



Full wwPDB X-ray Structure Validation Report i

Mar 18, 2024 – 04:36 pm GMT

PDB ID : 8ODO
Title : Structure of human guanylylated RTCB in complex with Archease
Authors : Kopp, J.; Gerber, J.L.; Peschek, J.
Deposited on : 2023-03-09
Resolution : 2.20 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 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
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
buster-report : 1.1.7 (2018)
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

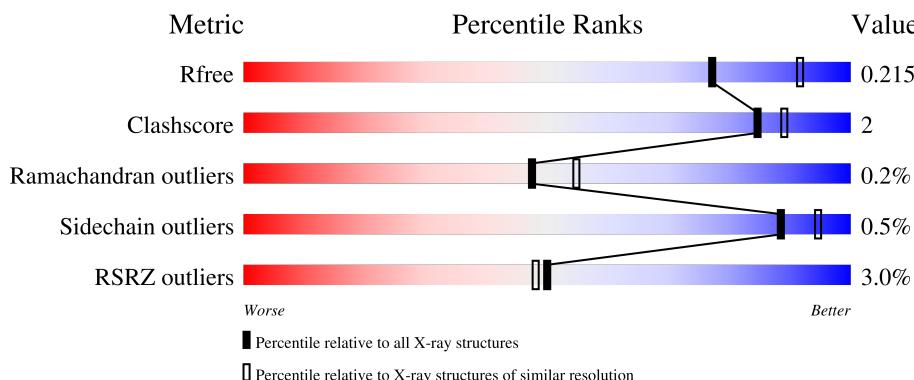
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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.



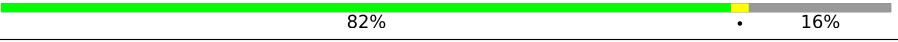
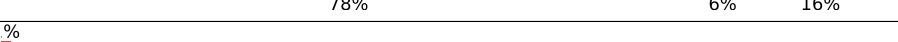
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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.



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Mol	Chain	Length	Quality of chain		
2	D	200		82%	• 16%
2	F	200		78%	6% 16%
2	H	200		84%	• 15%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 21728 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 RNA-splicing ligase RtcB homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	503	Total	C	N	O	S	0	0	0
			3855	2416	691	720	28			
1	C	503	Total	C	N	O	S	0	0	0
			3855	2416	691	720	28			
1	E	503	Total	C	N	O	S	0	0	0
			3855	2416	691	720	28			
1	G	503	Total	C	N	O	S	0	0	0
			3855	2416	691	720	28			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q9Y3I0
A	0	ALA	-	expression tag	UNP Q9Y3I0
C	-1	GLY	-	expression tag	UNP Q9Y3I0
C	0	ALA	-	expression tag	UNP Q9Y3I0
E	-1	GLY	-	expression tag	UNP Q9Y3I0
E	0	ALA	-	expression tag	UNP Q9Y3I0
G	-1	GLY	-	expression tag	UNP Q9Y3I0
G	0	ALA	-	expression tag	UNP Q9Y3I0

- Molecule 2 is a protein called Protein archease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	169	Total	C	N	O	S	0	0	0
			1387	886	219	276	6			
2	D	168	Total	C	N	O	S	0	0	0
			1382	883	218	275	6			
2	F	168	Total	C	N	O	S	0	0	0
			1382	883	218	275	6			
2	H	170	Total	C	N	O	S	0	0	0
			1394	891	220	277	6			

There are 84 discrepancies between the modelled and reference sequences:

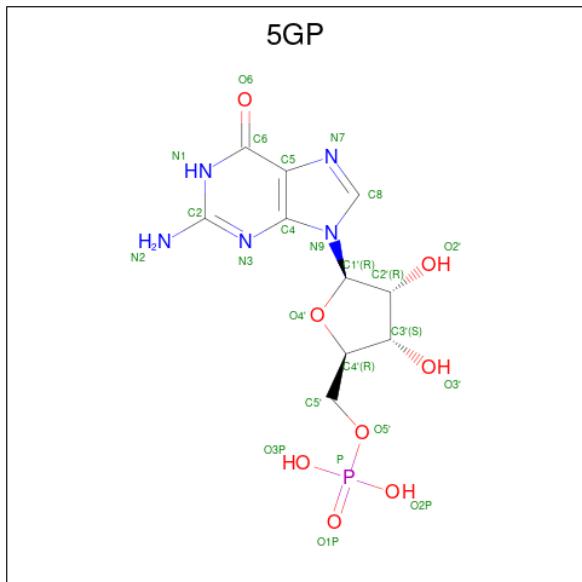
Chain	Residue	Modelled	Actual	Comment	Reference
B	-20	MET	-	initiating methionine	UNP A8K0B5
B	-19	GLY	-	expression tag	UNP A8K0B5
B	-18	SER	-	expression tag	UNP A8K0B5
B	-17	SER	-	expression tag	UNP A8K0B5
B	-16	HIS	-	expression tag	UNP A8K0B5
B	-15	HIS	-	expression tag	UNP A8K0B5
B	-14	HIS	-	expression tag	UNP A8K0B5
B	-13	HIS	-	expression tag	UNP A8K0B5
B	-12	HIS	-	expression tag	UNP A8K0B5
B	-11	HIS	-	expression tag	UNP A8K0B5
B	-10	SER	-	expression tag	UNP A8K0B5
B	-9	SER	-	expression tag	UNP A8K0B5
B	-8	GLY	-	expression tag	UNP A8K0B5
B	-7	LEU	-	expression tag	UNP A8K0B5
B	-6	VAL	-	expression tag	UNP A8K0B5
B	-5	PRO	-	expression tag	UNP A8K0B5
B	-4	ARG	-	expression tag	UNP A8K0B5
B	-3	GLY	-	expression tag	UNP A8K0B5
B	-2	SER	-	expression tag	UNP A8K0B5
B	-1	HIS	-	expression tag	UNP A8K0B5
B	0	MET	-	expression tag	UNP A8K0B5
D	-20	MET	-	initiating methionine	UNP A8K0B5
D	-19	GLY	-	expression tag	UNP A8K0B5
D	-18	SER	-	expression tag	UNP A8K0B5
D	-17	SER	-	expression tag	UNP A8K0B5
D	-16	HIS	-	expression tag	UNP A8K0B5
D	-15	HIS	-	expression tag	UNP A8K0B5
D	-14	HIS	-	expression tag	UNP A8K0B5
D	-13	HIS	-	expression tag	UNP A8K0B5
D	-12	HIS	-	expression tag	UNP A8K0B5
D	-11	HIS	-	expression tag	UNP A8K0B5
D	-10	SER	-	expression tag	UNP A8K0B5
D	-9	SER	-	expression tag	UNP A8K0B5
D	-8	GLY	-	expression tag	UNP A8K0B5
D	-7	LEU	-	expression tag	UNP A8K0B5
D	-6	VAL	-	expression tag	UNP A8K0B5
D	-5	PRO	-	expression tag	UNP A8K0B5
D	-4	ARG	-	expression tag	UNP A8K0B5
D	-3	GLY	-	expression tag	UNP A8K0B5
D	-2	SER	-	expression tag	UNP A8K0B5
D	-1	HIS	-	expression tag	UNP A8K0B5
D	0	MET	-	expression tag	UNP A8K0B5

