



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 10:06 AM UTC

PDB ID : 4ID5 / pdb_00004id5
Title : HIV-1 reverse transcriptase with bound fragment at the RNase H primer grip site
Authors : Bauman, J.D.; Patel, D.; Arnold, E.
Deposited on : 2012-12-11
Resolution : 1.95 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

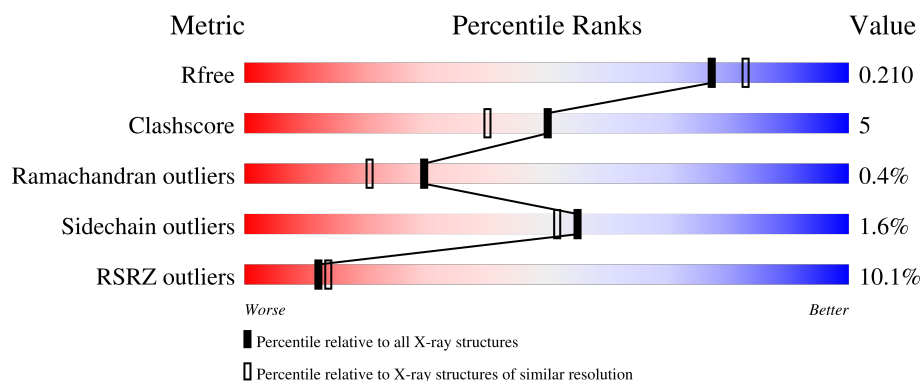
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

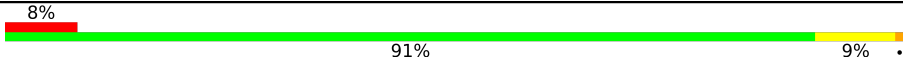
The reported resolution of this entry is 1.95 Å.

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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	557	 8% 91% 9% .
2	B	429	 12% 84% 12% .

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
4	DMS	A	606	-	-	X	-
4	DMS	B	505	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 8944 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	556	Total	C	N	O	S	9	1	0
			4525	2928	752	837	8			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P03366
A	0	VAL	-	expression tag	UNP P03366
A	172	ALA	LYS	engineered mutation	UNP P03366
A	173	ALA	LYS	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366

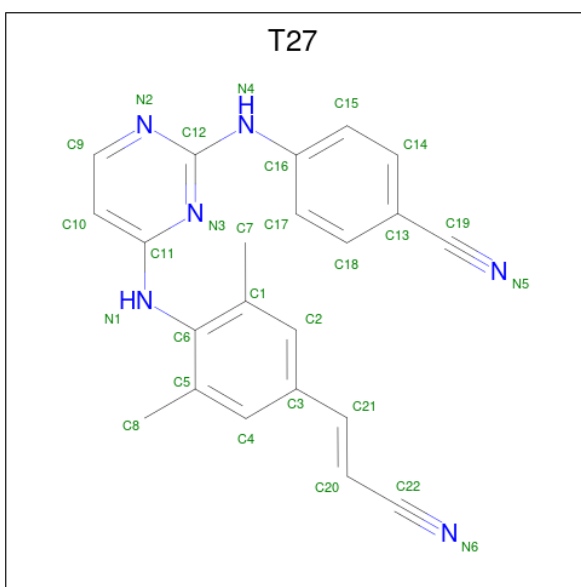
- Molecule 2 is a protein called P51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	412	Total	C	N	O	S	0	1	0
			3418	2228	565	618	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	GLY	-	expression tag	UNP P03366
B	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 3 is 4-{[4-({4-[(E)-2-cyanoethenyl]-2,6-dimethylphenyl}amino)pyrimidin-2-yl]amino}benzonitrile (CCD ID: T27) (formula: C₂₂H₁₈N₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			28	22	6		

- Molecule 4 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C_2H_6OS).



