



wwPDB X-ray Structure Validation Summary Report ⓘ

May 28, 2020 – 09:28 pm BST

PDB ID : 2D6F
Title : Crystal structure of Glu-tRNA(Gln) amidotransferase in the complex with tRNA(Gln)
Authors : Nureki, O.
Deposited on : 2005-11-13
Resolution : 3.15 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

<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
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

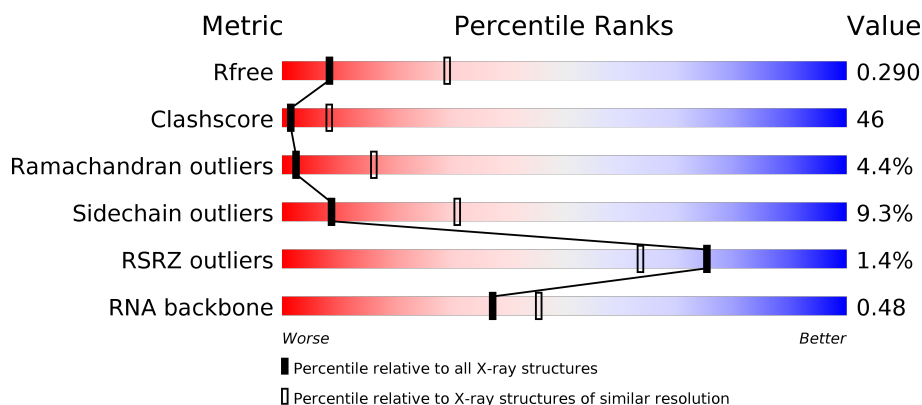
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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}	130704	1665 (3.20-3.12)
Clashscore	141614	1804 (3.20-3.12)
Ramachandran outliers	138981	1770 (3.20-3.12)
Sidechain outliers	138945	1769 (3.20-3.12)
RSRZ outliers	127900	1616 (3.20-3.12)
RNA backbone	3102	1073 (3.50-2.82)

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 respectively. 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	E	74	<div> <div>7%</div> <div>18%</div> <div>58%</div> <div>22%</div> <div>.</div> </div>
1	F	74	<div> <div>5%</div> <div>27%</div> <div>47%</div> <div>24%</div> <div>.</div> </div>
2	A	435	<div> <div>%</div> <div>37%</div> <div>51%</div> <div>9%</div> <div>.</div> </div>
2	B	435	<div> <div>37%</div> <div>51%</div> <div>9%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
3	C	619	<div><div><div></div><div></div><div></div><div></div></div><div><div>2%</div><div>26%</div><div>47%</div><div>6%</div><div>22%</div></div></div>
3	D	619	<div><div><div></div><div></div><div></div><div></div></div><div><div>%</div><div>30%</div><div>46%</div><div>8%</div><div>16%</div></div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 17816 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 RNA chain called tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	72	Total	C	N	O	P	0	0	0
			1539	684	272	511	72			
1	F	74	Total	C	N	O	P	0	0	0
			1579	702	278	525	74			

- Molecule 2 is a protein called Glutamyl-tRNA(Gln) amidotransferase subunit D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	424	Total	C	N	O	S	0	0	0
			3268	2028	575	641	24			
2	B	424	Total	C	N	O	S	0	0	0
			3274	2032	575	643	24			

- Molecule 3 is a protein called Glutamyl-tRNA(Gln) amidotransferase subunit E.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	485	Total	C	N	O	S	0	0	0
			3847	2390	690	752	15			
3	D	522	Total	C	N	O	S	0	0	0
			4127	2563	741	808	15			

