



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2018 – 09:02 pm GMT

PDB ID : 4I2P
Title : Crystal structure of HIV-1 reverse transcriptase in complex with rilpivirine (TMC278) based analogue
Authors : Patel, D.; Bauman, J.D.; Das, K.; Arnold, E.
Deposited on : 2012-11-22
Resolution : 2.30 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 ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : trunk30967
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk30967

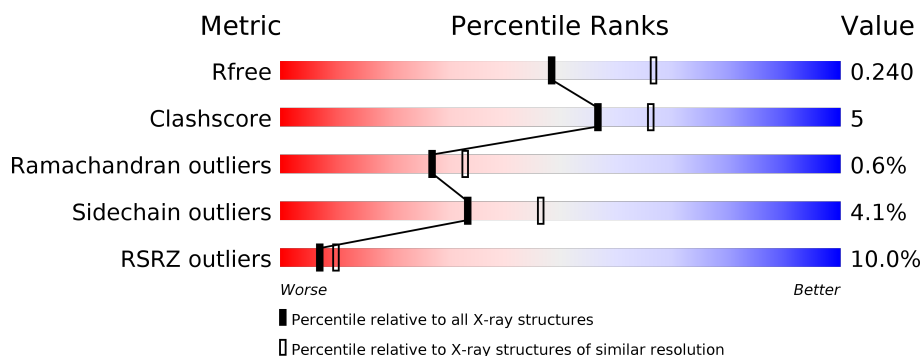
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

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 ≥ 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>7%</div> <div>84%</div> <div>14%</div> <div>..</div> </div>
2	B	428	<div> <div>13%</div> <div>81%</div> <div>15%</div> <div>..</div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8249 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 Gag-Pol polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	554	Total	C	N	O	S	0	0	0
			4505	2917	748	832	8			

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

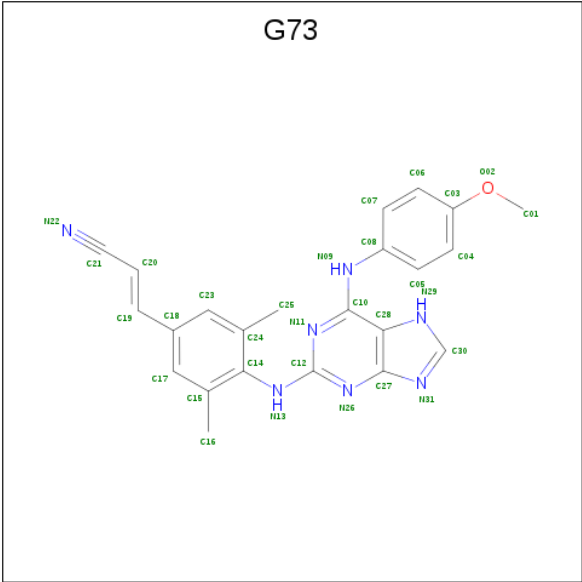
- Molecule 2 is a protein called Gag-Pol polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	412	Total	C	N	O	S	0	0	0
			3413	2225	564	617	7			

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-[4-({6-[(4-methoxyphenyl)amino]-7H-purin-2-yl}amino)-3,5-dimethylphenyl]prop-2-enenitrile (three-letter code: G73) (formula: C₂₃H₂₁N₇O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			31	23	7	1		

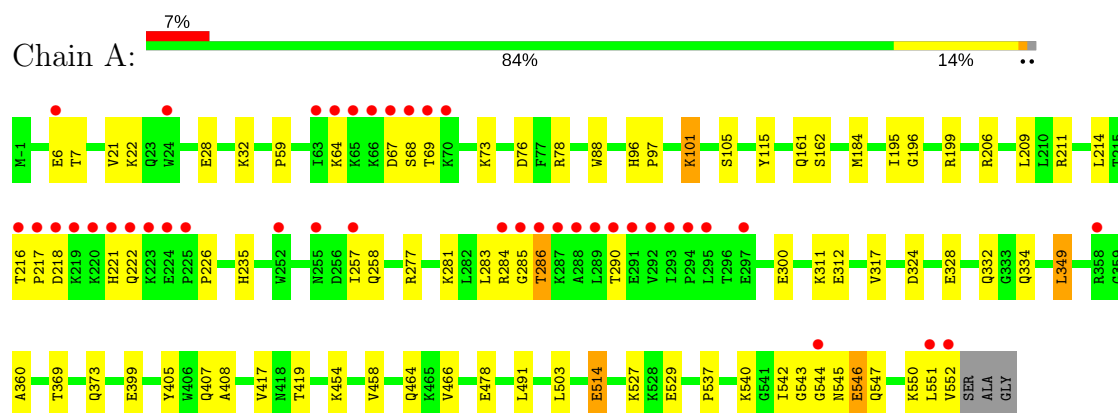
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	178	Total	O	0	0
			178	178		
4	B	122	Total	O	0	0
			122	122		

