



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:18 PM UTC

PDB ID : 4JJS / pdb_00004jjs
Title : Crystal structure of HCV NS5B polymerase in complex with COMPOUND 2
Authors : Coulombe, R.
Deposited on : 2013-03-08
Resolution : 2.20 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

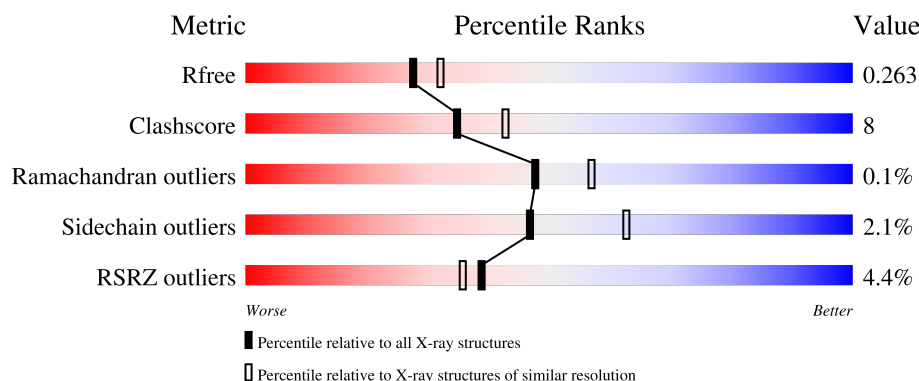
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

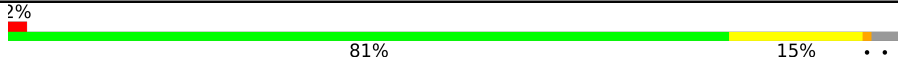
The reported resolution of this entry is 2.20 Å.

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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	576	
1	B	576	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9002 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.

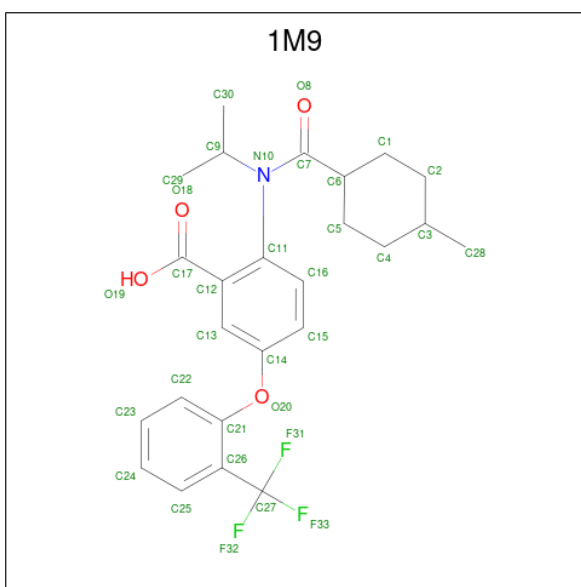
- Molecule 1 is a protein called Genome polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	559	Total	C	N	O	S	0	0	0
			4358	2745	770	811	32			
1	B	558	Total	C	N	O	S	0	0	0
			4346	2737	768	809	32			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	571	HIS	-	expression tag	UNP O92972
A	572	HIS	-	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
B	571	HIS	-	expression tag	UNP O92972
B	572	HIS	-	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

- Molecule 2 is 2-[[[(trans-4-methylcyclohexyl)carbonyl](propan-2-yl)amino]-5-[2-(trifluoromethyl)phenoxy]benzoic acid (CCD ID: 1M9) (formula: C₂₅H₂₈F₃NO₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			33	25	3	1	4		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