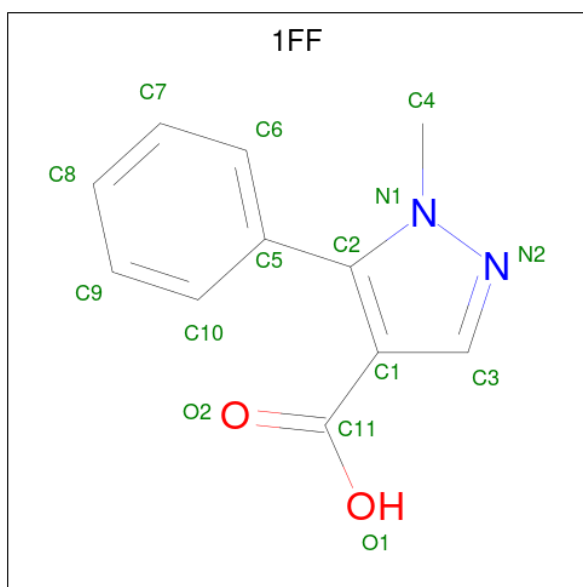
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	A	1	Total	C	O	S	0	0
			4	2	1	1		
4	A	1	Total	C	O	S	0	0
			4	2	1	1		

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

- Molecule 5 is 1-methyl-5-phenyl-1H-pyrazole-4-carboxylic acid (CCD ID: 1FF) (formula: $C_{11}H_{10}N_2O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			15	11	2	2		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Mg	0	0
			1	1		

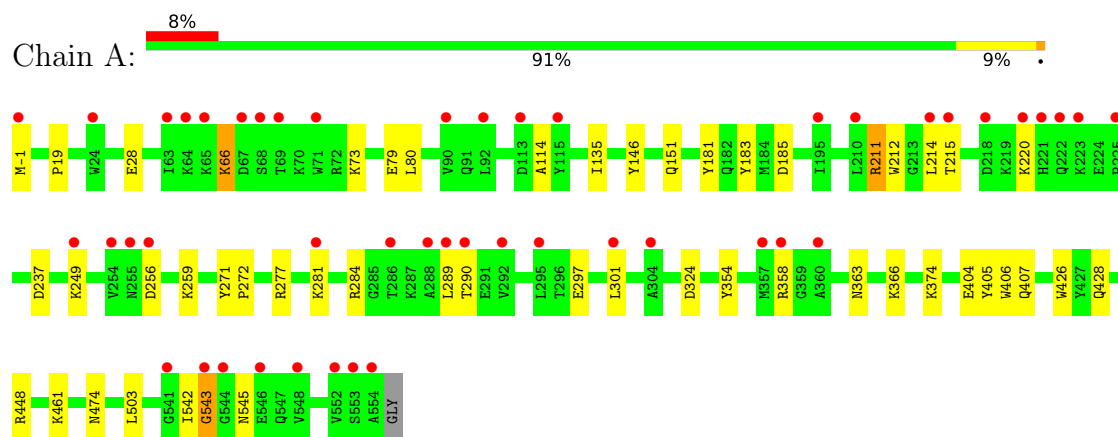
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	536	Total	O	0	0
			536	536		
7	B	353	Total	O	0	0
			353	353		

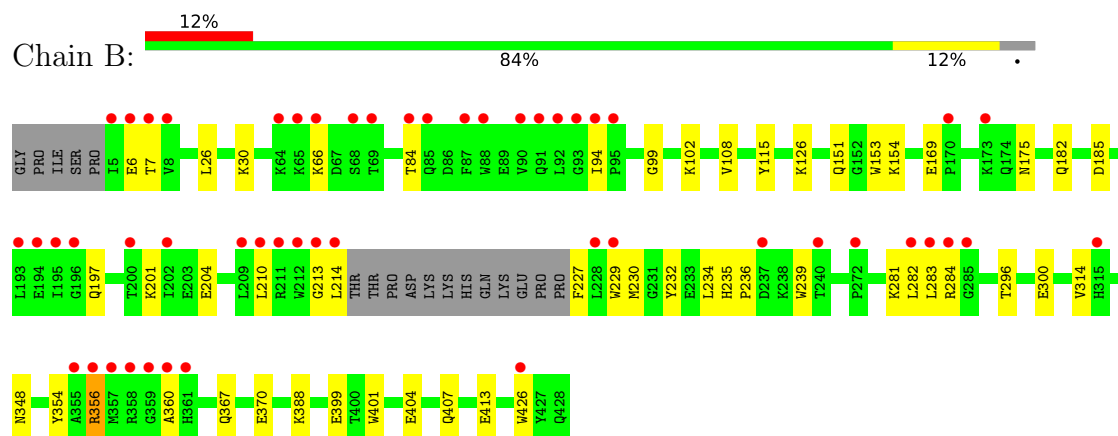
3 Residue-property plots

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: Reverse transcriptase/ribonuclease H