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Chain	Residue	Modelled	Actual	Comment	Reference
F	-20	MET	-	initiating methionine	UNP A8K0B5
F	-19	GLY	-	expression tag	UNP A8K0B5
F	-18	SER	-	expression tag	UNP A8K0B5
F	-17	SER	-	expression tag	UNP A8K0B5
F	-16	HIS	-	expression tag	UNP A8K0B5
F	-15	HIS	-	expression tag	UNP A8K0B5
F	-14	HIS	-	expression tag	UNP A8K0B5
F	-13	HIS	-	expression tag	UNP A8K0B5
F	-12	HIS	-	expression tag	UNP A8K0B5
F	-11	HIS	-	expression tag	UNP A8K0B5
F	-10	SER	-	expression tag	UNP A8K0B5
F	-9	SER	-	expression tag	UNP A8K0B5
F	-8	GLY	-	expression tag	UNP A8K0B5
F	-7	LEU	-	expression tag	UNP A8K0B5
F	-6	VAL	-	expression tag	UNP A8K0B5
F	-5	PRO	-	expression tag	UNP A8K0B5
F	-4	ARG	-	expression tag	UNP A8K0B5
F	-3	GLY	-	expression tag	UNP A8K0B5
F	-2	SER	-	expression tag	UNP A8K0B5
F	-1	HIS	-	expression tag	UNP A8K0B5
F	0	MET	-	expression tag	UNP A8K0B5
H	-20	MET	-	initiating methionine	UNP A8K0B5
H	-19	GLY	-	expression tag	UNP A8K0B5
H	-18	SER	-	expression tag	UNP A8K0B5
H	-17	SER	-	expression tag	UNP A8K0B5
H	-16	HIS	-	expression tag	UNP A8K0B5
H	-15	HIS	-	expression tag	UNP A8K0B5
H	-14	HIS	-	expression tag	UNP A8K0B5
H	-13	HIS	-	expression tag	UNP A8K0B5
H	-12	HIS	-	expression tag	UNP A8K0B5
H	-11	HIS	-	expression tag	UNP A8K0B5
H	-10	SER	-	expression tag	UNP A8K0B5
H	-9	SER	-	expression tag	UNP A8K0B5
H	-8	GLY	-	expression tag	UNP A8K0B5
H	-7	LEU	-	expression tag	UNP A8K0B5
H	-6	VAL	-	expression tag	UNP A8K0B5
H	-5	PRO	-	expression tag	UNP A8K0B5
H	-4	ARG	-	expression tag	UNP A8K0B5
H	-3	GLY	-	expression tag	UNP A8K0B5
H	-2	SER	-	expression tag	UNP A8K0B5
H	-1	HIS	-	expression tag	UNP A8K0B5
H	0	MET	-	expression tag	UNP A8K0B5

- Molecule 3 is GUANOSINE-5'-MONOPHOSPHATE (three-letter code: 5GP) (formula: C₁₀H₁₄N₅O₈P) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

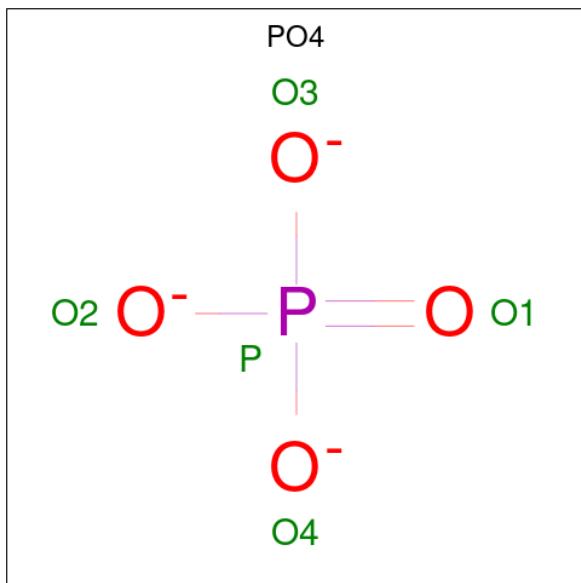
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mn	0	0
			1	1		
4	B	1	Total	Mn	0	0
			1	1		
4	C	1	Total	Mn	0	0
			1	1		
4	D	1	Total	Mn	0	0
			1	1		
4	E	1	Total	Mn	0	0
			1	1		
4	F	1	Total	Mn	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	G	1	Total Mn 1 1	0	0
4	H	1	Total Mn 1 1	0	0

