



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:00 AM UTC

PDB ID : 8EV1 / pdb_00008ev1
Title : Dual Modulators
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Deposited on : 2022-10-19
Resolution : 1.83 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

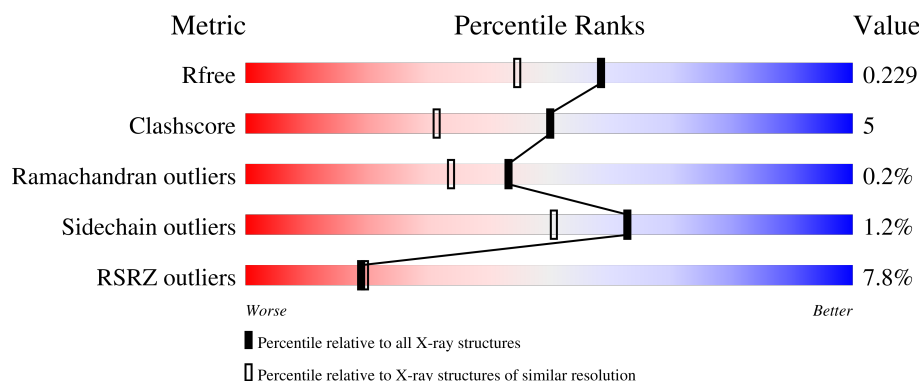
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

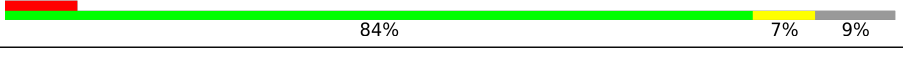
The reported resolution of this entry is 1.83 Å.

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	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	257	
2	B	257	
3	C	13	
3	D	13	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4087 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 Estrogen Receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	237	Total	C	N	O	S	0	0	0
			1890	1210	323	338	19			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	537	SER	TYR	engineered mutation	UNP P03372

- Molecule 2 is a protein called Estrogen receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	233	Total	C	N	O	S	0	0	0
			1838	1175	318	328	17			

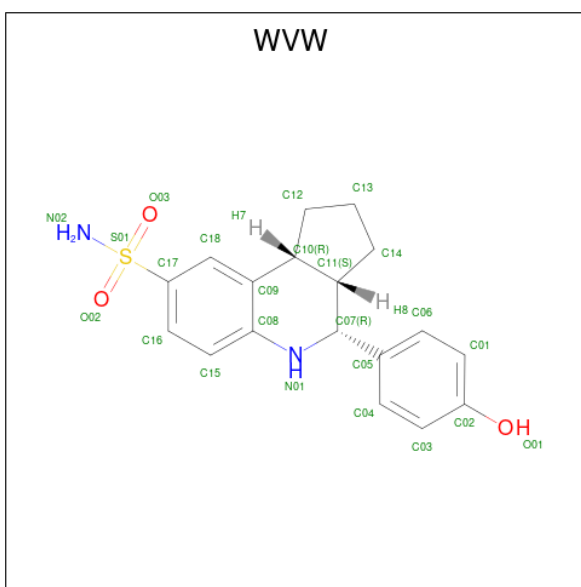
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	537	SER	TYR	engineered mutation	UNP P03372

- Molecule 3 is a protein called Nuclear receptor coactivator 2.

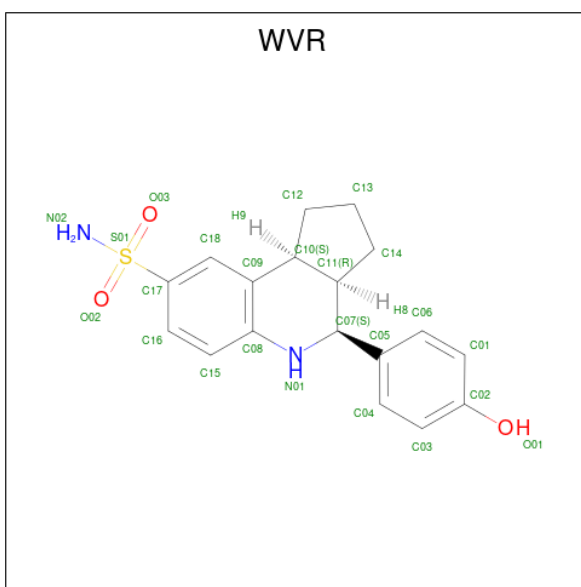
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			79	51	16	12			
3	D	9	Total	C	N	O	0	0	0
			79	51	16	12			

- Molecule 4 is (3aS,4R,9bR)-4-(4-hydroxyphenyl)-2,3,3a,4,5,9b-hexahydro-1H-cyclopenta[c]quinoline-8-sulfonamide (CCD ID: WVV) (formula: C₁₈H₂₀N₂O₃S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	1
			24	18	2	3	1		
4	B	1	Total	C	N	O	S	0	1
			24	18	2	3	1		

