Full wwPDB X-ray Structure Validation Report (i)

Feb 18, 2024 – 11:39 PM EST

PDB ID	:	4IFY
Title	:	HIV-1 reverse transcriptase with bound fragment at the Knuckles site
Authors	:	Bauman, J.D.; Patel, D.; Arnold, E.
Deposited on	:	2012-12-15
Resolution	:	2.10 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 (i) 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 (i)) were used in the production of this report:

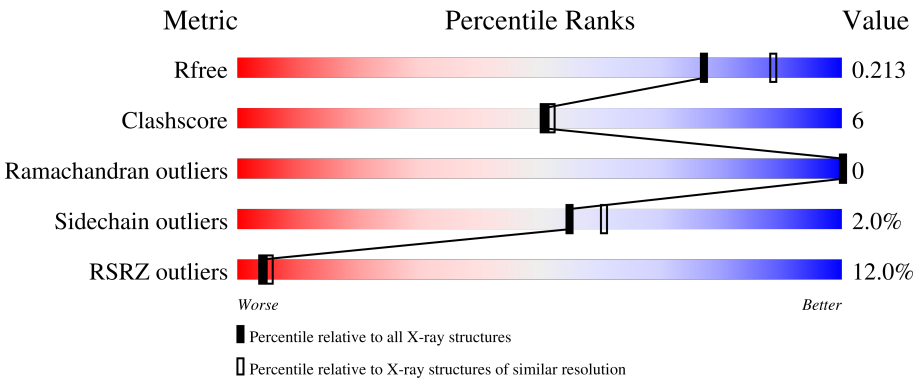
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	9% 89% 11% •
2	B	429	15% 83% 12% • •

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 8703 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
			Total	C	N	O	S			
1	A	556	4516	2923	750	835	8	0	0	0

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

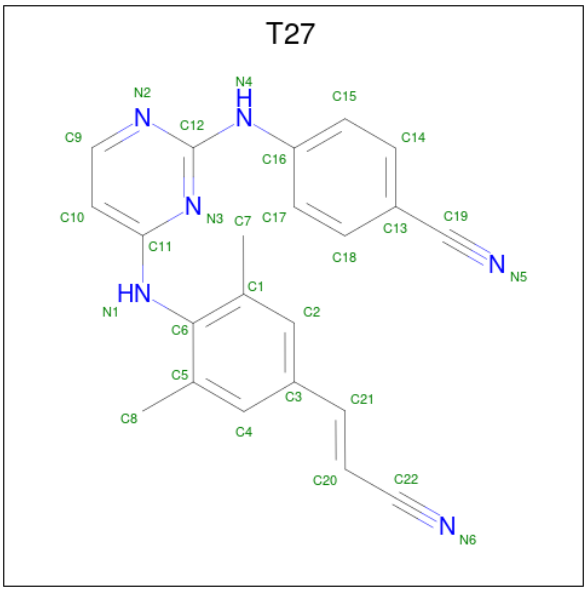
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	412	3419	2228	565	619	7	0	1	0

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 (three-letter code: T27) (formula: $C_{22}H_{18}N_6$).

