



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2017 – 01:01 PM EST

PDB ID : 4RW7  
Title : Crystal Structure of HIV-1 Reverse Transcriptase (K103N, Y181C) variant in complex with (E)-3-(3-chloro-5-(2-(2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy)phenoxy)phenyl)acrylonitrile (JLJ532), a non-nucleoside inhibitor  
Authors : Frey, K.M.; Anderson, K.S.  
Deposited on : unknown  
Resolution : 3.01 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20030345  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

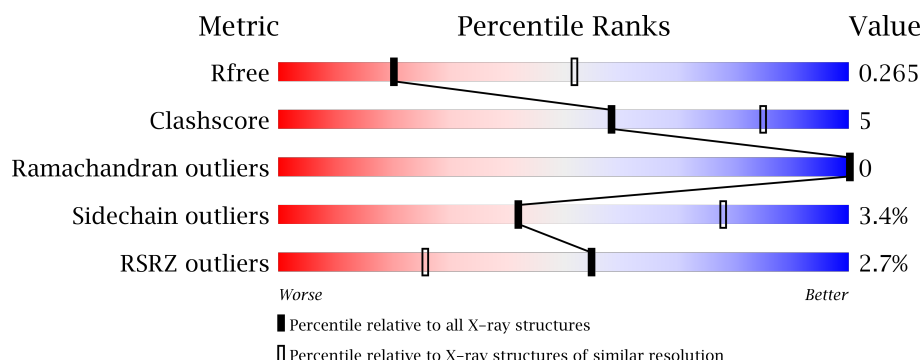
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.01 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))
$R_{free}$	100719	1924 (3.04-3.00)
Clashscore	112137	2279 (3.04-3.00)
Ramachandran outliers	110173	2207 (3.04-3.00)
Sidechain outliers	110143	2210 (3.04-3.00)
RSRZ outliers	101464	1948 (3.04-3.00)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>3%</div> <div>81%</div> <div>15%</div> <div>• •</div> </div>
2	B	428	<div> <div>3%</div> <div>79%</div> <div>15%</div> <div>• 5%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7744 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, p66 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	538	Total	C	N	O	S	0	0	0
			4359	2823	721	806	9			

There are 7 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	103	ASN	LYS	ENGINEERED MUTATION	UNP P03366
A	172	ALA	LYS	ENGINEERED MUTATION	UNP P03366
A	173	ALA	LYS	ENGINEERED MUTATION	UNP P03366
A	181	CYS	TYR	ENGINEERED MUTATION	UNP P03366
A	280	SER	CYS	ENGINEERED MUTATION	UNP P03366

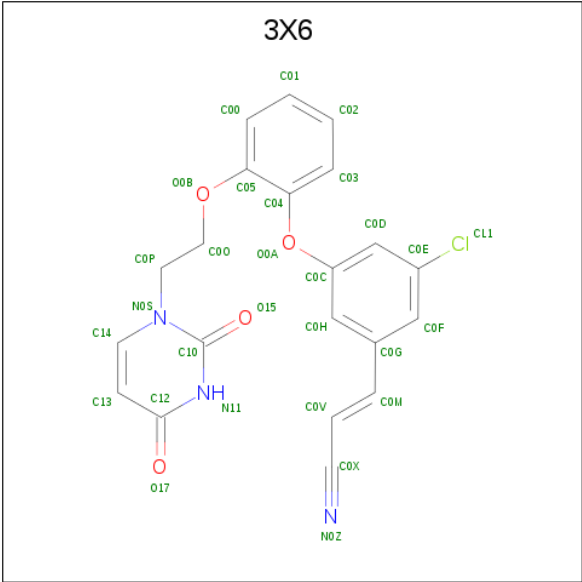
- Molecule 2 is a protein called Reverse transcriptase/ribonuclease H, p51 subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	405	Total	C	N	O	S	0	0	0
			3356	2184	556	610	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	ENGINEERED MUTATION	UNP P03366

- Molecule 3 is (2E)-3-(3-chloro-5-{2-[2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy]phenoxy}phenyl)prop-2-enenitrile (three-letter code: 3X6) (formula: C<sub>21</sub>H<sub>16</sub>ClN<sub>3</sub>O<sub>4</sub>).