• Molecule 2: P51 RT



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.05Å 72.87Å 109.15Å 90.00° 100.47° 90.00°	Depositor
Resolution (Å)	29.20 – 1.95 29.20 – 1.95	Depositor EDS
% Data completeness (in resolution range)	99.7 (29.20-1.95) 93.9 (29.20-1.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.19 (at 1.85Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8_1069)	Depositor
R, R_{free}	0.187 , 0.209 0.189 , 0.210	Depositor DCC
R_{free} test set	2125 reflections (1.99%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 59.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8944	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.10% 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: 1FF, T27, DMS, 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	0.46	0/4643	0.74	1/6311 (0.0%)
2	B	0.45	0/3516	0.77	4/4776 (0.1%)
All	All	0.46	0/8159	0.76	5/11087 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	7	THR	N-CA-C	7.13	119.50	110.24
1	A	289	LEU	N-CA-C	6.50	118.36	111.28
2	B	175	ASN	CA-C-N	5.29	124.90	119.56
2	B	175	ASN	C-N-CA	5.29	124.90	119.56
2	B	401	TRP	N-CA-C	5.11	120.16	113.88

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	4525	0	4579	41	0
2	B	3418	0	3447	41	0
3	A	28	0	18	1	0
4	A	28	0	42	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	40	0	60	17	0
5	A	15	0	9	0	0
6	A	1	0	0	0	0
7	A	536	0	0	7	0
7	B	353	0	0	6	0
All	All	8944	0	8155	86	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 (86) 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:26:LEU:H	4:B:503:DMS:H11	1.20	1.06
1:A:428:GLN:H	4:A:604:DMS:H23	1.24	1.00
1:A:426:TRP:H	4:A:603:DMS:H23	1.37	0.90
2:B:227:PHE:N	7:B:839:HOH:O	2.08	0.85
2:B:84:THR:HG21	2:B:153:TRP:HE1	1.43	0.84
1:A:259:LYS:NZ	7:A:1234:HOH:O	2.10	0.80
4:B:502:DMS:H23	7:B:805:HOH:O	1.84	0.77
1:A:151:GLN:H	4:A:605:DMS:H23	1.52	0.75
1:A:428:GLN:N	4:A:604:DMS:H23	2.05	0.69
1:A:281:LYS:HG2	1:A:284:ARG:HH22	1.57	0.69
2:B:30:LYS:NZ	7:B:808:HOH:O	2.27	0.68
1:A:474:ASN:HD22	4:A:606:DMS:H23	1.60	0.67
2:B:354:TYR:HA	2:B:356:ARG:HH11	1.63	0.64
1:A:448:ARG:HE	4:A:606:DMS:H11	1.63	0.62
1:A:73:LYS:NZ	1:A:146:TYR:OH	2.30	0.62
2:B:235:HIS:H	4:B:505:DMS:H21	1.65	0.62
2:B:399:GLU:HB3	4:B:506:DMS:H12	1.84	0.59
1:A:79:GLU:OE1	7:A:1096:HOH:O	2.17	0.59
1:A:404:GLU:HA	4:A:607:DMS:H21	1.83	0.59
1:A:211:ARG:HG2	1:A:212:TRP:CE3	2.37	0.59
2:B:26:LEU:N	4:B:503:DMS:H11	2.04	0.59
1:A:542:ILE:HA	2:B:283:LEU:HD11	1.84	0.58
1:A:543:GLY:N	2:B:283:LEU:HD11	2.18	0.58
2:B:239:TRP:HE1	4:B:505:DMS:H23	1.68	0.57
1:A:181:TYR:CE2	1:A:183:TYR:HB2	2.39	0.57
2:B:210:LEU:HA	2:B:214:LEU:HD11	1.88	0.55
2:B:115:TYR:OH	2:B:182:GLN:NE2	2.40	0.55
