



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 21, 2021 – 02:05 PM EDT

PDB ID : 7R7I
Title : Structure of human SHP2 in complex with compound 27
Authors : Leonard, P.G.; Cross, J.
Deposited on : 2021-06-24
Resolution : 2.85 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 : 2.23.2
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) : 2.23.2

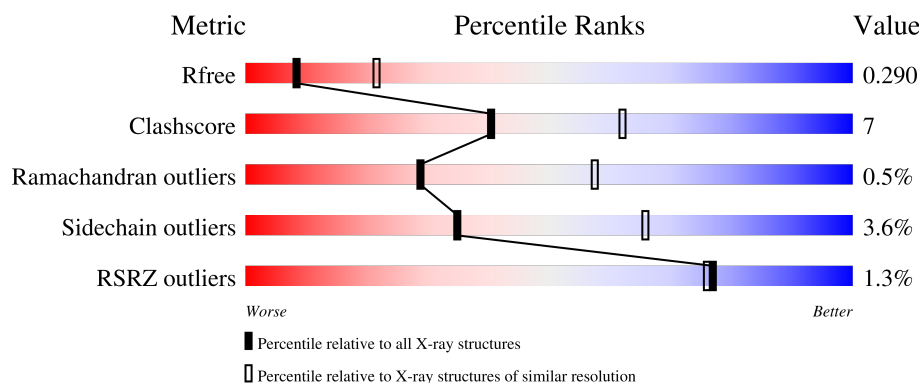
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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	536	<div> <div></div> <div>73%</div> <div>17%</div> <div>• 9%</div> </div>
1	B	536	<div> <div></div> <div>72%</div> <div>18%</div> <div>• 9%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7963 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.

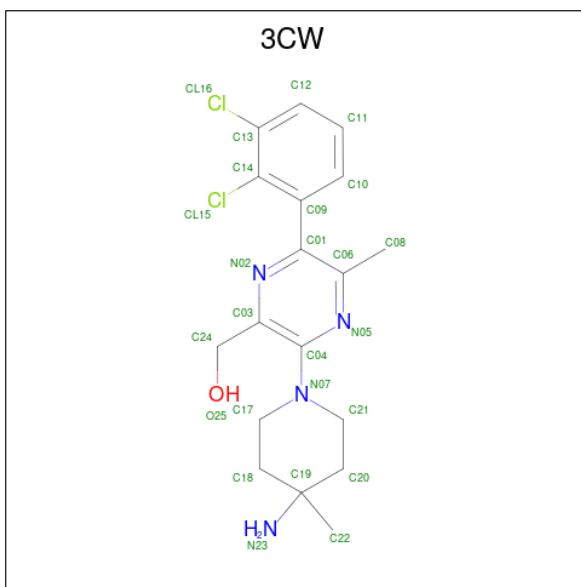
- Molecule 1 is a protein called Tyrosine-protein phosphatase non-receptor type 11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	489	Total	C	N	O	S	0	0	0
			3955	2492	707	738	18			
1	B	488	Total	C	N	O	S	0	0	0
			3952	2487	704	743	18			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP Q06124
A	-4	ALA	-	expression tag	UNP Q06124
A	-3	MET	-	expression tag	UNP Q06124
A	-2	ALA	-	expression tag	UNP Q06124
A	-1	ASP	-	expression tag	UNP Q06124
A	0	ILE	-	expression tag	UNP Q06124
B	-5	GLY	-	expression tag	UNP Q06124
B	-4	ALA	-	expression tag	UNP Q06124
B	-3	MET	-	expression tag	UNP Q06124
B	-2	ALA	-	expression tag	UNP Q06124
B	-1	ASP	-	expression tag	UNP Q06124
B	0	ILE	-	expression tag	UNP Q06124

- Molecule 2 is [3-(4-amino-4-methylpiperidin-1-yl)-6-(2,3-dichlorophenyl)-5-methylpyrazin-2-yl]methanol (three-letter code: 3CW) (formula: C₁₈H₂₂Cl₂N₄O) (labeled as "Ligand of Interest" by depositor).

