wwPDB X-ray Structure Validation Summary Report (i)

Dec 6, 2023 – 07:28 am GMT

PDB ID	:	2W89
Title	:	Crystal structure of the E.coli tRNAArg aminoacyl stem issoacceptor RR-1660 at 2.0 Angstroem resolution
Authors	:	Eichert, A.; Schreiber, A.; Fuerste, J.P.; Perbandt, M.; Betzel, C.; Erdmann, V.A.; Foerster, C.
Deposited on	:	2009-01-15
Resolution	:	2.00 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
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)	:	2.36

PERCENTILES INFOmissingINFO

1 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 680 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.

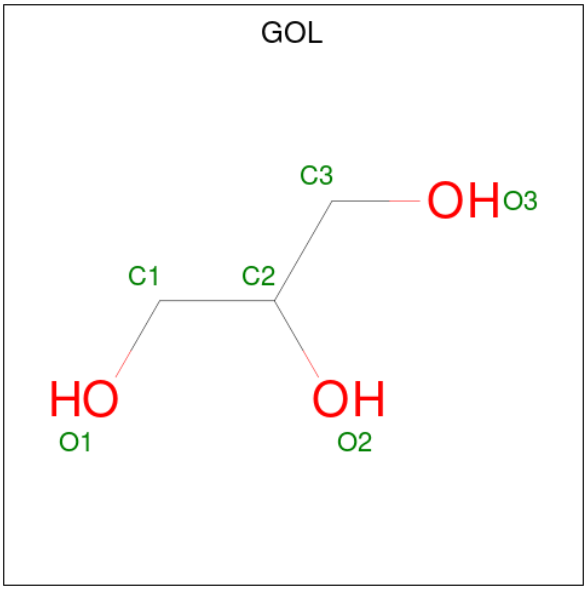
- Molecule 1 is a RNA chain called 5'-R(*GP*CP*AP*UP*CP*CP*GP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	7	Total	C	N	O	P	0	0	0
			145	66	26	47	6			
1	C	7	Total	C	N	O	P	0	0	0
			145	66	26	47	6			

- Molecule 2 is a RNA chain called 5'-R(*CP*GP*GP*AP*UP*GP*CP)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	7	Total	C	N	O	P	0	0	0
			148	67	28	47	6			
2	D	7	Total	C	N	O	P	0	0	0
			148	67	28	47	6			

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 6 3 3	0	0

- Molecule 4 is water.

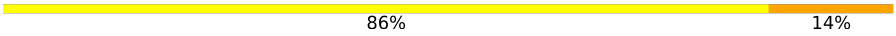
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	24	Total O 24 24	0	0
4	B	23	Total O 23 23	0	0
4	C	23	Total O 23 23	0	0
4	D	18	Total O 18 18	0	0

2 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

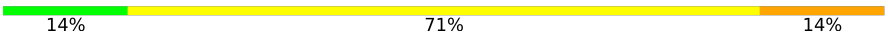
• Molecule 1: 5'-R(*GP*CP*AP*UP*CP*CP*GP)-3'

Chain A:



• Molecule 1: 5'-R(*GP*CP*AP*UP*CP*CP*GP)-3'

Chain C:

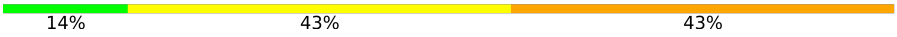


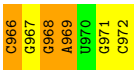
• Molecule 2: 5'-R(*CP*GP*GP*AP*UP*GP*CP)-3'

Chain B:

• Molecule 2: 5'-R(*CP*GP*GP*AP*UP*GP*CP)-3'

Chain D:





3 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	26.37Å 28.98Å 29.13Å 105.89° 98.76° 97.85°	Depositor
Resolution (Å)	20.92 – 2.00 20.74 – 2.00	Depositor EDS
% Data completeness (in resolution range)	97.9 (20.92-2.00) 82.2 (20.74-2.00)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.99 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.212 , 0.255 0.216 , 0.193	Depositor DCC
R_{free} test set	214 reflections (4.64%)	wwPDB-VP
Wilson B-factor (Å^2)	25.8	Xtriage
Anisotropy	0.119	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 52.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.53$, $< L^2 > = 0.38$	Xtriage
Estimated twinning fraction	0.450 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	680	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 22.53 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.5991e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