1:A:28:GLU:HG3	1:A:135:ILE:HD12	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:601:T27:H15	3:A:601:T27:N3	2.23	0.54
2:B:239:TRP:HE1	4:B:505:DMS:C2	2.21	0.53
1:A:474:ASN:H	4:A:606:DMS:H23	1.74	0.52
1:A:426:TRP:H	4:A:603:DMS:C2	2.17	0.51
1:A:151:GLN:H	4:A:605:DMS:C2	2.21	0.51
1:A:237:ASP:OD1	7:A:1112:HOH:O	2.19	0.50
1:A:277:ARG:HH12	1:A:358:ARG:HH12	1.59	0.50
1:A:542:ILE:O	1:A:545:ASN:HB3	2.11	0.50
2:B:348:ASN:HD22	4:B:509:DMS:H13	1.77	0.49
1:A:324:ASP:H	4:A:608:DMS:H13	1.77	0.48
2:B:30:LYS:NZ	2:B:404:GLU:OE2	2.46	0.47
2:B:197:GLN:O	2:B:201:LYS:HG2	2.14	0.47
1:A:324:ASP:H	4:A:608:DMS:C1	2.27	0.47
4:A:605:DMS:H21	7:A:1153:HOH:O	2.15	0.47
2:B:94:ILE:O	7:B:863:HOH:O	2.21	0.47
2:B:108:VAL:HB	2:B:232:TYR:HB3	1.97	0.47
4:A:603:DMS:H22	7:A:784:HOH:O	2.15	0.47
2:B:227:PHE:HD1	2:B:230:MET:HE1	1.79	0.47
2:B:281:LYS:O	2:B:284:ARG:HG3	2.14	0.47
2:B:426:TRP:HZ3	4:B:507:DMS:O	1.98	0.47
2:B:66:LYS:NZ	2:B:407:GLN:OE1	2.48	0.47
2:B:99:GLY:HA2	2:B:102:LYS:HD2	1.98	0.46
1:A:277:ARG:HH12	1:A:358:ARG:NH1	2.14	0.46
2:B:354:TYR:HB3	2:B:356:ARG:HG2	1.98	0.46
2:B:399:GLU:HB3	4:B:506:DMS:C1	2.46	0.45
1:A:211:ARG:HG2	1:A:212:TRP:CZ3	2.51	0.45
1:A:428:GLN:H	4:A:604:DMS:C2	2.10	0.45
7:A:894:HOH:O	4:B:510:DMS:H13	2.16	0.45
1:A:19:PRO:HG3	1:A:80:LEU:HB2	1.98	0.45
1:A:114:ALA:HB2	1:A:214:LEU:HD13	1.98	0.44
2:B:360:ALA:HB1	2:B:367:GLN:HG3	1.99	0.44
1:A:448:ARG:HG2	4:A:606:DMS:H21	1.99	0.44
2:B:126:LYS:NZ	4:B:502:DMS:H21	2.32	0.44
2:B:314:VAL:HG21	4:B:509:DMS:H12	2.00	0.43
1:A:354:TYR:HD1	1:A:374:LYS:HD2	1.83	0.43
2:B:235:HIS:H	4:B:505:DMS:C2	2.30	0.43
1:A:461:LYS:NZ	7:A:1005:HOH:O	2.51	0.43
2:B:234:LEU:HA	4:B:505:DMS:H22	2.00	0.43
2:B:413:GLU:OE1	7:B:849:HOH:O	2.21	0.43
1:A:474:ASN:ND2	4:A:606:DMS:H23	2.30	0.43
1:A:363:ASN:ND2	1:A:366:LYS:HE3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.54	0.42
2:B:281:LYS:HE2	2:B:284:ARG:HH22	1.84	0.42
1:A:354:TYR:CD1	1:A:374:LYS:HD2	2.55	0.42
2:B:229:TRP:CZ2	2:B:230:MET:HE2	2.54	0.42
1:A:366:LYS:HE2	1:A:405:TYR:OH	2.20	0.42
2:B:84:THR:HG1	2:B:154:LYS:HE2	1.85	0.42
1:A:297:GLU:O	1:A:301:LEU:HG	2.19	0.41
2:B:84:THR:OG1	2:B:154:LYS:HE2	2.20	0.41
4:B:501:DMS:H13	7:B:929:HOH:O	2.20	0.41
2:B:26:LEU:O	4:B:503:DMS:H21	2.21	0.41
2:B:151:GLN:HB3	2:B:185:ASP:OD2	2.21	0.41
1:A:277:ARG:NH1	1:A:358:ARG:HH12	2.17	0.41
1:A:406:TRP:CE2	1:A:407:GLN:HG3	2.55	0.41
1:A:249:LYS:HE2	1:A:256:ASP:OD2	2.21	0.41
1:A:271:TYR:HA	1:A:272:PRO:HD3	1.98	0.40
2:B:282:LEU:HD21	2:B:296:THR:H	1.85	0.40
2:B:281:LYS:HE2	2:B:284:ARG:NH2	2.36	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	555/557 (100%)	538 (97%)	15 (3%)	2 (0%)	30	21
2	B	409/429 (95%)	397 (97%)	10 (2%)	2 (0%)	24	16
All	All	964/986 (98%)	935 (97%)	25 (3%)	4 (0%)	30	21