- Molecule 5 is (3aR,4S,9bS)-4-(4-hydroxyphenyl)-2,3,3a,4,5,9b-hexahydro-1H-cyclopenta[c]quinoline-8-sulfonamide (CCD ID: WVR) (formula: $C_{18}H_{20}N_2O_3S$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	1
			24	18	2	3	1		

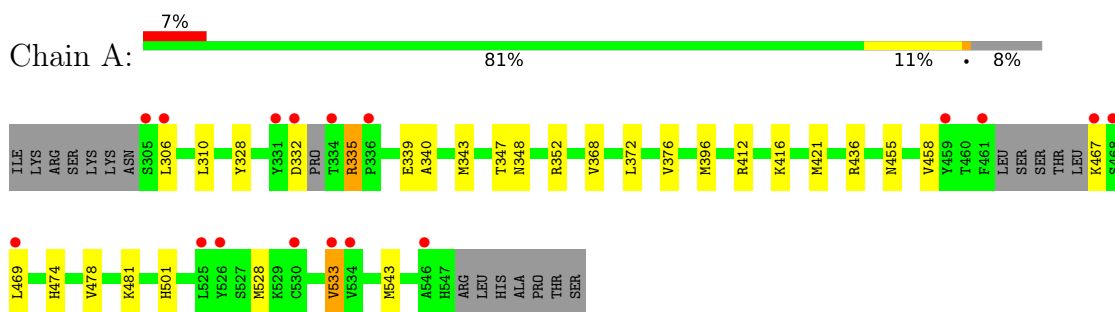
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	77	Total 77	O 77	0	0
6	B	50	Total 50	O 50	0	0
6	C	2	Total 2	O 2	0	0

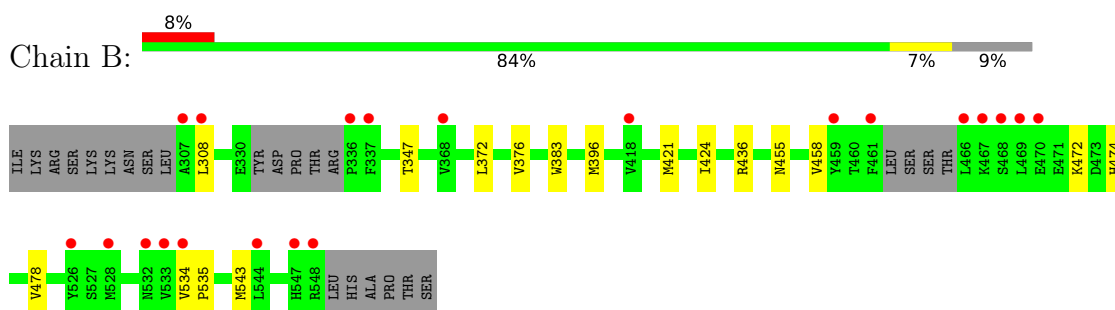
3 Residue-property plots

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.

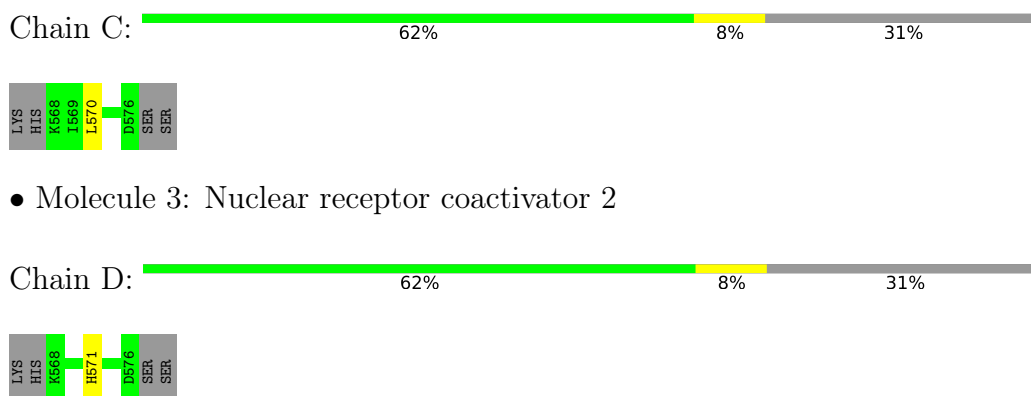
• Molecule 1: Estrogen Receptor



• Molecule 2: Estrogen receptor



• Molecule 3: Nuclear receptor coactivator 2



• Molecule 3: Nuclear receptor coactivator 2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	54.05Å 82.63Å 58.55Å 90.00° 110.93° 90.00°	Depositor
Resolution (Å)	50.54 – 1.83 50.54 – 1.83	Depositor EDS
% Data completeness (in resolution range)	64.8 (50.54-1.83) 65.2 (50.54-1.83)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.24 (at 1.83Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.176 , 0.224 0.190 , 0.229	Depositor DCC
R_{free} test set	30777 reflections (53.76%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtriage
Anisotropy	0.063	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4087	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 6.70% 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: YCM, WVR, WWV

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	0.65	1/1912 (0.1%)	0.91	0/2578
2	B	0.59	0/1848	0.91	1/2492 (0.0%)
3	C	0.48	0/79	0.91	0/104
3	D	0.56	0/79	1.00	0/104
All	All	0.62	1/3918 (0.0%)	0.91	1/5278 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	348	ASN	C-O	-5.60	1.17	1.24

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	472	LYS	N-CA-C	-6.23	104.59	111.82

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	1890	0	1937	28	0
2	B	1838	0	1857	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	79	0	88	3	0
3	D	79	0	88	2	0
4	A	24	0	0	2	0
4	B	24	0	0	5	0
5	A	24	0	0	2	0
6	A	77	0	0	3	0
6	B	50	0	0	0	0
6	C	2	0	0	0	0
All	All	4087	0	3970	42	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 5.

