



wwPDB X-ray Structure Validation Summary Report

Mar 1, 2014 – 12:28 AM GMT

PDB ID : 1C0A
Title : CRYSTAL STRUCTURE OF THE E. COLI ASPARTYL-TRNA SYN-
THETASE : TRNAASP : ASPARTYL-ADENYLATE COMPLEX
Authors : Eiler, S.; Dock-Bregeon, A.-C.; Moulinier, L.; Thierry, J.-C.; Moras, D.
Deposited on : 1999-07-15
Resolution : 2.40 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

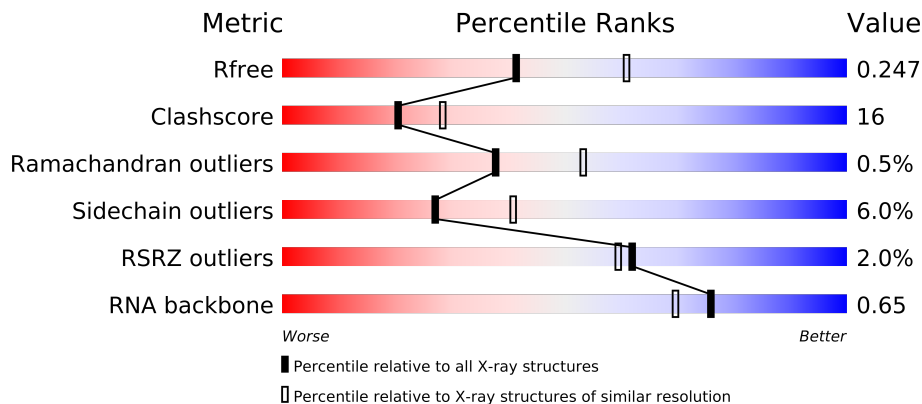
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.15 2013
Xtriage (Phenix)	:	dev-1323
EDS	:	stable22639
Percentile statistics	:	21963
Refmac	:	5.8.0049
CCP4	:	6.3.0 (Settle)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.40 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}	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)
RNA backbone	1838	1029 (3.00-1.80)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	B	77	
2	A	585	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	SO4	B	701	-	X
4	AMP	A	800	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6820 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

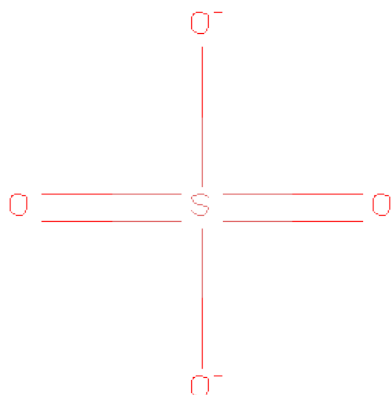
- Molecule 1 is a RNA chain called ASPARTYL TRNA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	77	Total	C	N	O	P	S	0	0	0
			1655	740	290	547	77	1			

- Molecule 2 is a protein called ASPARTYL TRNA SYNTHETASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	585	Total	C	N	O	S	0	0	0
			4592	2900	804	862	26			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



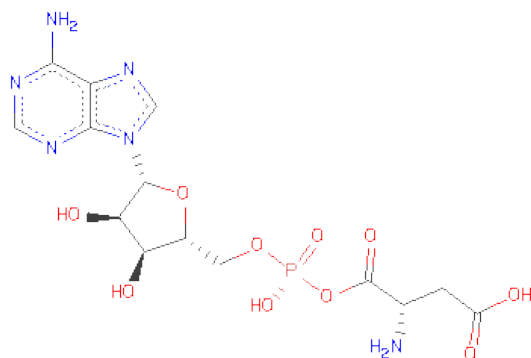
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 5 is ASPARTYL-ADENOSINE-5'-MONOPHOSPHATE (three-letter code: AMO) (formula: $C_{14}H_{19}N_6O_{10}P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			31	14	6	10	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	407	Total 407	O 407	0	0
6	B	107	Total 107	O 107	0	0

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 errors 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.

