



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2020 – 02:20 pm BST

PDB ID : 3HKY
Title : HCV NS5B polymerase genotype 1b in complex with 1,5 benzodiazepine 6
Authors : Nyanguile, O.; De Bondt, H.L.
Deposited on : 2009-05-26
Resolution : 1.90 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 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 : 2.11
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

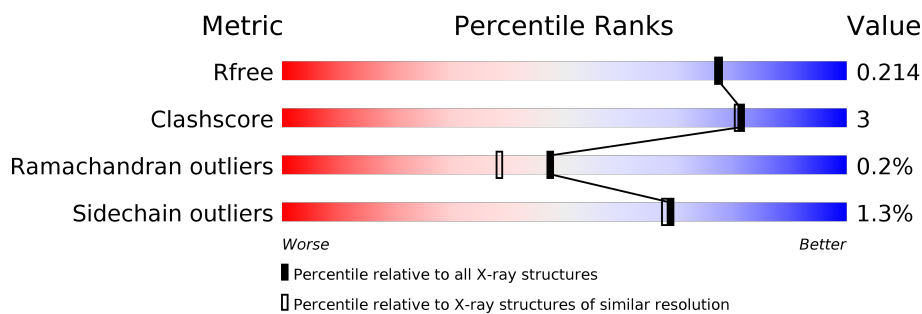
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	581	
1	B	581	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	581	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9585 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 RNA-directed RNA polymerase.

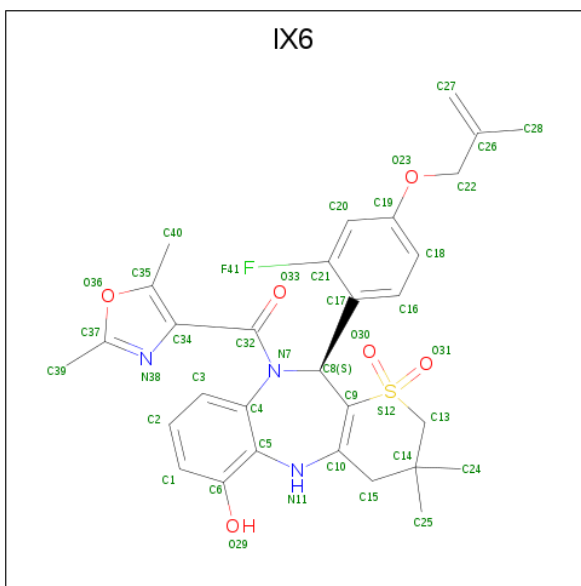
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	564	Total	C	N	O	S	0	5	0
			4426	2783	785	825	33			
1	B	560	Total	C	N	O	S	0	1	0
			4362	2747	771	812	32			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	EXPRESSION TAG	UNP O92972
A	-1	ALA	-	EXPRESSION TAG	UNP O92972
A	0	SER	-	EXPRESSION TAG	UNP O92972
A	571	LEU	-	EXPRESSION TAG	UNP O92972
A	572	GLU	-	EXPRESSION TAG	UNP O92972
A	573	HIS	-	EXPRESSION TAG	UNP O92972
A	574	HIS	-	EXPRESSION TAG	UNP O92972
A	575	HIS	-	EXPRESSION TAG	UNP O92972
A	576	HIS	-	EXPRESSION TAG	UNP O92972
A	577	HIS	-	EXPRESSION TAG	UNP O92972
A	578	HIS	-	EXPRESSION TAG	UNP O92972
B	-2	MET	-	EXPRESSION TAG	UNP O92972
B	-1	ALA	-	EXPRESSION TAG	UNP O92972
B	0	SER	-	EXPRESSION TAG	UNP O92972
B	571	LEU	-	EXPRESSION TAG	UNP O92972
B	572	GLU	-	EXPRESSION TAG	UNP O92972
B	573	HIS	-	EXPRESSION TAG	UNP O92972
B	574	HIS	-	EXPRESSION TAG	UNP O92972
B	575	HIS	-	EXPRESSION TAG	UNP O92972
B	576	HIS	-	EXPRESSION TAG	UNP O92972
B	577	HIS	-	EXPRESSION TAG	UNP O92972
B	578	HIS	-	EXPRESSION TAG	UNP O92972

