



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:50 AM GMT

PDB ID : 3NBP  
Title : HIV-1 reverse transcriptase with aminopyrimidine inhibitor 2  
Authors : Harris, S.F.; Villasenor, A.G.  
Deposited on : 2010-06-03  
Resolution : 2.95 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](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.

---

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
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) : trunk26865

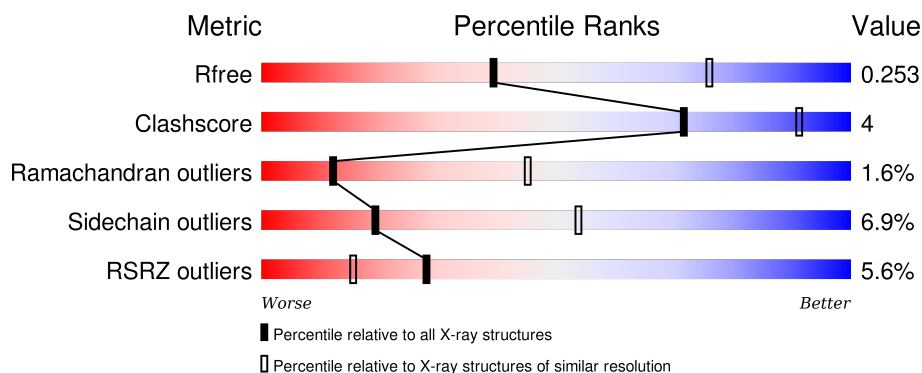
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.95 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))
$R_{free}$	91344	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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	561	<div> <div>4%</div> <div>80%</div> <div>18%</div> <div>..</div> </div>
2	B	440	<div> <div>7%</div> <div>77%</div> <div>13%</div> <div>• 9%</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	MN	A	601	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7939 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	554	Total	C	N	O	S	0	0	0
			4501	2909	751	833	8			

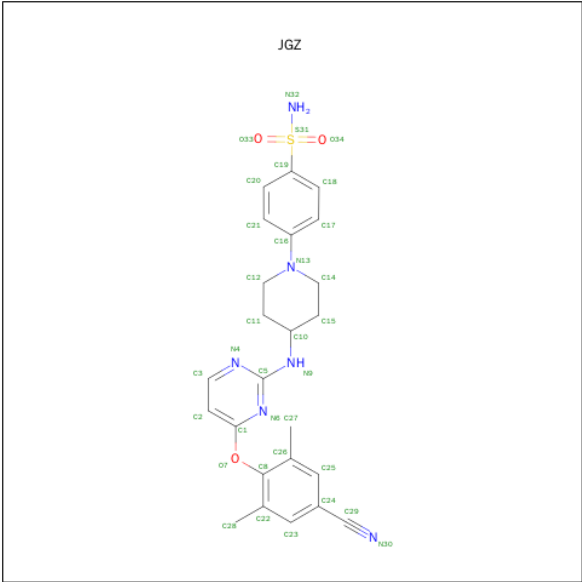
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	400	Total	C	N	O	S	0	0	0
			3311	2160	541	603	7			

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Mn	0	0
			2	2		

- Molecule 4 is 4-(4-{[4-(4-CYANO-2,6-DIMETHYLPHENOXY)PYRIMIDIN-2-YL]AMINO}PIPERIDIN-1-YL)BENZENESULFONAMIDE (three-letter code: JGZ) (formula: C<sub>24</sub>H<sub>26</sub>N<sub>6</sub>O<sub>3</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			34	24	6	3	1		

