



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 26, 2017 – 09:50 AM EDT

PDB ID : 1GJ8  
Title : ENGINEERING INHIBITORS HIGHLY SELECTIVE FOR THE S1 SITES  
OF SER190 TRYPSIN-LIKE SERINE PROTEASE DRUG TARGETS  
Authors : Katz, B.A.; Sprengeler, P.A.; Luong, C.; Verner, E.; Spencer, J.R.; Breiten-  
bucher, J.G.; Hui, H.; McGee, D.; Allen, D.; Martelli, A.; Mackman, R.L.  
Deposited on : unknown  
Resolution : 1.64 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

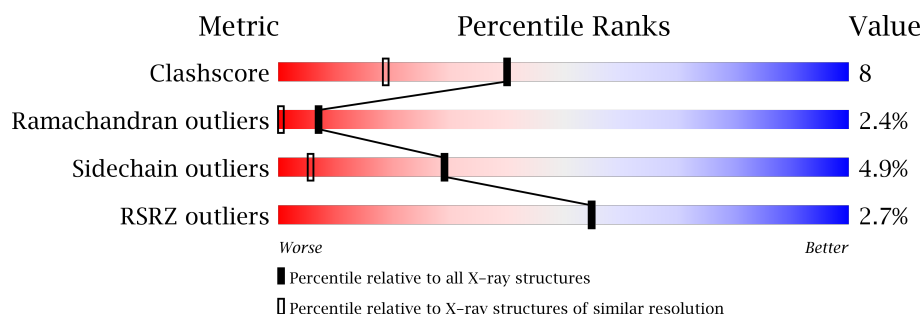
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.64 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))
Clashscore	112137	2356 (1.66-1.62)
Ramachandran outliers	110173	2315 (1.66-1.62)
Sidechain outliers	110143	2315 (1.66-1.62)
RSRZ outliers	101464	2219 (1.66-1.62)

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	23	<div> <div>13%</div> <div>30%</div> <div>22%</div> <div>.</div> <div>43%</div> </div>
2	B	253	<div> <div>2%</div> <div>76%</div> <div>15%</div> <div>5%</div> <div>..</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	CIT	B	2	-	-	-	X

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 4848 atoms, of which 2508 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 UROKINASE-TYPE PLASMINOGEN ACTIVATOR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	13	206	66	102	17	20	1	0	0	0

- Molecule 2 is a protein called UROKINASE-TYPE PLASMINOGEN ACTIVATOR.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
2	B	245	3881	1236	1923	337	366	19	0	7	0

There is a discrepancy between the modelled and reference sequences:

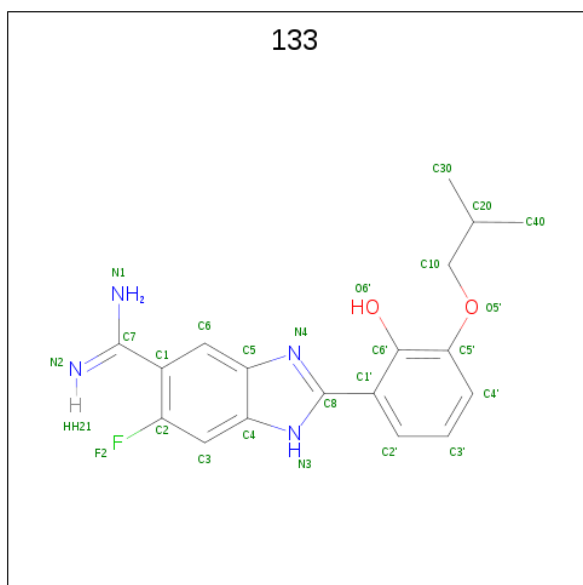
Chain	Residue	Modelled	Actual	Comment	Reference
B	145	ALA	ASN	CONFLICT	UNP P00749

- Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula: C<sub>6</sub>H<sub>8</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	H	O	0	0
			18	6	5	7		
3	B	1	Total	C	H	O	0	0
			18	6	5	7		

- Molecule 4 is 6-FLUORO-2-(2-HYDROXY-3-ISOBUTOXY-PHENYL)-1H-BENZOIMIDAZOLE-5-CARBOXAMIDINE (three-letter code: 133) (formula: C<sub>18</sub>H<sub>19</sub>FN<sub>4</sub>O<sub>2</sub>).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	B	1	Total	C	F	H	N	O	0	0
			44	18	1	19	4	2		