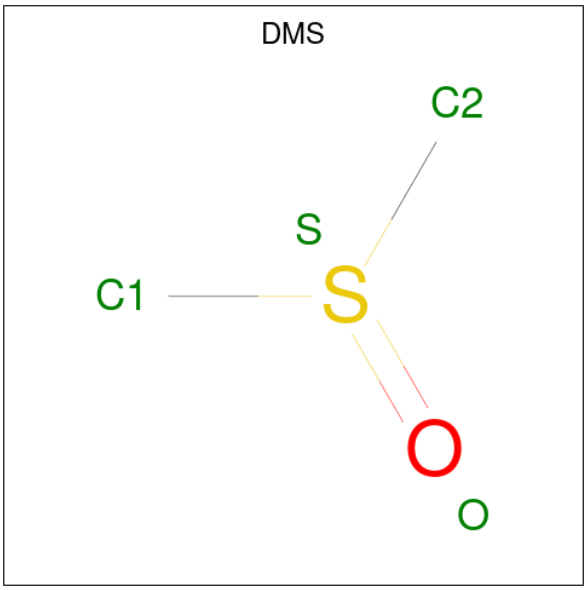


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	N		
3	A	1	28	22	6	0	0

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

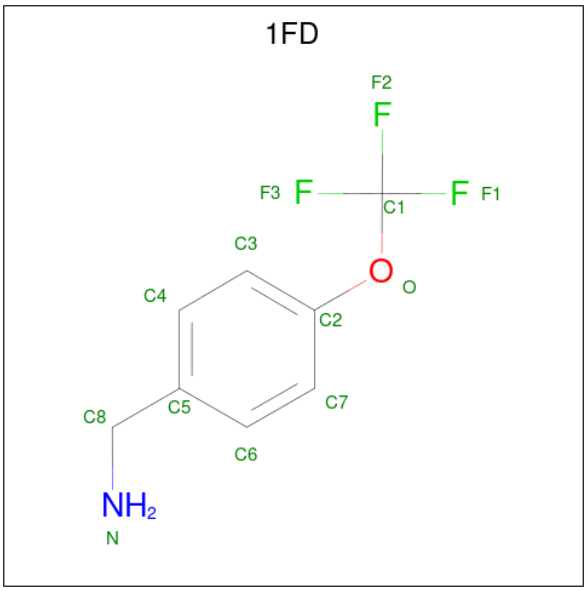
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
4	A	1	1	1	0	0

- Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



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

- Molecule 6 is 1-[4-(trifluoromethoxy)phenyl]methanamine (three-letter code: 1FD) (formula: $C_8H_8F_3NO$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
6	A	1	13	8	3	1	1	0	0

- Molecule 7 is water.

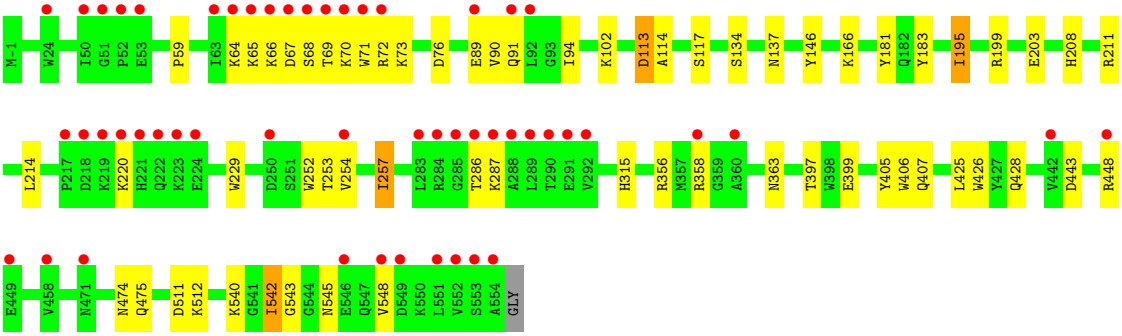
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	419	419	419	0	0
			Total	O		
7	B	243	243	243	0	0

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.

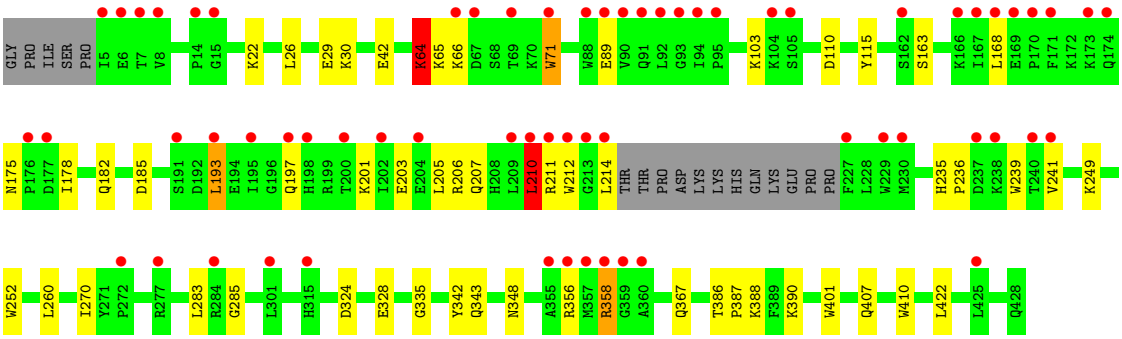
- Molecule 1: REVERSE TRANSCRIPTASE/RIBONUCLEASE H

Chain A:



