



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 21, 2017 – 08:15 AM EST

PDB ID : 5ON3
Title : Quaternary complex of mutant T252A of E. coli leucyl-tRNA synthetase with tRNA(leu), leucyl-adenylate analogue, and post-transfer editing analogue of leucine in the aminoacylation conformation
Authors : Palencia, A.; Cusack, S.
Deposited on : 2017-08-02
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

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 : rb-20030736
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-20030736

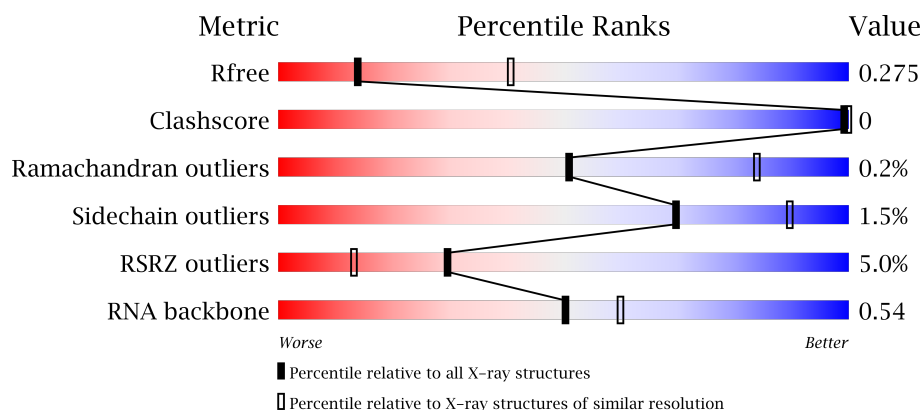
1 Overall quality at a glance

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}	100719	1001 (3.12-3.08)
Clashscore	112137	1099 (3.12-3.08)
Ramachandran outliers	110173	1057 (3.12-3.08)
Sidechain outliers	110143	1057 (3.12-3.08)
RSRZ outliers	101464	1006 (3.12-3.08)
RNA backbone	2435	1112 (3.50-2.70)

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	880	<div> <div>2%</div> <div>95%</div> <div>..</div> </div>
1	D	880	<div> <div>8%</div> <div>95%</div> <div>..</div> </div>
2	B	87	<div> <div>5%</div> <div>75%</div> <div>16%</div> <div>9%</div> </div>
2	E	87	<div> <div>9%</div> <div>77%</div> <div>14%</div> <div>9%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17061 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 Leucine-tRNA ligase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	860	Total	C	N	O	S	0	0	0
			6833	4338	1159	1291	45			
1	D	850	Total	C	N	O	S	0	0	0
			6761	4294	1148	1276	43			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP P07813
A	-18	GLY	-	expression tag	UNP P07813
A	-17	SER	-	expression tag	UNP P07813
A	-16	SER	-	expression tag	UNP P07813
A	-15	HIS	-	expression tag	UNP P07813
A	-14	HIS	-	expression tag	UNP P07813
A	-13	HIS	-	expression tag	UNP P07813
A	-12	HIS	-	expression tag	UNP P07813
A	-11	HIS	-	expression tag	UNP P07813
A	-10	HIS	-	expression tag	UNP P07813
A	-9	SER	-	expression tag	UNP P07813
A	-8	SER	-	expression tag	UNP P07813
A	-7	GLY	-	expression tag	UNP P07813
A	-6	LEU	-	expression tag	UNP P07813
A	-5	VAL	-	expression tag	UNP P07813
A	-4	PRO	-	expression tag	UNP P07813
A	-3	ARG	-	expression tag	UNP P07813
A	-2	GLY	-	expression tag	UNP P07813
A	-1	SER	-	expression tag	UNP P07813
A	0	HIS	-	expression tag	UNP P07813
A	252	ALA	THR	engineered mutation	UNP P07813
D	-19	MET	-	initiating methionine	UNP P07813
D	-18	GLY	-	expression tag	UNP P07813
D	-17	SER	-	expression tag	UNP P07813
D	-16	SER	-	expression tag	UNP P07813

