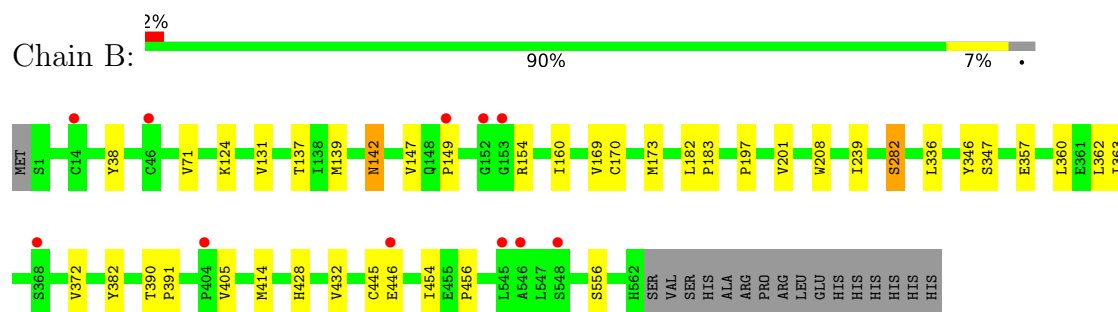
3 Residue-property plots

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: NS5B RNA-dependent RNA polymerase



- Molecule 1: NS5B RNA-dependent RNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.35Å 60.74Å 91.98Å 89.32° 86.64° 80.32°	Depositor
Resolution (Å)	29.94 – 2.45 29.94 – 2.45	Depositor EDS
% Data completeness (in resolution range)	98.5 (29.94-2.45) 98.5 (29.94-2.45)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.45Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.208 , 0.246 0.211 , 0.249	Depositor DCC
R_{free} test set	2945 reflections (7.16%)	wwPDB-VP
Wilson B-factor (Å ²)	24.1	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 24.4	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	0.92	EDS
Total number of atoms	8738	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.41% 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: SO4, 1PV

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	0.75	0/4387	0.88	3/5966 (0.1%)
1	B	0.74	0/4354	0.86	1/5930 (0.0%)
All	All	0.74	0/8741	0.87	4/11896 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	558	GLY	N-CA-C	8.70	125.45	114.66
1	A	553	ALA	N-CA-C	7.22	121.80	112.92
1	B	131	VAL	N-CA-C	6.24	117.36	112.12
1	A	131	VAL	N-CA-C	5.71	116.91	112.12

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	4291	0	4246	49	0
1	B	4257	0	4166	26	0
2	A	15	0	0	1	0
2	B	35	0	0	0	0
3	A	39	0	25	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	51	0	0	0	0
4	B	50	0	0	1	0
All	All	8738	0	8437	75	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 4.

