



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 3, 2017 – 04:42 PM EST

PDB ID : 5TEP  
Title : Crystal Structure of HIV-1 Reverse Transcriptase in Complex with 7-(2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy)phenoxy)-2-naphthonitrile (JLJ649), a Non-nucleoside Inhibitor  
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Deposited on : 2016-09-22  
Resolution : 3.10 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](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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20028442  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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-20028442

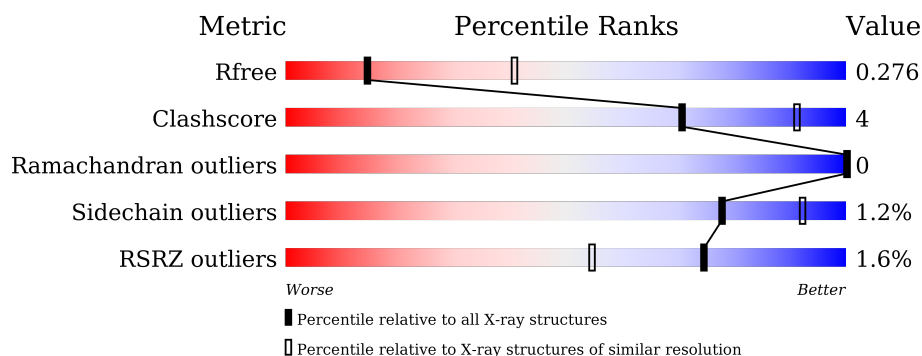
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.10 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))
$R_{free}$	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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>2%</div> <div> <div></div> <div>84%</div> <div>14%</div> <div>.</div> </div> </div>
2	B	428	<div> <div>84%</div> <div>11%</div> <div>5%</div> </div>

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
3	7AX	A	601	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7751 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 HIV-1 REVERSE TRANSCRIPTASE, P66 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	545	Total	C	N	O	S	0	0	0
			4396	2851	728	810	7			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	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

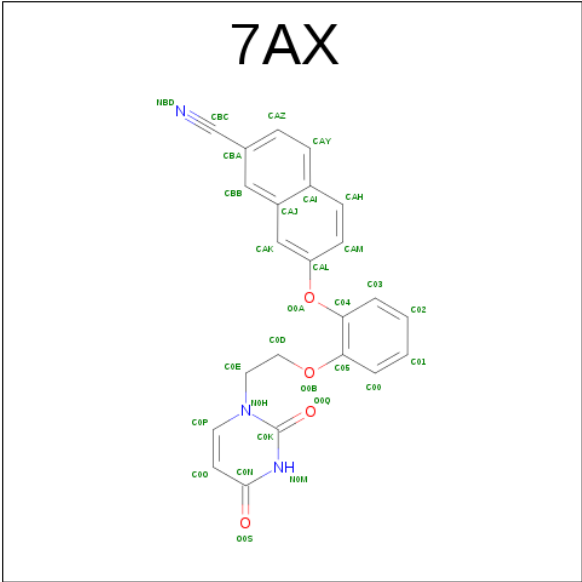
- Molecule 2 is a protein called HIV-1 REVERSE TRANSCRIPTASE, P51 SUBUNIT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	407	Total	C	N	O	S	0	0	0
			3324	2168	544	606	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 7-(2-(2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy)phenoxy)-2-naphtho nitrile (three-letter code: 7AX) (formula: C<sub>23</sub>H<sub>17</sub>N<sub>3</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			30	23	3	4		

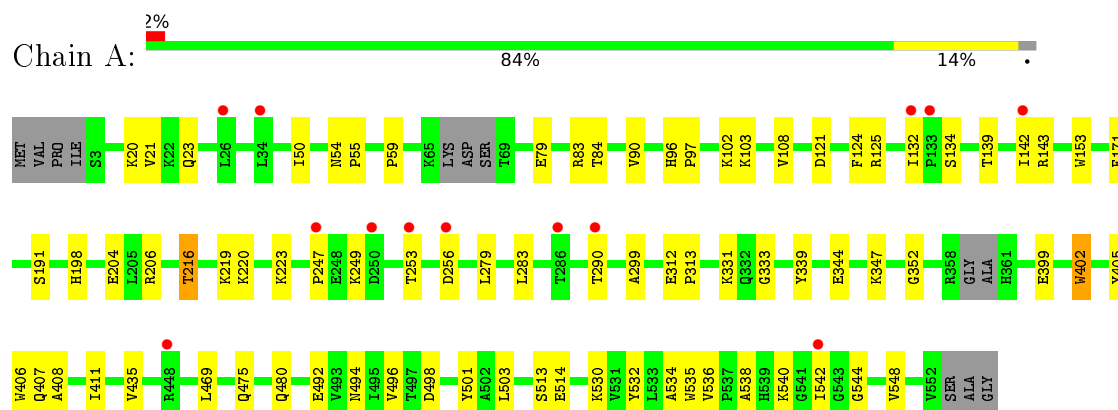
- Molecule 4 is water.