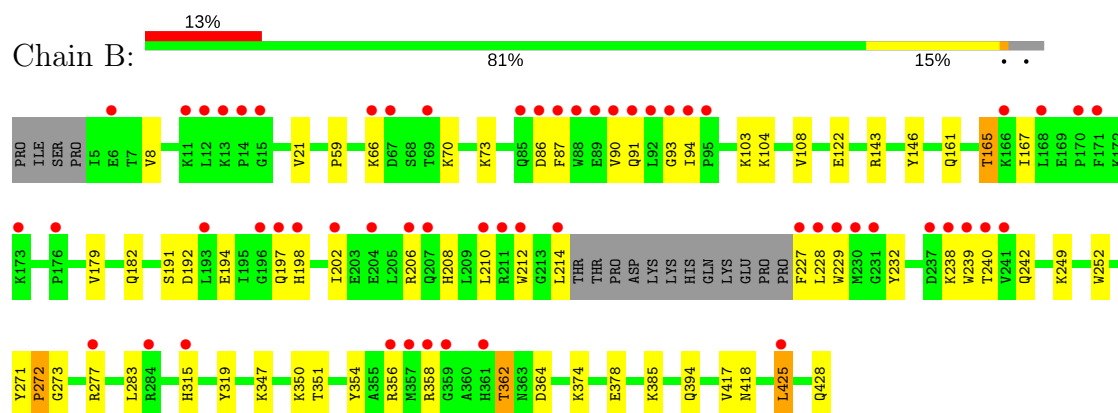
3 Residue-property plots

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: Gag-Pol polyprotein



• Molecule 2: Gag-Pol polyprotein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.65Å 72.99Å 109.60Å 90.00° 100.59° 90.00°	Depositor
Resolution (Å)	41.29 – 2.30 41.29 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.8 (41.29-2.30) 98.8 (41.29-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.29Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, R_{free}	0.216 , 0.260 0.205 , 0.240	Depositor DCC
R_{free} test set	897 reflections (1.60%)	wwPDB-VP
Wilson B-factor (Å ²)	36.0	Xtriage
Anisotropy	0.117	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	8249	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: G73

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	0.27	0/4623	0.45	0/6284
2	B	0.26	0/3511	0.45	0/4768
All	All	0.27	0/8134	0.45	0/11052