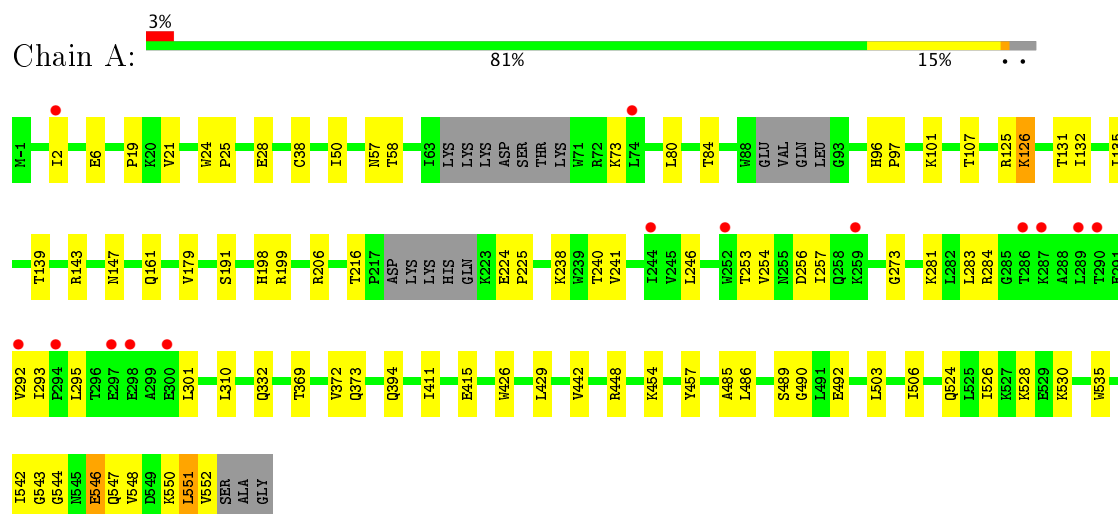


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	0	0
			29	21	1	3	4		

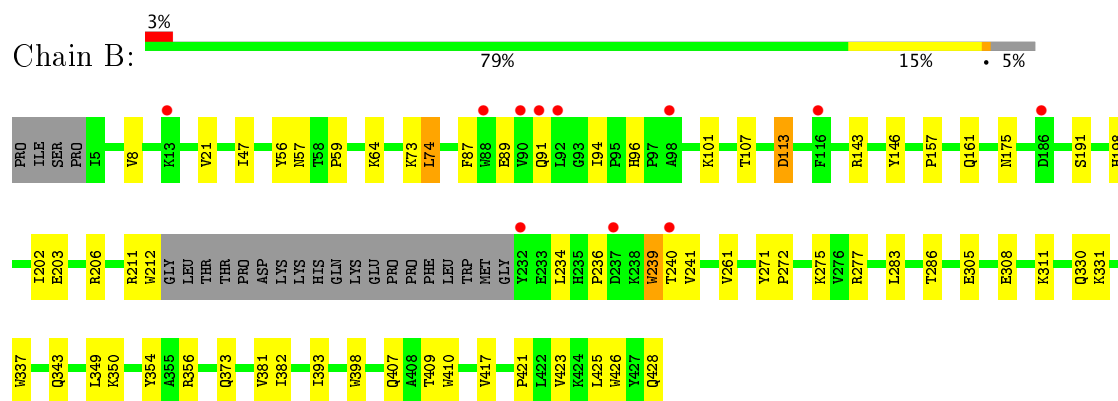
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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, p66 subunit