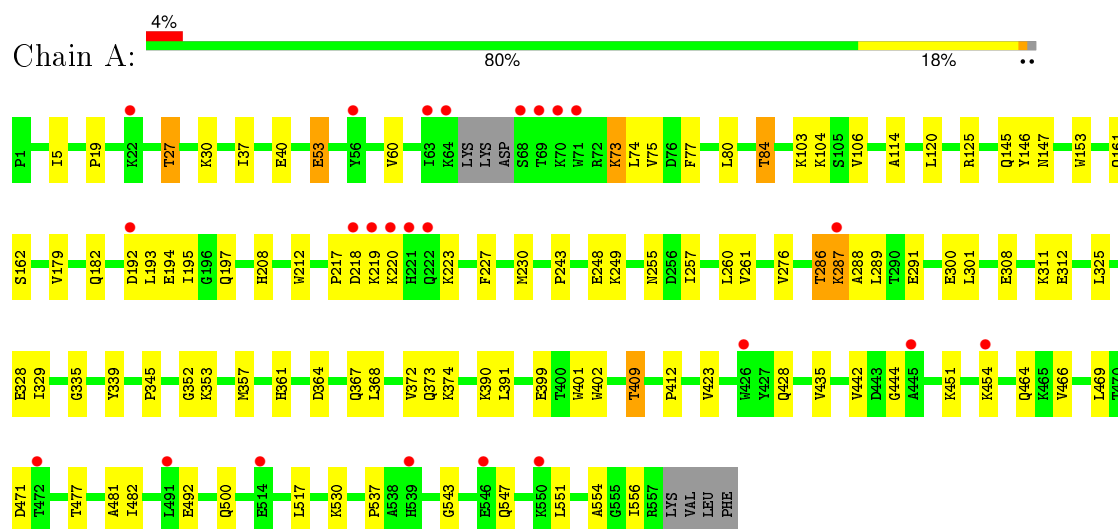
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	46	Total	O	0	0
			46	46		
5	B	45	Total	O	0	0
			45	45		

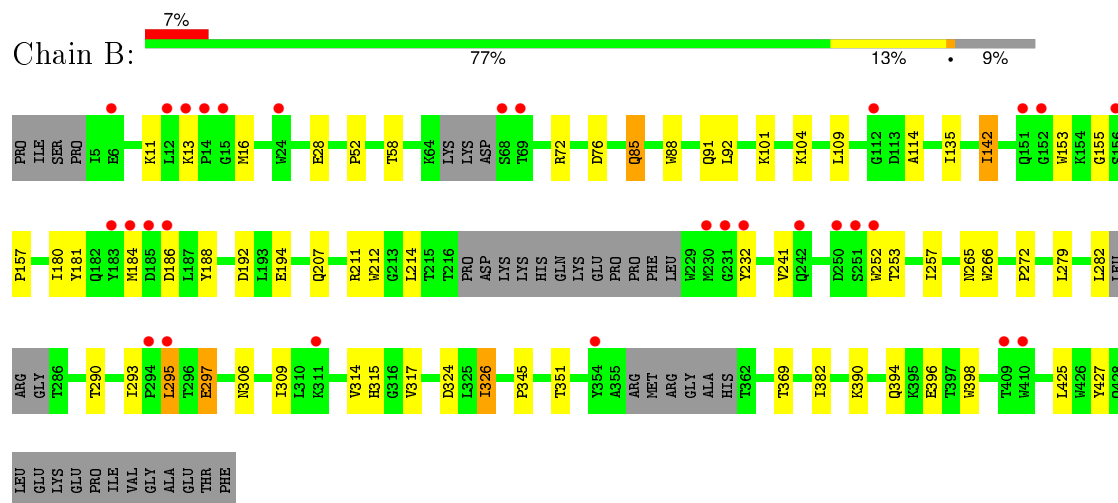
### 3 Residue-property plots [i](#)

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: Reverse transcriptase/ribonuclease H



- Molecule 2: p51 RT



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	118.69Å 152.87Å 154.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.14 – 2.95 29.80 – 2.95	Depositor EDS
% Data completeness (in resolution range)	95.7 (25.14-2.95) 95.8 (29.80-2.95)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.11 (at 2.95Å)	Xtriage
Refinement program	BUSTER 2.9.2	Depositor
R, $R_{free}$	0.194 , 0.244 0.201 , 0.253	Depositor DCC
$R_{free}$ test set	1463 reflections (5.39%)	DCC
Wilson B-factor (Å <sup>2</sup> )	70.6	Xtriage
Anisotropy	0.630	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 64.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 28616 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7939	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: JGZ, MN

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	0/4617	0.71	0/6274
2	B	0.48	0/3404	0.71	0/4627
All	All	0.47	0/8021	0.71	0/10901