- Molecule 2: p51 RT

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	161.95Å 73.05Å 108.75Å 90.00° 100.47° 90.00°	Depositor
Resolution (Å)	31.31 – 2.10 31.31 – 2.01	Depositor EDS
% Data completeness (in resolution range)	99.9 (31.31-2.10) 90.8 (31.31-2.01)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.11 (at 2.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1233)	Depositor
R, R_{free}	0.186 , 0.213 0.186 , 0.213	Depositor DCC
R_{free} test set	1643 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å^2)	29.5	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 49.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8703	wwPDB-VP
Average B, all atoms (Å^2)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: DMS, 1FD, T27, 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	0.42	0/4634	0.55	0/6299
2	B	0.42	1/3517 (0.0%)	0.60	4/4776 (0.1%)
All	All	0.42	1/8151 (0.0%)	0.57	4/11075 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	71	TRP	CE3-CZ3	-5.35	1.29	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	210	LEU	CA-CB-CG	5.92	128.90	115.30
2	B	285	GLY	N-CA-C	-5.63	99.03	113.10
2	B	401	TRP	N-CA-C	5.15	124.92	111.00
2	B	64	LYS	CB-CA-C	-5.12	100.16	110.40

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	4516	0	4572	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	3419	0	3447	41	0
3	A	28	0	18	1	0
4	A	1	0	0	0	0
5	A	32	0	48	7	0
5	B	32	0	48	9	0
6	A	13	0	8	0	0
7	A	419	0	0	5	2
7	B	243	0	0	11	1
All	All	8703	0	8141	92	2

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 6.