All (42) 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)
2:B:421:MET:HE1	4:B:601[A]:WVW:C13	1.85	1.06
1:A:543:MET:HE1	3:C:570:LEU:HD22	1.47	0.94
1:A:339:GLU:HG2	1:A:343:MET:HE2	1.56	0.87
2:B:347:THR:HG22	4:B:601[A]:WVW:C16	2.06	0.86
1:A:343:MET:HG2	4:A:601[A]:WVW:N02	1.95	0.82
2:B:421:MET:CE	4:B:601[A]:WVW:C13	2.59	0.81
1:A:343:MET:HG2	5:A:602[B]:WVR:O03	1.82	0.78
2:B:534:VAL:HG22	2:B:535:PRO:HD2	1.73	0.71
1:A:343:MET:HE1	1:A:533:VAL:HB	1.76	0.68
2:B:347:THR:CG2	4:B:601[A]:WVW:C16	2.74	0.66
1:A:412:ARG:NH1	1:A:416:LYS:NZ	2.47	0.62
1:A:528:MET:HG3	5:A:602[B]:WVR:N02	2.21	0.55
2:B:383:TRP:CD1	2:B:543:MET:HE3	2.41	0.55
1:A:412:ARG:NH1	1:A:416:LYS:HZ2	2.05	0.54
1:A:328:TYR:O	1:A:352:ARG:NH2	2.27	0.53
2:B:372:LEU:HD23	3:D:571:HIS:NE2	2.26	0.51
1:A:339:GLU:CG	1:A:343:MET:HE2	2.36	0.51
1:A:343:MET:SD	1:A:528:MET:HE3	2.50	0.50
1:A:310:LEU:O	1:A:481:LYS:HE3	2.10	0.50
1:A:528:MET:HG3	4:A:601[A]:WVW:O02	2.13	0.48
1:A:310:LEU:O	1:A:481:LYS:CE	2.62	0.48
2:B:421:MET:SD	4:B:601[A]:WVW:C12	3.02	0.47
1:A:376:VAL:HG13	3:C:570:LEU:HD23	1.97	0.47
1:A:396:MET:HE3	1:A:436:ARG:HA	1.97	0.47
2:B:474:HIS:O	2:B:478:VAL:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:HIS:O	1:A:478:VAL:HG23	2.15	0.46
1:A:412:ARG:NH1	1:A:416:LYS:HZ1	2.12	0.45
1:A:332:ASP:O	1:A:335:ARG:NH2	2.49	0.45
1:A:368:VAL:HG22	6:A:716:HOH:O	2.17	0.44
1:A:543:MET:CE	3:C:570:LEU:HD22	2.34	0.43
1:A:343:MET:HE1	1:A:533:VAL:CB	2.46	0.43
2:B:372:LEU:HD23	3:D:571:HIS:CE1	2.53	0.43
1:A:501:HIS:ND1	6:A:702:HOH:O	2.36	0.43
2:B:372:LEU:O	2:B:376:VAL:HG23	2.19	0.43
2:B:421:MET:HE3	2:B:424:ILE:HB	2.00	0.43
2:B:455:ASN:O	2:B:458:VAL:HG12	2.19	0.42
1:A:340:ALA:HA	1:A:343:MET:HE3	2.00	0.42
2:B:396:MET:HE3	2:B:436:ARG:HA	2.01	0.42
1:A:372:LEU:O	1:A:376:VAL:HG23	2.19	0.42
1:A:455:ASN:O	1:A:458:VAL:HG12	2.20	0.42
1:A:467:LYS:N	6:A:705:HOH:O	2.53	0.41
1:A:467:LYS:C	1:A:469:LEU:H	2.29	0.41

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	230/257 (90%)	224 (97%)	5 (2%)	1 (0%)	30	18
2	B	225/257 (88%)	223 (99%)	2 (1%)	0	100	100
3	C	7/13 (54%)	7 (100%)	0	0	100	100
3	D	7/13 (54%)	6 (86%)	1 (14%)	0	100	100
All	All	469/540 (87%)	460 (98%)	8 (2%)	1 (0%)	43	34

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	335	ARG

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	211/231 (91%)	207 (98%)	4 (2%)	50	34
2	B	198/230 (86%)	197 (100%)	1 (0%)	81	75
3	C	9/13 (69%)	9 (100%)	0	100	100
3	D	9/13 (69%)	9 (100%)	0	100	100
All	All	427/487 (88%)	422 (99%)	5 (1%)	63	51