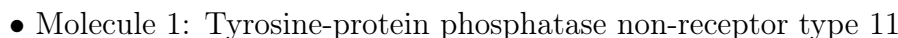


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Cl	N	O	0	0
			25	18	2	4	1		
2	B	1	Total	C	Cl	N	O	0	0
			25	18	2	4	1		

- Molecule 3 is water.

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

- Molecule 1: Tyrosine-protein phosphatase non-receptor type 11



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.18Å 83.63Å 217.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	54.78 – 2.85 54.78 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.6 (54.78-2.85) 99.7 (54.78-2.85)	Depositor EDS
R_{merge}	0.33	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.19.1-4122-000	Depositor
R, R_{free}	0.232 , 0.292 0.233 , 0.290	Depositor DCC
R_{free} test set	1293 reflections (5.33%)	wwPDB-VP
Wilson B-factor (Å ²)	37.5	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 29.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	7963	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 28.65 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.7763e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: 3CW

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	0.25	0/4036	0.49	0/5440
1	B	0.25	0/4032	0.50	0/5435
All	All	0.25	0/8068	0.50	0/10875

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3955	0	3904	60	0
1	B	3952	0	3884	54	0
2	A	25	0	0	1	0
2	B	25	0	0	0	0
3	A	3	0	0	0	0
3	B	3	0	0	0	0
All	All	7963	0	7788	114	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 7.