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-15	HIS	-	expression tag	UNP P07813
D	-14	HIS	-	expression tag	UNP P07813
D	-13	HIS	-	expression tag	UNP P07813
D	-12	HIS	-	expression tag	UNP P07813
D	-11	HIS	-	expression tag	UNP P07813
D	-10	HIS	-	expression tag	UNP P07813
D	-9	SER	-	expression tag	UNP P07813
D	-8	SER	-	expression tag	UNP P07813
D	-7	GLY	-	expression tag	UNP P07813
D	-6	LEU	-	expression tag	UNP P07813
D	-5	VAL	-	expression tag	UNP P07813
D	-4	PRO	-	expression tag	UNP P07813
D	-3	ARG	-	expression tag	UNP P07813
D	-2	GLY	-	expression tag	UNP P07813
D	-1	SER	-	expression tag	UNP P07813
D	0	HIS	-	expression tag	UNP P07813
D	252	ALA	THR	engineered mutation	UNP P07813

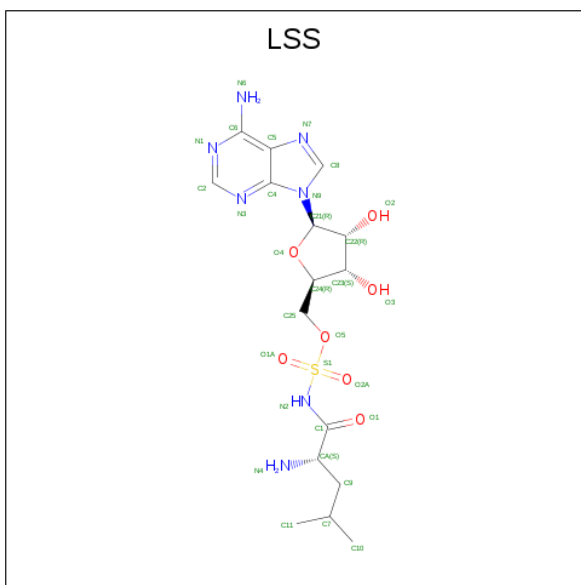
- Molecule 2 is a RNA chain called tRNA(leu).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	79	Total	C	N	O	P	0	0	0
			1675	743	303	550	79			
2	E	79	Total	C	N	O	P	0	0	0
			1675	743	303	550	79			

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

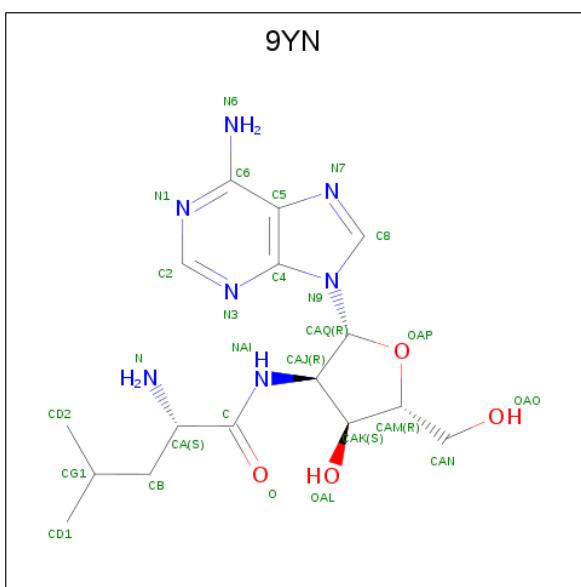
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is 5'-O-(L-leucylsulfamoyl)adenosine (three-letter code: LSS) (formula: C₁₆H₂₅N₇O₇S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 31	C 16	N 7	O 7	S 1	0	0
4	D	1	Total 31	C 16	N 7	O 7	S 1	0	0