- Molecule 5 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O P 5 4 1	0	0
5	C	1	Total O P 5 4 1	0	0
5	E	1	Total O P 5 4 1	0	0
5	G	1	Total O P 5 4 1	0	0

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	166	Total O 166 166	0	0
6	B	75	Total O 75 75	0	0
6	C	164	Total O 164 164	0	0

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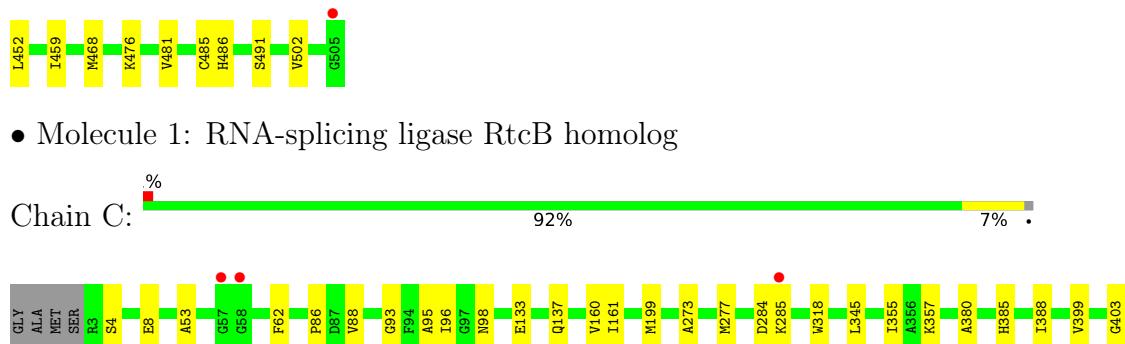
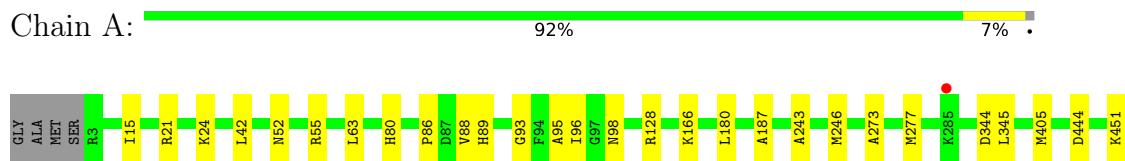
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	D	68	Total O 68 68	0	0
6	E	21	Total O 21 21	0	0
6	F	50	Total O 50 50	0	0
6	G	59	Total O 59 59	0	0
6	H	40	Total O 40 40	0	0

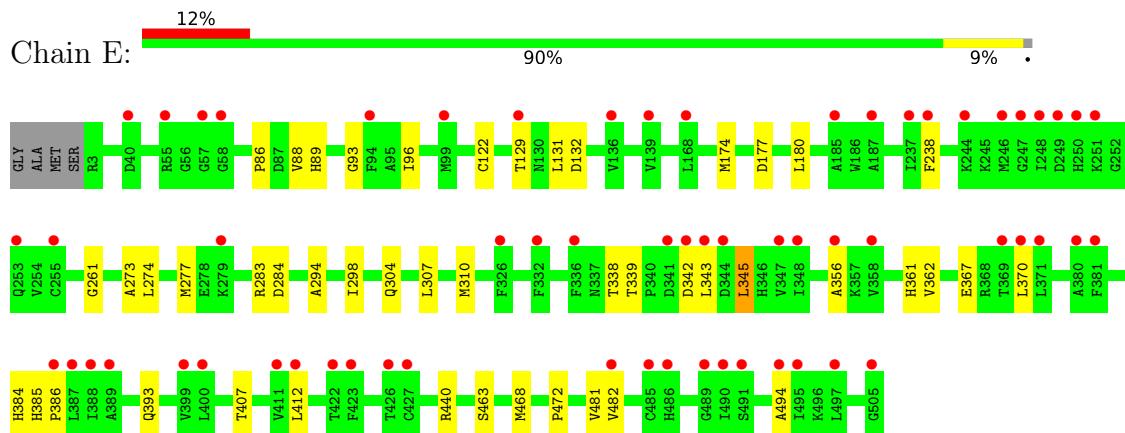
3 Residue-property plots

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.

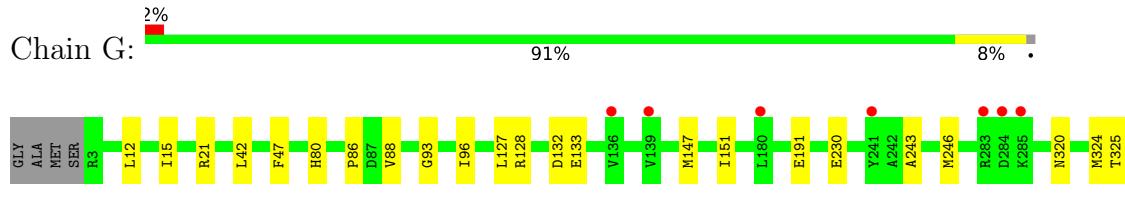
- Molecule 1: RNA-splicing ligase RtcB homolog



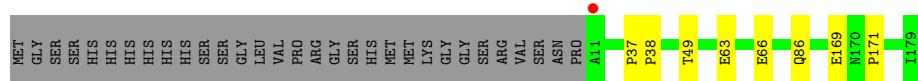
- Molecule 1: RNA-splicing ligase RtcB homolog



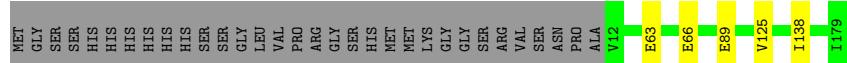
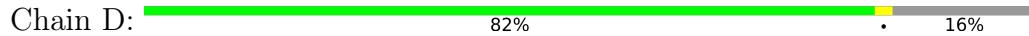
- Molecule 1: RNA-splicing ligase RtcB homolog