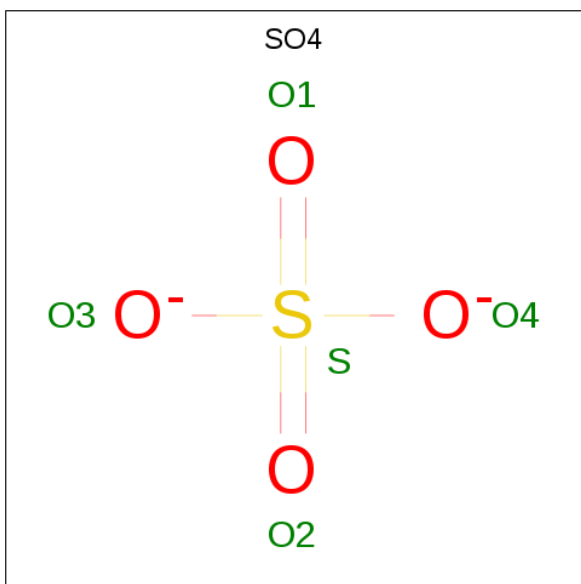
- Molecule 2 is (11S)-10-[(2,5-dimethyl-1,3-oxazol-4-yl)carbonyl]-11-{2-fluoro-4-[(2-methylprop-2-en-1-yl)oxy]phenyl}-3,3-dimethyl-2,3,4,5,10,11-hexahydrothiopyrano[3,2-b][1,5]benzodia

zepin-6-ol 1,1-dioxide (three-letter code: IX6) (formula: $C_{30}H_{32}FN_3O_6S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	S	0	0
			41	30	1	3	6	1		
2	B	1	Total	C	F	N	O	S	0	0
			41	30	1	3	6	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total Cl 1 1	0	0
4	A	1	Total Cl 1 1	0	0

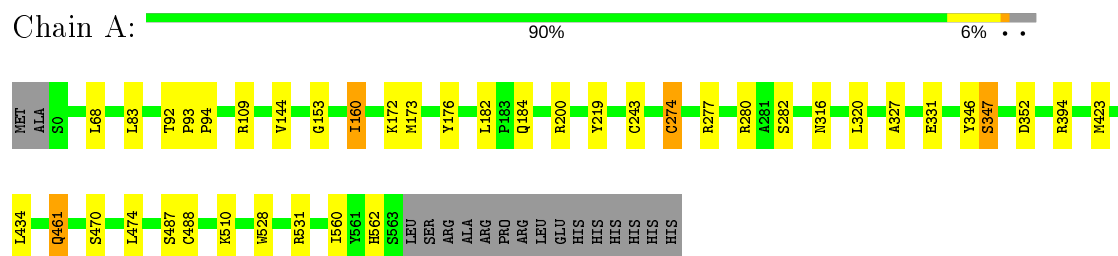
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	402	Total O 403 403	0	1
5	B	270	Total O 270 270	0	0

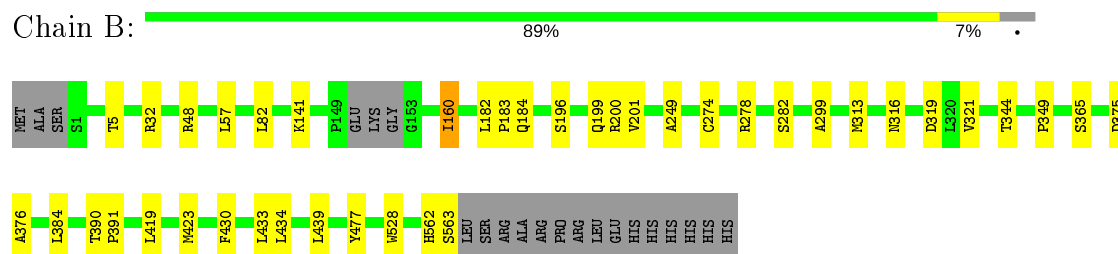
3 Residue-property plots

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. 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. 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: RNA-directed RNA polymerase