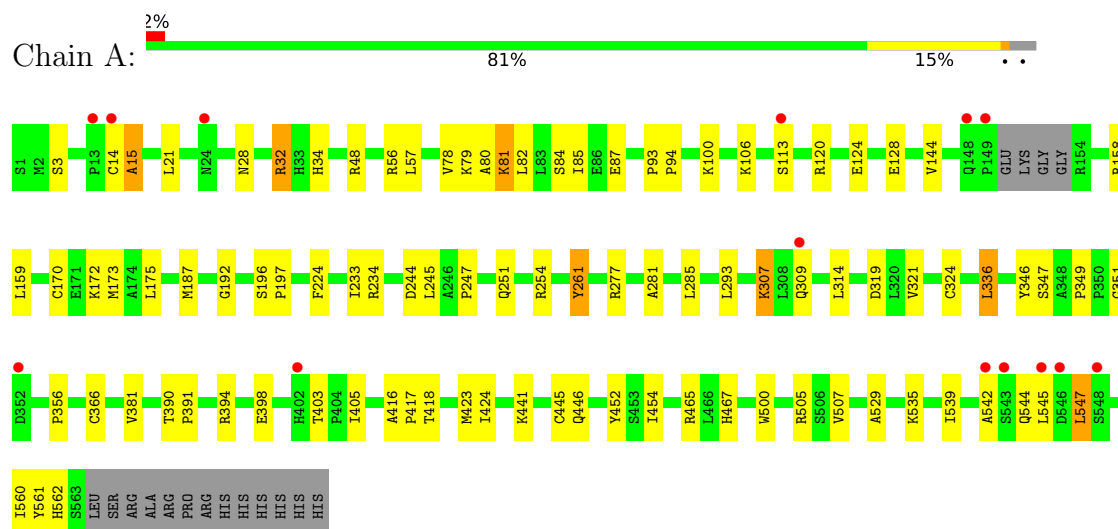
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	169	Total	O	0	0
			169	169		
4	B	94	Total	O	0	0
			94	94		

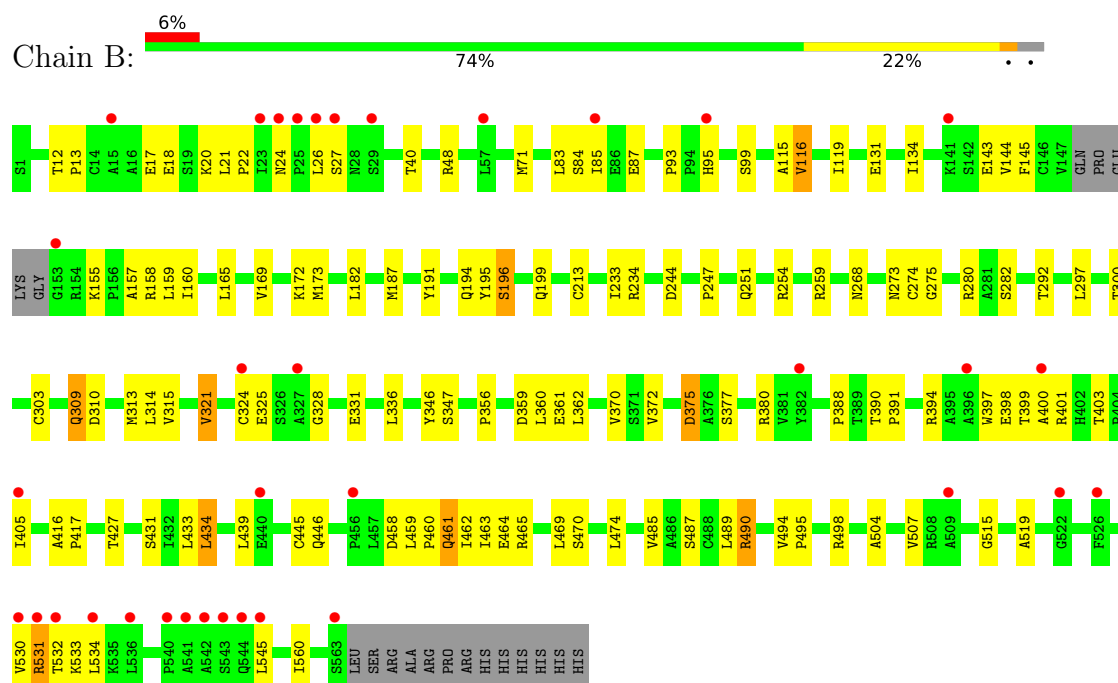
3 Residue-property plots [i](#)