4 Model quality (i)

4.1 Standard geometry (i)

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

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	2.10	6/161 (3.7%)	2.80	25/249 (10.0%)
1	C	1.86	4/161 (2.5%)	2.78	20/249 (8.0%)
2	B	1.96	5/165 (3.0%)	3.09	24/256 (9.4%)
2	D	1.97	6/165 (3.6%)	2.85	24/256 (9.4%)
All	All	1.98	21/652 (3.2%)	2.89	93/1010 (9.2%)

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	901	G	C2-N3	8.66	1.39	1.32
1	A	907	G	C2-N3	7.75	1.39	1.32
2	D	969	A	C6-N1	7.68	1.41	1.35
2	B	969	A	C5-C6	-7.50	1.34	1.41
2	D	971	G	C6-N1	7.16	1.44	1.39

The worst 5 of 93 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	969	A	N1-C6-N6	13.62	126.77	118.60
2	B	972	C	N3-C4-N4	-13.41	108.61	118.00
1	A	907	G	C5-C6-O6	-13.14	120.72	128.60
2	B	967	G	C5-C6-O6	-12.47	121.11	128.60
2	D	969	A	N1-C6-N6	11.85	125.71	118.60

There are no chirality outliers.

There are no planarity outliers.

4.2 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	145	0	78	3	0
1	C	145	0	78	1	0
2	B	148	0	78	3	0
2	D	148	0	78	2	0
3	B	6	0	8	1	0
4	A	24	0	0	0	0
4	B	23	0	0	0	0
4	C	23	0	0	0	0
4	D	18	0	0	0	0
All	All	680	0	320	8	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 13.

The worst 5 of 8 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:C:907:G:H1	2:D:966:C:H42	1.38	0.72
1:A:902:C:O2'	1:A:903:A:H5'	2.03	0.59
2:B:967:G:O2'	2:B:968:G:H5'	2.06	0.56
1:A:902:C:C2'	1:A:903:A:H5'	2.36	0.55
2:B:967:G:C2'	2:B:968:G:H5'	2.49	0.42

There are no symmetry-related clashes.

4.3 Torsion angles

4.3.1 Protein backbone

There are no protein molecules in this entry.

4.3.2 Protein sidechains

There are no protein molecules in this entry.

4.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	6/7 (85%)	0	0
1	C	6/7 (85%)	0	0
2	B	6/7 (85%)	0	0
2	D	6/7 (85%)	0	0
All	All	24/28 (85%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

4.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

4.5 Carbohydrates (i)

There are no monosaccharides in this entry.

4.6 Ligand geometry (i)

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	GOL	B	1973	-	5,5,5	0.42	0	5,5,5	0.42	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
3	GOL	B	1973	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1973	GOL	O1-C1-C2-C3
3	B	1973	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1973	GOL	1	0

4.7 Other polymers (i)

There are no such residues in this entry.

4.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

5 Fit of model and data

5.1 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, 95^{th} 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	7/7 (100%)	-1.00	0	100	100	18, 20, 26, 27	0
1	C	7/7 (100%)	-0.95	0	100	100	17, 19, 32, 33	0
2	B	7/7 (100%)	-1.02	0	100	100	19, 22, 28, 29	0
2	D	7/7 (100%)	-0.97	0	100	100	19, 22, 34, 34	0
All	All	28/28 (100%)	-0.98	0	100	100	17, 24, 33, 34	0

There are no RSRZ outliers to report.

5.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.3 Carbohydrates

There are no monosaccharides in this entry.

5.4 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, 95^{th} 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(Å^2)	Q<0.9
3	GOL	B	1973	6/6	0.82	0.15	36,39,40,43	0

5.5 Other polymers (i)

There are no such residues in this entry.