All (75) 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:170:CYS:HA	1:B:173:MET:HE3	1.49	0.92
1:A:193:PHE:HE2	1:A:552:THR:C	1.82	0.87
1:B:160:ILE:HD12	1:B:282:SER:HB2	1.55	0.86
1:B:208:TRP:CZ3	1:B:363:ILE:HD11	2.18	0.79
1:A:193:PHE:CD1	1:A:448:TYR:HD2	2.03	0.76
1:A:193:PHE:HE2	1:A:553:ALA:N	1.87	0.73
1:A:448:TYR:HE1	3:A:604:1PV:H9	1.56	0.70
1:B:208:TRP:CZ3	1:B:363:ILE:CD1	2.74	0.70
1:A:193:PHE:CE2	1:A:552:THR:C	2.68	0.70
1:A:193:PHE:CE1	1:A:448:TYR:HD2	2.11	0.69
1:A:141:LYS:HG3	1:A:160:ILE:CG2	2.24	0.68
1:B:445:CYS:SG	1:B:454:ILE:HD12	2.32	0.68
1:A:141:LYS:HG3	1:A:160:ILE:HG23	1.76	0.67
1:A:193:PHE:CZ	1:A:554:GLY:N	2.66	0.63
1:B:147:VAL:HG23	1:B:149:PRO:HD3	1.80	0.62
1:A:193:PHE:CD1	1:A:448:TYR:CD2	2.86	0.61
1:A:197:PRO:HG3	3:A:604:1PV:H8	1.85	0.58
1:B:169:VAL:HG12	1:B:173:MET:HE2	1.86	0.58
1:A:193:PHE:HE1	1:A:448:TYR:HB2	1.68	0.58
1:A:313:MET:HG2	1:A:322:VAL:HG22	1.85	0.58
1:B:428:HIS:O	1:B:432:VAL:HG23	2.04	0.57
1:B:346:TYR:O	1:B:347:SER:HB3	2.04	0.56
1:A:193:PHE:CE1	1:A:448:TYR:CD2	2.94	0.56
1:A:119:ILE:HD13	1:A:169:VAL:HG11	1.87	0.56
1:A:462:ILE:O	1:A:466:LEU:HG	2.06	0.56
1:A:96:SER:OG	1:A:168:ARG:NH2	2.40	0.55
1:B:208:TRP:CH2	1:B:363:ILE:HD11	2.43	0.54
1:A:193:PHE:CE2	1:A:553:ALA:N	2.73	0.54
1:A:201:VAL:HG22	1:A:384:LEU:HG	1.90	0.53
1:A:346:TYR:O	1:A:347:SER:HB3	2.08	0.52
1:B:182:LEU:HB3	1:B:183:PRO:HD3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:LEU:HB3	1:A:183:PRO:HD3	1.92	0.52
1:A:414:MET:HB3	3:A:604:1PV:H10	1.94	0.50
1:A:193:PHE:HE1	1:A:448:TYR:CB	2.25	0.50
1:A:285:LEU:HA	1:A:558:GLY:HA2	1.94	0.49
1:B:142:ASN:HD22	1:B:142:ASN:N	2.10	0.49
1:B:38:TYR:CE2	1:B:154:ARG:HB3	2.48	0.48
1:A:147:VAL:HG13	1:A:149:PRO:HD3	1.95	0.48
1:A:103:TYR:OH	1:A:118:HIS:ND1	2.42	0.48
1:B:360:LEU:HA	1:B:363:ILE:HD12	1.96	0.48
1:A:546:ALA:C	1:A:547:LEU:HD23	2.39	0.48
1:A:524:TYR:CD2	1:A:536:LEU:HD22	2.48	0.47
1:A:83:LEU:HB2	1:A:173:MET:HA	1.98	0.46
1:B:405:VAL:HG11	1:B:446:GLU:HG3	1.97	0.46
1:A:233:ILE:HD13	1:A:261:TYR:O	2.16	0.46
1:B:137:THR:HG21	1:B:139:MET:HE2	1.98	0.45
1:A:300:ARG:CB	1:A:313:MET:HE1	2.46	0.45
1:A:300:ARG:HB2	1:A:313:MET:HE1	1.99	0.45
1:A:428:HIS:O	1:A:432:VAL:HG23	2.17	0.45
1:A:321:VAL:HG21	3:A:604:1PV:C35	2.47	0.45
1:A:200:ARG:HD2	1:A:384:LEU:HD11	1.98	0.44
1:B:208:TRP:CZ3	1:B:363:ILE:HD13	2.52	0.44
1:A:450:ALA:HB3	1:A:452:TYR:CE1	2.53	0.44
1:A:359:ASP:HB3	1:A:362:LEU:HD12	1.99	0.44
1:A:517:ARG:NE	2:A:602:SO4:O4	2.42	0.43
1:A:141:LYS:HG3	1:A:160:ILE:HG21	1.98	0.43
1:A:465:ARG:NH2	1:A:545:LEU:O	2.46	0.43
1:B:336:LEU:HD12	1:B:336:LEU:HA	1.85	0.43
1:B:357:GLU:OE2	1:B:362:LEU:HD13	2.17	0.43
1:A:193:PHE:CE1	1:A:554:GLY:HA3	2.54	0.43
1:A:194:GLN:HA	1:A:551:PHE:O	2.18	0.43
1:B:38:TYR:CZ	1:B:154:ARG:HB3	2.54	0.43
1:B:71:VAL:HG11	1:B:239:ILE:HD13	2.01	0.42
1:A:193:PHE:CE1	1:A:448:TYR:CB	3.02	0.42
1:A:390:THR:HB	1:A:391:PRO:HD3	2.01	0.42
1:B:456:PRO:HD2	4:B:716:HOH:O	2.18	0.42
1:A:118:HIS:O	1:A:122:VAL:HG23	2.19	0.42
1:A:176:TYR:HE1	1:A:560:ILE:HD12	1.85	0.41
1:B:197:PRO:HG3	1:B:414:MET:SD	2.60	0.41
1:A:94:PRO:O	1:A:105:ALA:HB3	2.20	0.41
1:B:197:PRO:O	1:B:201:VAL:HG23	2.19	0.41
1:B:390:THR:HB	1:B:391:PRO:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:ARG:NH1	1:A:530:VAL:HG12	2.36	0.40
1:A:141:LYS:HE3	1:A:160:ILE:CG2	2.51	0.40
1:B:372:VAL:HG22	1:B:382:TYR:CD1	2.57	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	560/579 (97%)	556 (99%)	4 (1%)	0	100	100
1	B	560/579 (97%)	555 (99%)	5 (1%)	0	100	100
All	All	1120/1158 (97%)	1111 (99%)	9 (1%)	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	451/483 (93%)	448 (99%)	3 (1%)	76	84
1	B	444/483 (92%)	440 (99%)	4 (1%)	70	81
All	All	895/966 (93%)	888 (99%)	7 (1%)	73	83