All (92) 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	5:B:503:DMS:H13	1.21	1.01
1:A:428:GLN:H	5:A:604:DMS:H22	1.29	0.94
2:B:178:ILE:HD11	2:B:201:LYS:HD3	1.52	0.92
5:B:507:DMS:H13	7:B:781:HOH:O	1.75	0.84
1:A:65:LYS:HG3	1:A:72:ARG:HH12	1.43	0.81
1:A:426:TRP:H	5:A:603:DMS:H23	1.45	0.80
2:B:22:LYS:NZ	7:B:822:HOH:O	2.15	0.79
2:B:185:ASP:OD1	7:B:791:HOH:O	2.03	0.74
2:B:42:GLU:OE1	7:B:778:HOH:O	2.05	0.74
1:A:114:ALA:HB2	1:A:214:LEU:HD13	1.71	0.73
1:A:474:ASN:H	5:A:606:DMS:H22	1.53	0.71
1:A:203:GLU:OE1	7:A:1039:HOH:O	2.10	0.70
2:B:64:LYS:O	2:B:407:GLN:NE2	2.30	0.64
1:A:542:ILE:HG13	1:A:545:ASN:HB3	1.80	0.64
2:B:175:ASN:OD1	2:B:201:LYS:NZ	2.30	0.64
1:A:426:TRP:H	5:A:603:DMS:C2	2.10	0.64
2:B:207:GLN:HA	2:B:210:LEU:HG	1.79	0.63
1:A:428:GLN:H	5:A:604:DMS:C2	2.07	0.60
2:B:168:LEU:HD22	2:B:205:LEU:HD11	1.85	0.58
1:A:448:ARG:NE	7:A:975:HOH:O	2.15	0.57
2:B:163:SER:OG	7:B:829:HOH:O	2.17	0.57
1:A:195:ILE:HG13	1:A:199:ARG:NH1	2.20	0.55
5:B:502:DMS:H22	7:B:742:HOH:O	2.07	0.55
2:B:22:LYS:HG3	7:B:822:HOH:O	2.07	0.55
1:A:94:ILE:HD11	1:A:229:TRP:CZ2	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:113:ASP:O	1:A:117:SER:OG	2.19	0.55
2:B:26:LEU:N	5:B:503:DMS:H13	2.06	0.55
1:A:181:TYR:CE2	1:A:183:TYR:HB2	2.42	0.54
3:A:601:T27:H15	3:A:601:T27:N3	2.23	0.53
1:A:73:LYS:NZ	1:A:146:TYR:OH	2.42	0.53
2:B:65:LYS:NZ	2:B:110:ASP:OD2	2.42	0.52
1:A:195:ILE:HG13	1:A:199:ARG:HH12	1.73	0.52
1:A:64:LYS:HD3	1:A:71:TRP:CH2	2.44	0.52
1:A:69:THR:HG23	1:A:70:LYS:HE3	1.93	0.51
2:B:115:TYR:OH	2:B:182:GLN:NE2	2.44	0.50
2:B:203:GLU:OE2	2:B:207:GLN:NE2	2.38	0.48
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.14	0.48
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.50	0.47
1:A:315:HIS:HB2	5:A:608:DMS:O	2.15	0.47
1:A:287:LYS:HD3	1:A:287:LYS:HA	1.75	0.47
1:A:358:ARG:HA	1:A:358:ARG:HD3	1.57	0.46
2:B:29:GLU:OE2	7:B:743:HOH:O	2.20	0.46
1:A:356:ARG:HE	1:A:358:ARG:HH12	1.63	0.46
2:B:178:ILE:CD1	2:B:201:LYS:HD3	2.36	0.46
2:B:212:TRP:HE3	2:B:214:LEU:HD23	1.81	0.46
2:B:388:LYS:NZ	7:B:810:HOH:O	2.47	0.45
2:B:239:TRP:HE1	5:B:504:DMS:H23	1.81	0.45
1:A:542:ILE:HG13	1:A:542:ILE:O	2.16	0.45
1:A:66:LYS:O	1:A:67:ASP:HB2	2.16	0.45
1:A:64:LYS:HD2	1:A:64:LYS:HA	1.70	0.45
2:B:193:LEU:HD13	2:B:197:GLN:HG2	1.98	0.45
1:A:540:LYS:HD3	1:A:540:LYS:HA	1.78	0.45
1:A:134:SER:OG	1:A:137:ASN:HA	2.17	0.44
1:A:252:TRP:HB3	1:A:257:ILE:HD11	1.99	0.44
1:A:253:THR:HG22	1:A:254:VAL:N	2.33	0.44
1:A:542:ILE:HB	2:B:283:LEU:HD13	1.99	0.44
2:B:252:TRP:CZ3	2:B:260:LEU:HD22	2.53	0.44
1:A:59:PRO:HG2	1:A:76:ASP:HB3	2.00	0.43
1:A:65:LYS:HG3	1:A:72:ARG:NH1	2.21	0.43
1:A:70:LYS:HA	1:A:70:LYS:HD3	1.84	0.43
1:A:443:ASP:HB2	1:A:548:VAL:HG13	2.01	0.43
2:B:30:LYS:HG2	2:B:71:TRP:CZ3	2.53	0.43
1:A:65:LYS:HZ2	1:A:68:SER:HB3	1.83	0.43
1:A:252:TRP:HB3	1:A:257:ILE:CD1	2.48	0.43
2:B:235:HIS:H	5:B:504:DMS:H23	1.82	0.43
2:B:386:THR:HA	2:B:387:PRO:HD3	1.91	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:239:TRP:HE1	5:B:504:DMS:C2	2.30	0.43
2:B:249:LYS:HE3	7:B:831:HOH:O	2.17	0.43
1:A:397:THR:HG23	1:A:425:LEU:HG	2.01	0.43
1:A:89:GLU:OE1	1:A:91:GLN:NE2	2.50	0.42
1:A:425:LEU:HA	5:A:603:DMS:H22	2.01	0.42
1:A:475:GLN:NE2	7:A:892:HOH:O	2.12	0.42
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.54	0.42
2:B:26:LEU:O	5:B:503:DMS:H23	2.20	0.42
2:B:210:LEU:HD12	2:B:211:ARG:HG3	2.01	0.42
1:A:208:HIS:O	1:A:211:ARG:HG3	2.20	0.42
2:B:66:LYS:HE3	2:B:66:LYS:HB3	1.92	0.42
2:B:193:LEU:HD11	2:B:201:LYS:HD2	2.02	0.42
1:A:406:TRP:CE2	1:A:407:GLN:HG3	2.54	0.42
2:B:203:GLU:OE1	2:B:206:ARG:HD2	2.20	0.42
2:B:270:ILE:HG21	5:B:508:DMS:H23	2.00	0.41
2:B:324:ASP:O	2:B:343:GLN:HG2	2.20	0.41
2:B:335:GLY:HA2	2:B:367:GLN:OE1	2.21	0.41
1:A:286:THR:HG22	1:A:287:LYS:N	2.35	0.41
1:A:89:GLU:HA	7:A:854:HOH:O	2.20	0.41
1:A:166:LYS:HE3	1:A:166:LYS:HB2	1.80	0.41
1:A:543:GLY:HA3	2:B:283:LEU:O	2.21	0.41
2:B:328:GLU:HG2	2:B:390:LYS:HD3	2.03	0.41
1:A:90:VAL:HG13	7:B:770:HOH:O	2.21	0.40
1:A:211:ARG:HD2	7:A:990:HOH:O	2.20	0.40
2:B:342:TYR:HB3	2:B:348:ASN:HD22	1.86	0.40
2:B:356:ARG:HH22	2:B:358:ARG:HD2	1.86	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:1094:HOH:O	7:A:1107:HOH:O[4_556]	1.99	0.21
7:A:928:HOH:O	7:B:748:HOH:O[4_545]	2.18	0.02