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: Genome polypeptide



• Molecule 1: Genome polypeptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	107.27Å 105.74Å 134.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20 50.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 90.4 (50.00-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.20Å)	Xtriage
Refinement program	CNX	Depositor
R, R_{free}	0.236 , 0.272 0.228 , 0.263	Depositor DCC
R_{free} test set	7184 reflections (10.12%)	wwPDB-VP
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.674	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 24.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.018 for k,h,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9002	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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: 1M9, MG

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	2/4453 (0.0%)	0.99	16/6044 (0.3%)
1	B	0.62	1/4440 (0.0%)	0.96	14/6025 (0.2%)
All	All	0.63	3/8893 (0.0%)	0.97	30/12069 (0.2%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	349	PRO	CA-C	6.59	1.55	1.51
1	B	20	LYS	C-N	6.03	1.42	1.33
1	A	423	MET	SD-CE	-5.53	1.65	1.79

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	351	GLY	N-CA-C	-10.10	101.02	110.21
1	A	196	SER	N-CA-C	-8.58	100.26	110.13
1	B	196	SER	N-CA-C	-8.01	100.92	110.13
1	B	26	LEU	N-CA-C	-6.99	104.49	113.16
1	B	403	THR	CA-C-N	6.85	126.37	119.24
1	B	403	THR	C-N-CA	6.85	126.37	119.24
1	A	81	LYS	N-CA-C	6.50	122.16	113.72
1	A	539	ILE	CA-C-N	6.45	125.95	119.24
1	A	539	ILE	C-N-CA	6.45	125.95	119.24
1	A	261	TYR	N-CA-C	6.19	118.02	111.28
1	B	131	GLU	N-CA-C	6.02	120.42	112.72
1	B	244	ASP	N-CA-C	-6.02	100.19	109.76
1	A	418	THR	N-CA-C	5.96	118.46	110.35
1	A	192	GLY	N-CA-C	5.78	121.12	113.37
1	A	285	LEU	N-CA-C	5.54	118.08	111.71
1	A	100	LYS	N-CA-C	-5.54	106.19	113.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	244	ASP	N-CA-C	-5.53	101.46	109.59
1	B	495	PRO	CA-C-N	5.43	125.63	120.31
1	B	495	PRO	C-N-CA	5.43	125.63	120.31
1	B	24	ASN	CA-C-N	5.35	126.10	120.11
1	B	24	ASN	C-N-CA	5.35	126.10	120.11
1	B	213	CYS	CA-C-N	5.34	125.64	119.93
1	B	213	CYS	C-N-CA	5.34	125.64	119.93
1	A	175	LEU	N-CA-C	5.25	121.48	113.61
1	B	12	THR	N-CA-C	5.12	117.11	110.40
1	A	441	LYS	N-CA-C	5.12	116.53	109.15
1	A	224	PHE	N-CA-C	5.08	117.20	111.11
1	A	403	THR	CA-C-N	5.05	124.22	118.97
1	A	403	THR	C-N-CA	5.05	124.22	118.97
1	B	315	VAL	N-CA-C	5.01	115.19	108.17

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	4358	0	4371	48	0
1	B	4346	0	4359	88	0
2	A	33	0	27	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	169	0	0	0	0
4	B	94	0	0	0	0
All	All	9002	0	8757	132	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 8.