All (114) 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:221:ILE:HD11	1:A:229:ARG:HG2	1.66	0.77
1:A:355:MET:HG3	1:A:458:HIS:CE1	2.23	0.73
1:A:116:HIS:O	1:A:116:HIS:ND1	2.21	0.71
1:A:4:ARG:N	1:A:259:CYS:HG	1.89	0.70
1:A:397:THR:HG22	1:A:421:ARG:HD3	1.75	0.68
1:B:47:ARG:NH2	1:B:90:GLU:OE1	2.28	0.65
1:A:94:ASP:N	1:A:94:ASP:OD1	2.26	0.65
1:A:175:GLN:NE2	1:A:180:ASP:OD2	2.32	0.63
1:B:497:VAL:HG12	1:B:504:MET:HG3	1.81	0.62
1:A:495:GLN:HG3	2:A:601:3CW:CL16	2.37	0.61
1:A:497:VAL:HG12	1:A:504:MET:HG3	1.82	0.61
1:B:373:ASP:OD1	1:B:373:ASP:N	2.30	0.61
1:B:272:GLU:N	1:B:272:GLU:OE1	2.32	0.58
1:B:227:GLU:HG3	1:B:519:GLN:HG3	1.86	0.58
1:B:54:ILE:HD11	1:B:67:GLY:H	1.70	0.57
1:B:377:LEU:HD12	1:B:386:ARG:HB2	1.87	0.57
1:A:7:PHE:HA	1:A:31:ALA:HB3	1.88	0.56
1:B:131:LYS:HD3	1:B:132:HIS:N	2.22	0.55
1:A:386:ARG:HG2	1:A:388:VAL:HG12	1.89	0.54
1:B:90:GLU:HG2	1:B:92:ASN:H	1.72	0.54
1:A:290:VAL:HG11	1:A:344:MET:HG3	1.89	0.54
1:B:390:GLU:HG2	1:B:399:ARG:HG2	1.89	0.54
1:B:43:LEU:HB3	1:B:54:ILE:HG23	1.91	0.53
1:B:84:HIS:ND1	1:B:84:HIS:O	2.42	0.52
1:B:4:ARG:NH1	1:B:255:GLN:O	2.42	0.52
1:B:92:ASN:O	1:B:92:ASN:ND2	2.39	0.52
1:B:397:THR:OG1	1:B:421:ARG:NH2	2.43	0.52
1:A:325:LYS:HD3	1:A:446:GLN:HG2	1.92	0.51
1:B:222:ASN:OD1	1:B:485:ASP:HA	2.09	0.51
1:A:125:LEU:HB3	1:A:216:LEU:HD21	1.92	0.51
1:B:116:HIS:O	1:B:116:HIS:ND1	2.44	0.51
1:A:418:TYR:HB3	1:A:438:PHE:CE1	2.45	0.51
1:B:79:GLN:NE2	1:B:83:GLU:OE2	2.42	0.50
1:B:34:SER:HB2	1:B:40:ASP:HB3	1.93	0.50
1:B:125:LEU:HB3	1:B:216:LEU:HD21	1.92	0.50
1:A:351:ARG:HG3	1:A:449:ILE:HG21	1.93	0.50
1:A:225:GLU:N	1:A:225:GLU:OE1	2.42	0.49
1:A:330:THR:HG21	1:A:344:MET:HE1	1.93	0.49
1:A:65:LEU:HD23	1:A:77:LEU:HD11	1.94	0.49
1:A:307:ALA:HB2	1:A:330:THR:HG22	1.94	0.48
1:A:366:LYS:HD3	1:A:460:SER:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:ALA:HB2	1:A:484:VAL:HG22	1.96	0.48
1:A:269:GLN:HG3	1:A:283:LEU:HD13	1.95	0.48
1:B:293:HIS:O	1:B:294:ASP:HB2	2.14	0.48
1:A:352:VAL:HG11	1:A:442:VAL:HG13	1.96	0.48
1:A:203:VAL:HG22	1:A:209:VAL:HG12	1.95	0.48
1:A:8:HIS:CE1	1:A:102:LEU:HD12	2.49	0.48
1:A:377:LEU:HD21	1:A:384:ARG:HD2	1.96	0.48
1:B:62:TYR:CE1	1:B:70:LYS:HD3	2.49	0.47
1:B:78:VAL:HG12	1:B:82:MET:HE2	1.97	0.47
1:B:58:ASN:ND2	1:B:62:TYR:O	2.48	0.47
1:B:175:GLN:NE2	1:B:180:ASP:OD2	2.48	0.47
1:B:134:SER:HA	1:B:214:GLN:O	2.15	0.47
1:B:219:THR:HG21	1:B:491:PRO:HG2	1.97	0.47
1:B:423:TRP:CD1	1:B:465:ARG:HD3	2.50	0.46
1:B:352:VAL:HG11	1:B:442:VAL:HG13	1.97	0.46
1:A:7:PHE:CZ	1:A:33:PRO:HG3	2.51	0.46
1:A:287:HIS:ND1	1:A:288:THR:HG23	2.29	0.46
1:B:278:ARG:HG2	1:B:279:TYR:CE2	2.51	0.46
1:B:349:ASN:OD1	1:B:351:ARG:NH1	2.48	0.46
1:A:265:ARG:HH21	1:A:283:LEU:HD12	1.81	0.45
1:B:12:THR:OG1	1:B:15:GLU:HG3	2.16	0.45
1:B:355:MET:HB3	1:B:419:HIS:HA	1.98	0.45
1:A:178:LYS:HE3	1:A:178:LYS:HB3	1.68	0.45
1:B:233:LEU:HA	1:B:246:GLY:HA3	1.98	0.45
1:A:12:THR:OG1	1:A:15:GLU:OE2	2.35	0.45
1:A:272:GLU:H	1:A:272:GLU:CD	2.20	0.44
1:B:330:THR:HG23	1:B:458:HIS:HB3	1.98	0.44
1:B:199:LYS:O	1:B:201:PRO:HD3	2.18	0.44
1:B:418:TYR:HB3	1:B:438:PHE:CE1	2.53	0.44
1:A:383:MET:CE	1:A:405:LYS:HG3	2.47	0.44
1:A:379:GLU:HG2	1:A:384:ARG:HD3	2.00	0.44
1:B:81:TYR:CD1	1:B:88:LEU:HB2	2.53	0.43
1:B:73:THR:OG1	1:B:76:GLU:HG3	2.19	0.43
1:A:218:THR:O	1:A:229:ARG:NH2	2.51	0.43
1:A:226:ILE:HD12	1:A:488:ILE:HD11	2.01	0.43
1:A:288:THR:HG21	1:A:500:GLN:HG2	1.99	0.43
1:A:388:VAL:O	1:A:389:LYS:HD3	2.18	0.43
1:B:28:SER:HA	1:B:100:TYR:O	2.19	0.43
1:A:91:LYS:HA	1:A:91:LYS:HD2	1.54	0.43
1:B:436:LEU:HD22	1:B:521:TYR:HB2	2.01	0.42
1:B:355:MET:HG3	1:B:458:HIS:CE1	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:ARG:HH21	1:A:304:TYR:HA	1.84	0.42
1:A:330:THR:OG1	1:A:458:HIS:HB3	2.19	0.42
1:B:250:GLU:OE2	1:B:511:TYR:OH	2.32	0.42
1:B:47:ARG:HH12	1:B:52:THR:HG21	1.85	0.42
1:A:421:ARG:HE	1:A:421:ARG:HB2	1.66	0.41
1:A:495:GLN:HA	1:A:498:ARG:HB2	2.02	0.41
1:B:229:ARG:HA	1:B:229:ARG:HD3	1.86	0.41
1:A:32:ARG:HG2	1:A:32:ARG:HH11	1.85	0.41
1:A:109:SER:HB2	1:A:256:GLN:OE1	2.21	0.41
1:A:264:SER:OG	1:A:286:ASP:OD2	2.32	0.41
1:A:383:MET:HE1	1:A:405:LYS:HG3	2.02	0.41
1:B:265:ARG:O	1:B:269:GLN:HG3	2.20	0.41
1:A:459:CYS:SG	1:A:460:SER:N	2.94	0.41
1:B:26:ASP:HA	1:B:46:ARG:HD3	2.02	0.41
1:A:134:SER:HA	1:A:214:GLN:O	2.21	0.41
1:A:222:ASN:HB3	1:A:225:GLU:CD	2.41	0.41
1:A:266:LYS:HA	1:A:266:LYS:HE2	2.03	0.41
1:A:274:LYS:HE2	1:A:274:LYS:HB2	1.71	0.41
1:A:126:LEU:HD23	1:A:216:LEU:HD13	2.03	0.41
1:A:133:GLY:HA3	1:A:213:LYS:HB2	2.02	0.41
1:B:290:VAL:HG11	1:B:344:MET:HG3	2.02	0.41
1:B:291:VAL:O	1:B:347:GLN:NE2	2.40	0.41
1:A:198:LYS:HG2	1:A:212:LEU:HB2	2.02	0.40
1:A:294:ASP:O	1:A:343:ARG:NH2	2.54	0.40
1:B:221:ILE:HG21	1:B:229:ARG:HG2	2.02	0.40
1:A:124:LYS:HD3	1:A:125:LEU:HD12	2.02	0.40
1:A:389:LYS:HE2	1:A:389:LYS:HB2	1.90	0.40
1:B:131:LYS:HD3	1:B:132:HIS:HB3	2.04	0.40
1:A:355:MET:HG3	1:A:458:HIS:NE2	2.35	0.40
1:B:164:LYS:HA	1:B:164:LYS:HD3	1.86	0.40
1:B:358:LYS:HD2	1:B:358:LYS:HA	1.88	0.40
1:B:5:ARG:HB3	1:B:103:ASN:HB3	2.02	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	479/536 (89%)	441 (92%)	35 (7%)	3 (1%)	25	53
1	B	476/536 (89%)	443 (93%)	31 (6%)	2 (0%)	34	62
All	All	955/1072 (89%)	884 (93%)	66 (7%)	5 (0%)	29	57

