



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 01:39 am GMT

PDB ID : 1DE5
Title : L-RHAMNOSE ISOMERASE
Authors : Korndorfer, I.P.; Fessner, W.D.; Matthews, B.W.
Deposited on : 1999-11-12
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
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) : recalc28949

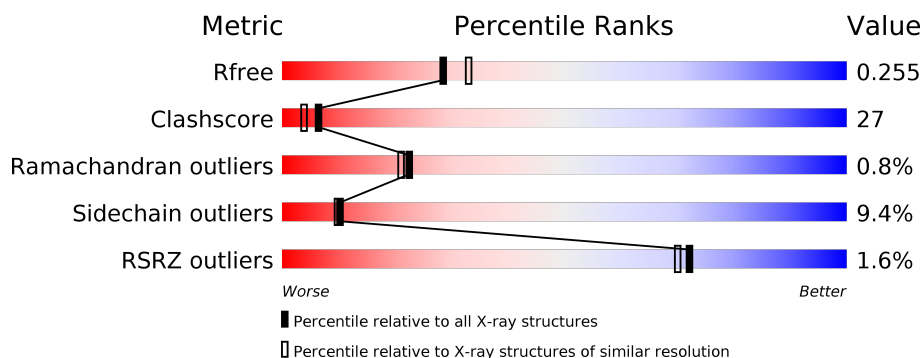
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	426	<div> <div>3%</div> <div> <div>48%</div> <div>37%</div> <div>11%</div> <div>..</div> </div> </div>
1	B	426	<div> <div>%</div> <div> <div>48%</div> <div>39%</div> <div>9%</div> <div>..</div> </div> </div>
1	C	426	<div> <div>%</div> <div> <div>47%</div> <div>41%</div> <div>8%</div> <div>..</div> </div> </div>
1	D	426	<div> <div>%</div> <div> <div>46%</div> <div>40%</div> <div>11%</div> <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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	RNT	A	1460	-	-	-	X
2	RNT	C	3460	-	-	-	X
2	RNT	D	4460	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14315 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 L-RHAMNOSE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	0	0	0
			3316	2094	588	621	13			
1	B	416	Total	C	N	O	S	0	0	0
			3309	2090	587	619	13			
1	C	416	Total	C	N	O	S	0	0	0
			3309	2090	587	619	13			
1	D	416	Total	C	N	O	S	0	0	0
			3309	2090	587	619	13			

There are 28 discrepancies between the modelled and reference sequences:

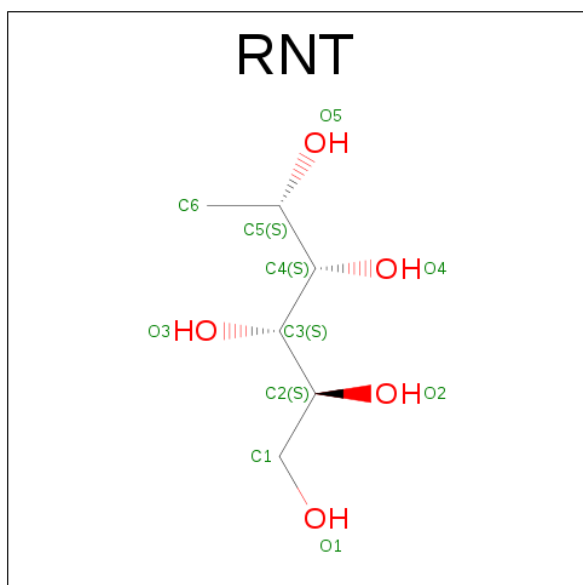
Chain	Residue	Modelled	Actual	Comment	Reference
A	2	GLY	-	RECOMBINANT HIS TAG	UNP P32170
A	3	HIS	-	RECOMBINANT HIS TAG	UNP P32170
A	4	HIS	-	RECOMBINANT HIS TAG	UNP P32170
A	5	HIS	-	RECOMBINANT HIS TAG	UNP P32170
A	6	HIS	-	RECOMBINANT HIS TAG	UNP P32170
A	7	HIS	-	RECOMBINANT HIS TAG	UNP P32170
A	8	HIS	-	RECOMBINANT HIS TAG	UNP P32170
B	2	GLY	-	RECOMBINANT HIS TAG	UNP P32170
B	3	HIS	-	RECOMBINANT HIS TAG	UNP P32170
B	4	HIS	-	RECOMBINANT HIS TAG	UNP P32170
B	5	HIS	-	RECOMBINANT HIS TAG	UNP P32170
B	6	HIS	-	RECOMBINANT HIS TAG	UNP P32170
B	7	HIS	-	RECOMBINANT HIS TAG	UNP P32170
B	8	HIS	-	RECOMBINANT HIS TAG	UNP P32170
C	2	GLY	-	RECOMBINANT HIS TAG	UNP P32170
C	3	HIS	-	RECOMBINANT HIS TAG	UNP P32170
C	4	HIS	-	RECOMBINANT HIS TAG	UNP P32170
C	5	HIS	-	RECOMBINANT HIS TAG	UNP P32170
C	6	HIS	-	RECOMBINANT HIS TAG	UNP P32170
C	7	HIS	-	RECOMBINANT HIS TAG	UNP P32170
C	8	HIS	-	RECOMBINANT HIS TAG	UNP P32170