- Molecule 5 is (2 {S})- {N}-[(2 {R},3 {R},4 {S},5 {R})-2-(6-aminopurin-9-yl)-5-(hydroxy methyl)-4-oxidanyl-oxolan-3-yl]-2-azanyl-4-methyl-pentanamide (three-letter code: 9YN) (formula: C₁₆H₂₅N₇O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			27	16	7	4		

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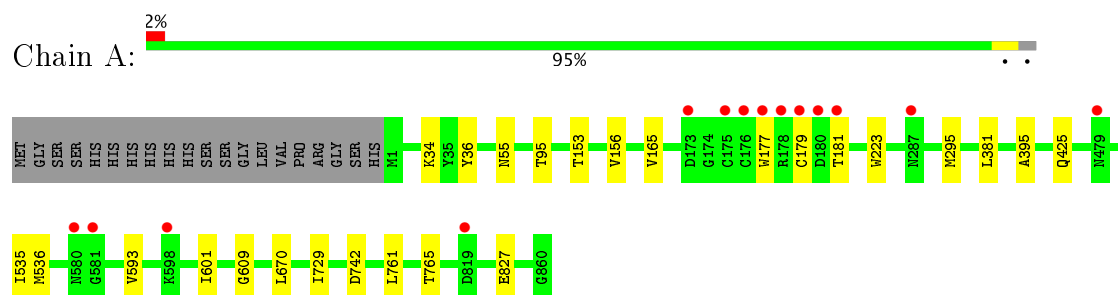
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	D	1	Total	C	N	O	0	0
			27	16	7	4		

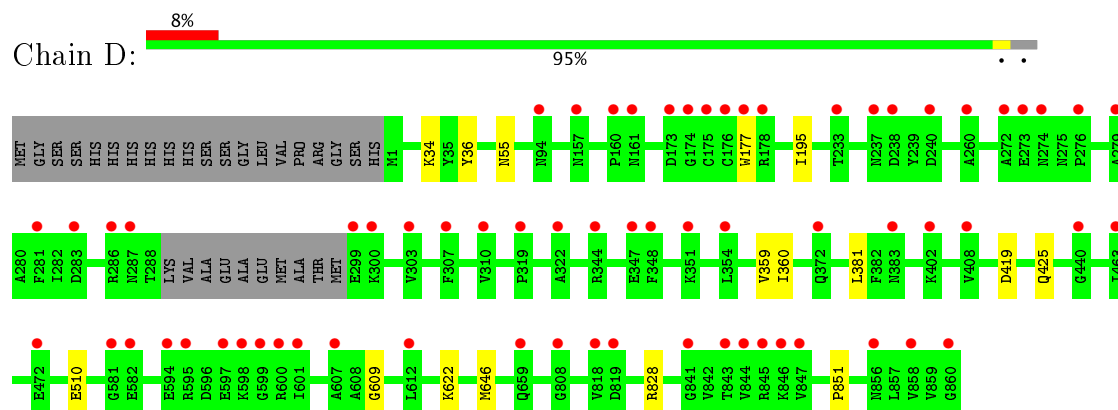
3 Residue-property plots

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.

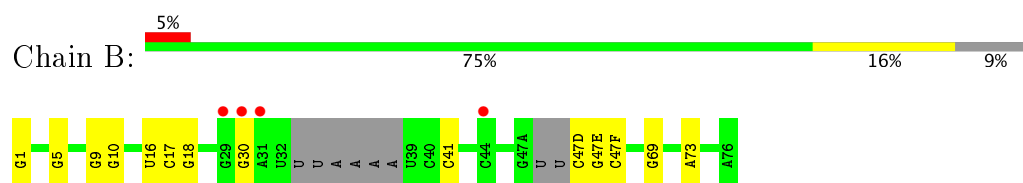
• Molecule 1: Leucine-tRNA ligase



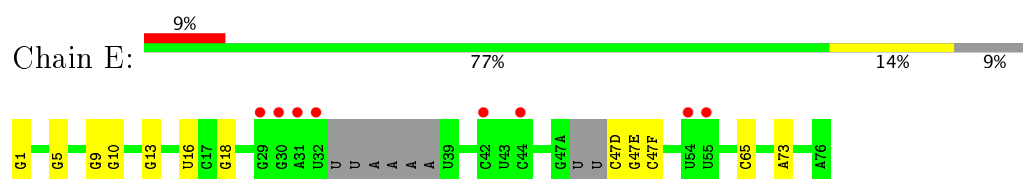
• Molecule 1: Leucine-tRNA ligase



• Molecule 2: tRNA(Leu)