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	66	LYS

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Mol	Chain	Res	Type
1	A	543	GLY
2	B	213	GLY
2	B	6	GLU

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	496/495 (100%)	488 (98%)	8 (2%)	55	52
2	B	375/390 (96%)	369 (98%)	6 (2%)	55	52
All	All	871/885 (98%)	857 (98%)	14 (2%)	55	52

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-1	MET
1	A	66	LYS
1	A	185	ASP
1	A	211	ARG
1	A	215	THR
1	A	220	LYS
1	A	290	THR
1	A	503	LEU
2	B	169	GLU
2	B	204	GLU
2	B	300	GLU
2	B	356	ARG
2	B	370	GLU
2	B	388	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	147	ASN

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Mol	Chain	Res	Type
1	A	174	GLN
1	A	278	GLN
1	A	487	GLN
2	B	182	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 20 ligands modelled in this entry, 1 is monoatomic - leaving 19 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	$\# Z > 2$
4	DMS	A	604	-	3,3,3	0.54	0	3,3,3	0.62	0
4	DMS	A	602	-	3,3,3	0.69	0	3,3,3	0.53	0
4	DMS	B	505	-	3,3,3	0.59	0	3,3,3	0.42	0
4	DMS	A	603	-	3,3,3	0.51	0	3,3,3	0.46	0
4	DMS	B	510	-	3,3,3	0.61	0	3,3,3	0.44	0
4	DMS	B	508	-	3,3,3	0.73	0	3,3,3	0.62	0
4	DMS	A	606	-	3,3,3	0.69	0	3,3,3	0.76	0
4	DMS	B	506	-	3,3,3	0.72	0	3,3,3	1.48	1 (33%)
4	DMS	B	501	-	3,3,3	0.66	0	3,3,3	0.61	0
4	DMS	A	608	-	3,3,3	0.67	0	3,3,3	0.59	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	1FF	A	609	-	16,16,16	0.99	1 (6%)	22,22,22	1.70	6 (27%)
3	T27	A	601	-	30,30,30	1.10	3 (10%)	37,40,40	1.85	4 (10%)
4	DMS	B	507	-	3,3,3	0.68	0	3,3,3	0.45	0
4	DMS	B	503	-	3,3,3	0.69	0	3,3,3	0.78	0
4	DMS	A	607	-	3,3,3	0.69	0	3,3,3	0.48	0
4	DMS	A	605	-	3,3,3	0.63	0	3,3,3	0.55	0
4	DMS	B	509	-	3,3,3	0.63	0	3,3,3	0.41	0
4	DMS	B	504	-	3,3,3	0.61	0	3,3,3	0.46	0
4	DMS	B	502	-	3,3,3	0.52	0	3,3,3	0.50	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
5	1FF	A	609	-	-	0/8/8/8	0/2/2/2
3	T27	A	601	-	-	0/13/14/14	0/3/3/3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	T27	C12-N4	3.66	1.44	1.36
3	A	601	T27	C11-N1	2.74	1.43	1.38
3	A	601	T27	C13-C19	2.33	1.49	1.44
5	A	609	1FF	C5-C2	-2.29	1.45	1.48