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	4505	0	4562	46	0
2	B	3413	0	3443	44	0
3	A	31	0	21	3	0
4	A	178	0	0	7	0
4	B	122	0	0	10	0
All	All	8249	0	8026	86	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 (86) 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:182:GLN:O	4:B:617:HOH:O	1.91	0.89
1:A:101:LYS:HE2	3:A:601:G73:H23	1.59	0.82
2:B:347:LYS:O	4:B:525:HOH:O	1.98	0.81
1:A:328:GLU:OE2	4:A:864:HOH:O	2.01	0.79
2:B:428:GLN:OXT	4:B:557:HOH:O	2.06	0.71
2:B:358:ARG:HH12	2:B:374:LYS:HD2	1.56	0.69
2:B:91:GLN:HG3	2:B:93:GLY:H	1.58	0.68
1:A:332:GLN:OE1	4:A:833:HOH:O	2.11	0.67
2:B:206:ARG:NH1	2:B:229:TRP:O	2.29	0.66
2:B:425:LEU:O	4:B:557:HOH:O	2.14	0.65
2:B:194:GLU:HB3	2:B:197:GLN:HG2	1.80	0.64
2:B:143:ARG:HD3	4:B:527:HOH:O	1.99	0.63
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.32	0.62
2:B:202:ILE:HG22	2:B:206:ARG:HE	1.64	0.62
1:A:216:THR:O	1:A:218:ASP:N	2.32	0.61
2:B:239:TRP:O	4:B:520:HOH:O	2.17	0.60
2:B:108:VAL:HB	2:B:232:TYR:HB3	1.83	0.59
1:A:311:LYS:HE3	1:A:312:GLU:HG2	1.85	0.59
1:A:527:LYS:NZ	4:A:808:HOH:O	2.36	0.59
2:B:240:THR:O	2:B:350:LYS:NZ	2.31	0.58
1:A:257:ILE:HB	1:A:283:LEU:HD21	1.86	0.58
1:A:6:GLU:CD	1:A:6:GLU:H	2.07	0.57
1:A:360:ALA:HA	1:A:514:GLU:HG3	1.86	0.57
1:A:218:ASP:OD1	4:A:843:HOH:O	2.18	0.56
1:A:206:ARG:HE	1:A:216:THR:HG1	1.54	0.55
3:A:601:G73:N11	3:A:601:G73:H5	2.22	0.55
1:A:206:ARG:CZ	1:A:218:ASP:HB2	2.37	0.54
1:A:88:TRP:CD1	2:B:143:ARG:HD2	2.43	0.54
1:A:101:LYS:H	3:A:601:G73:H22	1.55	0.54
1:A:88:TRP:NE1	2:B:143:ARG:HD2	2.22	0.54
2:B:425:LEU:HD13	2:B:428:GLN:HB3	1.90	0.54
2:B:103:LYS:HE3	2:B:179:VAL:HG23	1.91	0.53
2:B:161:GLN:O	2:B:165:THR:OG1	2.26	0.53
2:B:273:GLY:N	4:B:543:HOH:O	2.36	0.51
1:A:478:GLU:HG2	4:A:853:HOH:O	2.08	0.51
2:B:122:GLU:O	4:B:512:HOH:O	2.19	0.51
1:A:454:LYS:NZ	1:A:552:VAL:HB	2.26	0.51
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.47	0.50
2:B:198:HIS:O	2:B:202:ILE:HG12	2.11	0.50
1:A:277:ARG:HD2	1:A:334:GLN:HB3	1.93	0.50
1:A:28:GLU:HG2	1:A:32:LYS:HE3	1.93	0.50
1:A:491:LEU:HB3	1:A:529:GLU:HG2	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:ASP:OD1	1:A:78:ARG:HG3	2.12	0.49
2:B:70:LYS:O	4:B:536:HOH:O	2.20	0.49
2:B:208:HIS:O	2:B:212:TRP:HD1	1.95	0.49
1:A:258:GLN:HG2	1:A:283:LEU:HD13	1.93	0.49
1:A:543:GLY:N	2:B:283:LEU:O	2.46	0.48
1:A:317:VAL:HG23	1:A:349:LEU:HD12	1.94	0.48
1:A:458:VAL:HG12	1:A:464:GLN:HG2	1.94	0.48
2:B:239:TRP:N	4:B:520:HOH:O	2.46	0.48
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.95	0.48
1:A:544:GLY:O	1:A:546:GLU:N	2.48	0.47
1:A:369:THR:O	1:A:373:GLN:HG2	2.14	0.47
1:A:115:TYR:O	4:A:803:HOH:O	2.20	0.47
1:A:466:VAL:HG22	1:A:550:LYS:NZ	2.29	0.47
1:A:408:ALA:HB1	2:B:364:ASP:HB3	1.99	0.45
2:B:191:SER:HG	2:B:198:HIS:HD1	1.44	0.45
1:A:546:GLU:HA	4:A:750:HOH:O	2.17	0.45
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.99	0.45
1:A:547:GLN:O	1:A:551:LEU:N	2.47	0.44
2:B:191:SER:HG	2:B:198:HIS:CE1	2.35	0.44
1:A:542:ILE:HG23	2:B:283:LEU:HD13	1.99	0.44
1:A:466:VAL:HG22	1:A:550:LYS:HZ3	1.82	0.44
2:B:242:GLN:HB2	2:B:351:THR:OG1	2.17	0.44
1:A:196:GLY:HA2	1:A:199:ARG:HH21	1.83	0.44
1:A:68:SER:OG	1:A:69:THR:N	2.51	0.44
2:B:104:LYS:HB2	2:B:192:ASP:HA	2.00	0.44
2:B:208:HIS:O	2:B:208:HIS:ND1	2.51	0.43
2:B:91:GLN:HB2	2:B:94:ILE:HG13	2.00	0.43
1:A:537:PRO:HB2	1:A:540:LYS:HG3	2.01	0.43
1:A:226:PRO:HB3	1:A:235:HIS:CE1	2.54	0.43
1:A:417:VAL:HG22	1:A:419:THR:HG23	2.01	0.43
1:A:281:LYS:HA	1:A:284:ARG:HG3	2.01	0.42
1:A:64:LYS:HD2	1:A:68:SER:O	2.19	0.42
2:B:249:LYS:HB2	2:B:252:TRP:CE2	2.55	0.42
2:B:315:HIS:O	2:B:347:LYS:NZ	2.42	0.42
2:B:277:ARG:HD3	2:B:277:ARG:HA	1.81	0.42
1:A:454:LYS:HZ1	1:A:552:VAL:HB	1.84	0.41
2:B:271:TYR:HA	2:B:272:PRO:HD3	1.92	0.41
2:B:394:GLN:OE1	2:B:418:ASN:ND2	2.51	0.41
2:B:167:ILE:HG23	2:B:212:TRP:CG	2.56	0.41
2:B:354:TYR:OH	2:B:378:GLU:OE2	2.35	0.41
1:A:96:HIS:HA	1:A:97:PRO:HD3	1.96	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:362:THR:OG1	2:B:362:THR:O	2.38	0.40
1:A:209:LEU:HB3	1:A:214:LEU:HB2	2.03	0.40
2:B:319:TYR:OH	2:B:385:LYS:HE2	2.22	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	552/557 (99%)	529 (96%)	19 (3%)	4 (1%)	24	29
2	B	408/428 (95%)	388 (95%)	18 (4%)	2 (0%)	31	38
All	All	960/985 (98%)	917 (96%)	37 (4%)	6 (1%)	27	33