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	554/557 (100%)	546 (99%)	8 (1%)	0	100	100
2	B	409/429 (95%)	401 (98%)	8 (2%)	0	100	100
All	All	963/986 (98%)	947 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	495/495 (100%)	487 (98%)	8 (2%)	62	69
2	B	375/390 (96%)	366 (98%)	9 (2%)	49	53
All	All	870/885 (98%)	853 (98%)	17 (2%)	55	60

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	102	LYS
1	A	113	ASP
1	A	195	ILE
1	A	220	LYS
1	A	257	ILE
1	A	399	GLU
1	A	512	LYS
1	A	542	ILE
2	B	64	LYS
2	B	89	GLU
2	B	103	LYS
2	B	193	LEU
2	B	210	LEU
2	B	241	VAL

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Mol	Chain	Res	Type
2	B	358	ARG
2	B	410	TRP
2	B	422	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	348	ASN

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 19 ligands modelled in this entry, 1 is monoatomic - leaving 18 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	$\#\|Z\| > 2$
5	DMS	B	508	-	3,3,3	0.67	0	3,3,3	0.70	0
5	DMS	A	604	-	3,3,3	0.52	0	3,3,3	0.68	0
5	DMS	A	606	-	3,3,3	0.68	0	3,3,3	0.57	0
5	DMS	A	605	-	3,3,3	0.65	0	3,3,3	0.47	0
5	DMS	A	603	-	3,3,3	0.39	0	3,3,3	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
5	DMS	A	610	-	3,3,3	0.67	0	3,3,3	0.44	0
3	T27	A	601	-	30,30,30	1.18	3 (10%)	39,40,40	1.93	5 (12%)
5	DMS	B	505	-	3,3,3	0.71	0	3,3,3	0.96	0
5	DMS	B	507	-	3,3,3	0.64	0	3,3,3	0.60	0
5	DMS	A	608	-	3,3,3	0.64	0	3,3,3	0.75	0
5	DMS	B	506	-	3,3,3	0.67	0	3,3,3	0.68	0
5	DMS	B	501	-	3,3,3	0.67	0	3,3,3	0.45	0
5	DMS	B	503	-	3,3,3	0.64	0	3,3,3	0.71	0
5	DMS	B	502	-	3,3,3	0.53	0	3,3,3	0.44	0
5	DMS	B	504	-	3,3,3	0.62	0	3,3,3	0.45	0
5	DMS	A	609	-	3,3,3	0.63	0	3,3,3	0.71	0
5	DMS	A	607	-	3,3,3	0.65	0	3,3,3	0.61	0
6	1FD	A	611	-	13,13,13	0.48	0	18,18,18	0.59	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
3	T27	A	601	-	-	0/13/14/14	0/3/3/3
6	1FD	A	611	-	-	3/7/7/7	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	T27	C12-N4	3.42	1.43	1.36
3	A	601	T27	C11-N1	3.20	1.44	1.38
3	A	601	T27	C13-C19	2.37	1.49	1.44

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	601	T27	C9-N2-C12	6.14	120.90	115.45
3	A	601	T27	C9-C10-C11	5.06	120.07	116.76
3	A	601	T27	C10-C9-N2	-4.96	117.80	123.96
3	A	601	T27	N2-C12-N3	-3.98	122.78	126.55
3	A	601	T27	C10-C11-N3	-2.51	118.93	123.16