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	306	LEU
1	A	347	THR
1	A	421	MET
1	A	533	VAL
2	B	308	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	359	ASN
1	A	474	HIS
1	A	513	HIS
1	A	524	HIS
2	B	474	HIS
2	B	513	HIS
3	C	571	HIS
3	D	575	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	YCM	A	381	1	7,9,10	0.51	0	5,10,12	0.28	0
2	YCM	B	381	2	7,9,10	0.52	0	5,10,12	0.36	0
2	YCM	B	417	2	7,9,10	0.43	0	5,10,12	0.55	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
1	YCM	A	381	1	-	1/6/8/10	-
2	YCM	B	381	2	-	1/6/8/10	-
2	YCM	B	417	2	-	3/6/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	381	YCM	SG-CD-CE-NZ2
2	B	417	YCM	CA-CB-SG-CD
2	B	417	YCM	CE-CD-SG-CB
2	B	417	YCM	SG-CD-CE-NZ2
2	B	381	YCM	SG-CD-CE-NZ2

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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
5	WVR	A	602[B]	-	27,27,27	2.80	16 (59%)	39,41,41	4.59	17 (43%)
4	WWV	A	601[A]	-	27,27,27	2.85	15 (55%)	39,41,41	4.19	19 (48%)
4	WWV	B	601[A]	-	27,27,27	2.93	15 (55%)	39,41,41	4.93	20 (51%)

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
5	WVR	A	602[B]	-	-	6/10/32/32	0/4/4/4
4	WWV	A	601[A]	-	-	3/10/32/32	0/4/4/4
4	WWV	B	601[A]	-	-	1/10/32/32	0/4/4/4

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601[A]	WWV	C08-N01	-7.24	1.25	1.39
4	B	601[A]	WWV	C08-N01	-7.13	1.26	1.39
5	A	602[B]	WVR	C08-N01	-6.54	1.27	1.39
4	B	601[A]	WWV	C08-C09	-6.14	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	601[A]	WVW	C08-C09	-5.47	1.34	1.40
5	A	602[B]	WVR	C08-C09	-4.97	1.34	1.40
4	B	601[A]	WVW	C17-S01	4.78	1.84	1.77
5	A	602[B]	WVR	S01-N02	4.77	1.69	1.60
5	A	602[B]	WVR	C13-C12	-4.75	1.32	1.51
4	A	601[A]	WVW	S01-N02	4.69	1.69	1.60
4	B	601[A]	WVW	C13-C12	-4.57	1.33	1.51
4	A	601[A]	WVW	C13-C12	-4.41	1.34	1.51
4	B	601[A]	WVW	S01-N02	3.69	1.67	1.60
4	B	601[A]	WVW	C15-C08	-3.67	1.33	1.39
4	A	601[A]	WVW	C15-C08	-3.50	1.34	1.39
4	B	601[A]	WVW	C03-C02	-3.50	1.32	1.39
5	A	602[B]	WVR	C18-C09	-3.41	1.34	1.39
4	A	601[A]	WVW	C06-C05	-3.34	1.33	1.39
4	A	601[A]	WVW	C06-C01	-3.23	1.33	1.38
5	A	602[B]	WVR	C15-C08	-3.05	1.34	1.39
4	B	601[A]	WVW	C05-C07	3.04	1.55	1.52
4	A	601[A]	WVW	C16-C17	-2.94	1.34	1.38
4	A	601[A]	WVW	C16-C15	-2.89	1.34	1.38
5	A	602[B]	WVR	C06-C05	-2.87	1.34	1.39
5	A	602[B]	WVR	C12-C10	-2.78	1.49	1.54
5	A	602[B]	WVR	C04-C05	-2.75	1.34	1.39
5	A	602[B]	WVR	C04-C03	-2.72	1.34	1.38
5	A	602[B]	WVR	C06-C01	-2.72	1.34	1.38
5	A	602[B]	WVR	C01-C02	-2.70	1.33	1.39
5	A	602[B]	WVR	C18-C17	-2.67	1.34	1.39
4	A	601[A]	WVW	C01-C02	-2.66	1.34	1.39
4	B	601[A]	WVW	C04-C03	-2.52	1.34	1.38
5	A	602[B]	WVR	C16-C17	-2.45	1.35	1.38
4	B	601[A]	WVW	C01-C02	-2.44	1.34	1.39
4	A	601[A]	WVW	C18-C09	-2.40	1.35	1.39
5	A	602[B]	WVR	C17-S01	2.38	1.80	1.77
4	B	601[A]	WVW	C12-C10	-2.36	1.50	1.54
4	B	601[A]	WVW	C06-C01	-2.31	1.35	1.38
4	A	601[A]	WVW	C04-C05	-2.28	1.35	1.39
4	B	601[A]	WVW	C06-C05	-2.20	1.35	1.39
5	A	602[B]	WVR	C03-C02	-2.19	1.34	1.39
4	A	601[A]	WVW	C17-S01	2.15	1.80	1.77
4	A	601[A]	WVW	C03-C02	-2.14	1.35	1.39
4	B	601[A]	WVW	C16-C15	-2.04	1.35	1.38
4	A	601[A]	WVW	C04-C03	-2.03	1.35	1.38
4	B	601[A]	WVW	C04-C05	-2.00	1.36	1.39