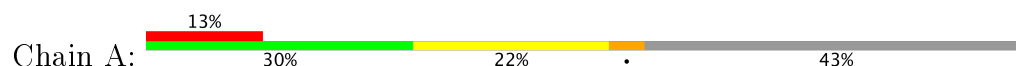
- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	8	Total	H	O	0	0
			24	16	8		
5	B	219	Total	H	O	0	0
			657	438	219		

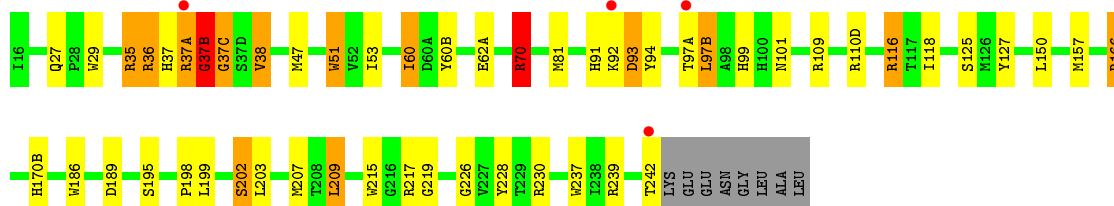
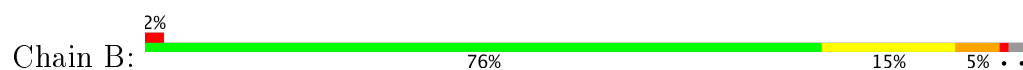
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: UROKINASE-TYPE PLASMINOGEN ACTIVATOR



#### • Molecule 2: UROKINASE-TYPE PLASMINOGEN ACTIVATOR



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.77Å 50.02Å 66.94Å 90.00° 113.76° 90.00°	Depositor
Resolution (Å)	7.00 – 1.64 25.01 – 1.36	Depositor EDS
% Data completeness (in resolution range)	69.3 (7.00-1.64) 45.8 (25.01-1.36)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.37 (at 1.36Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, $R_{free}$	0.188 , 0.221 0.194 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	11.5	Xtriage
Anisotropy	0.277	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.28 , 40.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.030 for 1/2*h+3/2*k,1/2*h-1/2*k,-1/2*h-1/2*k-l 0.007 for 1/2*h-3/2*k,-1/2*h-1/2*k,-1/2*h+1/2*k-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	4848	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.54% 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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 133, CIT

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	1.67	1/106 (0.9%)	1.80	3/140 (2.1%)
2	B	1.43	4/2035 (0.2%)	1.54	36/2755 (1.3%)
All	All	1.44	5/2141 (0.2%)	1.56	39/2895 (1.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	37(C)	GLY	N-CA	15.31	1.69	1.46
2	B	37(C)	GLY	CA-C	12.79	1.72	1.51
2	B	37(B)	GLY	CA-C	8.12	1.64	1.51
1	A	9	LEU	CA-CB	6.52	1.68	1.53
2	B	51	TRP	CG-CD2	-5.72	1.33	1.43

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	237	TRP	CD1-NE1-CE2	11.07	118.97	109.00
2	B	215	TRP	CD1-NE1-CE2	9.46	117.51	109.00
2	B	186	TRP	CD1-NE1-CE2	9.31	117.38	109.00
2	B	29	TRP	CD1-NE1-CE2	9.22	117.30	109.00
1	A	9	LEU	CB-CA-C	-8.79	93.51	110.20
2	B	51	TRP	CD1-NE1-CE2	8.64	116.78	109.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	237	TRP	NE1-CE2-CZ2	8.09	139.30	130.40
2	B	51	TRP	NE1-CE2-CZ2	7.91	139.10	130.40
2	B	35	ARG	NE-CZ-NH2	-7.82	116.39	120.30
2	B	29	TRP	NE1-CE2-CZ2	7.69	138.86	130.40
2	B	37	HIS	N-CA-C	-7.57	90.57	111.00
2	B	237	TRP	CG-CD1-NE1	-7.43	102.67	110.10
2	B	186	TRP	NE1-CE2-CZ2	7.33	138.46	130.40
2	B	36	ARG	NE-CZ-NH2	-7.24	116.68	120.30
2	B	215	TRP	CG-CD1-NE1	-7.14	102.96	110.10
2	B	237	TRP	NE1-CE2-CD2	-7.09	100.21	107.30
2	B	110(D)	ARG	NE-CZ-NH2	-6.95	116.83	120.30
2	B	51	TRP	CG-CD1-NE1	-6.87	103.23	110.10
2	B	29	TRP	CG-CD1-NE1	-6.85	103.25	110.10
2	B	199	LEU	N-CA-C	-6.84	92.53	111.00
2	B	186	TRP	CG-CD1-NE1	-6.82	103.28	110.10
2	B	166	ARG	NE-CZ-NH2	-6.66	116.97	120.30
2	B	109	ARG	NE-CZ-NH2	-6.60	117.00	120.30
2	B	215	TRP	NE1-CE2-CZ2	6.54	137.59	130.40
1	A	11	PHE	N-CA-CB	6.19	121.74	110.60
2	B	38	VAL	N-CA-C	-6.17	94.36	111.00
2	B	186	TRP	NE1-CE2-CD2	-6.15	101.15	107.30
2	B	207	MET	N-CA-C	-6.15	94.39	111.00
2	B	29	TRP	NE1-CE2-CD2	-6.10	101.20	107.30
2	B	51	TRP	NE1-CE2-CD2	-6.05	101.25	107.30
2	B	215	TRP	NE1-CE2-CD2	-5.89	101.41	107.30
2	B	226	GLY	N-CA-C	-5.72	98.81	113.10
2	B	239	ARG	NE-CZ-NH2	-5.63	117.48	120.30
2	B	70	ARG	NE-CZ-NH2	-5.46	117.57	120.30
2	B	37(A)	ARG	NE-CZ-NH2	-5.37	117.61	120.30
2	B	116	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	A	9	LEU	C-N-CA	-5.23	108.63	121.70
2	B	217	ARG	NE-CZ-NH2	-5.09	117.75	120.30
2	B	189	ASP	CB-CG-OD2	-5.02	113.78	118.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	230	ARG	Sidechain
2	B	36	ARG	Sidechain
2	B	70	ARG	Sidechain