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

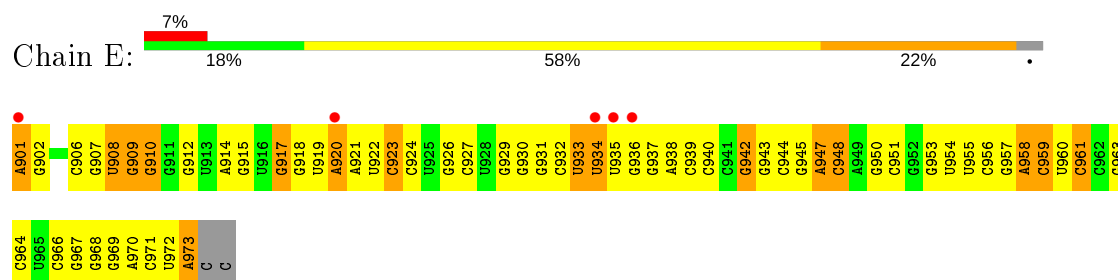
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	16	Total 16	O 16	0	0
5	F	24	Total 24	O 24	0	0
5	A	31	Total 31	O 31	0	0
5	B	24	Total 24	O 24	0	0
5	C	36	Total 36	O 36	0	0
5	D	49	Total 49	O 49	0	0

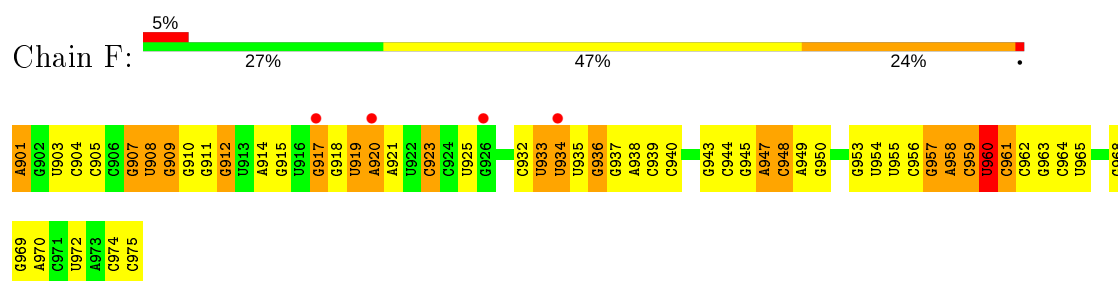
3 Residue-property plots [i](#)

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.