- Molecule 1: RNA-directed RNA polymerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	106.27Å 107.68Å 133.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.90 – 1.90 44.88 – 1.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.90-1.90) 99.9 (44.88-1.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.184 , 0.209 0.190 , 0.214	Depositor DCC
R_{free} test set	967 reflections (0.80%)	wwPDB-VP
Wilson B-factor (Å ²)	31.1	Xtriage
Anisotropy	0.330	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.023 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9585	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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: IX6, SO4, CL

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	0.62	1/4523 (0.0%)	0.70	3/6137 (0.0%)
1	B	0.52	1/4457 (0.0%)	0.61	0/6049
All	All	0.57	2/8980 (0.0%)	0.66	3/12186 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	274	CYS	CB-SG	-8.31	1.68	1.82
1	A	274	CYS	CB-SG	-8.15	1.68	1.82

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	277	ARG	NE-CZ-NH1	6.07	123.33	120.30
1	A	280	ARG	NE-CZ-NH1	-5.63	117.49	120.30
1	A	277	ARG	NE-CZ-NH2	-5.62	117.49	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	4426	0	4428	22	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	4362	0	4373	22	0
2	A	41	0	31	0	0
2	B	41	0	31	0	0
3	A	30	0	0	2	0
3	B	10	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	403	0	0	4	0
5	B	270	0	0	4	0
All	All	9585	0	8863	46	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 (46) 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:488:CYS:HB2	5:A:603:HOH:O	1.76	0.85
1:A:461:GLN:H	1:A:461:GLN:HE21	1.37	0.72
3:A:581:SO4:O1	5:A:616:HOH:O	2.14	0.63
3:A:581:SO4:O4	5:A:671:HOH:O	2.16	0.61
1:A:200:ARG:HH12	1:A:316:ASN:HD21	1.50	0.58
1:B:434:LEU:CD1	1:B:439:LEU:HD11	2.34	0.58
1:A:160:ILE:HD12	1:A:282:SER:OG	2.06	0.56
1:B:160:ILE:HD12	1:B:282:SER:OG	2.05	0.56
1:B:82:LEU:HD13	1:B:249:ALA:HB2	1.87	0.56
1:A:182:LEU:HD12	1:A:243:CYS:SG	2.45	0.56
1:B:5:THR:HG23	1:B:278:ARG:HH12	1.71	0.55
1:A:461:GLN:NE2	1:A:461:GLN:H	2.05	0.54
1:B:321:VAL:HG22	1:B:365:SER:HB3	1.89	0.54
1:B:299:ALA:C	1:B:313:MET:HE1	2.32	0.49
1:B:390:THR:HB	1:B:391:PRO:HD3	1.95	0.49
1:A:200:ARG:HH12	1:A:316:ASN:ND2	2.10	0.49
1:B:419:LEU:HG	1:B:423:MET:CE	2.43	0.48
1:B:201:VAL:HG22	1:B:384:LEU:HG	1.95	0.48
1:A:184:GLN:NE2	5:A:779:HOH:O	2.47	0.48
1:B:184:GLN:NE2	5:B:810:HOH:O	2.47	0.48
1:A:327:ALA:O	1:A:331:GLU:HG3	2.14	0.47
1:A:434:LEU:HD21	1:A:510:LYS:HB2	1.96	0.47
1:B:419:LEU:HD13	1:B:477:TYR:CD1	2.50	0.47
1:A:346:TYR:O	1:A:347:SER:HB3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:48:ARG:NH1	5:B:801:HOH:O	2.48	0.46
1:B:375:ASP:OD1	1:B:376:ALA:N	2.46	0.46
1:A:144:VAL:HB	1:A:394:ARG:HG2	1.97	0.45
1:B:196:SER:H	1:B:199:GLN:NE2	2.14	0.45
1:A:327:ALA:O	1:A:331:GLU:CG	2.65	0.45
1:A:172:LYS:HE3	1:A:560:ILE:HD13	1.99	0.45
1:A:219:TYR:HB3	1:A:320:LEU:HD23	1.97	0.44
1:B:562:HIS:O	1:B:563:SER:C	2.55	0.44
1:A:470:SER:O	1:A:474:LEU:HG	2.18	0.44
1:A:423:MET:HA	1:A:528:TRP:CZ2	2.53	0.44
1:A:176:TYR:OH	1:A:562:HIS:HE1	2.01	0.43
1:B:344:THR:HG23	1:B:349:PRO:HB3	2.01	0.43
1:B:200:ARG:HH22	1:B:316:ASN:HD21	1.67	0.43
1:B:430:PHE:O	1:B:434:LEU:HB2	2.19	0.42
1:B:141:LYS:NZ	5:B:585:HOH:O	2.53	0.42
1:A:83:LEU:HB2	1:A:173:MET:HA	2.01	0.42
1:B:182:LEU:N	1:B:183:PRO:CD	2.83	0.42
1:A:346:TYR:O	1:A:347:SER:CB	2.68	0.42
1:B:423:MET:HA	1:B:528:TRP:CZ2	2.55	0.42
1:A:93:PRO:HA	1:A:94:PRO:HD3	1.94	0.41
1:B:375:ASP:HB3	5:B:611:HOH:O	2.20	0.41
1:A:92:THR:O	1:A:109:ARG:HD2	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	566/581 (97%)	553 (98%)	11 (2%)	2 (0%)	34	24
1	B	556/581 (96%)	548 (99%)	8 (1%)	0	100	100
All	All	1122/1162 (97%)	1101 (98%)	19 (2%)	2 (0%)	47	38