- Molecule 2: Reverse transcriptase/ribonuclease H, p51 subunit



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	161.95Å 73.87Å 108.46Å 90.00° 99.87° 90.00°	Depositor
Resolution (Å)	34.97 – 3.01 34.97 – 3.01	Depositor EDS
% Data completeness (in resolution range)	99.4 (34.97-3.01) 99.4 (34.97-3.01)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.03 (at 3.00Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, $R_{free}$	0.229 , 0.266 0.228 , 0.265	Depositor DCC
$R_{free}$ test set	1999 reflections (7.99%)	DCC
Wilson B-factor (Å <sup>2</sup> )	85.8	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 33.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	7744	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.49% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: 3X6

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	0.23	0/4472	0.42	0/6083
2	B	0.22	0/3451	0.42	0/4687
All	All	0.22	0/7923	0.42	0/10770

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

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	4359	0	4390	50	0
2	B	3356	0	3387	38	0
3	A	29	0	16	1	0
All	All	7744	0	7793	85	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 (85) 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:373:GLN:HE22	2:B:407:GLN:H	1.35	0.72
1:A:131:THR:OG1	1:A:143:ARG:NH1	2.27	0.68
1:A:246:LEU:HD11	1:A:310:LEU:HD12	1.76	0.68
2:B:107:THR:HG1	2:B:198:HIS:HE2	1.39	0.66
2:B:89:GLU:HB2	2:B:91:GLN:HG2	1.77	0.64
2:B:91:GLN:HB2	2:B:94:ILE:HG13	1.79	0.64
2:B:373:GLN:HE22	2:B:407:GLN:N	1.96	0.63
2:B:74:LEU:HD21	2:B:409:THR:HA	1.83	0.60
2:B:56:TYR:O	2:B:143:ARG:NH2	2.33	0.60
1:A:544:GLY:HA2	2:B:286:THR:HG22	1.83	0.59
2:B:421:PRO:HB2	2:B:423:VAL:HG22	1.86	0.58
2:B:425:LEU:HD23	2:B:428:GLN:HB3	1.85	0.58
1:A:191:SER:OG	1:A:198:HIS:ND1	2.34	0.56
1:A:179:VAL:HG23	3:A:601:3X6:H4	1.87	0.56
1:A:372:VAL:HG11	1:A:411:ILE:HG23	1.86	0.56
1:A:28:GLU:HG3	1:A:135:ILE:HD12	1.87	0.56
1:A:442:VAL:HG12	1:A:457:TYR:HB3	1.87	0.55
1:A:292:VAL:HG12	1:A:293:ILE:H	1.72	0.55
1:A:50:ILE:HG13	1:A:143:ARG:HB3	1.88	0.54
2:B:211:ARG:HG3	2:B:212:TRP:HD1	1.73	0.54
1:A:19:PRO:HG3	1:A:80:LEU:HB2	1.90	0.53
1:A:490:GLY:O	1:A:528:LYS:NZ	2.32	0.53
1:A:369:THR:O	1:A:373:GLN:HG2	2.07	0.53
2:B:234:LEU:HD22	2:B:239:TRP:HZ2	1.74	0.53
1:A:253:THR:HG23	1:A:256:ASP:H	1.74	0.52
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.91	0.52
1:A:542:ILE:HD11	2:B:261:VAL:HG11	1.91	0.52
1:A:107:THR:OG1	1:A:198:HIS:NE2	2.33	0.52
1:A:546:GLU:HG3	1:A:548:VAL:HG22	1.92	0.52
2:B:47:ILE:HG22	2:B:146:TYR:HA	1.93	0.51
1:A:489:SER:O	1:A:528:LYS:NZ	2.44	0.51
2:B:21:VAL:O	2:B:57:ASN:ND2	2.38	0.51