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	217	PRO
1	A	545	ASN
1	A	285	GLY
2	B	272	PRO
1	A	286	THR
2	B	86	ASP

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	494/495 (100%)	472 (96%)	22 (4%)	30	42
2	B	374/390 (96%)	360 (96%)	14 (4%)	37	51
All	All	868/885 (98%)	832 (96%)	36 (4%)	33	46

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	THR
1	A	22	LYS
1	A	67	ASP
1	A	73	LYS
1	A	101	LYS
1	A	105	SER
1	A	161	GLN
1	A	162	SER
1	A	184	MET
1	A	195	ILE
1	A	211	ARG
1	A	221	HIS
1	A	222	GLN
1	A	286	THR
1	A	290	THR
1	A	300	GLU
1	A	324	ASP
1	A	349	LEU
1	A	399	GLU
1	A	503	LEU
1	A	514	GLU
1	A	546	GLU
2	B	8	VAL
2	B	66	LYS
2	B	87	PHE
2	B	90	VAL
2	B	165	THR
2	B	210	LEU
2	B	214	LEU
2	B	227	PHE
2	B	228	LEU
2	B	238	LYS
2	B	356	ARG
2	B	362	THR
2	B	417	VAL

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Mol	Chain	Res	Type
2	B	425	LEU

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 ⓘ

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 ⓘ

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	G73	A	601	-	31,34,34	1.46	3 (9%)	36,47,47	1.53	7 (19%)

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	G73	A	601	-	-	0/13/14/14	0/4/4/4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	G73	C27-N31	2.28	1.39	1.34
3	A	601	G73	C12-N13	4.28	1.44	1.36
3	A	601	G73	C10-N09	5.08	1.44	1.36