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	153	GLY
1	A	347	SER

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	484/495 (98%)	477 (99%)	7 (1%)	67	65
1	B	477/495 (96%)	472 (99%)	5 (1%)	76	76
All	All	961/990 (97%)	949 (99%)	12 (1%)	69	70

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	LEU
1	A	160	ILE
1	A	274	CYS
1	A	352	ASP
1	A	461	GLN
1	A	487	SER
1	A	531	ARG
1	B	32	ARG
1	B	57	LEU
1	B	160	ILE
1	B	319	ASP
1	B	433	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	35	ASN
1	A	49	GLN

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Mol	Chain	Res	Type
1	A	206	ASN
1	A	273	ASN
1	A	316	ASN
1	A	461	GLN
1	A	483	ASN
1	A	514	GLN
1	A	562	HIS
1	B	58	GLN
1	B	184	GLN
1	B	199	GLN
1	B	206	ASN
1	B	273	ASN
1	B	309	GLN
1	B	316	ASN
1	B	562	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 for Mogul analysis.

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	SO4	A	582	-	4,4,4	0.16	0	6,6,6	0.22	0
3	SO4	A	584	-	4,4,4	0.14	0	6,6,6	0.16	0
3	SO4	A	586	-	4,4,4	0.17	0	6,6,6	0.15	0
3	SO4	A	581	-	4,4,4	0.12	0	6,6,6	0.15	0
3	SO4	A	583	-	4,4,4	0.21	0	6,6,6	0.21	0
3	SO4	B	582	-	4,4,4	0.13	0	6,6,6	0.08	0
3	SO4	A	580	-	4,4,4	0.22	0	6,6,6	0.57	0
3	SO4	B	580	-	4,4,4	0.09	0	6,6,6	0.16	0
2	IX6	B	579	-	36,45,45	1.05	4 (11%)	51,70,70	2.23	13 (25%)
2	IX6	A	579	-	36,45,45	1.05	2 (5%)	51,70,70	2.29	14 (27%)