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.44	0.49
1:A:281:LYS:HD2	1:A:284:ARG:HH22	1.78	0.49
2:B:211:ARG:HG3	2:B:212:TRP:CD1	2.48	0.49
1:A:454:LYS:NZ	1:A:552:VAL:HB	2.28	0.48
2:B:354:TYR:CE1	2:B:356:ARG:HB3	2.48	0.48
1:A:253:THR:OG1	1:A:254:VAL:N	2.46	0.48
1:A:429:LEU:HD11	1:A:506:ILE:HG22	1.95	0.48
1:A:543:GLY:HA3	2:B:283:LEU:O	2.14	0.48
1:A:442:VAL:HG11	1:A:485:ALA:HB2	1.95	0.47
2:B:308:GLU:HA	2:B:311:LYS:HE2	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:THR:OG1	1:A:241:VAL:N	2.47	0.47
1:A:492:GLU:HG2	1:A:530:LYS:HB2	1.97	0.46
2:B:191:SER:OG	2:B:198:HIS:ND1	2.47	0.46
1:A:126:LYS:HE3	1:A:126:LYS:HB2	1.69	0.46
1:A:547:GLN:O	1:A:551:LEU:HB2	2.15	0.45
1:A:206:ARG:NH2	1:A:216:THR:O	2.48	0.45
1:A:292:VAL:O	1:A:293:ILE:HG13	2.16	0.45
2:B:271:TYR:HA	2:B:272:PRO:HD3	1.83	0.45
2:B:236:PRO:HA	2:B:239:TRP:CD1	2.52	0.45
2:B:113:ASP:N	2:B:113:ASP:OD2	2.50	0.44
1:A:426:TRP:HB3	1:A:526:ILE:HG12	1.99	0.44
2:B:89:GLU:OE1	2:B:91:GLN:NE2	2.51	0.44
1:A:21:VAL:O	1:A:57:ASN:ND2	2.34	0.44
1:A:80:LEU:O	1:A:84:THR:OG1	2.24	0.44
1:A:253:THR:O	1:A:257:ILE:HG13	2.18	0.44
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.99	0.44
1:A:273:GLY:HA2	1:A:332:GLN:HE22	1.82	0.44
1:A:547:GLN:HA	1:A:550:LYS:HE3	1.99	0.44
2:B:198:HIS:O	2:B:202:ILE:HG12	2.17	0.44
2:B:89:GLU:N	2:B:89:GLU:OE1	2.50	0.44
1:A:24:TRP:HE3	1:A:25:PRO:HD2	1.83	0.43
2:B:96:HIS:NE2	2:B:381:VAL:O	2.36	0.43
1:A:224:GLU:HB2	1:A:225:PRO:HD2	2.01	0.43
1:A:486:LEU:HB3	1:A:524:GLN:HB3	2.01	0.43
2:B:107:THR:OG1	2:B:198:HIS:NE2	2.34	0.43
1:A:126:LYS:H	1:A:126:LYS:HG3	1.56	0.43
2:B:393:ILE:HD13	2:B:398:TRP:HB2	2.00	0.43
2:B:331:LYS:HB2	2:B:337:TRP:CZ3	2.53	0.42
1:A:125:ARG:HD3	1:A:147:ASN:HA	2.01	0.42
1:A:73:LYS:HB3	1:A:73:LYS:HE2	1.91	0.42
2:B:203:GLU:HA	2:B:206:ARG:HG2	2.01	0.42
1:A:38:CYS:SG	1:A:132:ILE:HD11	2.60	0.42
2:B:101:LYS:HD3	2:B:382:ILE:HG23	2.00	0.42
1:A:547:GLN:HG3	1:A:550:LYS:NZ	2.34	0.42
1:A:80:LEU:O	1:A:84:THR:N	2.53	0.41
2:B:157:PRO:O	2:B:161:GLN:HG3	2.21	0.41
1:A:283:LEU:HD23	1:A:283:LEU:HA	1.94	0.41
1:A:96:HIS:HA	1:A:97:PRO:HD3	1.91	0.41
2:B:240:THR:O	2:B:350:LYS:NZ	2.54	0.41
2:B:423:VAL:HA	2:B:426:TRP:CE3	2.55	0.41
1:A:6:GLU:H	1:A:6:GLU:HG2	1.71	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:343:GLN:HG3	2:B:349:LEU:HD11	2.03	0.40
1:A:50:ILE:HD11	1:A:143:ARG:HH21	1.85	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	530/557 (95%)	514 (97%)	16 (3%)	0	100	100
2	B	401/428 (94%)	395 (98%)	6 (2%)	0	100	100
All	All	931/985 (94%)	909 (98%)	22 (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	477/495 (96%)	462 (97%)	15 (3%)	45	80
2	B	369/390 (95%)	355 (96%)	14 (4%)	38	75
All	All	846/885 (96%)	817 (97%)	29 (3%)	42	78