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	T27	C9-N2-C12	7.06	121.32	115.42
3	A	601	T27	C10-C9-N2	-5.05	117.79	123.97
5	A	609	1FF	C3-N2-N1	4.14	109.00	105.06
3	A	601	T27	N2-C12-N3	-4.07	122.49	126.42
5	A	609	1FF	C1-C3-N2	-3.37	108.27	112.45
5	A	609	1FF	C2-N1-N2	-3.16	108.81	112.19
5	A	609	1FF	C3-C1-C2	2.83	106.74	104.76
4	B	506	DMS	O-S-C1	2.27	117.84	106.49
5	A	609	1FF	C4-N1-N2	2.23	123.67	119.22
3	A	601	T27	C10-C11-N3	-2.12	119.59	123.15
5	A	609	1FF	O1-C11-O2	-2.02	119.10	123.90

There are no chirality outliers.

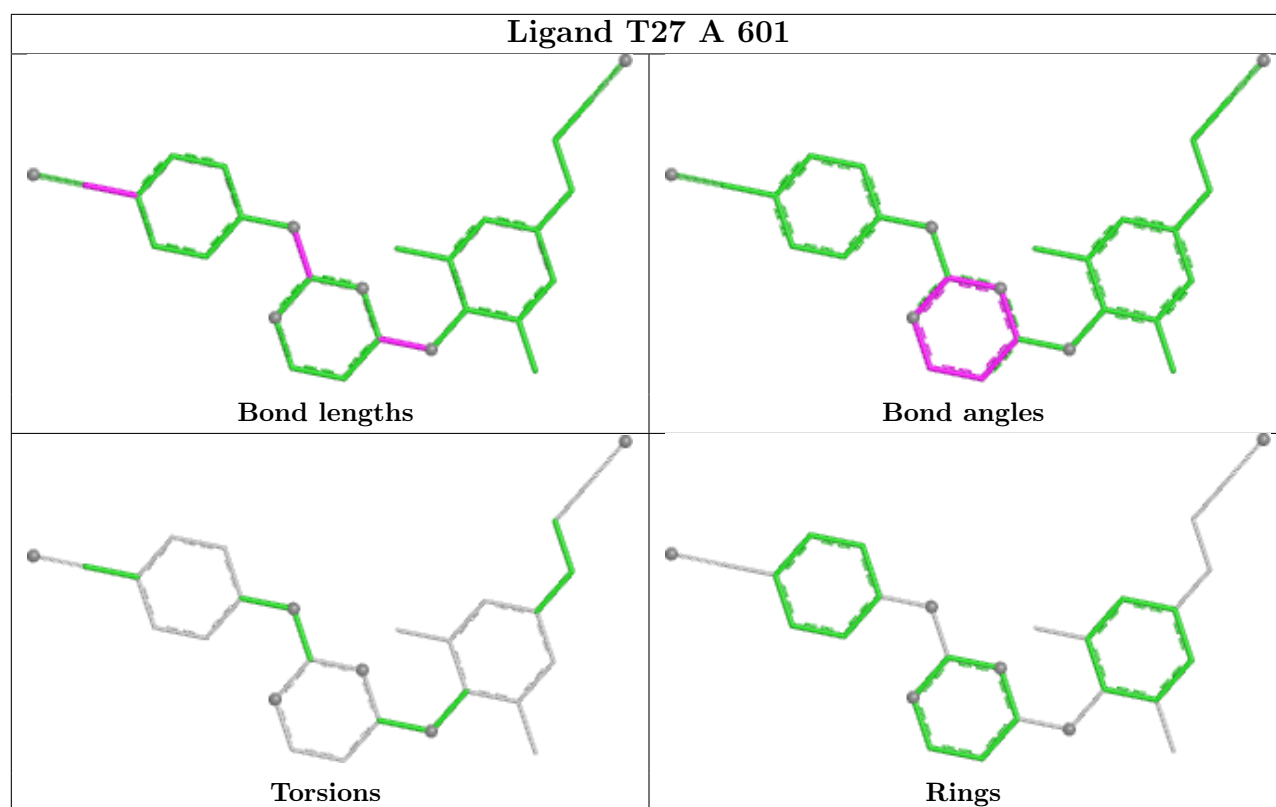
There are no torsion outliers.