All (56) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	601[A]	WVW	O03-S01-N02	-20.32	78.06	107.35
5	A	602[B]	WVR	O03-S01-N02	-17.97	81.45	107.35
5	A	602[B]	WVR	O02-S01-N02	-14.97	85.76	107.35
4	A	601[A]	WVW	O03-S01-N02	-13.29	88.19	107.35
4	A	601[A]	WVW	O02-S01-N02	-12.16	89.83	107.35
4	B	601[A]	WVW	O02-S01-N02	-11.14	91.30	107.35
4	B	601[A]	WVW	O03-S01-C17	11.11	119.90	107.35
4	A	601[A]	WVW	O02-S01-C17	8.97	117.49	107.35
5	A	602[B]	WVR	O03-S01-C17	8.92	117.44	107.35
5	A	602[B]	WVR	O02-S01-C17	8.80	117.29	107.35
4	A	601[A]	WVW	O03-S01-C17	8.07	116.47	107.35
4	B	601[A]	WVW	C17-S01-N02	6.65	117.66	108.40
4	A	601[A]	WVW	C11-C07-N01	5.58	114.86	108.69
4	B	601[A]	WVW	O02-S01-C17	5.26	113.29	107.35
4	A	601[A]	WVW	C05-C07-C11	5.21	123.83	113.00
4	B	601[A]	WVW	C05-C07-C11	5.05	123.49	113.00
4	A	601[A]	WVW	C17-S01-N02	4.71	114.96	108.40
4	B	601[A]	WVW	C16-C17-C18	-4.52	115.08	120.68
4	B	601[A]	WVW	C14-C11-C10	4.23	108.89	103.97
4	B	601[A]	WVW	C13-C14-C11	-4.18	96.74	104.85
4	A	601[A]	WVW	C13-C14-C11	-4.15	96.79	104.85
5	A	602[B]	WVR	O03-S01-O02	3.85	124.72	118.80
5	A	602[B]	WVR	C05-C07-N01	3.72	118.39	111.04
4	A	601[A]	WVW	C04-C05-C07	3.71	126.68	120.78
4	B	601[A]	WVW	O03-S01-O02	3.70	124.49	118.80
4	B	601[A]	WVW	C08-N01-C07	3.60	128.95	118.91
4	A	601[A]	WVW	C13-C12-C10	3.59	110.30	104.32
5	A	602[B]	WVR	C05-C07-C11	3.51	120.29	113.00
4	B	601[A]	WVW	C13-C12-C10	3.45	110.06	104.32
4	B	601[A]	WVW	C11-C07-N01	3.41	112.47	108.69
4	B	601[A]	WVW	C10-C11-C07	3.35	115.17	110.65
4	B	601[A]	WVW	C12-C10-C11	-3.20	98.57	103.63
4	A	601[A]	WVW	C14-C11-C07	3.10	120.88	115.14
4	A	601[A]	WVW	C15-C08-N01	-3.07	115.98	120.70
5	A	602[B]	WVR	C16-C17-S01	2.95	123.73	119.72
4	B	601[A]	WVW	C06-C05-C04	-2.92	114.68	118.30
5	A	602[B]	WVR	C10-C11-C07	-2.89	106.73	110.65
4	B	601[A]	WVW	C09-C18-C17	2.84	124.05	120.88
4	B	601[A]	WVW	C18-C17-S01	2.79	124.38	119.34
5	A	602[B]	WVR	C16-C17-C18	-2.69	117.34	120.68
4	A	601[A]	WVW	C06-C01-C02	2.67	122.71	119.88
4	A	601[A]	WVW	C08-N01-C07	2.67	126.35	118.91

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	601[A]	WVW	C06-C05-C07	-2.61	116.63	120.78
4	B	601[A]	WVW	C15-C08-N01	-2.53	116.82	120.70
4	A	601[A]	WVW	C18-C17-S01	2.41	123.69	119.34
5	A	602[B]	WVR	C04-C03-C02	2.39	122.41	119.88
5	A	602[B]	WVR	C17-S01-N02	2.36	111.68	108.40
5	A	602[B]	WVR	C03-C02-C01	-2.33	116.06	119.77
4	A	601[A]	WVW	C03-C02-C01	-2.31	116.10	119.77
4	A	601[A]	WVW	C14-C11-C10	2.31	106.65	103.97
4	A	601[A]	WVW	C12-C10-C11	-2.23	100.10	103.63
5	A	602[B]	WVR	C08-C09-C10	2.23	122.35	118.74
5	A	602[B]	WVR	C09-C18-C17	2.22	123.35	120.88
4	B	601[A]	WVW	C09-C08-N01	2.10	123.39	120.60
5	A	602[B]	WVR	C08-N01-C07	-2.08	113.10	118.91
5	A	602[B]	WVR	C06-C01-C02	2.03	122.03	119.88