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	412	GLU
1	B	132	HIS
1	A	413	ARG
1	A	505	VAL
1	B	505	VAL

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	433/475 (91%)	421 (97%)	12 (3%)	43	73
1	B	434/475 (91%)	415 (96%)	19 (4%)	28	58
All	All	867/950 (91%)	836 (96%)	31 (4%)	35	66

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	ASP
1	A	46	ARG
1	A	65	LEU
1	A	85	HIS
1	A	94	ASP
1	A	164	LYS
1	A	173	ARG

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Mol	Chain	Res	Type
1	A	199	LYS
1	A	234	SER
1	A	344	MET
1	A	389	LYS
1	A	397	THR
1	B	32	ARG
1	B	46	ARG
1	B	65	LEU
1	B	66	TYR
1	B	92	ASN
1	B	128	GLU
1	B	132	HIS
1	B	140	SER
1	B	205	THR
1	B	228	SER
1	B	229	ARG
1	B	335	GLN
1	B	364	LYS
1	B	373	ASP
1	B	431	ASP
1	B	477	ASP
1	B	484	VAL
1	B	485	ASP
1	B	523	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	175	GLN
1	B	132	HIS
1	B	211	GLN
1	B	273	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	3CW	A	601	-	24,27,27	2.51	8 (33%)	31,40,40	1.68	6 (19%)
2	3CW	B	601	-	24,27,27	2.42	7 (29%)	31,40,40	1.48	4 (12%)