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	IX6	B	579	-	-	2/13/54/54	0/3/5/5
2	IX6	A	579	-	-	3/13/54/54	0/3/5/5

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	579	IX6	C13-S12	2.71	1.80	1.76
2	B	579	IX6	C15-C10	2.59	1.53	1.50
2	B	579	IX6	C32-N7	2.48	1.40	1.37
2	A	579	IX6	C15-C10	2.40	1.53	1.50
2	B	579	IX6	C40-C35	2.25	1.51	1.48
2	A	579	IX6	C10-N11	2.02	1.39	1.35

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	579	IX6	O33-C32-N7	-6.71	112.95	121.48
2	B	579	IX6	C4-N7-C32	-6.45	116.33	122.94
2	B	579	IX6	C14-C15-C10	5.97	120.10	113.40
2	A	579	IX6	C14-C15-C10	5.72	119.82	113.40
2	A	579	IX6	C4-N7-C32	-5.71	117.09	122.94
2	A	579	IX6	C34-C32-N7	5.38	129.20	118.28
2	A	579	IX6	C22-O23-C19	4.93	126.33	117.67
2	A	579	IX6	C9-C10-N11	-4.86	123.89	126.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	579	IX6	C34-C32-N7	4.85	128.13	118.28
2	B	579	IX6	C9-C10-N11	-4.82	123.91	126.71
2	B	579	IX6	C22-O23-C19	4.61	125.78	117.67
2	B	579	IX6	O33-C32-N7	-4.56	115.68	121.48
2	A	579	IX6	C5-C4-N7	3.65	121.53	119.26
2	B	579	IX6	C5-C4-N7	3.57	121.48	119.26
2	B	579	IX6	C6-C5-N11	-2.79	114.56	118.92
2	B	579	IX6	O31-S12-O30	-2.74	114.44	117.06
2	B	579	IX6	C20-C21-C17	-2.63	120.68	123.83
2	B	579	IX6	O30-S12-C9	-2.59	104.27	109.39
2	B	579	IX6	C16-C17-C21	2.42	119.24	116.13
2	A	579	IX6	C1-C6-C5	2.38	122.64	118.89
2	A	579	IX6	C6-C5-N11	-2.33	115.28	118.92
2	A	579	IX6	C8-C9-C10	2.27	127.70	124.73
2	A	579	IX6	O30-S12-C9	-2.18	105.10	109.39
2	A	579	IX6	O31-S12-C9	-2.17	105.11	109.39
2	A	579	IX6	C20-C21-C17	-2.15	121.25	123.83
2	B	579	IX6	C4-C5-N11	2.13	126.35	122.29
2	A	579	IX6	C4-C5-N11	2.11	126.31	122.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	579	IX6	O23-C22-C26-C27
2	B	579	IX6	O23-C22-C26-C28
2	A	579	IX6	O23-C22-C26-C27
2	A	579	IX6	O23-C22-C26-C28
2	A	579	IX6	O33-C32-N7-C8