All (132) 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:531:ARG:HH11	1:B:531:ARG:H	1.25	0.83
1:A:170:CYS:HA	1:A:173:MET:HE3	1.68	0.76
1:A:81:LYS:O	1:A:82:LEU:HB3	1.86	0.73
1:B:300:THR:HA	1:B:313:MET:HE3	1.70	0.72
1:B:361:GLU:HG2	1:B:370:VAL:O	1.90	0.70
1:B:531:ARG:HD2	1:B:532:THR:H	1.57	0.68
1:B:394:ARG:O	1:B:398:GLU:HG3	1.94	0.68
1:B:434:LEU:HG	1:B:439:LEU:HD11	1.75	0.67
1:B:461:GLN:NE2	1:B:461:GLN:H	1.92	0.67
1:B:144:VAL:HB	1:B:394:ARG:HG2	1.77	0.67
1:B:27:SER:OG	1:B:399:THR:HB	1.97	0.64
1:B:158:ARG:HH11	1:B:158:ARG:HG3	1.63	0.63
1:B:187:MET:HE1	1:B:292:THR:HG22	1.81	0.63
1:B:460:PRO:HB2	1:B:461:GLN:HE21	1.65	0.62
1:B:465:ARG:HG3	1:B:545:LEU:HB3	1.81	0.61
1:B:314:LEU:HB3	1:B:321:VAL:HG13	1.82	0.60
1:B:328:GLY:HA3	1:B:331:GLU:OE1	2.02	0.60
1:A:394:ARG:O	1:A:398:GLU:HG3	2.02	0.59
1:A:465:ARG:NH1	1:A:545:LEU:HB2	2.18	0.58
1:A:390:THR:HB	1:A:391:PRO:HD3	1.85	0.58
1:A:535:LYS:HA	1:A:535:LYS:HE2	1.85	0.58
1:A:187:MET:HE2	1:A:293:LEU:HD23	1.86	0.58
1:B:22:PRO:HD2	1:B:400:ALA:HB1	1.86	0.56
1:A:120:ARG:O	1:A:124:GLU:HG2	2.06	0.55
1:B:416:ALA:HB3	1:B:417:PRO:HD3	1.89	0.55
1:B:375:ASP:CG	1:B:377:SER:H	2.14	0.55
1:B:515:GLY:HA2	1:B:519:ALA:HB2	1.88	0.55
1:A:172:LYS:HE3	1:A:560:ILE:HD13	1.89	0.55
1:B:490:ARG:HB3	1:B:490:ARG:HH11	1.72	0.53
1:A:93:PRO:HG3	1:A:561:TYR:HB2	1.91	0.53
1:B:309:GLN:O	1:B:324:CYS:HB2	2.08	0.53
1:B:160:ILE:HA	1:B:282:SER:OG	2.09	0.52
1:B:48:ARG:HG2	1:B:159:LEU:HG	1.92	0.52
1:B:172:LYS:HE3	1:B:560:ILE:HD13	1.91	0.52
1:A:170:CYS:HA	1:A:173:MET:CE	2.40	0.52
1:A:251:GLN:NE2	1:B:254:ARG:HG2	2.25	0.51
1:B:119:ILE:HD13	1:B:169:VAL:HG11	1.92	0.51
1:B:145:PHE:CZ	1:B:155:LYS:HD2	2.46	0.50
1:B:158:ARG:HG3	1:B:158:ARG:NH1	2.26	0.50
1:B:485:VAL:O	1:B:489:LEU:HG	2.12	0.49
1:A:452:TYR:OH	1:A:562:HIS:HD2	1.94	0.49
1:A:234:ARG:HD3	1:B:247:PRO:HG3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300:THR:HA	1:B:313:MET:CE	2.41	0.49
1:A:28:ASN:O	1:A:32:ARG:HD2	2.12	0.48
1:A:277:ARG:CZ	1:A:281:ALA:HB2	2.43	0.48