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ILE
1	A	58	THR
1	A	101	LYS
1	A	126	LYS
1	A	139	THR
1	A	161	GLN
1	A	199	ARG
1	A	238	LYS
1	A	295	LEU
1	A	301	LEU
1	A	394	GLN
1	A	415	GLU
1	A	448	ARG
1	A	546	GLU
1	A	551	LEU
2	B	8	VAL
2	B	64	LYS
2	B	74	LEU
2	B	87	PHE
2	B	113	ASP
2	B	175	ASN
2	B	239	TRP
2	B	241	VAL
2	B	275	LYS
2	B	277	ARG
2	B	305	GLU
2	B	330	GLN
2	B	410	TRP
2	B	417	VAL

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

Mol	Chain	Res	Type
1	A	103	ASN
1	A	197	GLN
1	A	258	GLN
1	A	332	GLN
1	A	394	GLN
1	A	475	GLN
1	A	520	GLN
1	A	539	HIS
2	B	151	GLN
2	B	182	GLN

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Mol	Chain	Res	Type
2	B	197	GLN
2	B	278	GLN
2	B	330	GLN
2	B	334	GLN
2	B	340	GLN
2	B	373	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z  > 2$
3	3X6	A	601	-	28,31,31	1.42	4 (14%)	33,41,41	3.11	6 (18%)

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	3X6	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	3X6	C0H-C0C	2.04	1.42	1.38
3	A	601	3X6	C0D-C0C	2.14	1.42	1.38
3	A	601	3X6	C0H-C0G	2.36	1.43	1.39
3	A	601	3X6	C14-N0S	3.68	1.42	1.36

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	3X6	C13-C12-N11	-3.53	114.70	123.12
3	A	601	3X6	C0C-C0D-C0E	2.04	120.53	118.17
3	A	601	3X6	C0G-C0F-C0E	2.22	121.55	119.65
3	A	601	3X6	C0G-C0H-C0C	2.52	121.99	119.88
3	A	601	3X6	O0B-C0O-C0P	2.69	110.03	107.28
3	A	601	3X6	C12-N11-C10	16.22	128.06	114.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	3X6	1	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	538/557 (96%)	-0.14	14 (2%) 56 27	17, 59, 122, 150	0
2	B	405/428 (94%)	-0.01	11 (2%) 55 26	19, 54, 116, 136	0
All	All	943/985 (95%)	-0.08	25 (2%) 55 26	17, 56, 118, 150	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	240	THR	5.6
1	A	294	PRO	5.1
1	A	286	THR	4.5
1	A	287	LYS	4.4
2	B	90	VAL	3.9
1	A	292	VAL	3.3
1	A	297	GLU	3.3
2	B	98	ALA	3.2
1	A	298	GLU	2.9
2	B	237	ASP	2.7
1	A	252	TRP	2.7
1	A	74	LEU	2.5
1	A	290	THR	2.5
1	A	289	LEU	2.5
2	B	13	LYS	2.4
2	B	92	LEU	2.3
1	A	2	ILE	2.3
2	B	232	TYR	2.2
2	B	116	PHE	2.2
2	B	88	TRP	2.2
1	A	244	ILE	2.2
1	A	259	LYS	2.1
2	B	91	GLN	2.1
2	B	186	ASP	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	300	GLU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	3X6	A	601	29/29	0.92	0.18	-0.40	32,45,52,57	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.