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	3CW	A	601	-	-	3/10/22/22	0/3/3/3
2	3CW	B	601	-	-	1/10/22/22	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	3CW	C09-C01	7.02	1.56	1.49
2	B	601	3CW	C09-C01	6.47	1.56	1.49
2	B	601	3CW	C04-N07	5.83	1.52	1.37
2	A	601	3CW	C04-N07	5.66	1.51	1.37
2	A	601	3CW	C14-CL15	3.93	1.81	1.72
2	B	601	3CW	C14-CL15	3.92	1.81	1.72
2	B	601	3CW	C13-CL16	3.34	1.81	1.73
2	A	601	3CW	C13-CL16	3.34	1.81	1.73
2	A	601	3CW	C22-C19	3.32	1.57	1.53
2	B	601	3CW	C22-C19	3.32	1.57	1.53
2	A	601	3CW	C24-C03	2.78	1.55	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	3CW	C09-C14	2.45	1.42	1.39
2	B	601	3CW	C24-C03	2.39	1.54	1.51
2	A	601	3CW	C20-C21	2.27	1.57	1.52
2	B	601	3CW	C20-C21	2.22	1.57	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	3CW	C21-N07-C17	4.98	122.50	111.52
2	B	601	3CW	C21-N07-C17	3.84	120.00	111.52
2	B	601	3CW	C04-N05-C06	3.80	121.76	117.23
2	A	601	3CW	C04-N05-C06	3.63	121.55	117.23
2	B	601	3CW	C03-C04-N05	-3.29	118.35	122.06
2	A	601	3CW	C03-C04-N05	-2.78	118.92	122.06
2	A	601	3CW	C20-C21-N07	2.71	115.14	110.34
2	A	601	3CW	C18-C17-N07	2.23	114.28	110.34
2	A	601	3CW	C09-C14-CL15	2.16	121.55	119.66
2	B	601	3CW	C18-C17-N07	2.11	114.08	110.34

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	601	3CW	C03-C04-N07-C21
2	A	601	3CW	N05-C04-N07-C21
2	B	601	3CW	N05-C04-N07-C21
2	A	601	3CW	C04-C03-C24-O25

