



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 4QRH
Title : Molecular mechanism and evolution of guanylate kinase regulation by (p)ppGpp
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Deposited on : 2014-07-01
Resolution : 1.65 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
<http://wwpdb.org/validation/2016/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
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

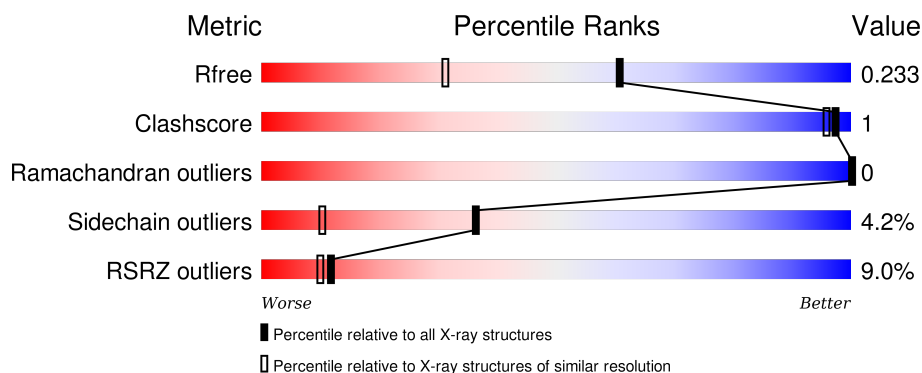
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.65 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}	91344	1226 (1.66-1.66)
Clashscore	102246	1323 (1.66-1.66)
Ramachandran outliers	100387	1295 (1.66-1.66)
Sidechain outliers	100360	1295 (1.66-1.66)
RSRZ outliers	91569	1227 (1.66-1.66)

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. 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	210	<div> <div>7%</div> <div>81%</div> <div>14%</div> </div>
1	B	210	<div> <div>8%</div> <div>83%</div> <div>5%</div> <div>11%</div> </div>
1	C	210	<div> <div>9%</div> <div>82%</div> <div>6%</div> <div>12%</div> </div>
1	D	210	<div> <div>8%</div> <div>81%</div> <div>6%</div> <div>12%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	EDO	D	303	-	-	-	X
6	EDO	D	305	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 6870 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 Guanylate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	180	Total	C	N	O	S	0	4	0
			1493	952	249	283	9			
1	B	186	Total	C	N	O	S	0	7	0
			1564	995	263	298	8			
1	C	185	Total	C	N	O	S	0	3	0
			1523	972	251	292	8			
1	D	184	Total	C	N	O	S	0	2	0
			1513	962	254	290	7			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP W6E076
A	-1	ASN	-	EXPRESSION TAG	UNP W6E076
A	0	ALA	-	EXPRESSION TAG	UNP W6E076
B	-2	SER	-	EXPRESSION TAG	UNP W6E076
B	-1	ASN	-	EXPRESSION TAG	UNP W6E076
B	0	ALA	-	EXPRESSION TAG	UNP W6E076
C	-2	SER	-	EXPRESSION TAG	UNP W6E076
C	-1	ASN	-	EXPRESSION TAG	UNP W6E076
C	0	ALA	-	EXPRESSION TAG	UNP W6E076
D	-2	SER	-	EXPRESSION TAG	UNP W6E076
D	-1	ASN	-	EXPRESSION TAG	UNP W6E076
D	0	ALA	-	EXPRESSION TAG	UNP W6E076

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

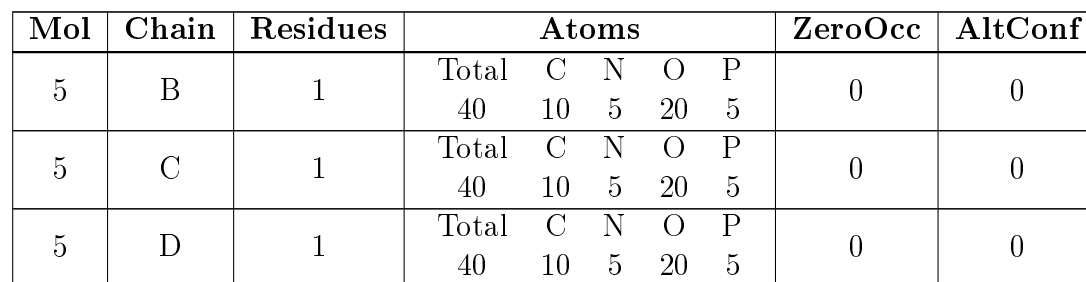
- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).


Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K).

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

- Molecule 5 is GUANOSINE 5'-(TETRAHYDROGEN TRIPHOSPHATE) 3'-(TRIHYDROGEN DIPHOSPHATE) (three-letter code: 0O2) (formula: C₁₀H₁₈N₅O₂₀P₅).



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- The diagram shows the chemical structure of 1,2-ethanediol (EDO). It consists of a two-carbon chain. The first carbon is labeled C1 and is bonded to a hydroxyl group (HO) labeled O1. The second carbon is labeled C2 and is bonded to a hydroxyl group (OH) labeled O2. The hydroxyl groups are shown in red, and the carbon labels are in green.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			4	2	2		



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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	0
			4	2	2		
6	D	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	151	Total	O	0	0
			151	151		
7	B	184	Total	O	0	0
			184	184		
7	C	161	Total	O	0	0
			161	161		
7	D	133	Total	O	0	0
			133	133		

K197	
Y198	
R199	
K200	
MET	
ILE	
LEU	
GLU	
ALA	
LYS	
LYS	

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.49 Å 93.96 Å 85.26 Å 90.00° 111.09° 90.00°	Depositor
Resolution (Å)	39.26 – 1.65 39.26 – 1.64	Depositor EDS
% Data completeness (in resolution range)	99.3 (39.26-1.65) 99.3 (39.26-1.64)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.62	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.09 (at 1.64 Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.201 , 0.227 0.212 , 0.233	Depositor DCC
R_{free} test set	6135 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.020	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.1	EDS
Estimated twinning fraction	0.013 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 123163 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6870	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.26% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: SO4, MG, OO2, K, EDO

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	0.35	0/1529	0.59	0/2054
1	B	0.35	0/1606	0.58	0/2156
1	C	0.35	0/1559	0.59	0/2096
1	D	0.35	0/1543	0.58	0/2074
All	All	0.35	0/6237	0.59	0/8380

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1493	0	1481	3	0
1	B	1564	0	1554	4	0
1	C	1523	0	1507	4	0
1	D	1513	0	1492	6	0
2	A	5	0	0	0	0
2	C	5	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	B	40	0	16	0	0
5	C	40	0	17	0	0
5	D	40	0	15	0	0
6	D	12	0	18	3	0
7	A	151	0	0	0	0
7	B	184	0	0	0	0
7	C	161	0	0	1	0
7	D	133	0	0	0	0
All	All	6870	0	6100	15	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 15 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:40[B]:MET:SD	1:A:58:LYS:HG3	2.37	0.65
1:D:44:GLN:HB2	6:D:305:EDO:HO2	1.72	0.54
1:C:129:LEU:HD21	1:C:157:GLU:HG2	1.90	0.53
1:C:25:ARG:HG3	1:C:177:LYS:HD3	1.91	0.52
1:A:182[B]:CYS:SG	1:B:182[B]:CYS:O	2.68	0.52

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	180/210 (86%)	177 (98%)	3 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	189/210 (90%)	187 (99%)	2 (1%)	0	100	100
1	C	184/210 (88%)	180 (98%)	4 (2%)	0	100	100
1	D	182/210 (87%)	179 (98%)	3 (2%)	0	100	100
All	All	735/840 (88%)	723 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	163/185 (88%)	157 (96%)	6 (4%)	41	13
1	B	171/185 (92%)	164 (96%)	7 (4%)	37	10
1	C	166/185 (90%)	157 (95%)	9 (5%)	27	6
1	D	165/185 (89%)	156 (94%)	9 (6%)	27	5
All	All	665/740 (90%)	634 (95%)	31 (5%)	36	8

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	105	GLU
1	C	155	ARG
1	D	147	ILE
1	C	128	SER
1	C	162	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	71	GLN
1	D	170	ASN
1	C	181	GLN

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Mol	Chain	Res	Type
1	A	152	ASN
1	D	81	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 14 ligands modelled in this entry, 6 are monoatomic - leaving 8 for Mogul analysis.