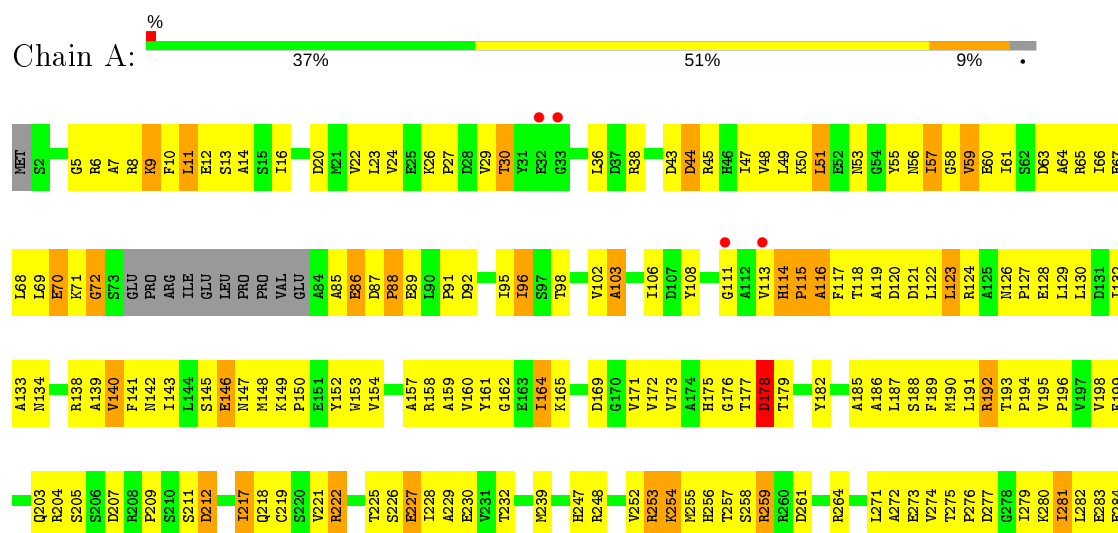
• Molecule 1: tRNA

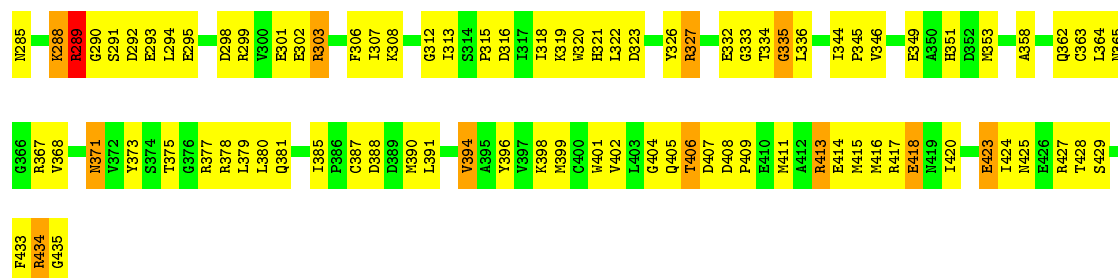


• Molecule 1: tRNA



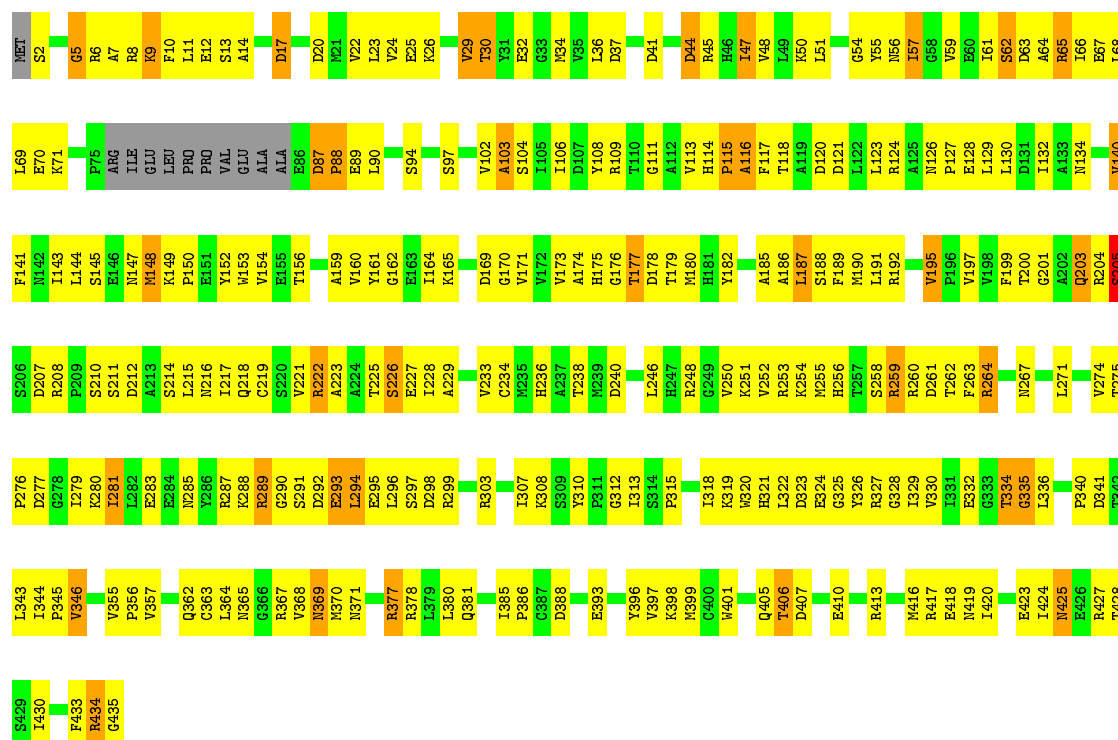
• Molecule 2: Glutamyl-tRNA(Gln) amidotransferase subunit D