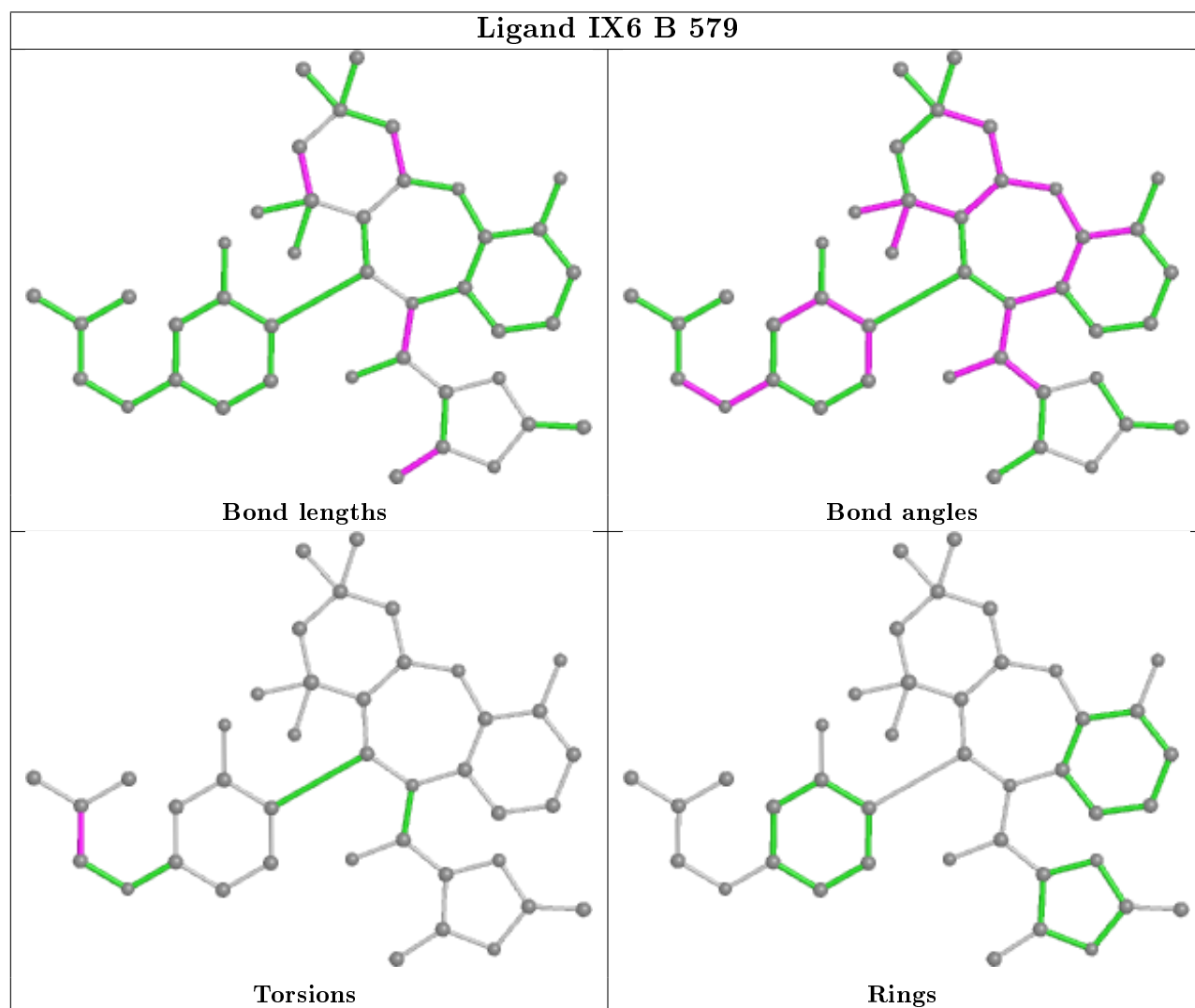
There are no ring outliers.