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	4501	0	4539	40	0
2	B	3311	0	3327	30	0
3	A	2	0	0	0	0
4	A	34	0	26	0	0
5	A	46	0	0	0	0
5	B	45	0	0	0	0
All	All	7939	0	7892	67	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 (67) 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:84:THR:HG21	1:A:153:TRP:HE1	1.38	0.87
1:A:255:ASN:HB2	1:A:289:LEU:HG	1.77	0.67
2:B:252:TRP:HD1	2:B:295:LEU:HD22	1.62	0.65
1:A:451:LYS:HB3	1:A:471:ASP:HA	1.80	0.63
1:A:162:SER:HB2	2:B:52:PRO:HG3	1.81	0.63
1:A:84:THR:HG21	1:A:153:TRP:NE1	2.11	0.62
1:A:364:ASP:HB3	1:A:423:VAL:HG13	1.79	0.62
2:B:295:LEU:HD23	2:B:295:LEU:H	1.66	0.61
1:A:401:TRP:HD1	1:A:402:TRP:CD1	2.18	0.60
1:A:339:TYR:CZ	1:A:352:GLY:HA3	2.37	0.59
2:B:394:GLN:HE21	2:B:396:GLU:HB2	1.66	0.59
1:A:80:LEU:O	1:A:84:THR:HG22	2.03	0.58
1:A:161:GLN:HE21	1:A:182:GLN:HE21	1.50	0.58
1:A:328:GLU:HG2	1:A:390:LYS:HB2	1.85	0.57
2:B:314:VAL:HB	2:B:317:VAL:HG12	1.87	0.55
1:A:19:PRO:HG3	1:A:80:LEU:HB2	1.90	0.54
2:B:266:TRP:HH2	2:B:427:TYR:CZ	2.25	0.54
1:A:193:LEU:HB3	1:A:197:GLN:HB2	1.90	0.52
1:A:335:GLY:HA2	1:A:367:GLN:HE22	1.75	0.52
1:A:75:VAL:HB	1:A:77:PHE:CE1	2.45	0.52
2:B:157:PRO:HG3	2:B:184:MET:HA	1.93	0.51
1:A:37:ILE:HG21	1:A:73:LYS:HB2	1.92	0.50
2:B:114:ALA:HB2	2:B:214:LEU:HD11	1.94	0.50
1:A:27:THR:HG22	1:A:30:LYS:HG3	1.94	0.50
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.93	0.49
2:B:266:TRP:CH2	2:B:427:TYR:CZ	3.01	0.49
1:A:402:TRP:CZ3	1:A:409:THR:HB	2.48	0.49
2:B:28:GLU:HA	2:B:135:ILE:HD11	1.94	0.48
2:B:241:VAL:HG12	2:B:351:THR:H	1.77	0.48
2:B:101:LYS:HD3	2:B:382:ILE:HG23	1.95	0.47
1:A:466:VAL:HG22	1:A:551:LEU:HD13	1.97	0.47
1:A:442:VAL:HB	1:A:481:ALA:HB1	1.96	0.46
1:A:442:VAL:HG21	1:A:482:ILE:HG13	1.98	0.46
2:B:326:ILE:HD11	2:B:390:LYS:HG3	1.97	0.46
1:A:435:VAL:HA	2:B:290:THR:HG21	1.99	0.45
2:B:207:GLN:O	2:B:211:ARG:HD3	2.15	0.45
2:B:180:ILE:HA	2:B:188:TYR:O	2.15	0.45
2:B:153:TRP:CZ2	2:B:155:GLY:HA3	2.51	0.45
1:A:368:LEU:O	1:A:372:VAL:HG23	2.17	0.44
2:B:58:THR:HG23	2:B:76:ASP:O	2.16	0.44
2:B:306:ASN:HA	2:B:309:ILE:HD12	1.99	0.44