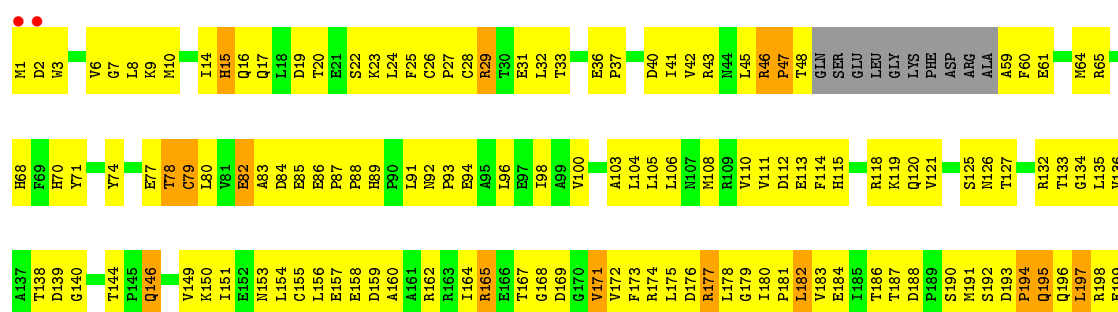
• Molecule 2: Glutamyl-tRNA(Gln) amidotransferase subunit D

Chain B: 37% 51% 9%



• Molecule 3: Glutamyl-tRNA(Gln) amidotransferase subunit E

Chain C: 26% 47% 6% 22%



S492	ARG	ARG
L493	LYS	GLU
L494	LEU	LYS
A495	ASN	ILE
Y496	LEU	GLN
T497	LEU	GLU
L498	LEU	ARG
R499	LEU	LEU
E500	ALA	
L501	GLU	
R502	ASP	
R503	GLU	
E504	ILE	
G505	GLU	
R506	SER	
D507	ILE	
V508	ILE	
D509	GLN	
G510	GLU	
L511	ILE	
G512	VAL	
L513	GLU	
D514	GLY	
E515	ASN	
L516	LEU	
R517	ASP	
D518	MET	
A519	ILE	
I520	SER	
R521	GLU	
L522	ARG	
L523	GLY	
E524	MET	
V525	GLY	
G526	ALA	
K527	MET	
I528	GLY	
S529	PRO	
R530	LEU	
D531	MET	
A532	GLY	
L533	GLN	
R534	ALA	
D535	MET	
I536	GLY	
V537	ARG	
A538	LEU	
CYS	ARG	
	MET	
	GLY	
	ARG	
	ALA	
	ASP	
	GLU	
	GLY	
	LYS	
	LEU	
	VAL	
	ALA	
	VAL	
	ASN	
	GLU	
	ASP	
	ARG	
	ILE	
	ALA	
	LEU	

ARG
GLU
LYS
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GLN
GLU
ARG
LEU

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	118.81Å 140.71Å 186.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.52 – 3.15 70.35 – 3.15	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.52-3.15) 98.9 (70.35-3.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 3.13Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.230 , 0.292 0.228 , 0.290	Depositor DCC
R_{free} test set	2728 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	60.0	Xtriage
Anisotropy	0.215	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 55.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	17816	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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

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	E	0.37	1/1718 (0.1%)	0.69	0/2676
1	F	0.40	1/1762 (0.1%)	0.72	0/2744
2	A	0.44	0/3323	0.71	1/4501 (0.0%)
2	B	0.45	0/3330	0.71	0/4511
3	C	0.36	0/3898	0.64	0/5265
3	D	0.44	0/4179	0.68	0/5642
All	All	0.42	2/18210 (0.0%)	0.69	1/25339 (0.0%)

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	F	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	901	A	OP3-P	-7.11	1.52	1.61
1	F	901	A	OP3-P	-6.87	1.52	1.61