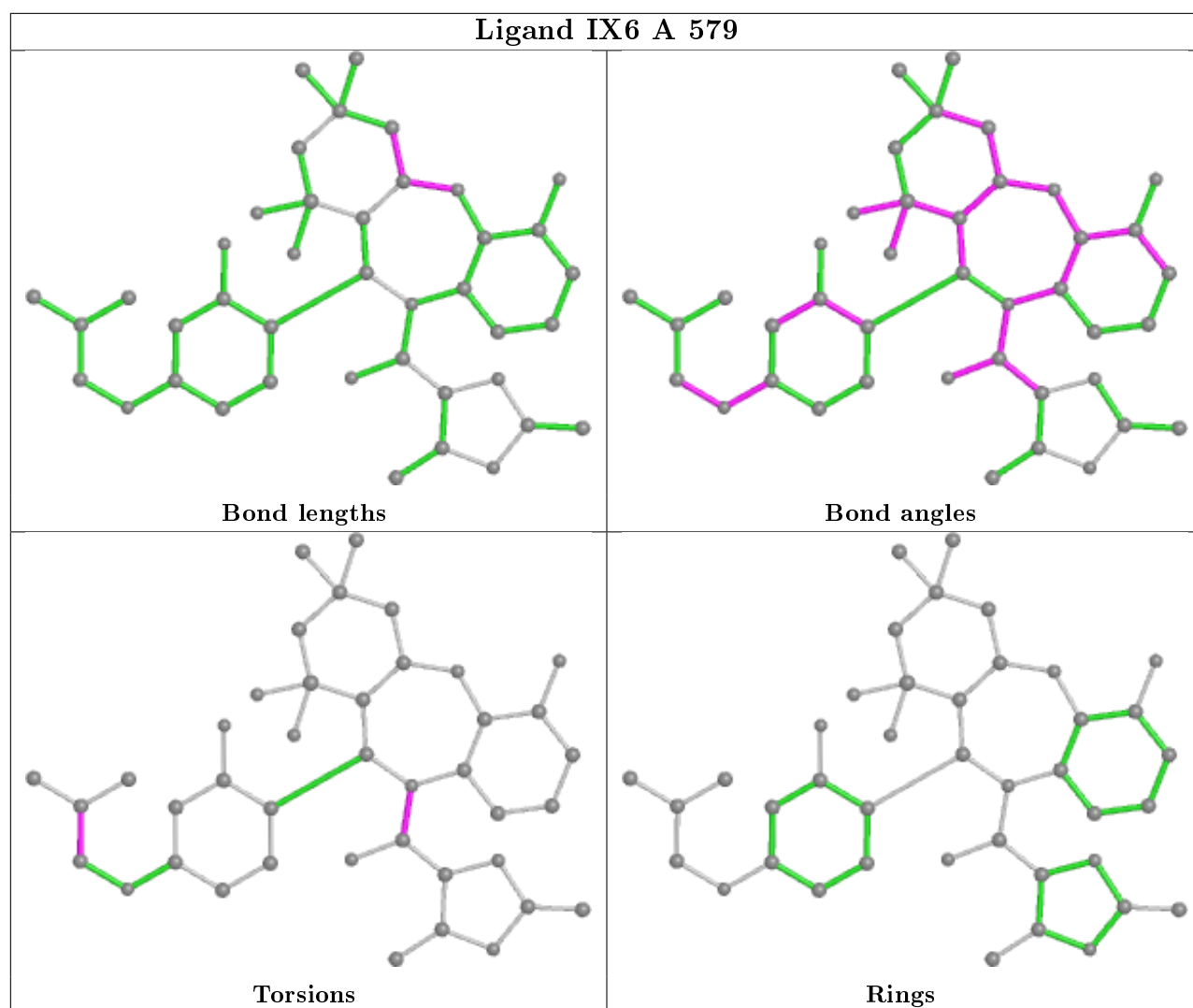
1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	581	SO4	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 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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