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

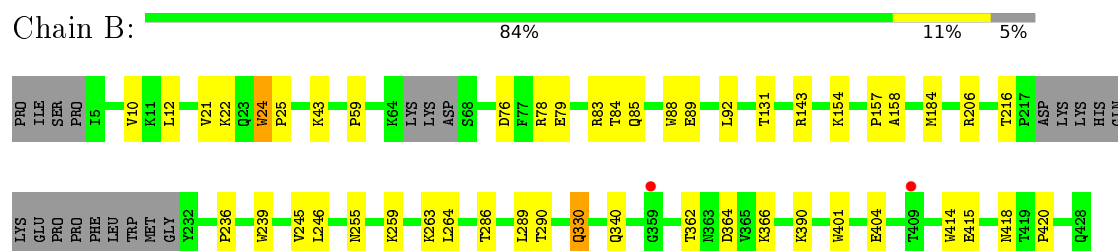
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: HIV-1 REVERSE TRANSCRIPTASE, P66 SUBUNIT



#### • Molecule 2: HIV-1 REVERSE TRANSCRIPTASE, P51 SUBUNIT



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	227.04Å 69.18Å 104.13Å 90.00° 106.62° 90.00°	Depositor
Resolution (Å)	38.22 – 3.10 38.22 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (38.22-3.10) 99.6 (38.22-3.10)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.04 (at 3.12Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.226 , 0.270 0.226 , 0.276	Depositor DCC
$R_{free}$ test set	1420 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	96.5	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 48.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7751	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	96.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.62% 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: 7AX

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	0.22	0/4511	0.40	0/6139
2	B	0.22	0/3419	0.40	0/4655
All	All	0.22	0/7930	0.40	0/10794

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	4396	0	4403	45	0
2	B	3324	0	3322	29	0
3	A	30	0	0	0	0
4	A	1	0	0	0	0
All	All	7751	0	7725	68	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 4.

All (68) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:LYS:HE2	1:A:333:GLY:HA2	1.68	0.76
2:B:85:GLN:HA	2:B:88:TRP:HB2	1.73	0.70
1:A:108:VAL:HG11	1:A:223:LYS:HD2	1.75	0.68
1:A:84:THR:HG21	1:A:153:TRP:HE1	1.59	0.68
1:A:492:GLU:HG2	1:A:530:LYS:HB2	1.77	0.66
1:A:191:SER:OG	1:A:198:HIS:ND1	2.26	0.64
2:B:245:VAL:O	2:B:263:LYS:NZ	2.33	0.59
1:A:23:GLN:OE1	1:A:23:GLN:N	2.36	0.59
2:B:92:LEU:HB3	2:B:158:ALA:HB1	1.86	0.56
1:A:102:LYS:NZ	1:A:103:LYS:O	2.40	0.54
2:B:157:PRO:HG3	2:B:184:MET:HA	1.90	0.53
1:A:84:THR:HG22	1:A:124:PHE:HZ	1.73	0.53
1:A:344:GLU:HB2	1:A:347:LYS:HB2	1.90	0.52
1:A:206:ARG:HH21	1:A:216:THR:HG23	1.75	0.51
2:B:131:THR:OG1	2:B:143:ARG:NH1	2.43	0.51
1:A:498:ASP:HB2	1:A:538:ALA:HB2	1.93	0.50
1:A:513:SER:OG	1:A:514:GLU:N	2.46	0.49
1:A:54:ASN:HB3	1:A:143:ARG:HH11	1.78	0.49
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.48	0.48
1:A:408:ALA:HB1	2:B:364:ASP:HB3	1.94	0.48
2:B:362:THR:HA	2:B:366:LYS:HD3	1.95	0.48
2:B:206:ARG:NH1	2:B:216:THR:OG1	2.46	0.48
2:B:79:GLU:OE2	2:B:83:ARG:NH1	2.47	0.48
1:A:132:ILE:HB	1:A:142:ILE:HB	1.97	0.47
1:A:536:VAL:HB	1:A:542:ILE:HD12	1.96	0.47
2:B:12:LEU:HD23	2:B:84:THR:HG22	1.96	0.47
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.97	0.47
1:A:469:LEU:HD11	1:A:480:GLN:HG2	1.98	0.46
2:B:246:LEU:HD11	2:B:264:LEU:HD21	1.97	0.45
1:A:312:GLU:HA	1:A:313:PRO:HD3	1.86	0.45
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.99	0.45
2:B:85:GLN:HG3	2:B:154:LYS:HB3	1.97	0.45
1:A:406:TRP:CE2	2:B:420:PRO:HB3	2.52	0.45
1:A:219:LYS:HG3	1:A:220:LYS:O	2.17	0.44
2:B:236:PRO:HA	2:B:239:TRP:CD2	2.52	0.44
1:A:20:LYS:HE2	1:A:55:PRO:HB2	1.98	0.44
1:A:532:TYR:CE1	1:A:534:ALA:HB2	2.52	0.44
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.52	0.44
1:A:79:GLU:OE2	1:A:83:ARG:NH1	2.50	0.44
2:B:76:ASP:OD1	2:B:78:ARG:NE	2.51	0.43
2:B:10:VAL:HA	2:B:88:TRP:HZ2	1.83	0.43
1:A:279:LEU:HD23	1:A:299:ALA:HB1	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:330:GLN:OE1	2:B:340:GLN:NE2	2.36	0.43
1:A:247:PRO:HB2	1:A:249:LYS:HE3	2.01	0.43
1:A:544:GLY:HA2	2:B:286:THR:HG22	2.01	0.43
1:A:402:TRP:CE3	1:A:411:ILE:HG13	2.53	0.43
2:B:43:LYS:HE3	2:B:43:LYS:HB2	1.79	0.43
1:A:134:SER:OG	1:A:139:THR:O	2.26	0.43
1:A:171:PHE:HE1	1:A:204:GLU:HG2	1.84	0.43
1:A:399:GLU:HA	1:A:402:TRP:CD2	2.53	0.43
2:B:255:ASN:O	2:B:259:LYS:HG2	2.19	0.43
1:A:435:VAL:HG22	2:B:290:THR:HG21	2.01	0.42
1:A:399:GLU:HA	1:A:402:TRP:CE2	2.55	0.42
2:B:22:LYS:HE3	2:B:24:TRP:CD1	2.54	0.42
1:A:496:VAL:HG21	2:B:289:LEU:HD21	2.02	0.42
2:B:401:TRP:HE3	2:B:404:GLU:HG3	1.85	0.42
1:A:121:ASP:O	1:A:125:ARG:HG3	2.20	0.42
2:B:85:GLN:O	2:B:89:GLU:N	2.52	0.42
1:A:540:LYS:HA	1:A:540:LYS:HD3	1.89	0.41
1:A:54:ASN:O	1:A:143:ARG:NH1	2.54	0.41
2:B:390:LYS:NZ	2:B:415:GLU:OE2	2.50	0.41
1:A:253:THR:HG23	1:A:256:ASP:H	1.85	0.41
2:B:21:VAL:HB	2:B:59:PRO:HD3	2.02	0.41
1:A:96:HIS:HA	1:A:97:PRO:HD3	1.93	0.41
1:A:339:TYR:CZ	1:A:352:GLY:HA3	2.57	0.40
1:A:494:ASN:HB3	2:B:289:LEU:HD12	2.03	0.40
1:A:50:ILE:HG13	1:A:143:ARG:HB3	2.02	0.40
2:B:24:TRP:CE3	2:B:25:PRO:HD2	2.56	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	539/557 (97%)	524 (97%)	15 (3%)	0	100	100
2	B	401/428 (94%)	386 (96%)	15 (4%)	0	100	100
All	All	940/985 (95%)	910 (97%)	30 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	475/495 (96%)	469 (99%)	6 (1%)	76	91
2	B	362/390 (93%)	358 (99%)	4 (1%)	80	93
All	All	837/885 (95%)	827 (99%)	10 (1%)	78	92