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	192	ARG	N-CA-C	-5.15	97.09	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	F	960	U	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	E	1539	0	777	77	0
1	F	1579	0	799	68	0
2	A	3268	0	3217	332	0
2	B	3274	0	3220	318	0
3	C	3847	0	3861	425	1
3	D	4127	0	4152	399	1
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	31	0	0	11	0
5	B	24	0	0	5	0
5	C	36	0	0	9	0
5	D	49	0	0	14	0
5	E	16	0	0	2	0
5	F	24	0	0	6	0
All	All	17816	0	16026	1543	1

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 46.

The worst 5 of 1543 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)
3:D:133:THR:HG23	3:D:157:GLU:HB3	1.26	1.10
2:A:301:GLU:HG3	2:A:303:ARG:NH1	1.67	1.10
2:B:238:THR:HG23	2:B:240:ASP:H	1.12	1.08
3:D:43:ARG:HH11	3:D:43:ARG:HG2	1.19	1.06
3:C:233:ARG:HG3	3:C:397:GLU:HB3	1.37	1.06

All (1) 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)
3:C:169:ASP:OD2	3:D:268:GLU:OE1[4_556]	2.08	0.12

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	
2	A	420/435 (97%)	349 (83%)	50 (12%)	21 (5%)	2	14
2	B	420/435 (97%)	337 (80%)	65 (16%)	18 (4%)	2	17
3	C	479/619 (77%)	411 (86%)	52 (11%)	16 (3%)	4	22
3	D	516/619 (83%)	436 (84%)	55 (11%)	25 (5%)	2	15
All	All	1835/2108 (87%)	1533 (84%)	222 (12%)	80 (4%)	2	16

5 of 80 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	13	SER
2	A	115	PRO
2	A	140	VAL
2	A	281	ILE
2	B	44	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	
2	A	356/367 (97%)	320 (90%)	36 (10%)	7	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	358/367 (98%)	325 (91%)	33 (9%)	9	31
3	C	423/529 (80%)	388 (92%)	35 (8%)	11	37
3	D	452/529 (85%)	408 (90%)	44 (10%)	8	29
All	All	1589/1792 (89%)	1441 (91%)	148 (9%)	9	31

5 of 148 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	425	ASN
3	C	171	VAL
3	D	384	VAL
2	B	434	ARG
3	C	82	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 49 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	425	ASN
3	C	131	GLN
3	D	267	GLN
3	C	73	ASN
3	C	146	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	71/74 (95%)	16 (22%)	1 (1%)
1	F	73/74 (98%)	19 (26%)	4 (5%)
All	All	144/148 (97%)	35 (24%)	5 (3%)

5 of 35 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	E	908	U
1	E	909	G
1	E	910	G
1	E	917	G
1	E	920	A

All (5) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	E	958	A
1	F	907	G
1	F	909	G
1	F	958	A
1	F	960	U

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 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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	E	72/74 (97%)	0.29	5 (6%) 16 9	83, 122, 174, 192	0
1	F	74/74 (100%)	0.33	4 (5%) 25 13	55, 88, 139, 152	0
2	A	424/435 (97%)	-0.48	4 (0%) 84 75	7, 33, 81, 113	0
2	B	424/435 (97%)	-0.49	0 100 100	12, 36, 68, 93	0
3	C	485/619 (78%)	-0.07	12 (2%) 57 42	23, 76, 133, 143	0
3	D	522/619 (84%)	-0.43	4 (0%) 86 78	9, 41, 102, 122	0
All	All	2001/2256 (88%)	-0.31	29 (1%) 75 63	7, 46, 127, 192	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	935	U	13.7
3	D	511	LEU	8.4
1	E	934	U	6.5
3	C	359	VAL	6.4
1	E	936	G	5.3

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. 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
4	ZN	D	1900	1/1	1.00	0.13	35,35,35,35	0
4	ZN	C	900	1/1	1.00	0.14	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.