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	611	1FD	F1-C1-O-C2
6	A	611	1FD	F2-C1-O-C2
6	A	611	1FD	F3-C1-O-C2

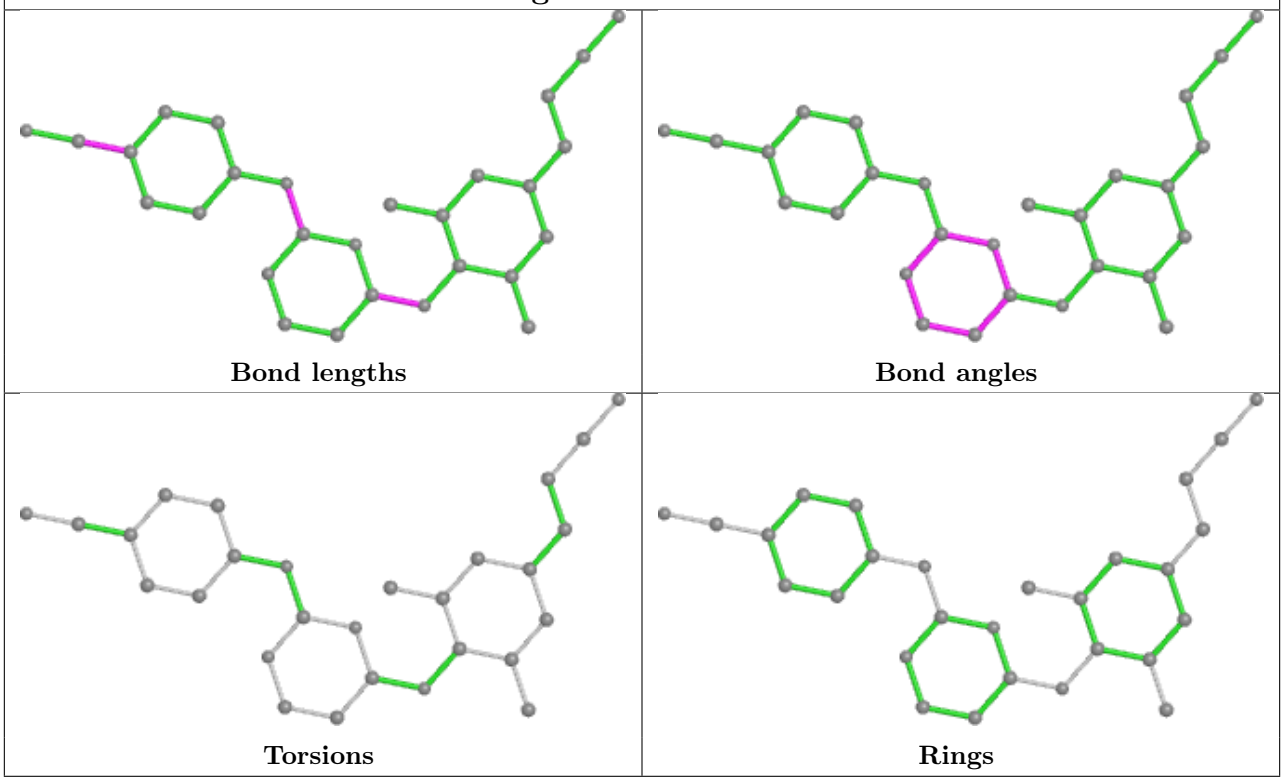
There are no ring outliers.

10 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	508	DMS	1	0
5	A	604	DMS	2	0
5	A	606	DMS	1	0
5	A	603	DMS	3	0
3	A	601	T27	1	0
5	B	507	DMS	1	0
5	A	608	DMS	1	0
5	B	503	DMS	3	0
5	B	502	DMS	1	0
5	B	504	DMS	3	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 then 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.