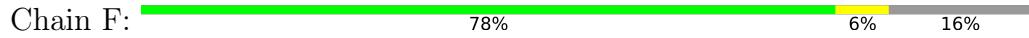
- Molecule 2: Protein archease



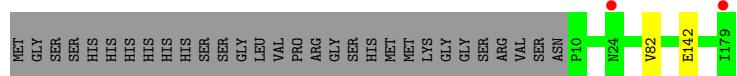
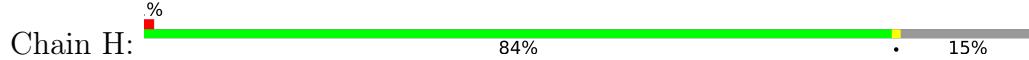
- Molecule 2: Protein archease



- Molecule 2: Protein archease



- Molecule 2: Protein archease



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	99.09 Å 125.55 Å 125.73 Å 90.00° 108.51° 90.00°	Depositor
Resolution (Å)	75.23 – 2.20 119.23 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.2 (75.23-2.20) 99.4 (119.23-2.20)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ ¹	1.62 (at 2.20 Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R , R_{free}	0.193 , 0.218 0.190 , 0.215	Depositor DCC
R_{free} test set	7204 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	43.1	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 43.8	EDS
L-test for twinning ²	$< L > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	21728	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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

Bond lengths and bond angles in the following residue types are not validated in this section: 5GP, MN, PO4

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	0.25	0/3927	0.48	0/5300
1	C	0.25	0/3927	0.49	0/5300
1	E	0.25	0/3927	0.48	0/5300
1	G	0.25	0/3927	0.49	0/5300
2	B	0.25	0/1420	0.46	0/1924
2	D	0.25	0/1415	0.46	0/1917
2	F	0.25	0/1415	0.46	0/1917
2	H	0.25	0/1428	0.46	0/1935
All	All	0.25	0/21386	0.48	0/28893