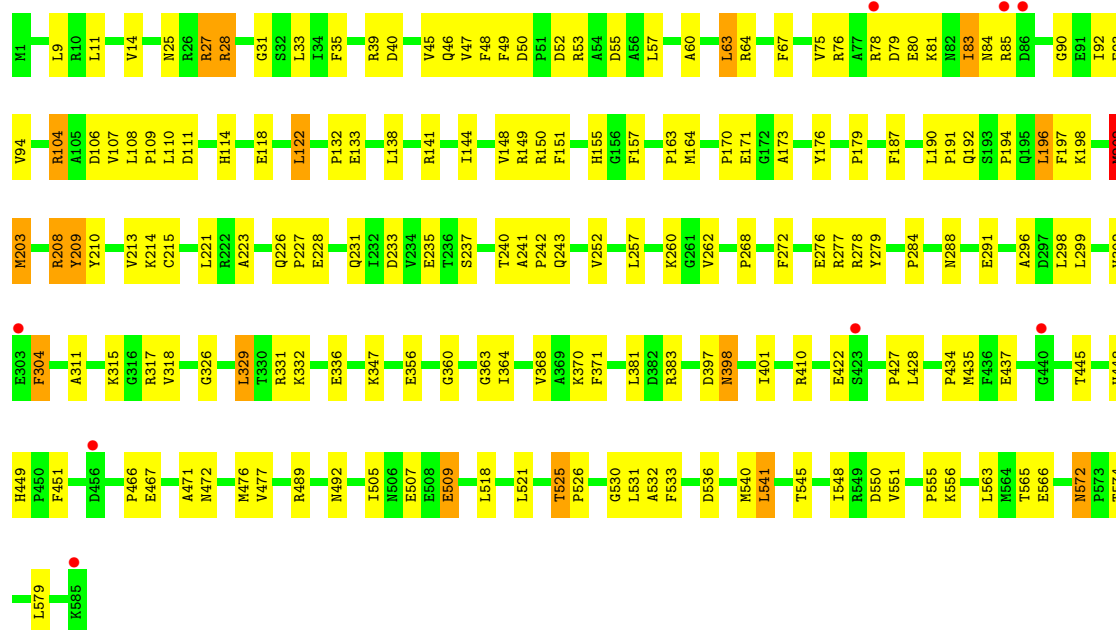
• Molecule 1: ASPARTYL TRNA

Chain B: 



• Molecule 2: ASPARTYL TRNA SYNTHETASE

Chain A: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	101.20Å 101.20Å 231.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 2.40 14.89 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.0 (12.00-2.40) 98.1 (14.89-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.78 (at 2.39Å)	Xtriage
Refinement program	CNS 0.4	Depositor
R, R_{free}	0.208 , 0.249 0.207 , 0.247	Depositor DCC
R_{free} test set	3555 reflections (8.22%)	DCC
Wilson B-factor (Å ²)	25.5	Xtriage
Anisotropy	0.172	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 29.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 46829 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6820	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.61% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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: 5MU, AMO, G7M, H2U, SO4, AMP, 4SU, QUO, PSU

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	B	0.73	3/1628 (0.2%)	0.99	6/2534 (0.2%)
2	A	0.52	1/4678 (0.0%)	0.79	7/6320 (0.1%)
All	All	0.58	4/6306 (0.1%)	0.85	13/8854 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	648	C	O3'-P	-18.15	1.39	1.61
1	B	646	G7M	O3'-P	-10.43	1.48	1.61
1	B	601	G	OP3-P	-7.26	1.52	1.61
2	A	398	ASN	C-N	-7.18	1.17	1.34

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	648	C	P-O3'-C3'	26.13	151.06	119.70
1	B	648	C	OP2-P-O3'	-13.40	75.72	105.20
2	A	398	ASN	O-C-N	-10.16	106.44	122.70
1	B	648	C	OP1-P-O3'	8.89	124.77	105.20
1	B	646	G7M	P-O3'-C3'	8.72	130.16	119.70

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit,

and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1655	0	850	43	0
2	A	4592	0	4589	144	0
3	B	5	0	0	0	0
4	A	23	0	12	2	0
5	A	31	0	17	0	0
6	A	407	0	0	12	0
6	B	107	0	0	1	0
All	All	6820	0	5468	185	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 16.

The worst 5 of 185 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:202:MET:HG3	2:A:237:SER:OG	1.65	0.96
2:A:78:ARG:HD2	2:A:83:ILE:HA	1.48	0.95
2:A:202:MET:HA	2:A:202:MET:HE2	1.50	0.94
2:A:505:ILE:HG23	2:A:509:GLU:HG2	1.51	0.92
1:B:647:U:H4'	1:B:648:C:H5'	1.56	0.86

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
2	A	583/585 (100%)	551 (94%)	29 (5%)	3 (0%)	38 53

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	80	GLU

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Mol	Chain	Res	Type
2	A	304	PHE
2	A	106	ASP

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	
2	A	486/486 (100%)	457 (94%)	29 (6%)	27	41

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	331	ARG
2	A	397	ASP
2	A	555	PRO
2	A	368	VAL
2	A	422	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
2	A	226	GLN
2	A	312	ASN
2	A	387	GLN
2	A	155	HIS
2	A	365	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	B	75/77 (97%)	8 (10%)	2 (2%)

5 of 8 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	B	609	A
1	B	617	C
1	B	618	G
1	B	619	G
1	B	620	H2U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	B	617	C
1	B	619	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

