wwPDB X-ray Structure Validation Summary Report (i)

Dec 3, 2023 – 09:34 pm GMT

PDB ID	:	2C46
Title	:	CRYSTAL STRUCTURE OF THE HUMAN RNA guanylyltransferase and 5'- phosphatase
Authors	:	Debreczeni, J.; Johansson, C.; Longman, E.; Gileadi, O.; SavitskySmee, P.; Smee, C.; Bunkoczi, G.; Ugochukwu, E.; von Delft, F.; Sundstrom, M.; Weigelt, J.; Arrowsmith, C.; Edwards, A.; Knapp, S.
Deposited on	:	2005-10-15
Resolution	:	1.60 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 (1)) were used in the production of this report:

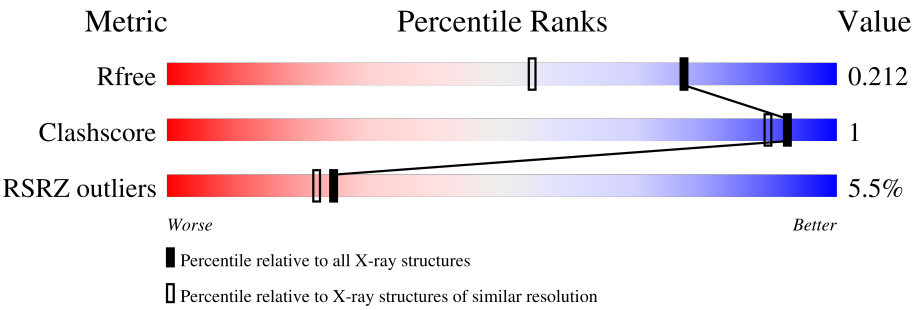
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 of 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 <=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	241	2%, 79%, •, 17%
1	B	241	2%, 80%, •, 17%
1	C	241	3%, 80%, •, 18%
1	D	241	10%, 74%, 5%, 22%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6719 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 MRNA CAPPING ENZYME.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	200	1603	1030	274	287	12	0	2	0
1	B	201	1628	1041	274	301	12	0	5	0
1	C	197	1553	995	262	285	11	0	0	0
1	D	189	1475	946	244	274	11	0	0	0

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-21	MET	-	expression tag	UNP O60942
A	-20	HIS	-	expression tag	UNP O60942
A	-19	HIS	-	expression tag	UNP O60942
A	-18	HIS	-	expression tag	UNP O60942
A	-17	HIS	-	expression tag	UNP O60942
A	-16	HIS	-	expression tag	UNP O60942
A	-15	HIS	-	expression tag	UNP O60942
A	-14	SER	-	expression tag	UNP O60942
A	-13	SER	-	expression tag	UNP O60942
A	-12	GLY	-	expression tag	UNP O60942
A	-11	VAL	-	expression tag	UNP O60942
A	-10	ASP	-	expression tag	UNP O60942
A	-9	LEU	-	expression tag	UNP O60942
A	-8	GLY	-	expression tag	UNP O60942
A	-7	THR	-	expression tag	UNP O60942
A	-6	GLU	-	expression tag	UNP O60942
A	-5	ASN	-	expression tag	UNP O60942
A	-4	LEU	-	expression tag	UNP O60942
A	-3	TYR	-	expression tag	UNP O60942
A	-2	PHE	-	expression tag	UNP O60942
A	-1	GLN	-	expression tag	UNP O60942

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP O60942
A	212	THR	PRO	conflict	UNP O60942
B	-21	MET	-	expression tag	UNP O60942
B	-20	HIS	-	expression tag	UNP O60942
B	-19	HIS	-	expression tag	UNP O60942
B	-18	HIS	-	expression tag	UNP O60942
B	-17	HIS	-	expression tag	UNP O60942
B	-16	HIS	-	expression tag	UNP O60942
B	-15	HIS	-	expression tag	UNP O60942
B	-14	SER	-	expression tag	UNP O60942
B	-13	SER	-	expression tag	UNP O60942
B	-12	GLY	-	expression tag	UNP O60942
B	-11	VAL	-	expression tag	UNP O60942
B	-10	ASP	-	expression tag	UNP O60942
B	-9	LEU	-	expression tag	UNP O60942
B	-8	GLY	-	expression tag	UNP O60942
B	-7	THR	-	expression tag	UNP O60942
B	-6	GLU	-	expression tag	UNP O60942
B	-5	ASN	-	expression tag	UNP O60942
B	-4	LEU	-	expression tag	UNP O60942
B	-3	TYR	-	expression tag	UNP O60942
B	-2	PHE	-	expression tag	UNP O60942
B	-1	GLN	-	expression tag	UNP O60942
B	0	SER	-	expression tag	UNP O60942
B	212	THR	PRO	conflict	UNP O60942
C	-21	MET	-	expression tag	UNP O60942
C	-20	HIS	-	expression tag	UNP O60942
C	-19	HIS	-	expression tag	UNP O60942
C	-18	HIS	-	expression tag	UNP O60942
C	-17	HIS	-	expression tag	UNP O60942
C	-16	HIS	-	expression tag	UNP O60942
C	-15	HIS	-	expression tag	UNP O60942
C	-14	SER	-	expression tag	UNP O60942
C	-13	SER	-	expression tag	UNP O60942
C	-12	GLY	-	expression tag	UNP O60942
C	-11	VAL	-	expression tag	UNP O60942
C	-10	ASP	-	expression tag	UNP O60942
C	-9	LEU	-	expression tag	UNP O60942
C	-8	GLY	-	expression tag	UNP O60942
C	-7	THR	-	expression tag	UNP O60942
C	-6	GLU	-	expression tag	UNP O60942
C	-5	ASN	-	expression tag	UNP O60942