## 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	104	102	102	2	0
2	B	1958	1923	1898	27	2
3	B	26	10	10	4	0
4	B	25	19	18	3	0
5	A	8	16	0	0	0
5	B	219	438	0	3	5
All	All	2340	2508	2028	34	5

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 8.

All (34) 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:37(C):GLY:CA	2:B:37(C):GLY:N	1.69	1.52
2:B:37(A):ARG:C	2:B:37(C):GLY:H	1.81	0.83
2:B:37(B):GLY:C	2:B:37(C):GLY:CA	2.54	0.76
2:B:92:LYS:HG2	5:B:469:HOH:O	1.89	0.72
2:B:70:ARG:HG2	5:B:445:HOH:O	1.89	0.71
2:B:37(A):ARG:C	2:B:37(C):GLY:N	2.44	0.69
2:B:195:SER:HG	4:B:251:133:HN3	1.44	0.66
2:B:195:SER:OG	5:B:347:HOH:O	2.15	0.64
3:B:1:CIT:O7	3:B:2:CIT:O7	2.16	0.62
3:B:1:CIT:HO7	3:B:2:CIT:HO7	1.45	0.61
2:B:37(A):ARG:O	2:B:37(C):GLY:N	2.35	0.60
2:B:51:TRP:CD1	2:B:242:THR:HG23	2.42	0.55
2:B:91:HIS:CD2	2:B:101:ASN:HB3	2.42	0.55
2:B:92:LYS:O	2:B:93:ASP:HB2	2.11	0.51
2:B:97(A):THR:O	2:B:97(B):LEU:HB2	2.10	0.51
2:B:92:LYS:O	2:B:93:ASP:CB	2.60	0.50
2:B:94:TYR:HH	2:B:99:HIS:HD1	1.59	0.50
2:B:170(B):HIS:H	2:B:170(B):HIS:CD2	2.29	0.50
2:B:47[B]:MET:SD	2:B:53:ILE:HB	2.54	0.48
1:A:8:GLU:H	1:A:8:GLU:CD	2.18	0.46
3:B:1:CIT:O6	3:B:2:CIT:O7	2.33	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:35:ARG:O	2:B:38:VAL:HA	2.17	0.44
2:B:228:TYR:N	2:B:228:TYR:CD1	2.84	0.44
2:B:198:PRO:HB3	2:B:209[B]:LEU:CD1	2.48	0.43
2:B:219:GLY:O	4:B:251:133:N1	2.51	0.43
4:B:251:133:O6'	4:B:251:133:N3	2.51	0.43
2:B:35:ARG:HD2	2:B:60(B):TYR:CD1	2.53	0.43
3:B:1:CIT:C5	3:B:2:CIT:O6	2.67	0.42
2:B:27:GLN:HG2	2:B:157:MET:CE	2.49	0.42
1:A:8:GLU:C	1:A:10:LYS:H	2.22	0.42
2:B:97(A):THR:O	2:B:97(B):LEU:CB	2.68	0.41
2:B:81[A]:MET:CE	2:B:118:ILE:HD12	2.51	0.40