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:HIS:O	1:A:212:TRP:HD1	2.01	0.44
1:A:469:LEU:HD13	1:A:477:THR:HG22	1.99	0.43
1:A:73:LYS:NZ	1:A:146:TYR:OH	2.45	0.43
2:B:253:THR:O	2:B:257:ILE:HD12	2.17	0.43
2:B:314:VAL:HB	2:B:317:VAL:CG1	2.48	0.43
1:A:257:ILE:O	1:A:261:VAL:HG23	2.19	0.43
1:A:492:GLU:HG2	1:A:530:LYS:HB2	2.00	0.43
1:A:53:GLU:HG3	1:A:53:GLU:H	1.54	0.42
1:A:162:SER:CB	2:B:52:PRO:HG3	2.49	0.42
2:B:85:GLN:HA	2:B:88:TRP:CE2	2.53	0.42
1:A:288:ALA:HB3	1:A:291:GLU:HB2	2.02	0.42
2:B:211:ARG:O	2:B:212:TRP:HB2	2.18	0.42
2:B:272:PRO:HG2	2:B:315:HIS:HB3	2.00	0.42
2:B:104:LYS:HB2	2:B:192:ASP:HA	2.02	0.42
1:A:401:TRP:CD1	1:A:402:TRP:CD1	3.03	0.41
2:B:297:GLU:H	2:B:297:GLU:HG3	1.63	0.41
1:A:194:GLU:H	1:A:197:GLN:NE2	2.18	0.41
1:A:27:THR:HG22	1:A:30:LYS:H	1.85	0.41
2:B:369:THR:HG22	2:B:398:TRP:CH2	2.55	0.41
1:A:104:LYS:HB2	1:A:192:ASP:HA	2.02	0.41
2:B:181:TYR:HB3	2:B:188:TYR:HB2	2.02	0.41
1:A:223:LYS:HE3	1:A:227:PHE:HA	2.03	0.41
2:B:142:ILE:HG13	2:B:142:ILE:H	1.67	0.41
1:A:329:ILE:HD12	1:A:391:LEU:CD2	2.51	0.40
1:A:120:LEU:HD23	1:A:125:ARG:HG2	2.02	0.40
1:A:311:LYS:HG3	1:A:312:GLU:HG2	2.03	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	550/561 (98%)	508 (92%)	30 (6%)	12 (2%)	8	35
2	B	390/440 (89%)	361 (93%)	26 (7%)	3 (1%)	24	64
All	All	940/1001 (94%)	869 (92%)	56 (6%)	15 (2%)	12	45

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	85	GLN
1	A	195	ILE
1	A	217	PRO
1	A	286	THR
1	A	287	LYS
1	A	543	GLY
1	A	243	PRO
1	A	554	ALA
1	A	114	ALA
1	A	412	PRO
2	B	13	LYS
1	A	345	PRO
1	A	556	ILE
2	B	345	PRO
1	A	444	GLY

### 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	492/501 (98%)	452 (92%)	40 (8%)	15	44
2	B	365/400 (91%)	346 (95%)	19 (5%)	29	66
All	All	857/901 (95%)	798 (93%)	59 (7%)	19	54

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ILE

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	27	THR
1	A	40	GLU
1	A	53	GLU
1	A	60	VAL
1	A	73	LYS
1	A	74	LEU
1	A	84	THR
1	A	103	LYS
1	A	106	VAL
1	A	145	GLN
1	A	179	VAL
1	A	218	ASP
1	A	219	LYS
1	A	220	LYS
1	A	230	MET
1	A	248	GLU
1	A	249	LYS
1	A	260	LEU
1	A	276	VAL
1	A	286	THR
1	A	287	LYS
1	A	300	GLU
1	A	301	LEU
1	A	308	GLU
1	A	325	LEU
1	A	353	LYS
1	A	357	MET
1	A	361	HIS
1	A	373	GLN
1	A	374	LYS
1	A	399	GLU
1	A	409	THR
1	A	428	GLN
1	A	454	LYS
1	A	464	GLN
1	A	500	GLN
1	A	517	LEU
1	A	537	PRO
1	A	547	GLN
2	B	11	LYS
2	B	16	MET
2	B	72	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	B	91	GLN
2	B	92	LEU
2	B	109	LEU
2	B	142	ILE
2	B	186	ASP
2	B	194	GLU
2	B	232	TYR
2	B	265	ASN
2	B	279	LEU
2	B	282	LEU
2	B	293	ILE
2	B	295	LEU
2	B	297	GLU
2	B	324	ASP
2	B	326	ILE
2	B	425	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	161	GLN
1	A	175	ASN
1	A	197	GLN
1	A	198	HIS
1	A	336	GLN
1	A	509	GLN
2	B	151	GLN
2	B	182	GLN
2	B	394	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 [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
4	JGZ	A	562	-	37,37,37	1.25	3 (8%)	53,53,53	2.59	16 (30%)