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	147	VAL
1	A	282	SER
1	A	560	ILE
1	B	124	LYS
1	B	142	ASN
1	B	282	SER
1	B	556	SER

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	34	HIS
1	A	35	ASN
1	A	95	HIS
1	A	142	ASN
1	A	441	GLN
1	B	35	ASN
1	B	118	HIS
1	B	273	ASN
1	B	438	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

11 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	SO4	B	606	-	4,4,4	0.51	0	6,6,6	0.19	0
3	1PV	A	604	-	43,43,43	3.55	7 (16%)	54,65,65	2.67	16 (29%)
2	SO4	B	602	-	4,4,4	0.48	0	6,6,6	0.33	0
2	SO4	B	607	-	4,4,4	0.49	0	6,6,6	0.18	0
2	SO4	A	603	-	4,4,4	0.50	0	6,6,6	0.23	0
2	SO4	A	601	-	4,4,4	0.45	0	6,6,6	0.26	0
2	SO4	A	602	-	4,4,4	0.44	0	6,6,6	0.36	0
2	SO4	B	603	-	4,4,4	0.46	0	6,6,6	0.24	0
2	SO4	B	601	-	4,4,4	0.49	0	6,6,6	0.30	0
2	SO4	B	605	-	4,4,4	0.48	0	6,6,6	0.41	0
2	SO4	B	604	-	4,4,4	0.48	0	6,6,6	0.18	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	1PV	A	604	-	-	6/32/34/34	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	604	1PV	C5-C6	11.00	1.49	1.36
3	A	604	1PV	B17-O18	10.91	1.54	1.36
3	A	604	1PV	B17-O19	10.59	1.53	1.36
3	A	604	1PV	S23-N11	-9.78	1.54	1.64
3	A	604	1PV	C24-S23	-5.26	1.64	1.75
3	A	604	1PV	C10-N11	-5.13	1.40	1.44
3	A	604	1PV	O7-C8	-3.83	1.32	1.38

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	604	1PV	O7-C6-C5	-8.73	103.30	111.18
3	A	604	1PV	O26-S23-O25	-7.41	107.38	118.46
3	A	604	1PV	O7-C6-C33	7.10	122.52	114.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	604	1PV	C8-O7-C6	6.45	112.45	106.25
3	A	604	1PV	C32-C30-C27	-5.21	112.00	121.75
3	A	604	1PV	O25-S23-N11	4.83	113.15	107.39
3	A	604	1PV	C8-C29-C5	-4.07	102.16	105.64
3	A	604	1PV	O7-C8-C29	3.54	114.31	110.84
3	A	604	1PV	C9-C8-C29	-3.23	121.02	124.70
3	A	604	1PV	C15-C16-C20	2.89	118.49	115.80
3	A	604	1PV	C13-C12-N11	2.86	117.71	112.02
3	A	604	1PV	C38-C36-C35	-2.52	119.50	122.80
3	A	604	1PV	C13-C22-C20	2.46	120.99	119.37
3	A	604	1PV	C39-C38-C36	2.36	120.80	118.38
3	A	604	1PV	C24-S23-N11	2.29	110.02	106.41
3	A	604	1PV	C28-C29-C8	2.12	121.36	119.28

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	604	1PV	O19-B17-C16-C20
3	A	604	1PV	O18-B17-C16-C20
3	A	604	1PV	C12-N11-S23-O26
3	A	604	1PV	C10-N11-S23-O26
3	A	604	1PV	O18-B17-C16-C15
3	A	604	1PV	O19-B17-C16-C15