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Chain	Residue	Modelled	Actual	Comment	Reference
D	2	GLY	-	RECOMBINANT HIS TAG	UNP P32170
D	3	HIS	-	RECOMBINANT HIS TAG	UNP P32170
D	4	HIS	-	RECOMBINANT HIS TAG	UNP P32170
D	5	HIS	-	RECOMBINANT HIS TAG	UNP P32170
D	6	HIS	-	RECOMBINANT HIS TAG	UNP P32170
D	7	HIS	-	RECOMBINANT HIS TAG	UNP P32170
D	8	HIS	-	RECOMBINANT HIS TAG	UNP P32170

- Molecule 2 is L-RHAMNITOL (three-letter code: RNT) (formula: $C_6H_{14}O_5$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 11 6 5	0	0
2	B	1	Total C O 11 6 5	0	0
2	C	1	Total C O 11 6 5	0	0
2	D	1	Total C O 11 6 5	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Zn 1 1	0	0

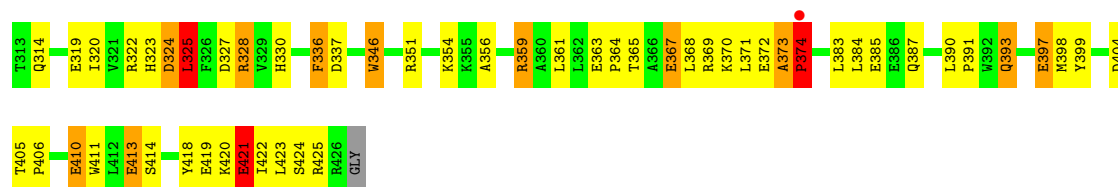
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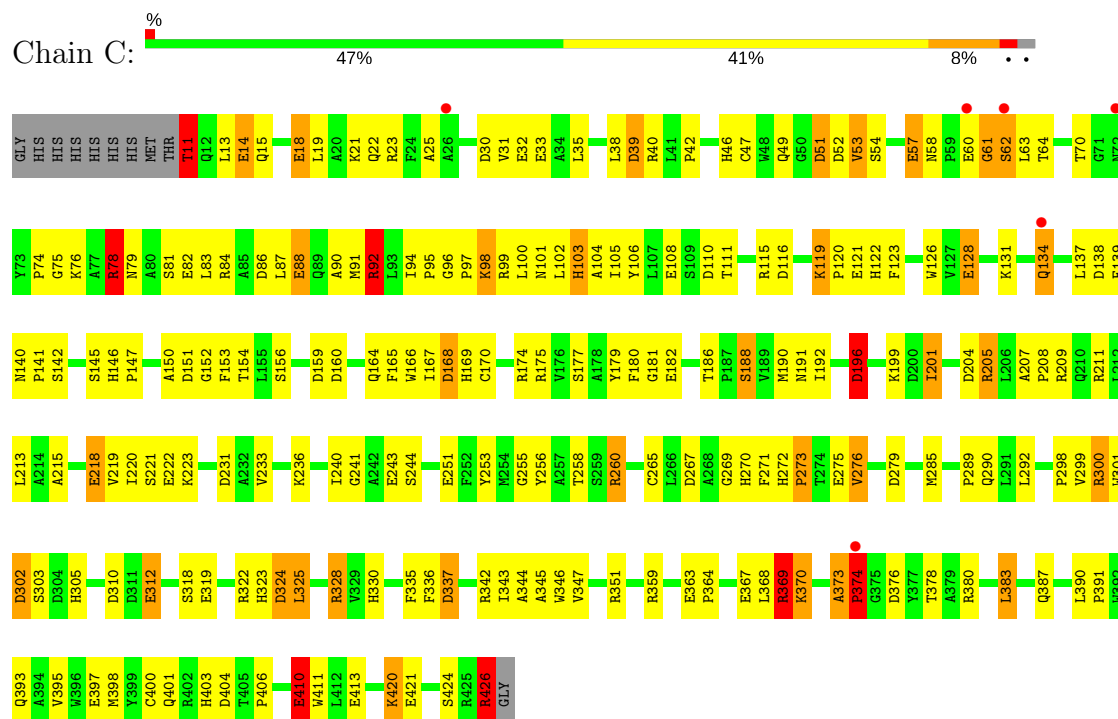
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Zn 1	0	0
3	D	1	Total 1	Zn 1	0	0
3	C	1	Total 1	Zn 1	0	0

- Molecule 4 is water.

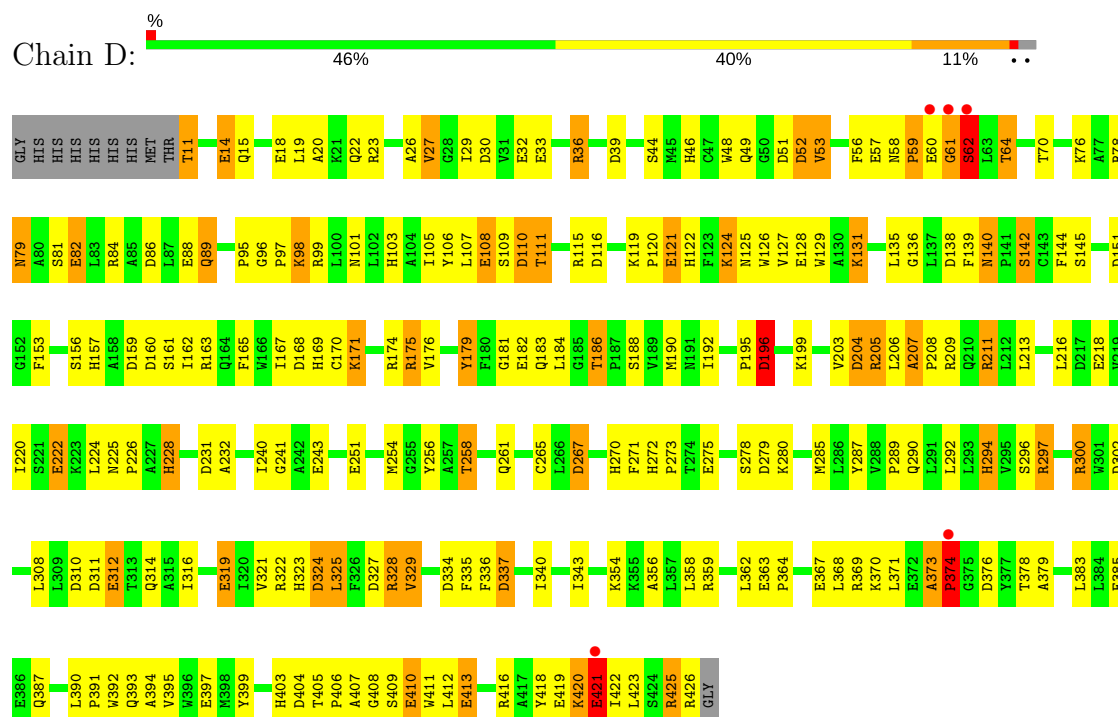
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	247	Total 247	O 247	0	0
4	B	286	Total 286	O 286	0	0
4	C	254	Total 254	O 254	0	0
4	D	237	Total 237	O 237	0	0