1:B:489:LEU:HD22	1:B:494:VAL:HB	1.95	0.48
1:A:80:ALA:HB3	1:A:245:LEU:HD23	1.95	0.48
1:A:94:PRO:HB3	1:A:106:LYS:HE2	1.95	0.48
1:B:27:SER:HG	1:B:399:THR:HB	1.79	0.47
1:A:254:ARG:HG2	1:B:251:GLN:NE2	2.30	0.47
1:B:459:LEU:N	1:B:460:PRO:CD	2.77	0.47
1:B:530:VAL:HA	1:B:531:ARG:NH1	2.29	0.47
1:A:505:ARG:HD2	1:A:529:ALA:O	2.14	0.47
1:A:465:ARG:HH12	1:A:545:LEU:C	2.23	0.47
1:B:372:VAL:HG21	1:B:380:ARG:HE	1.79	0.47
1:B:71:MET:SD	1:B:297:LEU:HD13	2.55	0.47
1:B:115:ALA:O	1:B:119:ILE:HG13	2.15	0.47
1:A:336:LEU:HD12	1:A:356:PRO:HD3	1.97	0.47
1:B:303:CYS:SG	1:B:313:MET:HE1	2.55	0.47
1:A:14:CYS:O	1:A:15:ALA:HB2	2.15	0.47
1:A:57:LEU:C	1:A:57:LEU:HD23	2.40	0.47
1:B:273:ASN:ND2	1:B:275:GLY:H	2.13	0.46
1:B:388:PRO:C	1:B:391:PRO:HD2	2.41	0.46
1:A:314:LEU:HB3	1:A:321:VAL:CG1	2.45	0.46
1:B:84:SER:OG	1:B:87:GLU:HG3	2.16	0.46
1:A:309:GLN:O	1:A:324:CYS:HB2	2.16	0.46
1:B:405:ILE:HD13	1:B:446:GLN:HG3	1.98	0.46
1:A:21:LEU:HD23	1:A:34:HIS:HB2	1.98	0.46
1:B:22:PRO:HG3	1:B:401:ARG:CZ	2.46	0.46
1:B:268:ASN:HB3	1:B:274:CYS:SG	2.56	0.46
1:B:143:GLU:OE1	1:B:158:ARG:HD2	2.16	0.46
1:A:405:ILE:HD12	1:A:446:GLN:HG3	1.97	0.45
1:B:145:PHE:CE2	1:B:155:LYS:HD2	2.51	0.45
1:B:21:LEU:HD21	1:B:397:TRP:HA	1.97	0.45
1:B:83:LEU:HB2	1:B:173:MET:HA	1.97	0.45
1:B:531:ARG:NH1	1:B:531:ARG:HG3	2.32	0.45
1:A:233:ILE:HD13	1:A:261:TYR:O	2.16	0.45
1:A:124:GLU:O	1:A:128:GLU:HG3	2.17	0.45
1:B:498:ARG:HG2	1:B:498:ARG:NH1	2.32	0.45
1:A:445:CYS:SG	1:A:454:ILE:HD12	2.57	0.45
1:B:405:ILE:HD13	1:B:446:GLN:CD	2.41	0.44
1:A:346:TYR:O	1:A:347:SER:HB3	2.18	0.44
1:A:84:SER:OG	1:A:87:GLU:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:470:SER:O	1:B:474:LEU:HG	2.18	0.44
1:B:531:ARG:HH11	1:B:531:ARG:HG3	1.81	0.44
1:B:464:GLU:HG3	1:B:469:LEU:HG	2.00	0.44
1:B:196:SER:OG	1:B:199:GLN:HG3	2.17	0.43
1:B:359:ASP:HB3	1:B:362:LEU:HG	1.99	0.43
1:B:490:ARG:HB3	1:B:490:ARG:NH1	2.33	0.43
1:B:134:ILE:HG13	1:B:259:ARG:HB3	2.01	0.43
1:A:307:LYS:N	1:A:307:LYS:HD3	2.34	0.43
1:B:93:PRO:HB3	1:B:95:HIS:CE1	2.53	0.43