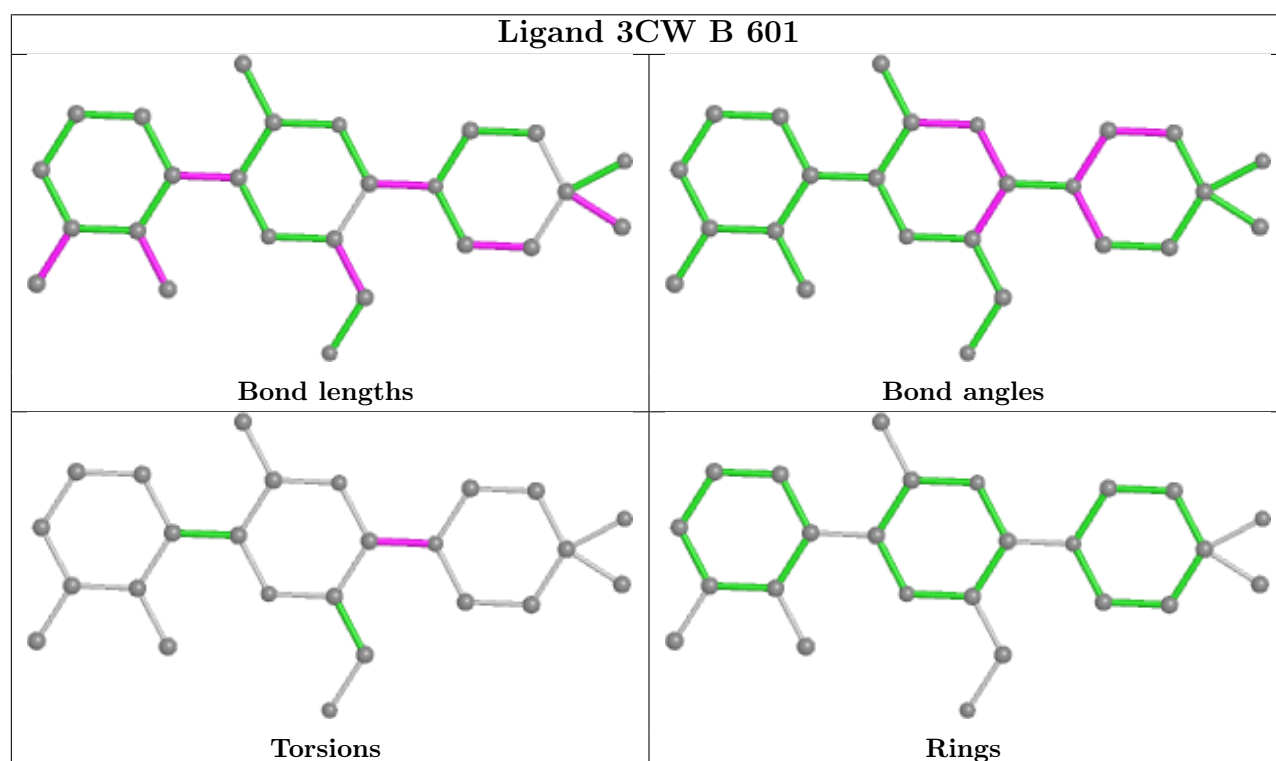
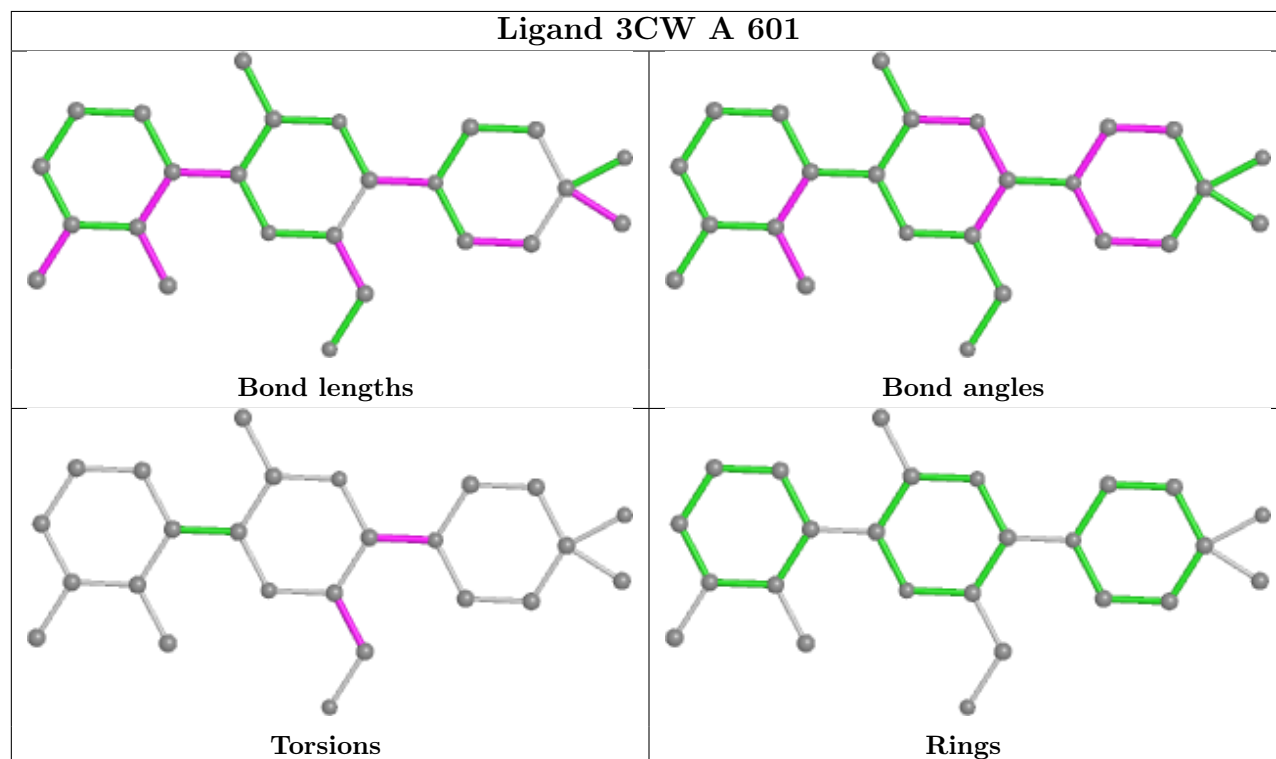
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	3CW	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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	489/536 (91%)	-0.07	5 (1%) 82 81	18, 37, 65, 81	0
1	B	488/536 (91%)	-0.04	8 (1%) 72 70	17, 40, 68, 94	0
All	All	977/1072 (91%)	-0.05	13 (1%) 77 76	17, 38, 66, 94	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	86	GLY	3.2
1	B	85	HIS	2.6
1	B	36	SER	2.3
1	B	157	LYS	2.3
1	B	116	HIS	2.3
1	A	86	GLY	2.2
1	B	87	GLN	2.2
1	A	123	GLU	2.2
1	B	177	LEU	2.2
1	B	142	SER	2.2
1	A	324	LYS	2.2
1	A	85	HIS	2.1
1	A	119	GLY	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