• Molecule 1: L-RHAMNOSE ISOMERASE



• Molecule 1: L-RHAMNOSE ISOMERASE



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	169.44Å 162.69Å 77.02Å 90.00° 110.68° 90.00°	Depositor
Resolution (Å)	15.00 – 2.20 14.91 – 2.20	Depositor EDS
% Data completeness (in resolution range)	81.0 (15.00-2.20) 86.4 (14.91-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.98 (at 2.20Å)	Xtriage
Refinement program	TNT V. 5-E	Depositor
R, R_{free}	0.156 , 0.275 0.152 , 0.255	Depositor DCC
R_{free} test set	4333 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	21.3	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 90.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	14315	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.41% 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 i

5.1 Standard geometry i

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

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	1.11	23/3396 (0.7%)	1.66	65/4612 (1.4%)
1	B	1.11	24/3389 (0.7%)	1.65	60/4602 (1.3%)
1	C	1.07	22/3389 (0.6%)	1.57	64/4602 (1.4%)
1	D	1.09	21/3389 (0.6%)	1.60	65/4602 (1.4%)
All	All	1.09	90/13563 (0.7%)	1.62	254/18418 (1.4%)

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
1	A	1	0
1	C	1	0
1	D	1	0
All	All	3	0

The worst 5 of 90 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	251	GLU	CD-OE2	9.14	1.35	1.25
1	D	222	GLU	CD-OE2	8.16	1.34	1.25
1	A	397	GLU	CD-OE2	7.99	1.34	1.25
1	B	128	GLU	CD-OE2	7.37	1.33	1.25
1	A	32	GLU	CD-OE2	7.09	1.33	1.25

The worst 5 of 254 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	373	ALA	C-N-CD	-18.31	80.31	120.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	373	ALA	C-N-CD	-17.93	81.16	120.60
1	C	373	ALA	C-N-CD	-14.10	89.57	120.60
1	B	175	ARG	NE-CZ-NH2	-13.54	113.53	120.30
1	D	328	ARG	NE-CZ-NH2	-13.45	113.58	120.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	10	THR	CA
1	C	150	ALA	CA
1	D	70	THR	CB

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	3316	0	3238	214	0
1	B	3309	0	3231	181	0
1	C	3309	0	3231	166	0
1	D	3309	0	3231	180	0
2	A	11	0	12	4	0
2	B	11	0	13	1	0
2	C	11	0	12	1	0
2	D	11	0	12	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	247	0	0	17	0
4	B	286	0	0	22	0
4	C	254	0	0	12	2
4	D	237	0	0	10	0
All	All	14315	0	12980	699	2

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 27.

The worst 5 of 699 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:B:269:GLY:HA2	1:B:298:PRO:HG3	1.38	1.04
1:A:369:ARG:HH11	1:A:369:ARG:HG3	1.25	1.00
1:D:64:THR:HG22	1:D:145:SER:H	1.27	1.00
1:D:422:ILE:HG22	1:D:423:LEU:HD23	1.41	0.99
1:C:272:HIS:HE1	4:D:4640:HOH:O	1.44	0.98

All (2) 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)
4:C:3475:HOH:O	4:C:3475:HOH:O[2_556]	1.99	0.21
4:C:3481:HOH:O	4:C:3481:HOH:O[2_556]	2.15	0.05