There are no ring outliers.

15 monomers are involved in 35 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	604	DMS	3	0
4	B	505	DMS	5	0
4	A	603	DMS	3	0
4	B	510	DMS	1	0
4	A	606	DMS	5	0
4	B	506	DMS	2	0
4	B	501	DMS	1	0
4	A	608	DMS	2	0
3	A	601	T27	1	0
4	B	507	DMS	1	0
4	B	503	DMS	3	0
4	A	607	DMS	1	0
4	A	605	DMS	3	0
4	B	509	DMS	2	0
4	B	502	DMS	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

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	555/557 (99%)	0.28	47 (8%) 16 19	15, 34, 81, 115	0
2	B	412/429 (96%)	0.52	51 (12%) 8 9	13, 37, 92, 134	1 (0%)
All	All	967/986 (98%)	0.38	98 (10%) 12 14	13, 35, 88, 134	1 (0%)

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	213	GLY	7.8
2	B	90	VAL	7.1
2	B	92	LEU	7.0
2	B	283	LEU	6.9
2	B	93	GLY	6.8
2	B	214	LEU	6.3
2	B	5	ILE	6.1
1	A	24	TRP	5.9
1	A	115	TYR	5.2
1	A	543	GLY	5.0
1	A	544	GLY	4.9
2	B	361	HIS	4.9
2	B	229	TRP	4.6
1	A	289	LEU	4.5
2	B	200	THR	4.2
2	B	360	ALA	4.2
1	A	541	GLY	4.1
1	A	552	VAL	4.1
2	B	355	ALA	4.1
2	B	357	MET	4.0
2	B	69	THR	3.8
1	A	90	VAL	3.8
2	B	196	GLY	3.7
2	B	84	THR	3.7

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Mol	Chain	Res	Type	RSRZ
2	B	202	ILE	3.7
1	A	92	LEU	3.7
2	B	94	ILE	3.6
2	B	95	PRO	3.6
2	B	212	TRP	3.6
1	A	288	ALA	3.6
2	B	358	ARG	3.6
2	B	195	ILE	3.6
2	B	88	TRP	3.5
2	B	282	LEU	3.5
1	A	69	THR	3.5
1	A	222	GLN	3.4
1	A	546	GLU	3.4
1	A	68	SER	3.4
1	A	292	VAL	3.3
2	B	7	THR	3.3
1	A	64	LYS	3.2
1	A	221	HIS	3.2
2	B	91	GLN	3.2
2	B	209	LEU	3.1
1	A	554	ALA	3.1
1	A	65	LYS	3.0
2	B	426	TRP	3.0
2	B	210	LEU	2.9
2	B	87	PHE	2.9
1	A	71	TRP	2.9
1	A	548	VAL	2.9
1	A	358	ARG	2.9
2	B	359	GLY	2.9
1	A	357	MET	2.8
2	B	315	HIS	2.7
2	B	6	GLU	2.6
2	B	68	SER	2.6
1	A	254	VAL	2.6
2	B	8	VAL	2.6
1	A	295	LEU	2.5
2	B	66	LYS	2.5
1	A	215	THR	2.5
1	A	220	LYS	2.5
1	A	249	LYS	2.5
1	A	67	ASP	2.5
2	B	237	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	290	THR	2.5
2	B	170	PRO	2.5
1	A	255	ASN	2.4
1	A	286	THR	2.4
1	A	218	ASP	2.4
2	B	211	ARG	2.4
2	B	85	GLN	2.3
1	A	195	ILE	2.3
1	A	281	LYS	2.3
2	B	240	THR	2.3
1	A	304	ALA	2.2
2	B	284	ARG	2.2
1	A	63	ILE	2.2
2	B	356	ARG	2.2
1	A	301	LEU	2.2
2	B	194	GLU	2.2
2	B	285	GLY	2.2
2	B	64	LYS	2.2
1	A	256	ASP	2.1
1	A	210	LEU	2.1
1	A	214	LEU	2.1
2	B	228	LEU	2.1
1	A	360	ALA	2.1
1	A	113	ASP	2.1
1	A	223	LYS	2.1
1	A	-1	MET	2.1
2	B	272	PRO	2.1
2	B	193	LEU	2.1
2	B	65	LYS	2.0
2	B	173	LYS	2.0
1	A	553	SER	2.0
1	A	225	PRO	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