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	G73	N26-C12-N11	-3.94	120.38	126.23
3	A	601	G73	C14-N13-C12	-2.42	117.94	127.99
3	A	601	G73	C27-C28-N29	-2.19	107.29	109.41
3	A	601	G73	C18-C19-C20	-2.14	113.61	125.39
3	A	601	G73	C28-C10-N11	-2.12	118.52	120.64
3	A	601	G73	C12-N11-C10	2.74	122.33	117.03
3	A	601	G73	C12-N26-C27	5.10	120.94	115.11

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	G73	3	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, 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	554/557 (99%)	0.46	40 (7%) 15 21	25, 46, 86, 129	0
2	B	412/428 (96%)	0.83	57 (13%) 3 4	26, 47, 95, 125	0
All	All	966/985 (98%)	0.62	97 (10%) 7 10	25, 47, 92, 129	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	90	VAL	9.9
1	A	67	ASP	8.9
2	B	88	TRP	8.7
2	B	357	MET	8.4
2	B	229	TRP	8.2
2	B	227	PHE	7.6
2	B	240	THR	7.0
1	A	219	LYS	6.7
1	A	286	THR	6.4
1	A	218	ASP	6.3
2	B	92	LEU	6.0
2	B	93	GLY	5.9
1	A	552	VAL	5.8
1	A	221	HIS	5.6
2	B	214	LEU	5.5
1	A	220	LYS	5.4
2	B	231	GLY	5.1
1	A	551	LEU	5.0
2	B	230	MET	4.9
1	A	290	THR	4.9
2	B	91	GLN	4.7
2	B	210	LEU	4.5
1	A	358	ARG	4.2
2	B	89	GLU	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	69	THR	4.1
1	A	293	ILE	4.0
1	A	292	VAL	4.0
1	A	68	SER	4.0
2	B	95	PRO	4.0
1	A	284	ARG	3.9
2	B	212	TRP	3.9
1	A	285	GLY	3.9
2	B	170	PRO	3.9
1	A	287	LYS	3.9
1	A	24	TRP	3.7
2	B	87	PHE	3.7
2	B	168	LEU	3.5
2	B	94	ILE	3.5
2	B	204	GLU	3.4
2	B	69	THR	3.4
2	B	171	PHE	3.4
1	A	289	LEU	3.4
2	B	14	PRO	3.4
1	A	288	ALA	3.4
2	B	196	GLY	3.3
2	B	197	GLN	3.3
1	A	66	LYS	3.3
2	B	202	ILE	3.2
2	B	86	ASP	3.2
1	A	295	LEU	3.2
1	A	70	LYS	3.2
2	B	173	LYS	3.1
2	B	211	ARG	3.1
2	B	358	ARG	3.1
1	A	217	PRO	3.0
2	B	11	LYS	2.9
2	B	15	GLY	2.9
2	B	67	ASP	2.9
2	B	166	LYS	2.9
2	B	239	TRP	2.9
2	B	237	ASP	2.8
1	A	63	ILE	2.8
2	B	12	LEU	2.7
2	B	206	ARG	2.6
2	B	238	LYS	2.6
2	B	241	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
2	B	85	GLN	2.6
1	A	65	LYS	2.6
1	A	252	TRP	2.6
1	A	255	ASN	2.5
2	B	356	ARG	2.5
1	A	6	GLU	2.5
2	B	13	LYS	2.5
2	B	6	GLU	2.5
2	B	284	ARG	2.5
1	A	224	GLU	2.5
2	B	361	HIS	2.4
1	A	257	ILE	2.4
2	B	193	LEU	2.4
2	B	228	LEU	2.4
2	B	359	GLY	2.4
1	A	222	GLN	2.3
2	B	66	LYS	2.3
2	B	315	HIS	2.3
1	A	297	GLU	2.2
1	A	544	GLY	2.2
1	A	294	PRO	2.2
2	B	277	ARG	2.2
2	B	425	LEU	2.2
1	A	291	GLU	2.2
2	B	198	HIS	2.1
1	A	216	THR	2.1
2	B	207	GLN	2.1
1	A	64	LYS	2.1
2	B	176	PRO	2.1
1	A	225	PRO	2.1
1	A	223	LYS	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

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(\AA^2)	Q<0.9
3	G73	A	601	31/31	0.96	0.16	31,38,49,52	0

6.5 Other polymers

There are no such residues in this entry.