All (5) 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)
5:B:314:HOH:H1	5:B:408:HOH:H2[4_546]	1.28	0.32
5:B:314:HOH:H2	5:B:408:HOH:H2[4_546]	1.34	0.26
5:B:371:HOH:O	5:B:373:HOH:H1[2_656]	1.53	0.07
2:B:202:SER:OG	5:B:470:HOH:H1[1_545]	1.59	0.01
2:B:37(C):GLY:O	5:B:433:HOH:H2[3_555]	1.59	0.01

## 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	11/23 (48%)	9 (82%)	1 (9%)	1 (9%)	1	0
2	B	250/253 (99%)	233 (93%)	12 (5%)	5 (2%)	9	0
All	All	261/276 (95%)	242 (93%)	13 (5%)	6 (2%)	7	0

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	97(B)	LEU
2	B	37(B)	GLY
2	B	60	ILE
2	B	93	ASP
1	A	9	LEU
2	B	127	TYR

### 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	12/22 (54%)	10 (83%)	2 (17%)	2	0
2	B	220/219 (100%)	210 (96%)	10 (4%)	32	7
All	All	232/241 (96%)	220 (95%)	12 (5%)	29	5

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	GLU
1	A	15	GLN
2	B	60	ILE
2	B	70	ARG
2	B	116	ARG
2	B	125	SER
2	B	150	LEU
2	B	166	ARG
2	B	202	SER
2	B	203	LEU
2	B	209[A]	LEU
2	B	209[B]	LEU

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

Mol	Chain	Res	Type
2	B	91	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

3 ligands are 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	CIT	B	1	-	3,12,12	3.32	1 (33%)	3,17,17	1.99	1 (33%)
3	CIT	B	2	-	3,12,12	3.92	2 (66%)	3,17,17	1.12	0
4	133	B	251	-	26,27,27	1.96	7 (26%)	31,39,39	1.73	9 (29%)

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	CIT	B	1	-	-	0/6/16/16	0/0/0/0
3	CIT	B	2	-	-	0/6/16/16	0/0/0/0
4	133	B	251	-	-	0/9/13/13	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	251	133	C1'-C8	-4.00	1.38	1.48
4	B	251	133	C1-C7	-3.46	1.40	1.47
4	B	251	133	C6-C5	-3.36	1.36	1.41
4	B	251	133	C5-N4	-2.35	1.31	1.39
4	B	251	133	C6-C1	3.04	1.41	1.37
3	B	2	CIT	C4-C3	3.38	1.59	1.54
4	B	251	133	C1-C2	3.65	1.44	1.38
4	B	251	133	C3-C2	3.68	1.41	1.35
3	B	1	CIT	C2-C3	5.40	1.62	1.54
3	B	2	CIT	C2-C3	5.87	1.63	1.54

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	251	133	C2-C3-C4	-4.40	114.72	119.19
4	B	251	133	F2-C2-C3	-3.52	115.40	120.31
4	B	251	133	C8-N4-C5	-2.98	98.18	103.89
4	B	251	133	C6-C5-N4	-2.72	122.88	130.75
4	B	251	133	C8-N3-C4	-2.43	104.43	107.84
4	B	251	133	C10-O5'-C5'	-2.33	113.38	118.04
4	B	251	133	C6-C5-C4	2.37	123.52	121.12
4	B	251	133	C4-C5-N4	2.60	113.55	108.08
4	B	251	133	C3-C4-C5	2.95	123.34	120.55
3	B	1	CIT	C3-C2-C1	3.31	120.13	114.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1	CIT	4	0
3	B	2	CIT	4	0
4	B	251	133	3	0

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	13/23 (56%)	1.86	3 (23%) <b>1</b> <b>1</b>	19, 37, 45, 46	5 (38%)
2	B	245/253 (96%)	-0.13	4 (1%) 72 74	9, 18, 36, 53	23 (9%)
All	All	258/276 (93%)	-0.03	7 (2%) 55 55	9, 19, 38, 53	28 (10%)

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	5	PRO	11.3
2	B	37(A)	ARG	10.5
1	A	17	THR	7.8
2	B	97(A)	THR	4.3
2	B	242	THR	3.0
2	B	92	LYS	2.7
1	A	6	PRO	2.3

### 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	CIT	B	2	13/13	0.82	0.17	3.27	38,47,58,61	0
3	CIT	B	1	13/13	0.94	0.08	0.03	15,22,29,29	0
4	133	B	251	25/25	0.95	0.07	-0.55	14,20,30,30	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.