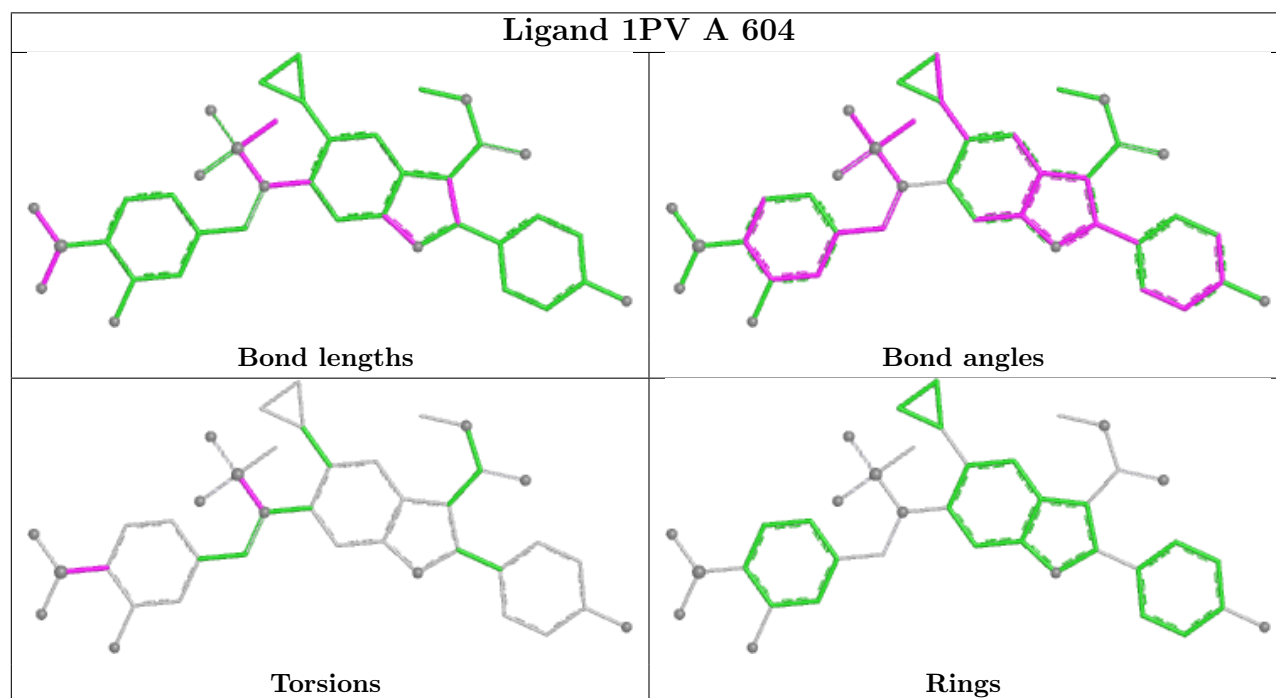
There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	604	1PV	4	0
2	A	602	SO4	1	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	562/579 (97%)	0.24	22 (3%)	43 43	16, 23, 35, 55	1 (0%)
1	B	562/579 (97%)	0.12	11 (1%)	65 66	13, 22, 36, 49	1 (0%)
All	All	1124/1158 (97%)	0.18	33 (2%)	53 55	13, 23, 35, 55	2 (0%)

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	558	GLY	7.1
1	A	548	SER	5.8
1	A	552	THR	5.5
1	A	556	SER	5.3
1	B	548	SER	5.1
1	A	557	GLY	5.0
1	A	545	LEU	3.9
1	A	150	GLU	3.8
1	A	543	GLY	3.6
1	A	153	GLY	3.5
1	A	553	ALA	3.4
1	A	352	ASP	3.1
1	A	550	TRP	3.1
1	B	153	GLY	3.1
1	B	14	CYS	3.1
1	A	406	ASN	3.0
1	A	549	GLY	2.9
1	A	544	GLN	2.7
1	B	545	LEU	2.6
1	A	555	TYR	2.6
1	B	546	ALA	2.6
1	A	347	SER	2.6
1	A	149	PRO	2.5
1	B	149	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	148	GLN	2.5
1	A	193	PHE	2.5
1	B	152	GLY	2.4
1	B	46	CYS	2.3
1	B	446	GLU	2.2
1	B	404	PRO	2.2
1	A	546	ALA	2.1
1	A	542	ALA	2.0
1	B	368	SER	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.