• Molecule 2: tRNA(Leu)



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	159.00Å 68.70Å 227.20Å 90.00° 102.80° 90.00°	Depositor
Resolution (Å)	221.55 – 3.10 48.39 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.6 (221.55-3.10) 98.6 (48.39-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.02	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.44 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.241 , 0.278 0.243 , 0.275	Depositor DCC
R_{free} test set	2144 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	62.1	Xtriage
Anisotropy	0.457	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 28.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	17061	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.85% 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, 9YN, LSS

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	0.34	0/6994	0.51	0/9494
1	D	0.35	0/6921	0.50	0/9395
2	B	0.31	1/1869 (0.1%)	0.66	0/2908
2	E	0.31	1/1869 (0.1%)	0.65	0/2908
All	All	0.34	2/17653 (0.0%)	0.54	0/24705

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	1	G	OP3-P	-10.12	1.49	1.61
2	B	1	G	OP3-P	-10.05	1.49	1.61

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	6833	0	6683	7	0
1	D	6761	0	6611	2	0
2	B	1675	0	847	1	0
2	E	1675	0	847	1	0
3	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	31	0	25	0	0
4	D	31	0	25	0	0
5	A	27	0	0	0	0
5	D	27	0	0	0	0
All	All	17061	0	15038	11	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 0.

All (11) 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:729:ILE:HG21	1:A:761:LEU:HD13	1.93	0.51
2:B:47(D):C:O2	2:B:47(D):C:O4'	2.30	0.46
1:A:593:VAL:HG13	1:A:601:ILE:HG23	2.00	0.44
1:A:223:TRP:CD2	1:A:535:ILE:HG21	2.53	0.44
1:A:729:ILE:HG21	1:A:761:LEU:CD1	2.48	0.43
1:A:156:VAL:CG1	1:A:165:VAL:HG13	2.50	0.41
1:D:360:ILE:HD13	1:D:381:LEU:HD23	2.02	0.41
1:A:670:LEU:HD21	1:A:765:THR:HG21	2.03	0.41
2:E:47(D):C:O4'	2:E:47(D):C:O2	2.35	0.41
1:D:195:ILE:HG22	1:D:419:ASP:HA	2.03	0.40
1:A:381:LEU:HD11	1:A:395:ALA:HB1	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	858/880 (98%)	829 (97%)	28 (3%)	1 (0%)	55 88
1	D	846/880 (96%)	808 (96%)	35 (4%)	3 (0%)	38 75

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1704/1760 (97%)	1637 (96%)	63 (4%)	4 (0%)	51 84

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	609	GLY
1	D	609	GLY
1	D	851	PRO
1	D	359	VAL

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	723/740 (98%)	710 (98%)	13 (2%)	64 87
1	D	716/740 (97%)	707 (99%)	9 (1%)	73 91
All	All	1439/1480 (97%)	1417 (98%)	22 (2%)	70 89

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	LYS
1	A	36	TYR
1	A	55	ASN
1	A	95	THR
1	A	153	THR
1	A	177	TRP
1	A	179	CYS
1	A	181	THR
1	A	295	MET
1	A	425	GLN
1	A	536	MET
1	A	742	ASP
1	A	827	GLU
1	D	34	LYS