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	LEU	-	expression tag	UNP O60942
C	-3	TYR	-	expression tag	UNP O60942
C	-2	PHE	-	expression tag	UNP O60942
C	-1	GLN	-	expression tag	UNP O60942
C	0	SER	-	expression tag	UNP O60942
C	212	THR	PRO	conflict	UNP O60942
D	-21	MET	-	expression tag	UNP O60942
D	-20	HIS	-	expression tag	UNP O60942
D	-19	HIS	-	expression tag	UNP O60942
D	-18	HIS	-	expression tag	UNP O60942
D	-17	HIS	-	expression tag	UNP O60942
D	-16	HIS	-	expression tag	UNP O60942
D	-15	HIS	-	expression tag	UNP O60942
D	-14	SER	-	expression tag	UNP O60942
D	-13	SER	-	expression tag	UNP O60942
D	-12	GLY	-	expression tag	UNP O60942
D	-11	VAL	-	expression tag	UNP O60942
D	-10	ASP	-	expression tag	UNP O60942
D	-9	LEU	-	expression tag	UNP O60942
D	-8	GLY	-	expression tag	UNP O60942
D	-7	THR	-	expression tag	UNP O60942
D	-6	GLU	-	expression tag	UNP O60942
D	-5	ASN	-	expression tag	UNP O60942
D	-4	LEU	-	expression tag	UNP O60942
D	-3	TYR	-	expression tag	UNP O60942
D	-2	PHE	-	expression tag	UNP O60942
D	-1	GLN	-	expression tag	UNP O60942
D	0	SER	-	expression tag	UNP O60942
D	212	THR	PRO	conflict	UNP O60942

- Molecule 2 is water.

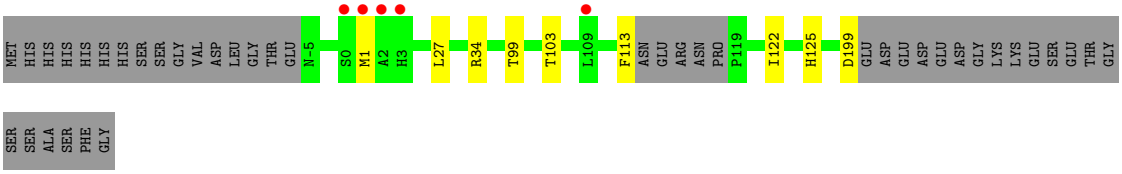
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	146	146	146	0	0
			Total	O		
2	B	147	147	147	0	0
			Total	O		
2	C	83	83	83	0	0
			Total	O		
2	D	84	84	84	0	0

3 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.

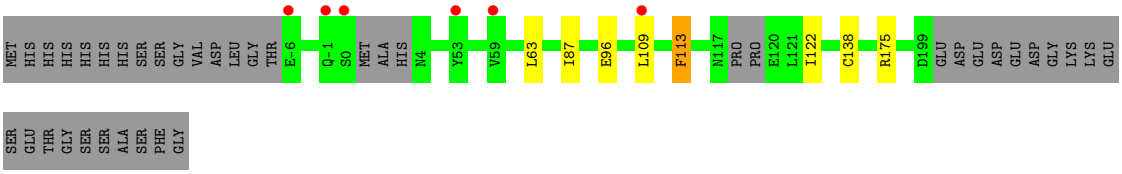
• Molecule 1: MRNA CAPPING ENZYME

Chain A:



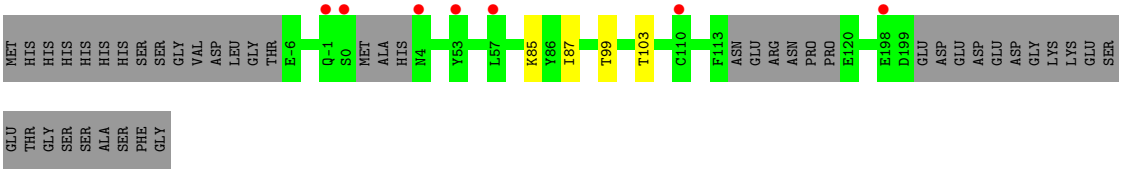
• Molecule 1: MRNA CAPPING ENZYME

Chain B:



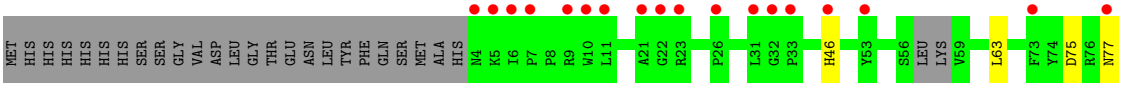
• Molecule 1: MRNA CAPPING ENZYME

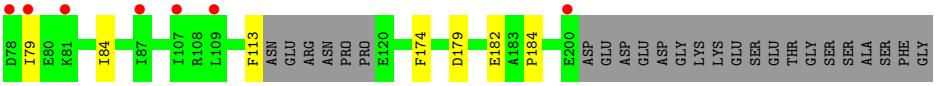
Chain C:



• Molecule 1: MRNA CAPPING ENZYME

Chain D:




D78
I79
E80
K81
I84
I87
I107
R108
L109
F113
ASN
GLU
ARG
ASN
PRO
PRO
E120
F174
D179
E182
A183
P184
E200
ASP
GLU
ASP
GLU
ASP
GLY
LYS
LYS
GLU
SER
GLU
THR
GLY
SER
SER
ALA
SER
PHE
GLY

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	60.40Å 161.60Å 60.70Å 90.00° 104.70° 90.00°	Depositor
Resolution (Å)	80.85 – 1.60 47.94 – 1.60	Depositor EDS
% Data completeness (in resolution range)	90.4 (80.85-1.60) 89.1 (47.94-1.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.07 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.204 , 0.234 0.202 , 0.212	Depositor DCC
R_{free} test set	6714 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å^2)	19.9	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 48.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.43$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	0.116 for l,-k,h	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6719	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% of the height of the origin peak. No significant pseudotranslation is detected.*

[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.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.58	0/1654	0.70	1/2242 (0.0%)
1	B	0.63	1/1683 (0.1%)	0.71	2/2281 (0.1%)
1	C	0.47	0/1594	0.61	0/2163
1	D	0.43	0/1515	0.59	0/2060
All	All	0.54	1/6446 (0.0%)	0.66	3/8746 (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	B	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	138	CYS	CB-SG	-5.03	1.73	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	175	ARG	NE-CZ-NH2	-5.83	117.38	120.30
1	B	175	ARG	NE-CZ-NH1	5.73	123.16	120.30
1	A	199	ASP	CB-CG-OD2	5.13	122.92	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	113	PHE	Peptide

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	1603	0	1542	5	0
1	B	1628	0	1563	4	0
1	C	1553	0	1464	2	0
1	D	1475	0	1373	7	0
2	A	146	0	0	0	0
2	B	147	0	0	1	0
2	C	83	0	0	0	0
2	D	84	0	0	0	0
All	All	6719	0	5942	18	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 1.

The worst 5 of 18 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:99:THR:O	1:A:103:THR:HG23	1.85	0.76
1:D:75:ASP:OD1	1:D:77:ASN:ND2	2.39	0.54
1:D:46:HIS:ND1	1:D:46:HIS:N	2.44	0.54
1:B:113:PHE:HB2	1:B:122:ILE:HD11	1.91	0.53
1:D:174:PHE:CE1	1:D:184:PRO:HD3	2.46	0.51

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains (i)

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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	200/241 (82%)	0.48	5 (2%)	57	55	21, 30, 42, 47	0
1	B	201/241 (83%)	0.47	6 (2%)	50	48	21, 30, 42, 52	0
1	C	197/241 (81%)	0.49	7 (3%)	42	40	21, 31, 39, 45	0
1	D	189/241 (78%)	1.00	25 (13%)	3	2	22, 32, 39, 46	0
All	All	787/964 (81%)	0.60	43 (5%)	25	22	21, 31, 41, 52	0

The worst 5 of 43 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ALA	6.0
1	D	6	ILE	5.7
1	A	1	MET	4.9
1	C	0	SER	4.4
1	A	3	HIS	4.4

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 monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.