1:B:346:TYR:O	1:B:347:SER:HB3	2.19	0.43
1:B:431:SER:HB2	1:B:507:VAL:HG21	1.99	0.43
1:B:13:PRO:HB3	1:B:17:GLU:CD	2.43	0.43
1:B:360:LEU:HD12	1:B:360:LEU:HA	1.89	0.43
1:A:424:ILE:HG23	1:A:500:TRP:CZ2	2.54	0.43
1:B:458:ASP:O	1:B:462:ILE:HG13	2.19	0.43
1:A:78:VAL:HG12	1:A:79:LYS:N	2.33	0.43
1:A:416:ALA:N	1:A:417:PRO:CD	2.82	0.43
1:B:487:SER:O	1:B:490:ARG:HG2	2.19	0.43
1:A:93:PRO:HA	1:A:94:PRO:HD3	1.93	0.42
1:B:99:SER:HB2	1:B:165:LEU:HB3	2.01	0.42
1:B:390:THR:HB	1:B:391:PRO:HD3	2.00	0.42
1:B:498:ARG:HG2	1:B:498:ARG:HH11	1.84	0.42
1:B:18:GLU:OE2	1:B:18:GLU:HA	2.18	0.42
1:B:459:LEU:O	1:B:463:ILE:HG13	2.19	0.42
1:A:144:VAL:HB	1:A:394:ARG:HG2	2.01	0.42
1:A:247:PRO:HG3	1:B:234:ARG:HD3	2.00	0.42
1:A:187:MET:HE2	1:A:293:LEU:CD2	2.47	0.42
1:B:233:ILE:HD13	1:B:280:ARG:NH1	2.35	0.42
1:B:405:ILE:HG23	1:B:445:CYS:HA	2.02	0.42
1:A:416:ALA:HB3	1:A:467:HIS:CD2	2.55	0.42
1:B:531:ARG:HH11	1:B:531:ARG:N	2.04	0.41
1:A:48:ARG:HG2	1:A:159:LEU:HG	2.01	0.41
1:B:21:LEU:CD2	1:B:397:TRP:HA	2.50	0.41
1:B:187:MET:HE1	1:B:292:THR:CG2	2.49	0.41
1:A:542:ALA:C	1:A:544:GLN:H	2.29	0.41
1:B:433:LEU:HB3	1:B:439:LEU:HD23	2.02	0.41
1:B:416:ALA:N	1:B:417:PRO:CD	2.84	0.41
1:B:191:TYR:O	1:B:194:GLN:HG2	2.20	0.41
1:A:314:LEU:HB3	1:A:321:VAL:HG12	2.02	0.41
1:A:545:LEU:HB3	1:A:547:LEU:HD13	2.03	0.41
1:B:427:THR:HG23	1:B:504:ALA:HA	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:ILE:HD11	1:B:116:VAL:HG22	2.03	0.41
1:B:309:GLN:HB3	1:B:325:GLU:HB3	2.02	0.41
1:B:195:TYR:HB3	1:B:199:GLN:HB2	2.02	0.40
1:B:40:THR:HB	1:B:157:ALA:HB2	2.03	0.40
1:B:336:LEU:HD23	1:B:356:PRO:HD3	2.03	0.40
1:A:3:SER:HB3	1:A:56:ARG:HD2	2.04	0.40
1:B:533:LYS:C	1:B:534:LEU:HD23	2.46	0.40
1:A:319:ASP:CG	1:A:366:CYS:H	2.29	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	555/576 (96%)	541 (98%)	13 (2%)	1 (0%)	43	51
1	B	554/576 (96%)	534 (96%)	20 (4%)	0	100	100
All	All	1109/1152 (96%)	1075 (97%)	33 (3%)	1 (0%)	48	57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	15	ALA