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	3855	0	3841	20	0
1	C	3855	0	3841	18	0
1	E	3855	0	3841	24	0
1	G	3855	0	3841	22	0
2	B	1387	0	1311	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1382	0	1306	3	0
2	F	1382	0	1306	9	0
2	H	1394	0	1319	1	0
3	A	23	0	12	0	0
3	C	23	0	12	0	0
3	E	23	0	12	0	0
3	G	23	0	12	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	5	0	0	0	0
5	C	5	0	0	0	0
5	E	5	0	0	0	0
5	G	5	0	0	0	0
6	A	166	0	0	1	0
6	B	75	0	0	0	0
6	C	164	0	0	0	0
6	D	68	0	0	0	0
6	E	21	0	0	0	0
6	F	50	0	0	0	0
6	G	59	0	0	3	0
6	H	40	0	0	0	0
All	All	21728	0	20654	97	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 (97) 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:E:131:LEU:HD11	1:E:343:LEU:HD22	1.71	0.71
1:G:127:LEU:HD21	1:G:325:THR:HG23	1.79	0.64
1:G:436:ARG:HG2	1:G:469:GLU:HB3	1.81	0.61
1:E:298:ILE:O	1:E:304:GLN:NE2	2.25	0.61
1:G:399:VAL:HB	1:G:412:LEU:HB2	1.81	0.60
1:E:384:HIS:HA	1:E:393:GLN:HG3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:440:ARG:NH1	2:F:19:ASP:OD1	2.38	0.56
1:A:88:VAL:HA	1:A:96:ILE:O	2.08	0.53
1:A:24:LYS:NZ	6:A:708:HOH:O	2.40	0.53
1:E:89:HIS:HB2	2:F:49:THR:HG21	1.91	0.53
1:E:362:VAL:HA	1:E:367:GLU:HA	1.90	0.52
1:A:52:ASN:HA	1:A:55:ARG:HG3	1.92	0.52
1:C:88:VAL:HA	1:C:96:ILE:O	2.09	0.52
1:G:461:VAL:HG12	1:G:504:LYS:HB2	1.91	0.52
1:C:273:ALA:O	1:C:277:MET:HG2	2.11	0.51
1:A:405:MET:HB2	1:A:502:VAL:HG11	1.92	0.51
1:G:320:ASN:O	1:G:324:MET:HG2	2.11	0.51
1:E:177:ASP:HA	1:E:180:LEU:HD12	1.94	0.50
1:G:88:VAL:HA	1:G:96:ILE:O	2.11	0.50
1:G:42:LEU:HD22	1:G:476:LYS:HD3	1.94	0.49
1:A:95:ALA:H	1:A:98:ASN:HD22	1.61	0.49
1:A:273:ALA:O	1:A:277:MET:HG2	2.13	0.49
1:G:128:ARG:O	1:G:345:LEU:HA	2.13	0.49
1:A:86:PRO:HB2	1:A:481:VAL:HG13	1.95	0.48
1:E:122:CYS:HA	1:E:261:GLY:HA2	1.96	0.47
1:G:15:ILE:HD11	1:G:21:ARG:HB2	1.96	0.47
1:G:405:MET:HB2	1:G:502:VAL:HG11	1.96	0.47
1:E:361:HIS:HB2	1:E:370:LEU:HD12	1.95	0.47
1:E:273:ALA:O	1:E:277:MET:HG2	2.15	0.47
1:E:385:HIS:CD2	1:E:386:PRO:HD2	2.49	0.47
1:G:389:ALA:HB1	6:G:754:HOH:O	2.15	0.47
1:E:88:VAL:HA	1:E:96:ILE:O	2.15	0.46
1:E:129:THR:HG22	1:E:345:LEU:HG	1.97	0.46
1:E:412:LEU:HD21	1:E:482:VAL:HG13	1.96	0.46
1:E:283:ARG:HG3	1:E:284:ASP:N	2.30	0.46
1:C:355:ILE:HG12	1:C:357:LYS:HE3	1.97	0.46
1:E:440:ARG:NH2	2:F:21:ARG:HA	2.30	0.46
1:E:238:PHE:N	1:E:494:ALA:O	2.43	0.46
1:A:452:LEU:HB3	1:A:459:ILE:HD11	1.97	0.46
1:G:243:ALA:HA	1:G:246:MET:HE3	1.97	0.46
1:C:380:ALA:HB2	1:C:426:THR:HG22	1.97	0.45
2:F:36:TYR:HE2	2:F:83:GLU:HG2	1.80	0.45
2:F:42:LYS:HB2	2:F:67:GLN:HG3	1.98	0.45
1:A:451:LYS:HB2	1:A:451:LYS:HE3	1.69	0.45
2:D:89:GLU:HG2	2:D:138:ILE:HG22	1.98	0.45
2:F:66:GLU:HB3	2:F:125:VAL:HG23	1.97	0.45
1:A:128:ARG:O	1:A:345:LEU:HA	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:486:HIS:HA	1:G:491:SER:O	2.17	0.45
1:G:128:ARG:HB3	1:G:348:ILE:HD11	1.99	0.45
1:E:307:LEU:HD23	1:E:310:MET:HE1	1.99	0.44
1:G:147:MET:O	1:G:151:ILE:HG12	2.16	0.44
1:C:4:SER:O	1:C:8:GLU:HG2	2.17	0.44
1:C:86:PRO:HG2	1:C:485:CYS:SG	2.57	0.44
1:G:132:ASP:OD1	1:G:133:GLU:N	2.50	0.44
1:C:403:GLY:HA3	1:C:408:CYS:O	2.18	0.44
1:E:174:MET:HB3	1:E:177:ASP:HB2	1.99	0.44
1:E:310:MET:HE1	1:E:356:ALA:HB3	1.99	0.43
1:G:86:PRO:HB2	1:G:481:VAL:HG13	2.00	0.43
1:C:460:ARG:HB2	1:C:503:ILE:HG22	1.99	0.43
1:G:151:ILE:O	1:G:151:ILE:HG13	2.17	0.43
1:C:284:ASP:O	1:C:285:LYS:HG2	2.18	0.43
1:E:338:THR:HG22	1:E:342:ASP:HB2	2.00	0.43
1:C:86:PRO:HB2	1:C:481:VAL:HG13	2.01	0.43
1:C:399:VAL:HB	1:C:412:LEU:HB2	2.01	0.43
1:E:86:PRO:HB2	1:E:481:VAL:HG13	2.00	0.43
2:F:63:GLU:HA	2:F:66:GLU:HG2	2.00	0.43
1:G:191:GLU:HG3	6:G:754:HOH:O	2.19	0.43
1:A:166:LYS:HD2	1:A:166:LYS:HA	1.85	0.43
2:F:36:TYR:CE2	2:F:83:GLU:HG2	2.53	0.43
1:E:407:THR:HG23	1:E:472:PRO:HB3	2.01	0.42
1:A:485:CYS:HB3	1:A:491:SER:HB2	2.01	0.42
2:B:169:GLU:O	2:B:171:PRO:HD3	2.19	0.42
1:A:89:HIS:HB2	2:B:49:THR:HG21	2.00	0.42
1:E:274:LEU:HD12	1:E:294:ALA:HB3	2.01	0.42
2:F:169:GLU:H	2:F:169:GLU:HG2	1.61	0.42
1:C:95:ALA:H	1:C:98:ASN:HD22	1.68	0.42
2:H:82:VAL:HG13	2:H:142:GLU:HG2	2.01	0.42
1:A:128:ARG:NH1	1:A:344:ASP:OD2	2.53	0.42
1:A:486:HIS:HA	1:A:491:SER:O	2.20	0.42
1:A:42:LEU:HD22	1:A:476:LYS:HD3	2.02	0.41
1:C:385:HIS:O	1:C:388:ILE:HG12	2.20	0.41
2:D:63:GLU:O	2:D:66:GLU:HG2	2.21	0.41
1:G:12:LEU:HD23	1:G:47:PHE:CE1	2.55	0.41
1:A:15:ILE:HD11	1:A:21:ARG:HB2	2.02	0.41
1:A:63:LEU:HD23	1:A:63:LEU:HA	1.93	0.41
1:C:405:MET:HB2	1:C:502:VAL:HG11	2.03	0.41
1:C:199:MET:HG3	1:C:318:TRP:CZ3	2.56	0.41
1:G:80:HIS:ND1	6:G:703:HOH:O	2.37	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:133:GLU:O	1:C:137:GLN:HG2	2.21	0.40
2:B:37:PRO:HA	2:B:38:PRO:HD3	1.94	0.40
1:G:230:GLU:CD	1:G:499:PRO:HB3	2.42	0.40
1:A:180:LEU:HD21	1:A:187:ALA:N	2.37	0.40
2:B:63:GLU:O	2:B:66:GLU:HG2	2.22	0.40
1:C:53:ALA:HB1	1:C:62:PHE:O	2.22	0.40
1:C:160:VAL:HG23	1:C:161:ILE:HD12	2.04	0.40
1:A:243:ALA:HA	1:A:246:MET:HE3	2.03	0.40
2:D:66:GLU:HB3	2:D:125:VAL:HG23	2.04	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	501/507 (99%)	488 (97%)	11 (2%)	2 (0%)	34 37
1	C	501/507 (99%)	490 (98%)	10 (2%)	1 (0%)	47 55
1	E	501/507 (99%)	487 (97%)	13 (3%)	1 (0%)	47 55
1	G	501/507 (99%)	485 (97%)	15 (3%)	1 (0%)	47 55
2	B	167/200 (84%)	161 (96%)	6 (4%)	0	100 100
2	D	166/200 (83%)	158 (95%)	8 (5%)	0	100 100
2	F	166/200 (83%)	161 (97%)	5 (3%)	0	100 100
2	H	168/200 (84%)	160 (95%)	8 (5%)	0	100 100
All	All	2671/2828 (94%)	2590 (97%)	76 (3%)	5 (0%)	47 55