Ligand T27 A 601



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 (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	556/557 (99%)	0.38	52 (9%) 8 11	17, 36, 87, 129	0
2	B	412/429 (96%)	0.71	64 (15%) 2 2	19, 42, 101, 145	0
All	All	968/986 (98%)	0.52	116 (11%) 4 5	17, 39, 96, 145	0

All (116) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	92	LEU	14.6
2	B	90	VAL	14.0
2	B	88	TRP	10.1
1	A	67	ASP	9.7
2	B	357	MET	8.3
2	B	89	GLU	8.1
1	A	68	SER	7.9
2	B	359	GLY	7.8
1	A	69	THR	7.7
2	B	67	ASP	7.2
1	A	65	LYS	7.1
1	A	219	LYS	7.0
2	B	356	ARG	6.9
2	B	93	GLY	6.8
1	A	289	LEU	6.5
2	B	94	ILE	6.2
2	B	214	LEU	5.9
1	A	285	GLY	5.9
1	A	287	LYS	5.9
1	A	222	GLN	5.8
1	A	24	TRP	5.8
1	A	546	GLU	5.7
1	A	218	ASP	5.7
1	A	220	LYS	5.6

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Mol	Chain	Res	Type	RSRZ
1	A	221	HIS	5.6
1	A	91	GLN	5.5
1	A	286	THR	5.4
2	B	6	GLU	5.2
1	A	66	LYS	5.2
1	A	554	ALA	5.1
2	B	358	ARG	5.1
1	A	51	GLY	5.1
1	A	92	LEU	5.0
2	B	5	ILE	4.9
1	A	288	ALA	4.8
1	A	548	VAL	4.8
2	B	170	PRO	4.8
2	B	7	THR	4.6
1	A	552	VAL	4.6
2	B	213	GLY	4.6
2	B	209	LEU	4.5
2	B	284	ARG	4.3
1	A	64	LYS	4.2
1	A	52	PRO	4.1
1	A	283	LEU	4.1
1	A	70	LYS	4.1
2	B	197	GLN	3.9
1	A	224	GLU	3.8
1	A	290	THR	3.8
1	A	551	LEU	3.7
2	B	355	ALA	3.6
2	B	91	GLN	3.6
1	A	553	SER	3.6
1	A	254	VAL	3.5
2	B	166	LYS	3.5
1	A	223	LYS	3.5
2	B	193	LEU	3.3
2	B	240	THR	3.3
1	A	53	GLU	3.3
2	B	171	PHE	3.2
1	A	448	ARG	3.2
2	B	229	TRP	3.2
2	B	195	ILE	3.2
1	A	72	ARG	3.2
2	B	69	THR	3.2
2	B	95	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
2	B	211	ARG	3.1
2	B	241	VAL	3.0
2	B	198	HIS	3.0
1	A	291	GLU	3.0
1	A	292	VAL	2.9
2	B	237	ASP	2.9
2	B	200	THR	2.9
2	B	167	ILE	2.8
2	B	230	MET	2.8
2	B	210	LEU	2.8
1	A	449	GLU	2.7
1	A	284	ARG	2.7
2	B	202	ILE	2.6
2	B	14	PRO	2.6
2	B	168	LEU	2.6
2	B	104	LYS	2.5
1	A	71	TRP	2.5
2	B	173	LYS	2.5
2	B	212	TRP	2.5
2	B	176	PRO	2.5
1	A	458	VAL	2.4
2	B	204	GLU	2.4
2	B	301	LEU	2.4
2	B	174	GLN	2.4
2	B	169	GLU	2.4
2	B	162	SER	2.4
2	B	238	LYS	2.4
2	B	277	ARG	2.4
1	A	471	ASN	2.3
1	A	50	ILE	2.3
2	B	425	LEU	2.3
2	B	15	GLY	2.3
1	A	360	ALA	2.3
2	B	66	LYS	2.3
1	A	358	ARG	2.2
2	B	177	ASP	2.2
1	A	217	PRO	2.2
2	B	272	PRO	2.2
1	A	549	ASP	2.2
2	B	360	ALA	2.2
1	A	89	GLU	2.2
2	B	315	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
2	B	191	SER	2.2
1	A	250	ASP	2.2
1	A	442	VAL	2.1
2	B	71	TRP	2.1
2	B	105	SER	2.0
1	A	63	ILE	2.0
2	B	8	VAL	2.0
2	B	227	PHE	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 (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
5	DMS	A	606	4/4	0.72	0.23	71,91,94,95	0
4	MG	A	602	1/1	0.77	0.15	54,54,54,54	0
5	DMS	B	503	4/4	0.85	0.17	19,19,71,71	0
5	DMS	B	504	4/4	0.85	0.33	40,92,100,102	0
6	1FD	A	611	13/13	0.87	0.20	70,77,80,80	0
5	DMS	A	609	4/4	0.89	0.20	47,62,75,77	0
5	DMS	A	603	4/4	0.91	0.21	11,45,55,61	0
5	DMS	B	506	4/4	0.94	0.24	50,72,75,96	0
5	DMS	B	508	4/4	0.94	0.15	48,56,76,77	0
5	DMS	A	610	4/4	0.94	0.12	52,54,68,71	0
5	DMS	B	502	4/4	0.95	0.13	23,28,46,50	0
3	T27	A	601	28/28	0.95	0.12	19,26,30,33	0
5	DMS	A	608	4/4	0.95	0.12	63,69,81,81	0
5	DMS	B	501	4/4	0.96	0.12	37,37,51,55	0
5	DMS	A	604	4/4	0.97	0.12	18,34,34,41	0