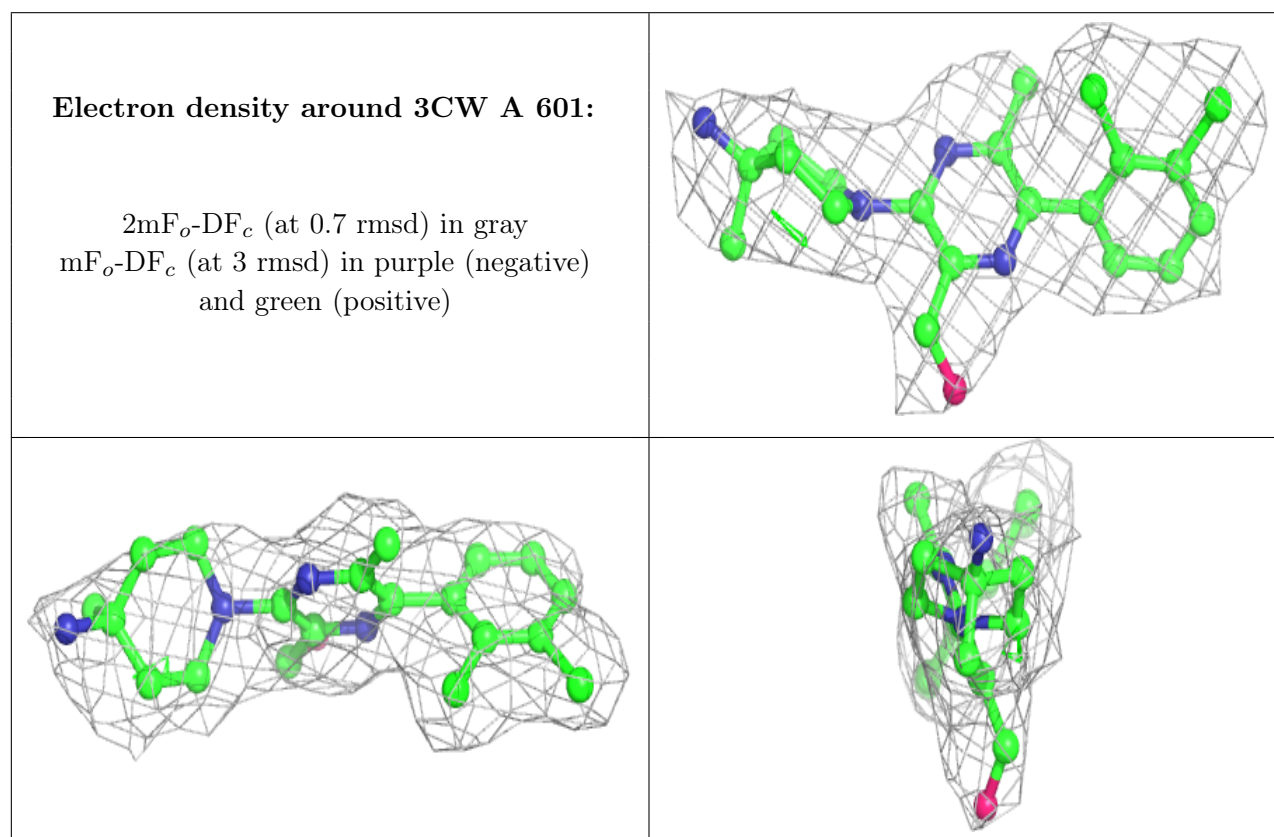
There are no monosaccharides in this entry.