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	602[B]	WVR	C04-C05-C07-C11
5	A	602[B]	WVR	C06-C05-C07-C11
5	A	602[B]	WVR	C18-C17-S01-N02
5	A	602[B]	WVR	C06-C05-C07-N01
5	A	602[B]	WVR	C16-C17-S01-N02
5	A	602[B]	WVR	C04-C05-C07-N01
4	A	601[A]	WVW	C18-C17-S01-N02
4	A	601[A]	WVW	C16-C17-S01-O02
4	A	601[A]	WVW	C16-C17-S01-N02
4	B	601[A]	WVW	C16-C17-S01-O02

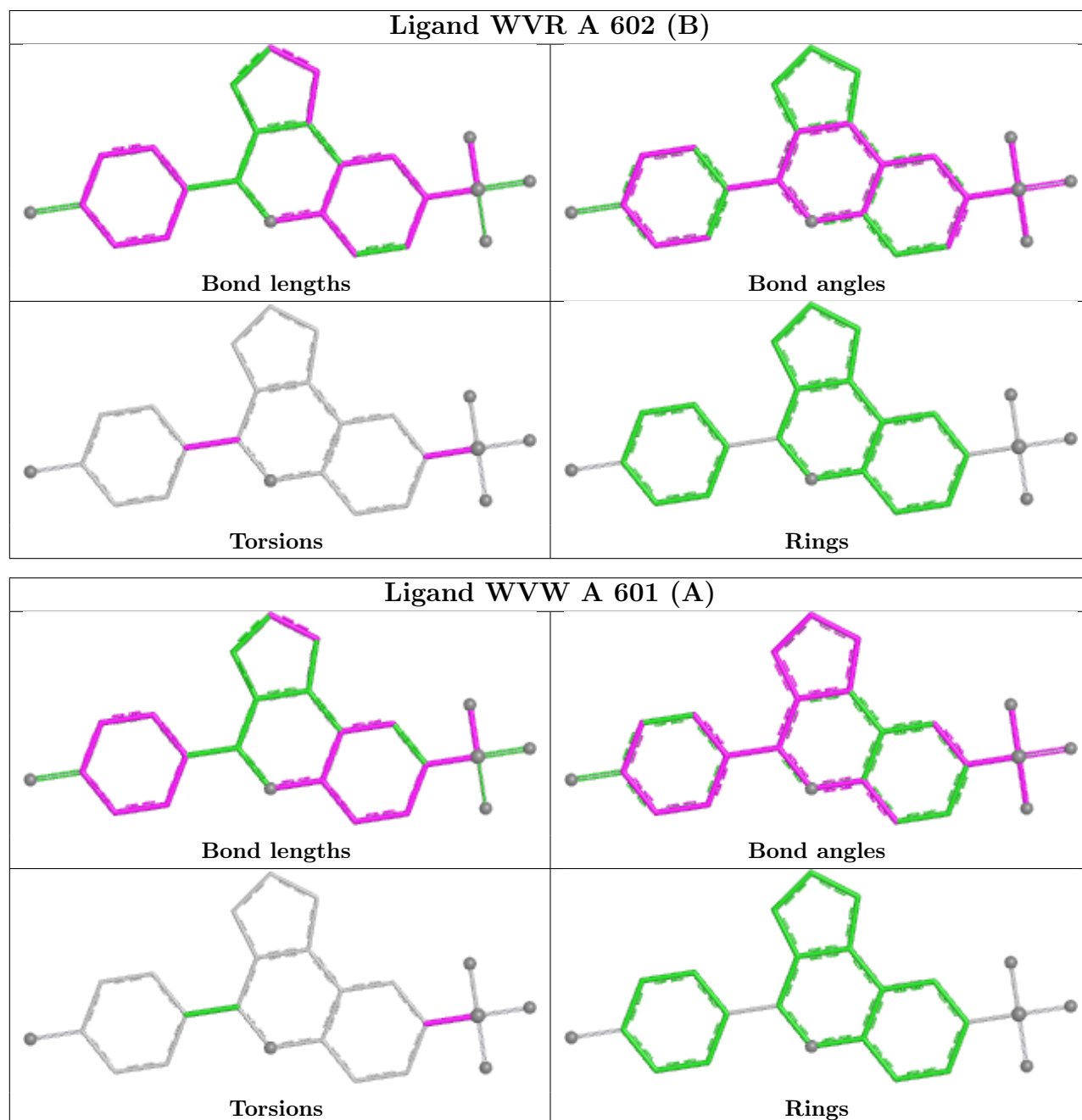
There are no ring outliers.