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	477/491 (97%)	467 (98%)	10 (2%)	47	63
1	B	475/491 (97%)	465 (98%)	10 (2%)	47	63
All	All	952/982 (97%)	932 (98%)	20 (2%)	47	63

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	ARG
1	A	85	ILE
1	A	113	SER
1	A	158	ARG
1	A	197	PRO
1	A	307	LYS
1	A	336	LEU
1	A	381	VAL
1	A	507	VAL
1	A	547	LEU
1	B	116	VAL
1	B	182	LEU
1	B	309	GLN
1	B	310	ASP
1	B	321	VAL
1	B	375	ASP
1	B	434	LEU
1	B	461	GLN
1	B	490	ARG
1	B	531	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	251	GLN
1	A	273	ASN
1	A	374	HIS
1	A	436	GLN
1	A	446	GLN
1	A	544	GLN
1	A	562	HIS
1	B	24	ASN
1	B	34	HIS

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Mol	Chain	Res	Type
1	B	117	ASN
1	B	251	GLN
1	B	273	ASN
1	B	438	GLN
1	B	461	GLN
1	B	544	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](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z > 2$
2	1M9	A	601	-	35,35,35	2.22	13 (37%)	49,51,51	1.21	3 (6%)

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	1M9	A	601	-	-	4/30/40/40	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	1M9	C7-N10	5.42	1.43	1.36
2	A	601	1M9	O18-C17	5.11	1.37	1.22
2	A	601	1M9	C25-C26	4.50	1.45	1.39
2	A	601	1M9	C12-C11	3.55	1.46	1.41
2	A	601	1M9	C15-C14	2.93	1.44	1.38
2	A	601	1M9	C24-C25	2.72	1.43	1.38
2	A	601	1M9	C16-C11	2.65	1.43	1.39
2	A	601	1M9	O19-C17	-2.64	1.22	1.30
2	A	601	1M9	C6-C7	2.57	1.55	1.51
2	A	601	1M9	C9-N10	2.52	1.52	1.48
2	A	601	1M9	C22-C21	2.43	1.44	1.39
2	A	601	1M9	C21-C26	2.09	1.43	1.39
2	A	601	1M9	C23-C22	2.06	1.42	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	1M9	C29-C9-N10	4.46	117.41	111.11
2	A	601	1M9	O18-C17-C12	-3.84	112.80	121.97
2	A	601	1M9	O19-C17-C12	3.75	125.94	115.28

There are no chirality outliers.

All (4) torsion outliers are listed below:

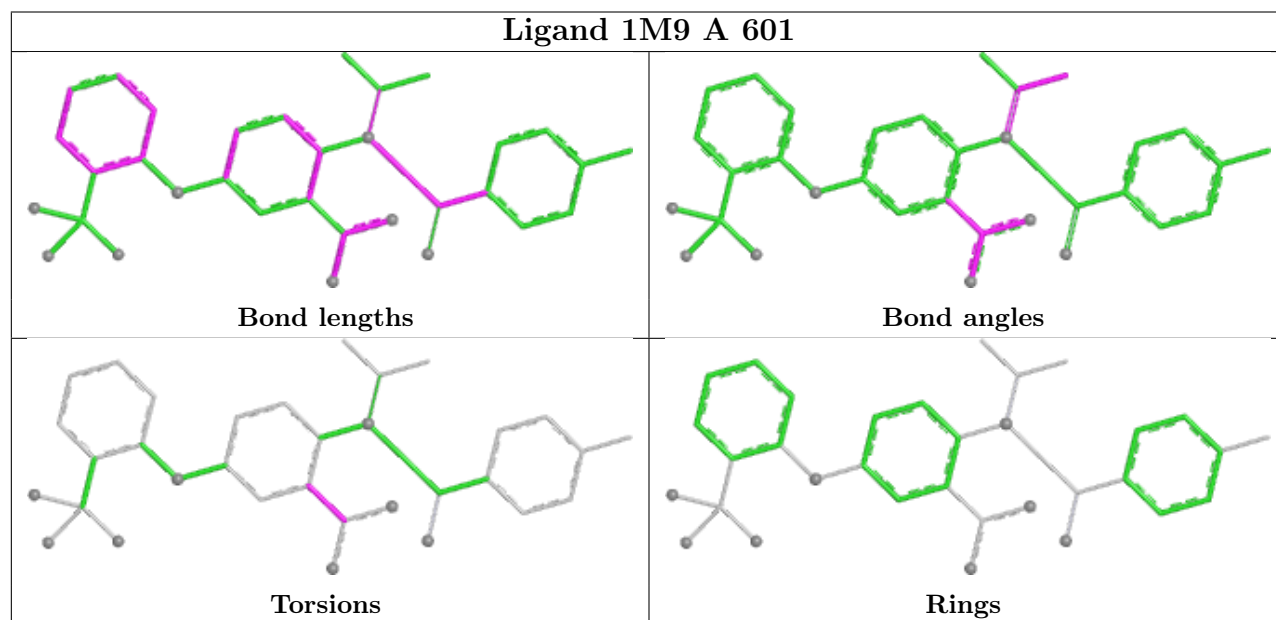
Mol	Chain	Res	Type	Atoms
2	A	601	1M9	C11-C12-C17-O18
2	A	601	1M9	C11-C12-C17-O19
2	A	601	1M9	C13-C12-C17-O18
2	A	601	1M9	C13-C12-C17-O19

There are no ring outliers.

No monomer is involved in short contacts.