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	80	HIS

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Mol	Chain	Res	Type
1	A	93	GLY
1	G	93	GLY
1	C	93	GLY
1	E	93	GLY

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	406/408 (100%)	404 (100%)	2 (0%)	88 94
1	C	406/408 (100%)	404 (100%)	2 (0%)	88 94
1	E	406/408 (100%)	401 (99%)	5 (1%)	71 83
1	G	406/408 (100%)	404 (100%)	2 (0%)	88 94
2	B	150/176 (85%)	149 (99%)	1 (1%)	84 91
2	D	150/176 (85%)	150 (100%)	0	100 100
2	F	150/176 (85%)	150 (100%)	0	100 100
2	H	151/176 (86%)	151 (100%)	0	100 100
All	All	2225/2336 (95%)	2213 (100%)	12 (0%)	88 94

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

Mol	Chain	Res	Type
1	A	444	ASP
1	A	468	MET
2	B	86	GLN
1	C	345	LEU
1	C	468	MET
1	E	132	ASP
1	E	339	THR
1	E	345	LEU
1	E	463	SER
1	E	468	MET
1	G	408	CYS

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Mol	Chain	Res	Type
1	G	468	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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)

Of 16 ligands modelled in this entry, 8 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
5	PO4	E	603	4	4,4,4	0.94	0	6,6,6	0.44	0
3	5GP	E	601	1,4	18,25,26	1.92	5 (27%)	19,37,40	1.56	4 (21%)
5	PO4	A	603	4	4,4,4	0.93	0	6,6,6	0.40	0
3	5GP	A	601	1,4	18,25,26	1.96	5 (27%)	19,37,40	1.56	3 (15%)
5	PO4	C	603	4	4,4,4	0.93	0	6,6,6	0.44	0
3	5GP	C	601	1,4	18,25,26	1.89	5 (27%)	19,37,40	1.58	4 (21%)
5	PO4	G	603	4	4,4,4	0.94	0	6,6,6	0.43	0
3	5GP	G	601	1,4	18,25,26	1.98	5 (27%)	19,37,40	1.52	4 (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
3	5GP	G	601	1,4	-	1/3/25/26	0/3/3/3
3	5GP	E	601	1,4	-	1/3/25/26	0/3/3/3
3	5GP	A	601	1,4	-	1/3/25/26	0/3/3/3
3	5GP	C	601	1,4	-	1/3/25/26	0/3/3/3

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	5GP	O5'-C5'	-4.38	1.34	1.44
3	E	601	5GP	O5'-C5'	-4.27	1.34	1.44
3	G	601	5GP	O5'-C5'	-4.24	1.34	1.44
3	C	601	5GP	O5'-C5'	-4.23	1.34	1.44
3	G	601	5GP	C6-N1	4.21	1.44	1.37
3	E	601	5GP	C6-N1	4.10	1.44	1.37
3	A	601	5GP	C6-N1	4.06	1.43	1.37
3	C	601	5GP	C6-N1	3.98	1.43	1.37
3	G	601	5GP	O4'-C1'	-2.96	1.36	1.41
3	A	601	5GP	O4'-C1'	-2.86	1.37	1.41
3	A	601	5GP	O3'-C3'	-2.57	1.36	1.43
3	C	601	5GP	O4'-C1'	-2.56	1.37	1.41
3	E	601	5GP	O4'-C1'	-2.55	1.37	1.41
3	G	601	5GP	O3'-C3'	-2.52	1.37	1.43
3	C	601	5GP	O3'-C3'	-2.46	1.37	1.43
3	E	601	5GP	O3'-C3'	-2.44	1.37	1.43
3	G	601	5GP	C5-C6	-2.37	1.42	1.47
3	A	601	5GP	C5-C6	-2.22	1.42	1.47
3	C	601	5GP	C5-C6	-2.20	1.42	1.47
3	E	601	5GP	C5-C6	-2.15	1.43	1.47

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	601	5GP	O6-C6-C5	3.85	131.90	124.37
3	A	601	5GP	O6-C6-C5	3.82	131.84	124.37
3	E	601	5GP	O6-C6-C5	3.75	131.69	124.37
3	G	601	5GP	O6-C6-C5	3.68	131.56	124.37
3	E	601	5GP	O6-C6-N1	-3.39	116.65	120.65
3	A	601	5GP	O6-C6-N1	-3.27	116.79	120.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	601	5GP	O6-C6-N1	-3.17	116.91	120.65
3	G	601	5GP	O6-C6-N1	-3.13	116.95	120.65
3	C	601	5GP	N2-C2-N3	-2.30	115.25	119.74
3	E	601	5GP	N2-C2-N3	-2.23	115.39	119.74
3	A	601	5GP	N2-C2-N3	-2.20	115.45	119.74
3	G	601	5GP	N2-C2-N3	-2.20	115.46	119.74
3	E	601	5GP	O3'-C3'-C4'	2.08	117.07	111.05
3	G	601	5GP	O3'-C3'-C4'	2.07	117.03	111.05
3	C	601	5GP	O3'-C3'-C4'	2.05	116.98	111.05

There are no chirality outliers.