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	415/426 (97%)	383 (92%)	32 (8%)	0	100	100
1	B	414/426 (97%)	386 (93%)	23 (6%)	5 (1%)	15	12
1	C	414/426 (97%)	387 (94%)	23 (6%)	4 (1%)	18	16
1	D	414/426 (97%)	384 (93%)	26 (6%)	4 (1%)	18	16
All	All	1657/1704 (97%)	1540 (93%)	104 (6%)	13 (1%)	22	21

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	62	SER

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Mol	Chain	Res	Type
1	D	62	SER
1	B	61	GLY
1	B	59	PRO
1	C	61	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	352/359 (98%)	315 (90%)	37 (10%)	8	7
1	B	351/359 (98%)	318 (91%)	33 (9%)	10	10
1	C	351/359 (98%)	322 (92%)	29 (8%)	13	13
1	D	351/359 (98%)	318 (91%)	33 (9%)	10	10
All	All	1405/1436 (98%)	1273 (91%)	132 (9%)	10	10

5 of 132 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	324	ASP
1	C	57	GLU
1	D	258	THR
1	B	336	PHE
1	B	414	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 42 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	393	GLN
1	C	122	HIS
1	D	228	HIS
1	C	15	GLN
1	C	49	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\# Z > 2$
2	RNT	A	1460	3	9,10,10	0.85	0	10,13,13	1.16	1 (10%)
2	RNT	B	2460	3	9,10,10	0.94	0	10,13,13	1.27	2 (20%)
2	RNT	C	3460	3	9,10,10	1.06	2 (22%)	10,13,13	1.14	1 (10%)
2	RNT	D	4460	3	9,10,10	1.07	0	10,13,13	0.86	0

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
2	RNT	A	1460	3	-	0/14/14/14	0/0/0/0
2	RNT	B	2460	3	-	0/14/14/14	0/0/0/0
2	RNT	C	3460	3	-	0/14/14/14	0/0/0/0
2	RNT	D	4460	3	-	0/14/14/14	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3460	RNT	O4-C4	2.11	1.47	1.43
2	C	3460	RNT	C2-C3	2.14	1.57	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1460	RNT	C1-C2-C3	2.01	116.89	112.41
2	C	3460	RNT	C1-C2-C3	2.09	117.08	112.41
2	B	2460	RNT	C1-C2-C3	2.20	117.31	112.41
2	B	2460	RNT	O3-C3-C2	2.64	115.37	108.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1460	RNT	4	0
2	B	2460	RNT	1	0
2	C	3460	RNT	1	0
2	D	4460	RNT	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 [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, 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	417/426 (97%)	-0.55	11 (2%) 56 54	11, 25, 55, 94	0
1	B	416/426 (97%)	-0.63	5 (1%) 79 77	13, 24, 48, 84	0
1	C	416/426 (97%)	-0.57	6 (1%) 75 73	12, 24, 49, 97	0
1	D	416/426 (97%)	-0.50	5 (1%) 79 77	12, 27, 57, 93	0
All	All	1665/1704 (97%)	-0.56	27 (1%) 72 70	11, 25, 52, 97	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	61	GLY	5.9
1	D	60	GLU	4.9
1	A	10	THR	4.0
1	C	134	GLN	3.5
1	D	62	SER	3.4

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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	RNT	A	1460	11/11	0.92	0.15	3.36	25,26,40,44	0
2	RNT	C	3460	11/11	0.91	0.16	2.99	22,25,37,42	0
2	RNT	D	4460	11/11	0.92	0.15	2.46	21,22,34,40	0
2	RNT	B	2460	11/11	0.94	0.14	1.82	19,23,35,39	0
3	ZN	A	450	1/1	1.00	0.06	-	34,34,34,34	0
3	ZN	B	450	1/1	0.99	0.04	-	35,35,35,35	0
3	ZN	C	450	1/1	1.00	0.03	-	33,33,33,33	0
3	ZN	D	450	1/1	1.00	0.05	-	34,34,34,34	0

6.5 Other polymers [i](#)

There are no such residues in this entry.