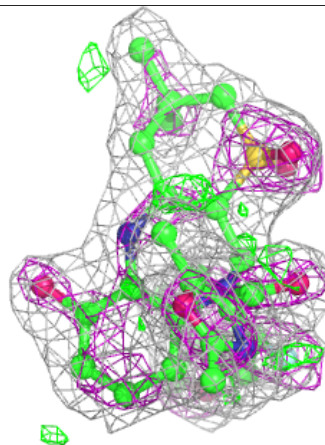
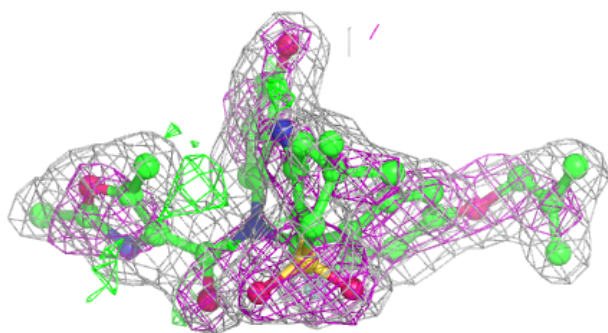
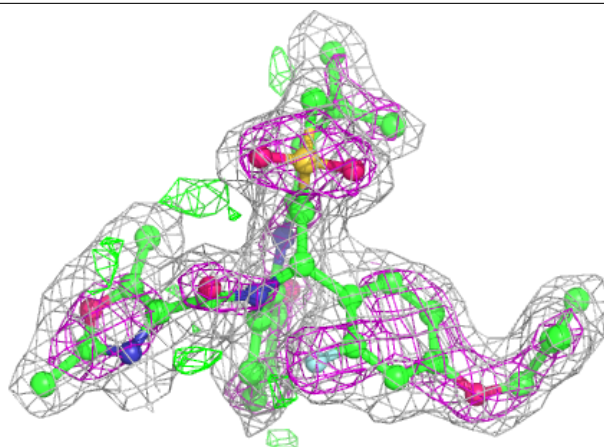
6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

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.

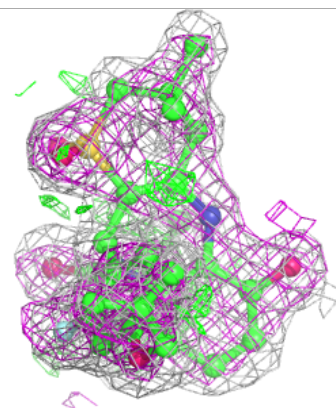
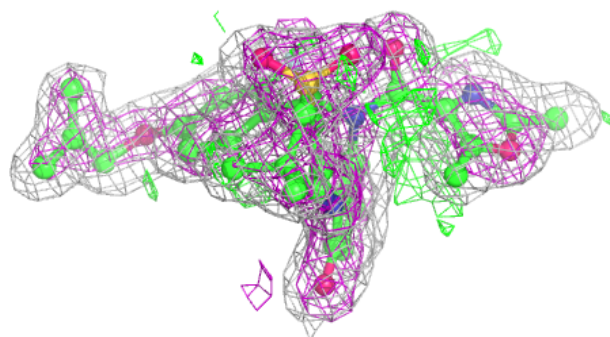
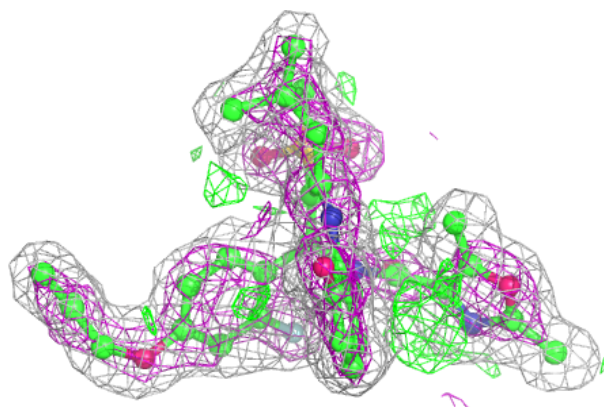
Electron density around IX6 B 579:

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



Electron density around IX6 A 579:

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



6.5 Other polymers [i](#)

Unable to reproduce the depositors R factor - this section is therefore empty.