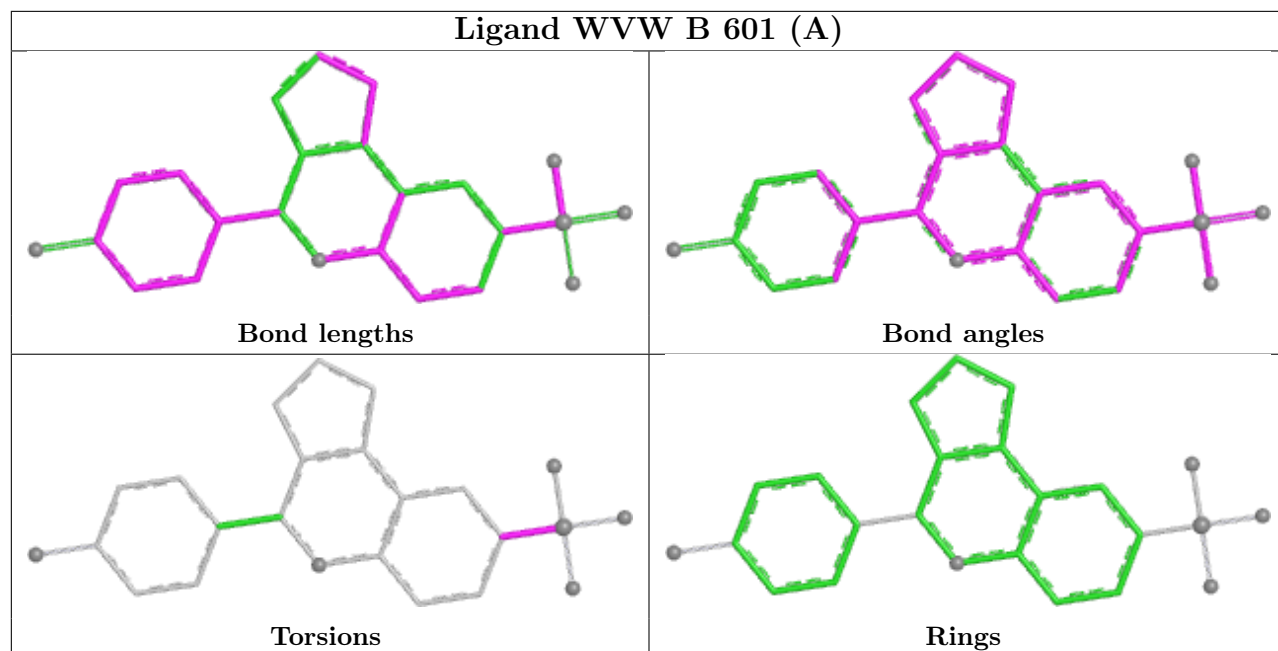
3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	602[B]	WVR	2	0
4	A	601[A]	WVW	2	0
4	B	601[A]	WVW	5	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	236/257 (91%)	0.24	17 (7%) 21 22	17, 36, 88, 142	0
2	B	231/257 (89%)	0.59	21 (9%) 15 16	22, 46, 91, 125	0
3	C	9/13 (69%)	0.42	0 100 100	32, 38, 68, 91	0
3	D	9/13 (69%)	1.21	0 100 100	52, 62, 91, 106	0
All	All	485/540 (89%)	0.43	38 (7%) 19 20	17, 41, 91, 142	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	466	LEU	5.5
2	B	533	VAL	5.5
2	B	468	SER	5.2
2	B	337	PHE	4.5
2	B	336	PRO	4.5
2	B	469	LEU	4.1
1	A	332	ASP	4.1
1	A	461	PHE	4.0
1	A	336	PRO	3.8
1	A	334	THR	3.6
1	A	459	TYR	3.6
1	A	533	VAL	3.5
2	B	534	VAL	3.4
2	B	544	LEU	3.3
1	A	530	CYS	3.3
1	A	469	LEU	3.2
2	B	547	HIS	3.1
2	B	548	ARG	3.0
1	A	526	TYR	2.9
2	B	532	ASN	2.9
2	B	418	VAL	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	307	ALA	2.6
2	B	368	VAL	2.6
2	B	461	PHE	2.6
1	A	331	TYR	2.5
2	B	470	GLU	2.4
1	A	534	VAL	2.4
2	B	526	TYR	2.4
1	A	306	LEU	2.3
1	A	467	LYS	2.3
1	A	546	ALA	2.2
2	B	528	MET	2.2
1	A	305	SER	2.2
1	A	468	SER	2.2
2	B	459	TYR	2.2
1	A	525	LEU	2.1
2	B	467	LYS	2.0
2	B	308	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	YCM	B	417	10/11	0.77	0.11	84,86,97,98	0
2	YCM	B	381	10/11	0.90	0.12	28,43,69,81	0
1	YCM	A	381	10/11	0.95	0.10	22,28,75,78	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