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
4	JGZ	A	562	-	-	0/20/30/30	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	562	JGZ	C1-N6	2.26	1.37	1.33
4	A	562	JGZ	S31-N32	2.71	1.66	1.60
4	A	562	JGZ	C5-N9	4.01	1.39	1.34

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	562	JGZ	N4-C5-N6	-9.24	116.82	126.67
4	A	562	JGZ	C15-C10-N9	-6.06	100.22	110.55
4	A	562	JGZ	C5-N9-C10	-3.70	119.39	123.51
4	A	562	JGZ	C14-N13-C16	-3.30	109.06	117.92
4	A	562	JGZ	O34-S31-N32	-2.23	104.39	107.28
4	A	562	JGZ	C17-C16-N13	-2.12	118.54	121.38

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	562	JGZ	C2-C1-N6	-2.06	117.83	123.12
4	A	562	JGZ	C26-C8-C22	-2.06	117.72	122.12
4	A	562	JGZ	N9-C5-N6	2.36	120.40	116.95
4	A	562	JGZ	O33-S31-N32	2.43	110.42	107.28
4	A	562	JGZ	C25-C26-C8	2.44	121.41	117.78
4	A	562	JGZ	O7-C1-C2	2.59	120.80	115.61
4	A	562	JGZ	O34-S31-O33	2.66	122.54	118.80
4	A	562	JGZ	N9-C5-N4	4.10	122.78	116.95
4	A	562	JGZ	C3-N4-C5	6.17	120.85	115.49
4	A	562	JGZ	C5-N6-C1	8.15	126.05	114.96

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

### 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	554/561 (98%)	0.13	24 (4%) 39 23	50, 77, 111, 138	0
2	B	400/440 (90%)	0.27	29 (7%) 18 9	45, 76, 114, 133	0
All	All	954/1001 (95%)	0.19	53 (5%) 28 15	45, 77, 112, 138	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	232	TYR	6.0
1	A	222	GLN	5.9
2	B	12	LEU	5.1
1	A	70	LYS	4.6
1	A	220	LYS	4.3
2	B	14	PRO	4.2
2	B	231	GLY	3.9
2	B	13	LYS	3.7
2	B	409	THR	3.6
1	A	491	LEU	3.6
1	A	539	HIS	3.5
2	B	69	THR	3.4
1	A	71	TRP	3.2
1	A	69	THR	3.2
1	A	221	HIS	3.1
2	B	6	GLU	3.1
2	B	15	GLY	3.1
2	B	230	MET	3.0
1	A	514	GLU	3.0
2	B	242	GLN	3.0
1	A	218	ASP	2.9
2	B	152	GLY	2.9
1	A	445	ALA	2.9
2	B	24	TRP	2.9

*Continued on next page...*



*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
2	B	295	LEU	2.9
2	B	184	MET	2.8
1	A	426	TRP	2.8
1	A	546	GLU	2.7
2	B	68	SER	2.7
1	A	550	LYS	2.6
1	A	192	ASP	2.6
2	B	251	SER	2.6
1	A	219	LYS	2.6
2	B	250	ASP	2.6
2	B	151	GLN	2.5
1	A	63	ILE	2.5
2	B	156	SER	2.4
2	B	186	ASP	2.3
2	B	294	PRO	2.3
2	B	311	LYS	2.3
2	B	354	TYR	2.2
1	A	22	LYS	2.2
2	B	185	ASP	2.2
2	B	112	GLY	2.2
2	B	183	TYR	2.2
1	A	56	TYR	2.2
1	A	68	SER	2.1
2	B	252	TRP	2.1
1	A	287	LYS	2.1
1	A	454	LYS	2.1
1	A	64	LYS	2.1
2	B	410	TRP	2.0
1	A	472	THR	2.0

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

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

## 6.3 Carbohydrates ⓘ

There are no 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	MN	A	601	1/1	0.92	0.31	2.30	239,239,239,239	0
4	JGZ	A	562	34/34	0.94	0.20	0.13	60,67,93,94	0
3	MN	A	602	1/1	0.81	0.17	-	157,157,157,157	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.