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Mol	Chain	Res	Type
1	D	36	TYR
1	D	55	ASN
1	D	177	TRP
1	D	425	GLN
1	D	510	GLU
1	D	622	LYS
1	D	646	MET
1	D	828	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	659	GLN
1	A	745	GLN
1	D	93	ASN
1	D	222	ASN
1	D	287	ASN
1	D	659	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	75/87 (86%)	12 (16%)	1 (1%)
2	E	75/87 (86%)	10 (13%)	1 (1%)
All	All	150/174 (86%)	22 (14%)	2 (1%)

All (22) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	5	G
2	B	9	G
2	B	10	G
2	B	16	U
2	B	17	C
2	B	18	G
2	B	30	G
2	B	41	C
2	B	47(E)	G
2	B	47(F)	C
2	B	69	G

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Mol	Chain	Res	Type
2	B	73	A
2	E	5	G
2	E	9	G
2	E	10	G
2	E	13	G
2	E	16	U
2	E	18	G
2	E	47(E)	G
2	E	47(F)	C
2	E	65	C
2	E	73	A

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	17	C
2	E	9	G

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](#)

Of 5 ligands modelled in this entry, 1 is 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	$\# Z > 2$
4	LSS	A	901	-	29,33,33	1.52	3 (10%)	31,49,49	2.97	4 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	9YN	A	902	-	26,29,29	2.53	3 (11%)	24,42,42	3.39	4 (16%)
4	LSS	D	901	-	29,33,33	1.60	3 (10%)	31,49,49	2.83	3 (9%)
5	9YN	D	902	-	26,29,29	2.52	3 (11%)	24,42,42	3.40	3 (12%)

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	LSS	A	901	-	-	0/18/39/39	0/3/3/3
5	9YN	A	902	-	-	0/14/34/34	0/3/3/3
4	LSS	D	901	-	-	0/18/39/39	0/3/3/3
5	9YN	D	902	-	-	0/14/34/34	0/3/3/3

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	901	LSS	S1-N2	-6.18	1.52	1.59
4	A	901	LSS	S1-N2	-5.69	1.53	1.59
4	D	901	LSS	O5-S1	-3.72	1.53	1.59
4	A	901	LSS	O5-S1	-3.55	1.54	1.59
4	A	901	LSS	O1A-S1	2.02	1.44	1.42
4	D	901	LSS	O1A-S1	2.07	1.44	1.42
5	D	902	9YN	C5-C4	3.27	1.47	1.40
5	A	902	9YN	C5-C4	3.28	1.47	1.40
5	D	902	9YN	C2-N1	7.47	1.47	1.33
5	A	902	9YN	C2-N1	7.51	1.48	1.33
5	D	902	9YN	C2-N3	9.49	1.47	1.32
5	A	902	9YN	C2-N3	9.51	1.48	1.32

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	902	9YN	N3-C2-N1	-15.82	115.08	128.86
5	A	902	9YN	N3-C2-N1	-15.63	115.24	128.86
4	A	901	LSS	O2A-S1-O1A	-13.15	107.86	121.30
4	D	901	LSS	O2A-S1-O1A	-12.32	108.71	121.30
4	A	901	LSS	N3-C2-N1	-8.42	121.53	128.86
4	D	901	LSS	N3-C2-N1	-8.29	121.64	128.86
5	A	902	9YN	C4-C5-N7	-2.92	106.59	109.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	902	9YN	C4-C5-N7	-2.65	106.85	109.41
4	A	901	LSS	O5-S1-N2	2.00	110.60	106.34
5	A	902	9YN	CAM-OAP-CAQ	2.14	112.05	109.77
4	A	901	LSS	C25-O5-S1	2.70	123.28	118.03
4	D	901	LSS	C25-O5-S1	2.85	123.58	118.03
5	A	902	9YN	C2-N1-C6	2.86	123.77	118.77
5	D	902	9YN	C2-N1-C6	2.95	123.92	118.77