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$
2	SO4	A	301	-	4,4,4	0.31	0	6,6,6	0.28	0
5	OO2	B	303	3	31,42,42	1.64	4 (12%)	46,68,68	1.85	8 (17%)
2	SO4	C	303	-	4,4,4	0.31	0	6,6,6	0.24	0
5	OO2	C	304	3	31,42,42	1.62	4 (12%)	46,68,68	1.77	11 (23%)
6	EDO	D	303	-	3,3,3	0.58	0	2,2,2	0.19	0
6	EDO	D	304	-	3,3,3	0.49	0	2,2,2	0.39	0
6	EDO	D	305	-	3,3,3	0.48	0	2,2,2	0.64	0
5	OO2	D	306	3	31,42,42	1.54	4 (12%)	46,68,68	1.88	10 (21%)

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
2	SO4	A	301	-	-	0/0/0/0	0/0/0/0
5	OO2	B	303	3	-	0/29/49/49	0/3/3/3
2	SO4	C	303	-	-	0/0/0/0	0/0/0/0
5	OO2	C	304	3	-	0/29/49/49	0/3/3/3
6	EDO	D	303	-	-	0/1/1/1	0/0/0/0
6	EDO	D	304	-	-	0/1/1/1	0/0/0/0
6	EDO	D	305	-	-	0/1/1/1	0/0/0/0
5	OO2	D	306	3	-	0/29/49/49	0/3/3/3

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	306	OO2	C2'-C3'	-3.06	1.46	1.53
5	B	303	OO2	C2'-C3'	-2.73	1.46	1.53
5	C	304	OO2	C2'-C3'	-2.55	1.47	1.53
5	B	303	OO2	O4'-C4'	2.14	1.50	1.45
5	D	306	OO2	O4'-C4'	2.27	1.50	1.45

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	306	OO2	C4'-O4'-C1'	-5.80	103.34	109.72
5	B	303	OO2	C4'-O4'-C1'	-5.62	103.55	109.72
5	C	304	OO2	C4'-O4'-C1'	-4.69	104.57	109.72
5	D	306	OO2	C4-C5-N7	-4.25	105.57	109.48
5	C	304	OO2	N3-C2-N1	-4.21	121.03	127.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	D	305	EDO	3	0

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 [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	180/210 (85%)	0.36	15 (8%) 14 12	14, 25, 55, 75	0
1	B	186/210 (88%)	0.35	16 (8%) 13 11	14, 23, 53, 73	0
1	C	185/210 (88%)	0.44	19 (10%) 9 7	14, 24, 63, 89	0
1	D	184/210 (87%)	0.47	16 (8%) 13 11	14, 23, 59, 86	0
All	All	735/840 (87%)	0.41	66 (8%) 12 10	14, 24, 59, 89	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	147	ILE	15.2
1	D	198	TYR	8.2
1	C	151	ILE	8.2
1	A	3	ASN	7.2
1	C	132	LEU	6.9

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 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. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	EDO	D	303	4/4	0.91	0.24	13.22	27,27,27,29	0
6	EDO	D	305	4/4	0.93	0.16	2.34	19,21,23,23	0
5	0O2	B	303	40/40	0.94	0.10	0.80	13,22,58,59	0
5	0O2	C	304	40/40	0.95	0.09	0.57	14,21,57,59	0
5	0O2	D	306	40/40	0.96	0.10	0.39	12,17,55,57	0
4	K	D	302	1/1	1.00	0.08	-0.15	15,15,15,15	0
6	EDO	D	304	4/4	0.94	0.09	-0.50	23,24,24,25	0
4	K	B	302	1/1	1.00	0.07	-0.58	14,14,14,14	0
2	SO4	A	301	5/5	0.97	0.07	-0.69	31,32,34,34	0
4	K	C	302	1/1	0.99	0.06	-1.07	15,15,15,15	0
2	SO4	C	303	5/5	0.98	0.06	-2.75	24,24,25,26	0
3	MG	B	301	1/1	0.98	0.08	-	21,21,21,21	0
3	MG	C	301	1/1	0.99	0.07	-	22,22,22,22	0
3	MG	D	301	1/1	0.96	0.12	-	23,23,23,23	0

6.5 Other polymers

There are no such residues in this entry.