



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 2C46 / pdb_00002c46
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 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

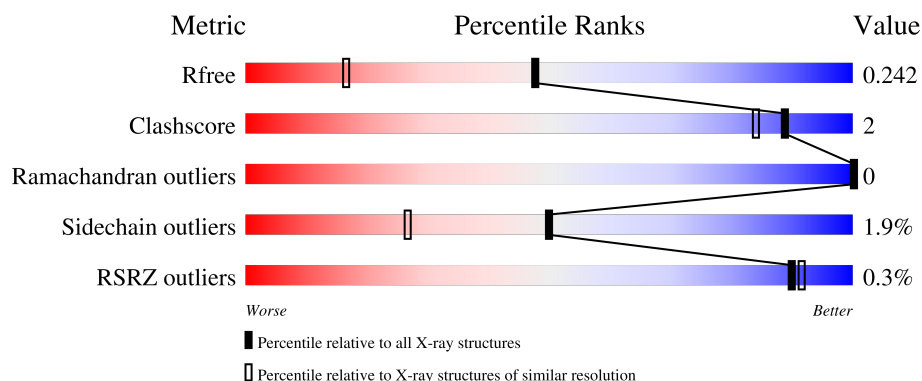
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (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 $\leq 5\%$. 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	241	 78% 5% 17%
1	B	241	 78% 5% 17%
1	C	241	 79% . 18%
1	D	241	 72% 6% 22%

2 Entry composition

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

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
2	A	146	Total O 146 146	0	0
2	B	147	Total O 147 147	0	0
2	C	83	Total O 83 83	0	0
2	D	84	Total O 84 84	0	0

- Molecule 1: MRNA CAPPING ENZYME

[illegible]

- Molecule 1: MRNA CAPPING ENZYME

GLU	ASP	GLY	LYS	GLU	SER	THR	GLY	SER	SER	ALA	SER	PHE	GLY	MET	HIS	HIS	HIS	HIS	HIS	SER	VAL	GLY	ASP	LEU	GLY	THR															
														E-6	SQ	MET	HIS	N4	Q18	R23	L27	N49	S56	L63	I87	R88	L89	E96	L109	F113	N114	N117	PRO	E120	L121	I122	M145	D199	ASP	GLU	ASP

- Molecule 1: MRNA CAPPING ENZYME

[illegible]

- Molecule 1: MRNA CAPPING ENZYME

[illegible]

4 Data and refinement statistics

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 80.80 – 1.60	Depositor EDS
% Data completeness (in resolution range)	90.4 (80.85-1.60) 89.1 (80.80-1.60)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.204 , 0.234 (Not available) , 0.242	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)	0.37 , 38.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	0.116 for l,-k,h	Xtriage
F_o, F_c correlation	0.96	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.*

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

5.1 Standard geometry

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	0.76	1/1654 (0.1%)	0.86	2/2242 (0.1%)
1	B	0.78	0/1683	0.90	2/2281 (0.1%)
1	C	0.59	0/1594	0.80	2/2163 (0.1%)
1	D	0.57	0/1515	0.79	0/2060
All	All	0.69	1/6446 (0.0%)	0.84	6/8746 (0.1%)

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	A	157	ALA	CA-CB	-5.21	1.44	1.53

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	18	GLN	CA-C-N	-6.08	113.50	119.76
1	B	18	GLN	C-N-CA	-6.08	113.50	119.76
1	A	183	ALA	CA-C-N	-6.06	114.14	120.38
1	A	183	ALA	C-N-CA	-6.06	114.14	120.38
1	C	32	GLY	CA-C-N	5.01	125.28	119.47
1	C	32	GLY	C-N-CA	5.01	125.28	119.47

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 ⓘ

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	6	0
1	B	1628	0	1563	6	0
1	C	1553	0	1464	2	0
1	D	1475	0	1373	9	0
2	A	146	0	0	1	0
2	B	147	0	0	2	0
2	C	83	0	0	0	0
2	D	84	0	0	0	0
All	All	6719	0	5942	23	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 2.

All (23) 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
1:A:1:MET:HE2	1:A:34:ARG:CB	2.42	0.50
1:A:27:LEU:HG	1:A:125:HIS:HB3	1.93	0.50
1:B:23:ARG:CZ	1:B:145[B]:MET:HE3	2.42	0.50
1:B:96:GLU:OE1	2:B:2074:HOH:O	2.19	0.49
1:A:49:MET:HE3	2:A:2036:HOH:O	2.13	0.48
1:D:63:LEU:HB2	1:D:113:PHE:CZ	2.49	0.48
1:A:1:MET:CE	1:A:34:ARG:CB	2.92	0.47
1:B:49:MET:HE3	2:B:2034:HOH:O	2.17	0.45
1:C:99:THR:O	1:C:103:THR:HG23	2.17	0.45
1:B:87[B]:ILE:HG21	1:B:109:LEU:HD21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:ILE:HG22	1:D:84:ILE:HB	2.00	0.43
1:C:85:LYS:HZ3	1:C:87:ILE:CG1	2.32	0.42
1:D:134:GLY:C	1:D:164:ILE:HD11	2.44	0.42
1:A:113:PHE:HB2	1:A:122:ILE:HD11	2.03	0.41
1:D:179:ASP:HB3	1:D:182:GLU:HG3	2.02	0.41
1:D:75:ASP:CG	1:D:77:ASN:ND2	2.79	0.40
1:B:63:LEU:HD11	1:B:87[B]:ILE:HG22	2.03	0.40
1:D:179:ASP:HB3	1:D:182:GLU:CG	2.51	0.40

There are no symmetry-related clashes.

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	
1	A	198/241 (82%)	189 (96%)	9 (4%)	0	100	100
1	B	200/241 (83%)	194 (97%)	6 (3%)	0	100	100
1	C	191/241 (79%)	185 (97%)	6 (3%)	0	100	100
1	D	183/241 (76%)	177 (97%)	6 (3%)	0	100	100
All	All	772/964 (80%)	745 (96%)	27 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	168/212 (79%)	166 (99%)	2 (1%)	63	43
1	B	173/212 (82%)	169 (98%)	4 (2%)	44	20
1	C	160/212 (76%)	158 (99%)	2 (1%)	61	40
1	D	152/212 (72%)	148 (97%)	4 (3%)	40	17
All	All	653/848 (77%)	641 (98%)	12 (2%)	50	28

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	88	LYS
1	A	188	LEU
1	B	27	LEU
1	B	56	SER
1	B	89	LEU
1	B	114	ASN
1	C	4	ASN
1	C	27	LEU
1	D	27	LEU
1	D	46	HIS
1	D	51	SER
1	D	89	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	90	GLN
1	A	158	GLN
1	B	90	GLN
1	B	158	GLN
1	C	69	ASN
1	C	90	GLN
1	D	77	ASN

5.3.3 RNA ⓘ

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 oligosaccharides 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%)	-0.68	0	100 100	16, 30, 42, 47	2 (1%)
1	B	201/241 (83%)	-0.70	0	100 100	16, 30, 42, 52	5 (2%)
1	C	197/241 (81%)	-0.71	1 (0%)	87 90	21, 31, 39, 45	0
1	D	189/241 (78%)	-0.49	1 (0%)	87 90	22, 32, 39, 46	0
All	All	787/964 (81%)	-0.65	2 (0%)	90 91	16, 31, 41, 52	7 (0%)

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	196	ASP	2.1
1	D	59	VAL	2.0

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 oligosaccharides 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.