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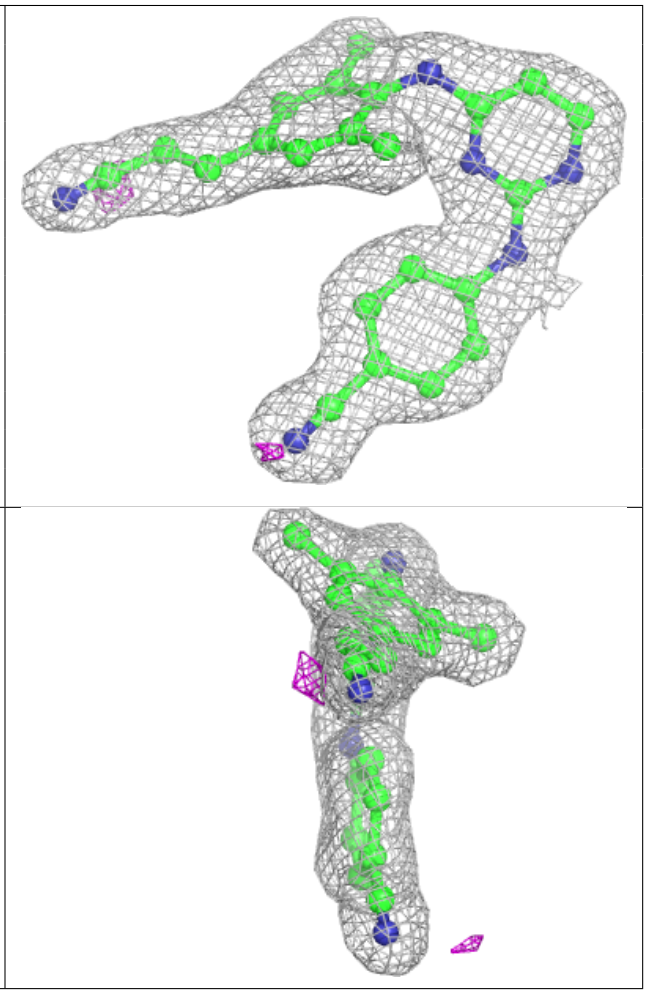
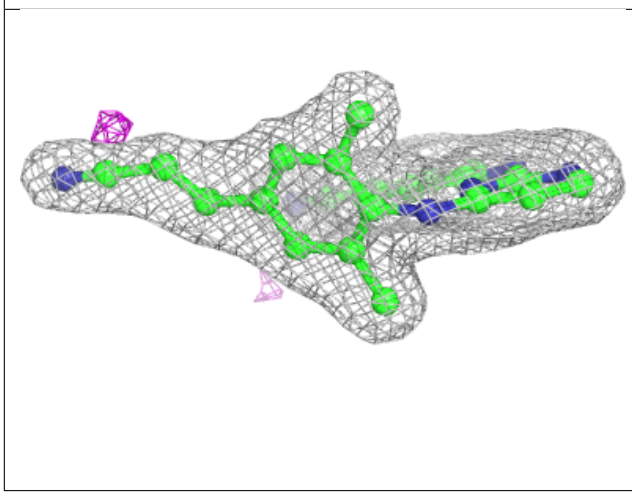
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	DMS	B	507	4/4	0.97	0.14	38,48,54,79	0
5	DMS	A	607	4/4	0.97	0.19	44,70,72,74	0
5	DMS	A	605	4/4	0.97	0.09	43,49,54,59	0
5	DMS	B	505	4/4	0.98	0.17	33,37,42,92	0

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.