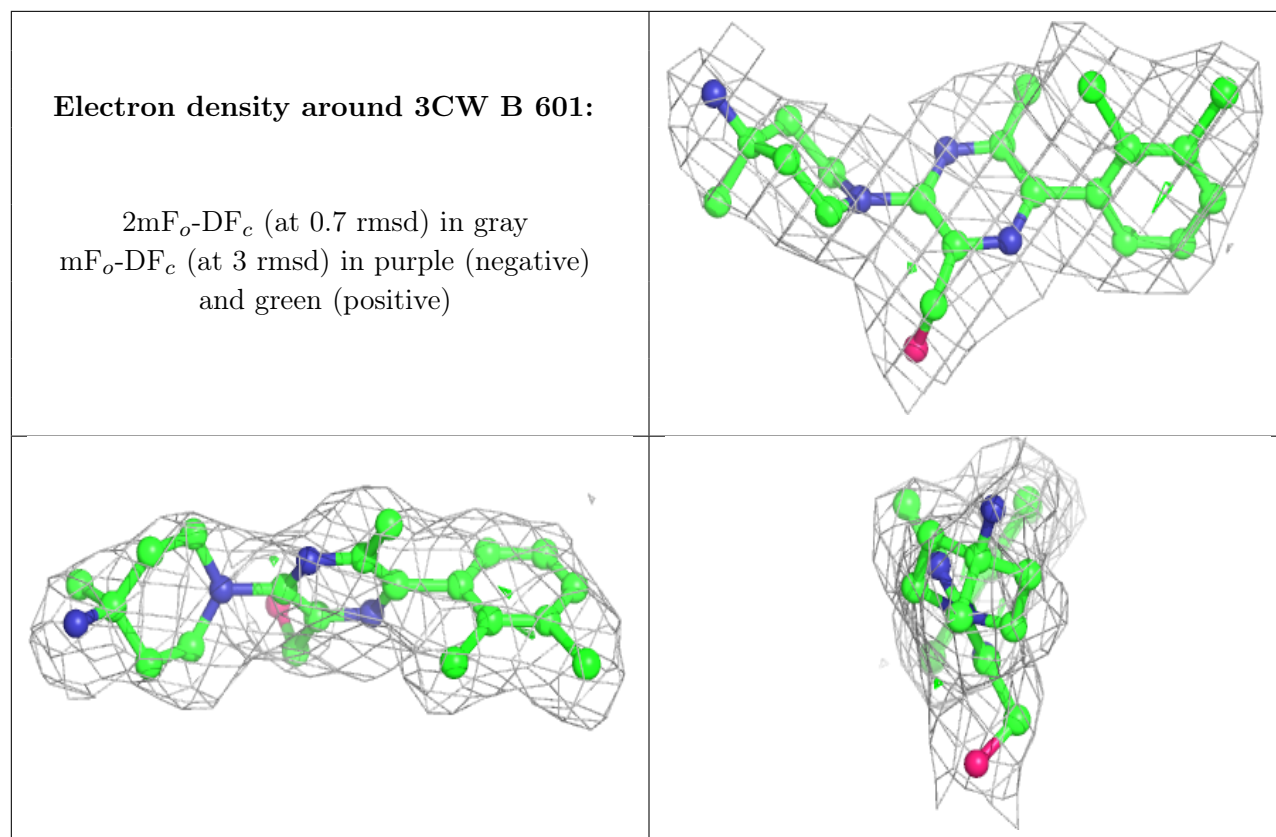
6.4 Ligands ⓘ

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	3CW	A	601	25/25	0.90	0.18	30,36,42,46	0
2	3CW	B	601	25/25	0.90	0.20	26,35,42,46	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.