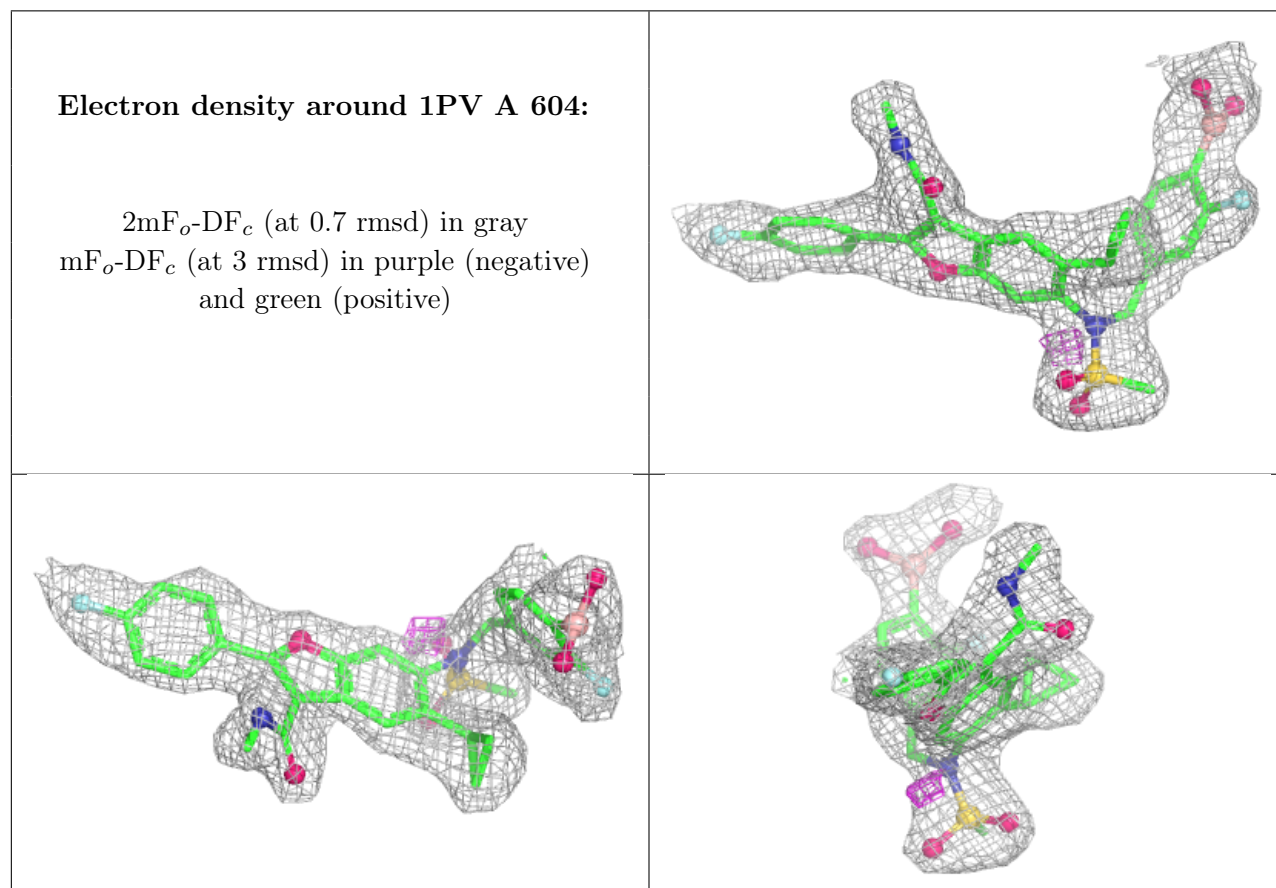
6.4 Ligands [i](#)

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($\text{\AA}^2$)	Q<0.9
2	SO4	B	607	5/5	0.81	0.13	52,54,56,58	0
2	SO4	B	606	5/5	0.85	0.17	57,59,60,63	0
3	1PV	A	604	39/39	0.87	0.12	36,39,44,44	0
2	SO4	A	603	5/5	0.89	0.17	42,42,43,44	0
2	SO4	B	603	5/5	0.91	0.12	40,41,41,41	0
2	SO4	B	604	5/5	0.92	0.14	44,44,45,46	0
2	SO4	B	605	5/5	0.94	0.17	41,42,42,42	0
2	SO4	A	602	5/5	0.94	0.11	38,39,39,40	0
2	SO4	A	601	5/5	0.95	0.09	32,33,34,35	0
2	SO4	B	602	5/5	0.95	0.12	30,31,33,34	0
2	SO4	B	601	5/5	0.97	0.06	23,24,24,25	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.