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	90	VAL
1	A	216	THR
1	A	283	LEU
1	A	290	THR
1	A	402	TRP
1	A	548	VAL
2	B	24	TRP
2	B	330	GLN
2	B	414	TRP
2	B	418	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA ⓘ

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	7AX	A	601	-	30,33,33	1.59	5 (16%)	38,45,45	2.58	6 (15%)

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	7AX	A	601	-	-	0/12/12/12	0/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	7AX	CAZ-CBA	2.22	1.44	1.39
3	A	601	7AX	C0E-C0D	2.65	1.56	1.51
3	A	601	7AX	O0A-CAL	2.66	1.45	1.39
3	A	601	7AX	CBA-CBC	3.07	1.52	1.44
3	A	601	7AX	C0P-N0H	3.92	1.42	1.36

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	7AX	C0O-C0N-N0M	-3.46	114.78	123.28
3	A	601	7AX	C0D-O0B-C05	2.45	123.45	117.66
3	A	601	7AX	C04-O0A-CAL	2.50	124.50	117.83
3	A	601	7AX	O0B-C0D-C0E	3.46	111.10	107.11
3	A	601	7AX	C0D-C0E-N0H	5.33	118.26	110.94
3	A	601	7AX	C0N-N0M-C0K	13.14	128.05	114.21

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 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, 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	545/557 (97%)	-0.08	13 (2%) 62 39	53, 98, 146, 179	0
2	B	407/428 (95%)	-0.20	2 (0%) 91 83	55, 85, 130, 167	0
All	All	952/985 (96%)	-0.14	15 (1%) 74 55	53, 94, 140, 179	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	133	PRO	5.2
1	A	247	PRO	4.0
2	B	359	GLY	3.2
1	A	253	THR	2.8
1	A	34	LEU	2.7
1	A	448	ARG	2.5
1	A	132	ILE	2.4
1	A	256	ASP	2.2
1	A	142	ILE	2.2
1	A	250	ASP	2.2
1	A	286	THR	2.2
1	A	26	LEU	2.1
1	A	542	ILE	2.1
1	A	290	THR	2.1
2	B	409	THR	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( $\text{\AA}^2$ )	Q<0.9
3	7AX	A	601	30/30	0.92	0.37	3.50	71,87,101,104	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.