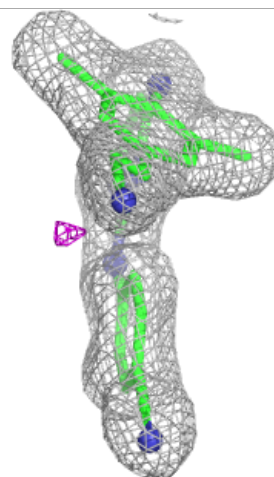
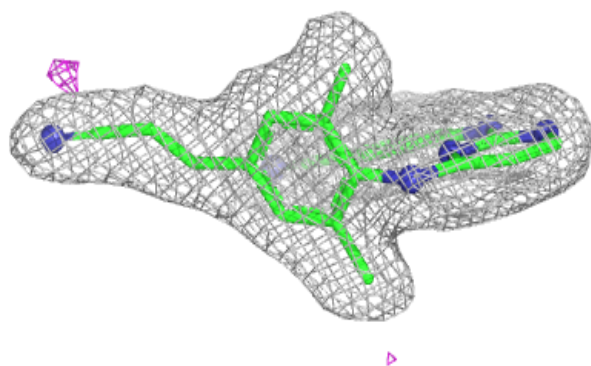
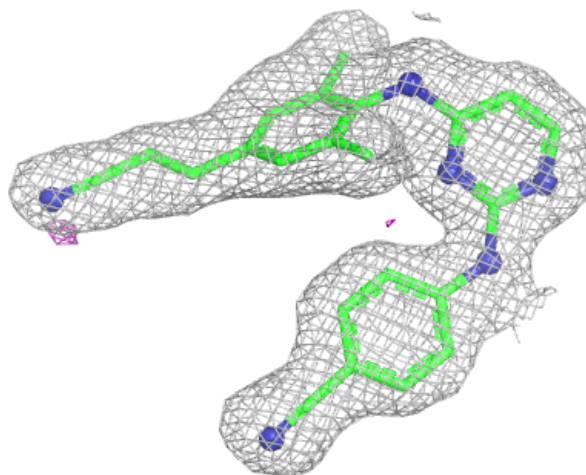
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	DMS	B	510	4/4	0.82	0.21	24,54,75,78	0
4	DMS	B	509	4/4	0.84	0.15	35,79,96,97	0
4	DMS	A	602	4/4	0.85	0.19	49,55,57,67	0
4	DMS	A	605	4/4	0.85	0.15	28,65,107,108	0
4	DMS	A	608	4/4	0.87	0.14	41,61,68,68	0
4	DMS	B	505	4/4	0.87	0.13	27,66,69,72	0
4	DMS	A	606	4/4	0.87	0.18	51,55,55,64	0
4	DMS	A	607	4/4	0.87	0.15	48,69,69,86	0
6	MG	A	610	1/1	0.87	0.11	43,43,43,43	0
4	DMS	B	504	4/4	0.88	0.36	31,103,160,161	0
4	DMS	A	603	4/4	0.90	0.21	14,39,72,74	0
4	DMS	B	503	4/4	0.90	0.13	16,21,75,78	0
4	DMS	B	507	4/4	0.90	0.15	42,55,60,93	0
4	DMS	B	508	4/4	0.92	0.17	30,47,48,56	0
5	1FF	A	609	15/15	0.94	0.07	26,28,32,33	0
3	T27	A	601	28/28	0.95	0.06	19,24,29,31	0
4	DMS	B	502	4/4	0.96	0.08	22,26,36,44	0
4	DMS	B	501	4/4	0.96	0.10	37,40,41,52	0
4	DMS	A	604	4/4	0.97	0.08	26,28,32,39	0
4	DMS	B	506	4/4	0.98	0.11	25,30,36,139	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 T27 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 [i](#)

There are no such residues in this entry.