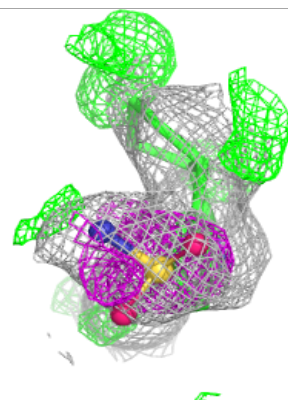
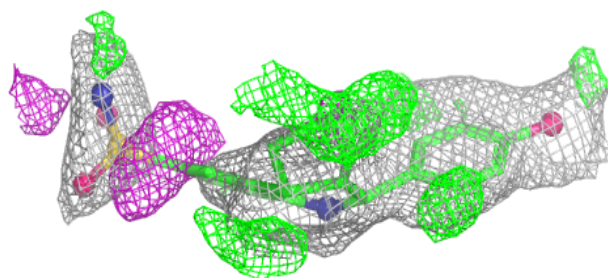
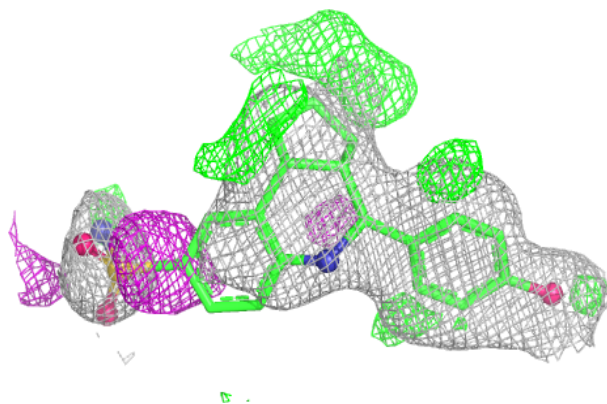
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
4	WVW	A	601[A]	24/24	0.70	0.30	60,82,124,127	24
4	WVW	B	601[A]	24/24	0.74	0.32	51,113,184,223	0
5	WVR	A	602[B]	24/24	0.78	0.18	19,55,71,74	24

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.

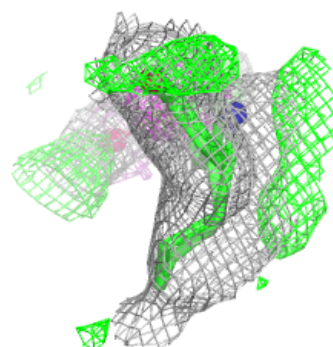
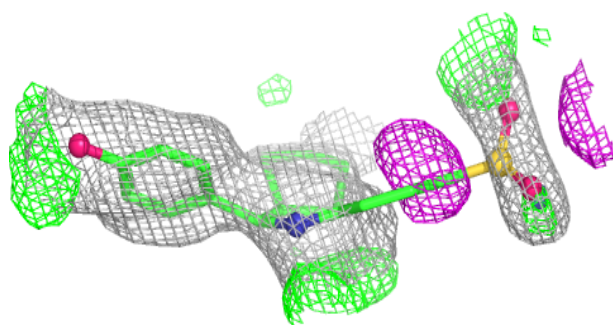
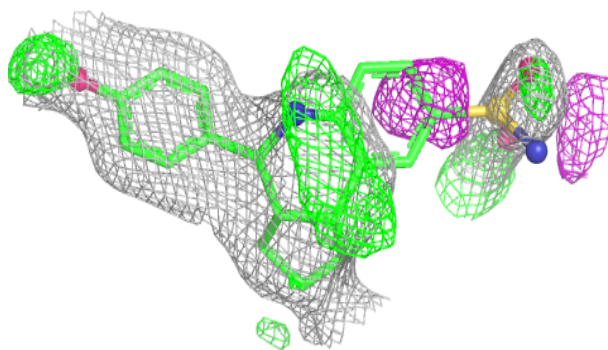
Electron density around WVW A 601 (A):

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

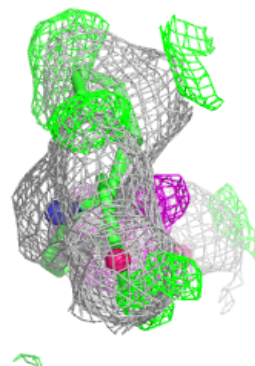
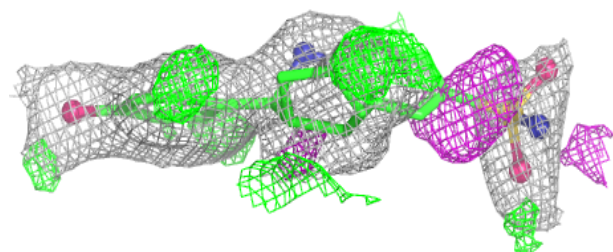
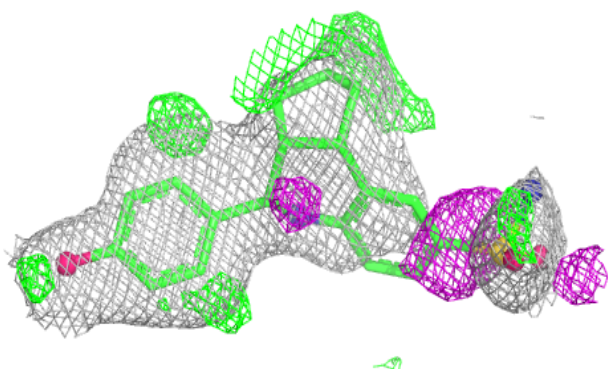


Electron density around WVV B 601 (A):

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

**Electron density around WVR A 602 (B):**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.