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, 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	860/880 (97%)	-0.09	14 (1%) 72 51	31, 51, 85, 148	0
1	D	850/880 (96%)	0.48	67 (7%) 13 5	54, 83, 127, 174	0
2	B	79/87 (90%)	0.17	4 (5%) 29 13	34, 53, 126, 137	0
2	E	79/87 (90%)	0.80	8 (10%) 8 2	60, 95, 135, 166	0
All	All	1868/1934 (96%)	0.22	93 (4%) 30 13	31, 68, 123, 174	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	177	TRP	7.4
2	E	32	U	6.4
1	D	808	GLY	5.4
1	A	177	TRP	5.1
1	D	860	GLY	4.9
1	D	178	ARG	4.9
1	D	176	CYS	4.8
1	D	273	GLU	4.7
1	D	272	ALA	4.7
1	D	175	CYS	4.7
1	D	174	GLY	4.6
1	D	260	ALA	4.6
1	D	600	ARG	4.5
1	D	847	VAL	4.3
1	A	180	ASP	4.3
1	D	276	PRO	4.3
1	D	846	LYS	4.2
2	E	31	A	4.1
1	A	580	ASN	3.8
1	A	173	ASP	3.7
1	D	599	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
1	D	845	ARG	3.5
1	D	594	GLU	3.5
1	D	303	VAL	3.5
1	D	281	PHE	3.5
1	D	598	LYS	3.4
2	E	44	C	3.4
1	A	181	THR	3.3
1	D	597	GLU	3.3
1	D	319	PRO	3.2
2	E	54	U	3.2
1	D	582	GLU	3.2
1	A	178	ARG	3.1
1	D	310	VAL	3.1
1	D	299	GLU	3.0
1	D	161	ASN	2.9
1	D	819	ASP	2.9
1	D	372	GLN	2.9
1	D	601	ILE	2.8
1	D	94	ASN	2.8
1	D	841	GLY	2.8
1	A	179	CYS	2.8
1	D	348	PHE	2.7
1	D	237	ASN	2.7
1	D	173	ASP	2.7
1	A	819	ASP	2.7
1	D	843	THR	2.7
2	E	29	G	2.7
1	A	175	CYS	2.7
1	D	856	ASN	2.7
1	D	351	LYS	2.6
1	D	274	ASN	2.6
1	D	818	VAL	2.6
1	D	612	LEU	2.6
2	E	30	G	2.6
1	A	287	ASN	2.6
1	D	595	ARG	2.6
1	D	408	VAL	2.6
1	D	463	ILE	2.5
1	D	607	ALA	2.5
1	D	157	ASN	2.5
2	B	30	G	2.5
1	D	240	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	279	ALA	2.4
1	D	287	ASN	2.4
1	D	307	PHE	2.4
1	D	238	ASP	2.4
1	D	347	GLU	2.4
1	D	283	ASP	2.4
2	E	55	U	2.3
1	D	286	ARG	2.3
1	D	472	GLU	2.3
2	B	31	A	2.3
1	A	176	CYS	2.3
1	D	344	ARG	2.3
1	D	858	VAL	2.3
1	D	844	VAL	2.2
1	D	659	GLN	2.2
1	D	402	LYS	2.2
1	A	598	LYS	2.1
2	B	44	C	2.1
1	A	581	GLY	2.1
1	D	322	ALA	2.1
1	D	300	LYS	2.1
2	E	42	C	2.1
1	D	233	THR	2.1
1	D	160	PRO	2.1
1	D	354	LEU	2.1
1	A	479	ASN	2.1
1	D	440	GLY	2.1
1	D	383	ASN	2.0
2	B	29	G	2.0
1	D	581	GLY	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, 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(Å ²)	Q<0.9
4	LSS	A	901	31/31	0.96	0.21	-0.23	35,36,37,37	0
5	9YN	D	902	27/27	0.82	0.26	-0.36	103,106,109,111	0
3	ZN	A	900	1/1	0.81	0.36	-0.47	138,138,138,138	0
5	9YN	A	902	27/27	0.93	0.20	-0.50	63,64,67,67	0
4	LSS	D	901	31/31	0.96	0.21	-0.95	51,53,54,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.