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	559/576 (97%)	0.20	14 (2%) 58 55	27, 38, 53, 68	0
1	B	558/576 (96%)	0.59	35 (6%) 26 23	27, 46, 63, 95	0
All	All	1117/1152 (96%)	0.39	49 (4%) 39 36	27, 41, 61, 95	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	26	LEU	5.4
1	B	24	ASN	5.4
1	A	149	PRO	5.1
1	B	541	ALA	4.5
1	B	522	GLY	4.3
1	B	23	ILE	4.2
1	A	543	SER	4.1
1	B	530	VAL	3.7
1	B	27	SER	3.7
1	A	402	HIS	3.6
1	B	400	ALA	3.6
1	B	153	GLY	3.5
1	A	548	SER	3.3
1	A	546	ASP	3.1
1	B	327	ALA	3.1
1	A	24	ASN	2.9
1	A	309	GLN	2.8
1	B	536	LEU	2.8
1	A	13	PRO	2.8
1	B	57	LEU	2.7
1	B	542	ALA	2.6
1	B	29	SER	2.6
1	B	526	PHE	2.6
1	B	95	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	544	GLN	2.6
1	B	545	LEU	2.6
1	B	405	ILE	2.6
1	B	440	GLU	2.5
1	B	509	ALA	2.5
1	B	532	THR	2.5
1	A	148	GLN	2.4
1	B	534	LEU	2.4
1	B	540	PRO	2.4
1	B	25	PRO	2.3
1	A	542	ALA	2.2
1	B	15	ALA	2.2
1	B	396	ALA	2.2
1	B	85	ILE	2.2
1	B	141	LYS	2.2
1	A	545	LEU	2.2
1	A	14	CYS	2.2
1	B	382	TYR	2.1
1	A	352	ASP	2.1
1	B	456	PRO	2.1
1	B	531	ARG	2.1
1	B	543	SER	2.1
1	B	563	SER	2.1
1	A	113	SER	2.0
1	B	324	CYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

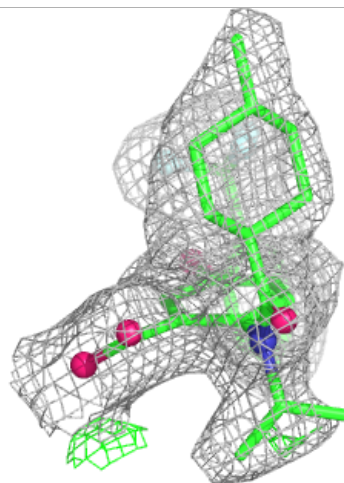
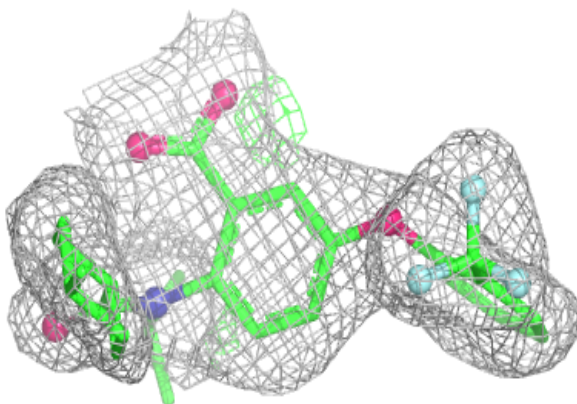
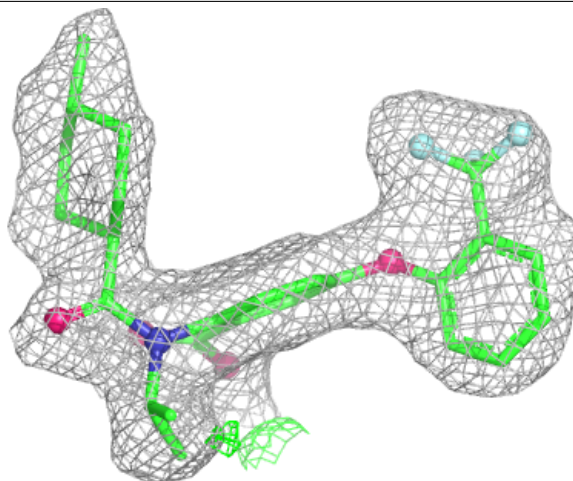
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	MG	A	602	1/1	0.71	0.20	67,67,67,67	0
3	MG	B	601	1/1	0.92	0.06	67,67,67,67	0
2	1M9	A	601	33/33	0.93	0.09	30,38,45,48	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 1M9 A 601:

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 ⓘ

There are no such residues in this entry.