9 non-standard protein/DNA/RNA residues are 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$
1	4SU	B	608	1	19,21,22	4.65	2 (10%)	23,30,33	28.48	1 (4%)
1	H2U	B	616	1	19,21,22	1.06	2 (10%)	27,30,33	1.28	2 (7%)
1	H2U	B	620	1	19,21,22	0.84	1 (5%)	27,30,33	1.22	2 (7%)
1	H2U	B	620(A)	1	19,21,22	0.74	0	27,30,33	1.05	2 (7%)
1	QUO	B	634	1	33,35,36	1.27	4 (12%)	45,52,55	2.17	10 (22%)
1	G7M	B	646	1	24,26,27	1.21	2 (8%)	32,39,42	1.70	8 (25%)
1	5MU	B	654	1	20,22,23	0.84	1 (5%)	25,32,35	1.21	4 (16%)
1	PSU	B	655	1	19,21,22	2.11	3 (15%)	23,30,33	2.91	3 (13%)
1	PSU	B	665	1	19,21,22	2.10	2 (10%)	23,30,33	2.76	3 (13%)

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
1	4SU	B	608	1	-	0/6/25/26	0/2/2/2
1	H2U	B	616	1	-	0/8/38/39	0/2/2/2
1	H2U	B	620	1	-	0/8/38/39	0/2/2/2
1	H2U	B	620(A)	1	-	0/8/38/39	0/2/2/2
1	QUO	B	634	1	-	0/13/43/44	0/2/4/4
1	G7M	B	646	1	-	0/8/25/26	0/1/3/3
1	5MU	B	654	1	-	0/6/25/26	0/2/2/2
1	PSU	B	655	1	-	0/8/25/26	0/2/2/2
1	PSU	B	665	1	-	0/8/25/26	0/2/2/2

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	608	4SU	C4-S4	-19.70	1.29	1.67
1	B	655	PSU	C6-N1	-8.43	1.24	1.32
1	B	665	PSU	C6-N1	-8.39	1.24	1.32
1	B	634	QUO	C8-C7	-4.36	1.31	1.38
1	B	608	4SU	C5-C4	3.50	1.44	1.38

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	608	4SU	C4-N3-C2	136.53	127.44	121.60
1	B	655	PSU	O4'-C1'-C5	13.03	125.76	109.55
1	B	665	PSU	O4'-C1'-C5	12.37	124.94	109.55
1	B	634	QUO	C10-N11-C12	10.79	132.38	114.94
1	B	616	H2U	C5-C6-N1	5.50	116.88	110.71

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

3 ligands are 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	$\# Z > 2$
4	AMP	A	800	-	25,25,25	0.64	0	38,38,38	0.87	1 (2%)
5	AMO	A	831	-	33,33,33	2.80	2 (6%)	49,49,49	2.05	5 (10%)
3	SO4	B	701	-	4,4,4	0.73	0	6,6,6	0.27	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
4	AMP	A	800	-	-	0/10/26/26	0/1/3/3
5	AMO	A	831	-	-	0/21/39/39	0/1/3/3
3	SO4	B	701	-	-	0/0/0/0	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	831	AMO	O3P-C	-15.21	1.16	1.37
5	A	831	AMO	P-O3P	3.93	1.68	1.61

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	831	AMO	O3P-C-O	10.45	130.38	122.11
5	A	831	AMO	O3P-P-O5'	6.20	121.70	102.91
5	A	831	AMO	O2P-P-O3P	-4.15	90.44	104.44
5	A	831	AMO	P-O3P-C	3.91	132.37	121.39
5	A	831	AMO	O3P-C-CA	-2.86	107.55	115.06

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	B	77/77 (100%)	0.48	5 (6%) 18 17	16, 39, 71, 89	0
2	A	585/585 (100%)	-0.40	8 (1%) 72 71	7, 22, 45, 65	0
All	All	662/662 (100%)	-0.29	13 (1%) 62 59	7, 25, 51, 89	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	617	C	8.5
1	B	643	G	4.4
2	A	585	LYS	3.6
1	B	637	A	2.7
1	B	676	A	2.7

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	H2U	B	620	20/21	0.38	3.01	72,82,83,83	0
1	5MU	B	654	21/22	0.23	1.24	37,44,47,50	0
1	PSU	B	655	20/21	0.21	1.12	35,46,51,52	0
1	H2U	B	616	20/21	0.36	0.83	51,79,83,83	0
1	PSU	B	665	20/21	0.14	0.34	27,33,36,38	0
1	QUO	B	634	32/33	0.23	0.27	59,65,76,76	0
1	G7M	B	646	24/25	0.14	0.16	42,45,47,48	0
1	4SU	B	608	20/21	0.09	-1.44	23,26,29,31	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	H2U	B	620(A)	20/21	0.38	-	72,80,83,83	0

6.3 Carbohydrates ⓘ

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. 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	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	SO4	B	701	5/5	0.17	9.26	50,51,51,52	0
4	AMP	A	800	23/23	0.25	2.66	77,79,89,89	0
5	AMO	A	831	31/31	0.15	1.31	8,15,32,40	0

6.5 Other polymers ⓘ

There are no such residues in this entry.