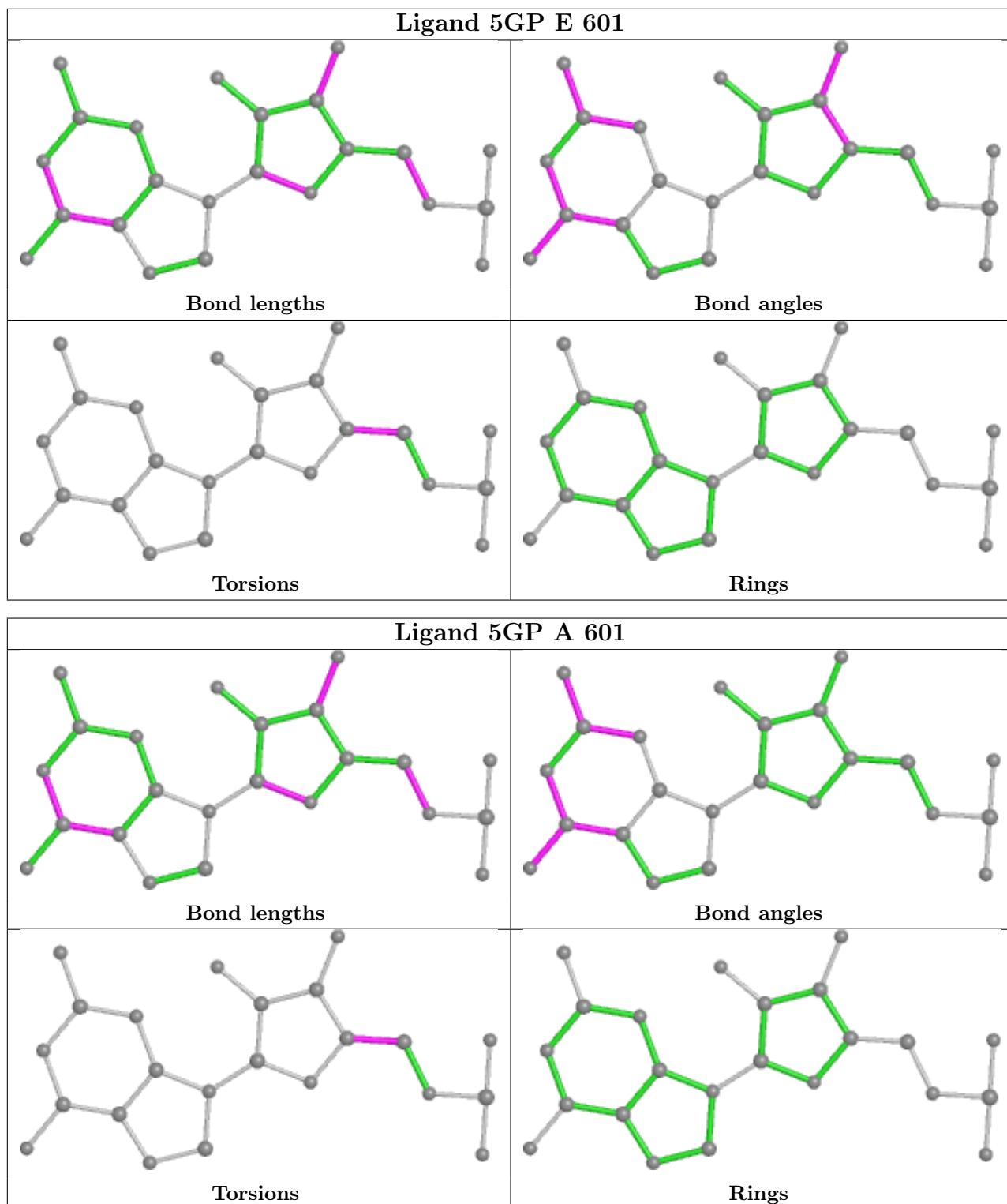
All (4) torsion outliers are listed below:

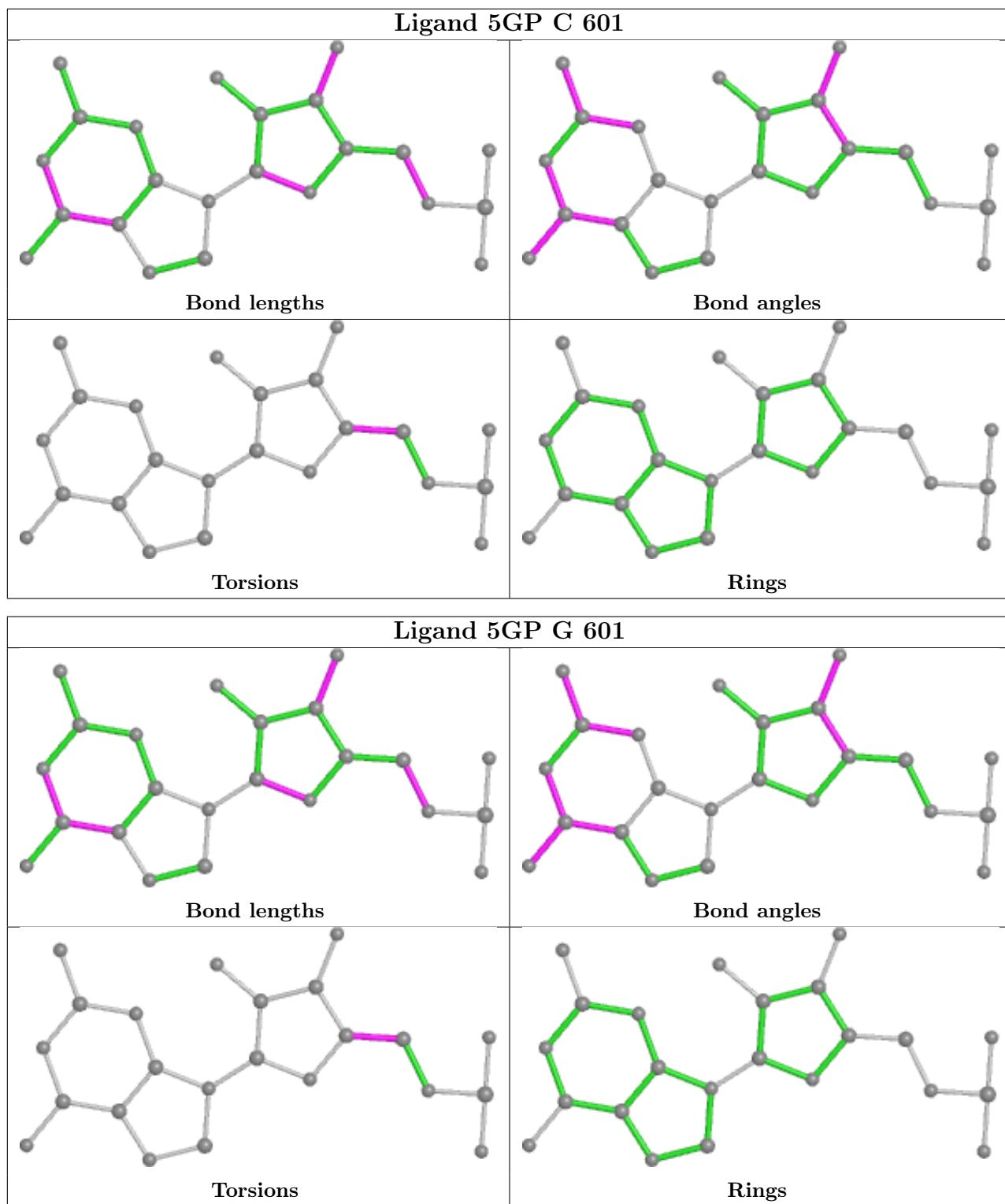
Mol	Chain	Res	Type	Atoms
3	A	601	5GP	O4'-C4'-C5'-O5'
3	C	601	5GP	O4'-C4'-C5'-O5'
3	E	601	5GP	O4'-C4'-C5'-O5'
3	G	601	5GP	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	503/507 (99%)	0.08	2 (0%) 92 91	37, 53, 70, 85	0
1	C	503/507 (99%)	0.04	4 (0%) 86 85	41, 52, 71, 99	0
1	E	503/507 (99%)	0.75	62 (12%) 4 3	54, 88, 125, 158	0
1	G	503/507 (99%)	0.26	9 (1%) 68 66	48, 71, 102, 133	0
2	B	169/200 (84%)	0.07	1 (0%) 89 88	38, 48, 70, 85	0
2	D	168/200 (84%)	0.07	0 100 100	39, 51, 82, 101	0
2	F	168/200 (84%)	0.04	1 (0%) 89 88	42, 55, 85, 109	0
2	H	170/200 (85%)	0.10	2 (1%) 79 77	45, 58, 88, 118	0
All	All	2687/2828 (95%)	0.23	81 (3%) 50 48	37, 59, 105, 158	0

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	400	LEU	6.6
1	E	347	VAL	5.8
1	E	248	ILE	5.2
1	E	427	CYS	4.6
1	E	356	ALA	4.4
1	E	387	LEU	4.2
1	E	399	VAL	4.2
1	E	341	ASP	3.8
1	E	369	THR	3.8
1	E	381	PHE	3.8
1	E	99	MET	3.7
1	E	136	VAL	3.7
1	E	505	GLY	3.6
1	E	495	ILE	3.5
1	E	238	PHE	3.5
1	E	426	THR	3.4

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Mol	Chain	Res	Type	RSRZ
1	C	58	GLY	3.3
2	H	24	ASN	3.3
1	E	246	MET	3.3
2	H	179	ILE	3.2
2	B	11	ALA	3.2
1	E	343	LEU	3.2
1	E	185	ALA	3.1
1	E	489	GLY	2.9
1	E	423	PHE	2.9
1	E	279	LYS	2.9
1	E	344	ASP	2.9
1	E	348	ILE	2.8
1	E	249	ASP	2.8
1	E	336	PHE	2.7
1	G	505	GLY	2.7
1	E	412	LEU	2.7
1	G	139	VAL	2.7
1	E	485	CYS	2.7
1	E	129	THR	2.7
1	E	482	VAL	2.7
1	E	497	LEU	2.7
1	G	284	ASP	2.6
1	E	253	GLN	2.6
1	E	389	ALA	2.6
1	C	285	LYS	2.6
1	E	332	PHE	2.6
1	G	378	THR	2.5
1	E	255	CYS	2.5
1	E	326	PHE	2.5
1	E	411	VAL	2.5
1	E	490	ILE	2.5
1	A	505	GLY	2.4
1	G	180	LEU	2.4
1	E	388	ILE	2.4
1	E	380	ALA	2.4
1	E	40	ASP	2.3
1	G	136	VAL	2.3
1	E	244	LYS	2.3
1	E	55	ARG	2.3
1	E	94	PHE	2.3
1	E	139	VAL	2.3
1	C	57	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	386	PRO	2.3
1	E	57	GLY	2.3
1	C	505	GLY	2.2
1	G	283	ARG	2.2
1	G	285	LYS	2.2
1	E	58	GLY	2.2
1	E	247	GLY	2.2
1	E	422	THR	2.2
1	E	370	LEU	2.2
1	E	371	LEU	2.2
1	E	358	VAL	2.1
1	E	342	ASP	2.1
1	E	187	ALA	2.1
2	F	167	ASN	2.1
1	E	237	ILE	2.1
1	E	168	LEU	2.1
1	E	250	HIS	2.1
1	G	241	TYR	2.1
1	A	285	LYS	2.1
1	E	494	ALA	2.1
1	E	491	SER	2.1
1	E	486	HIS	2.0
1	E	251	LYS	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 monosaccharides in this entry.

6.4 Ligands [\(i\)](#)

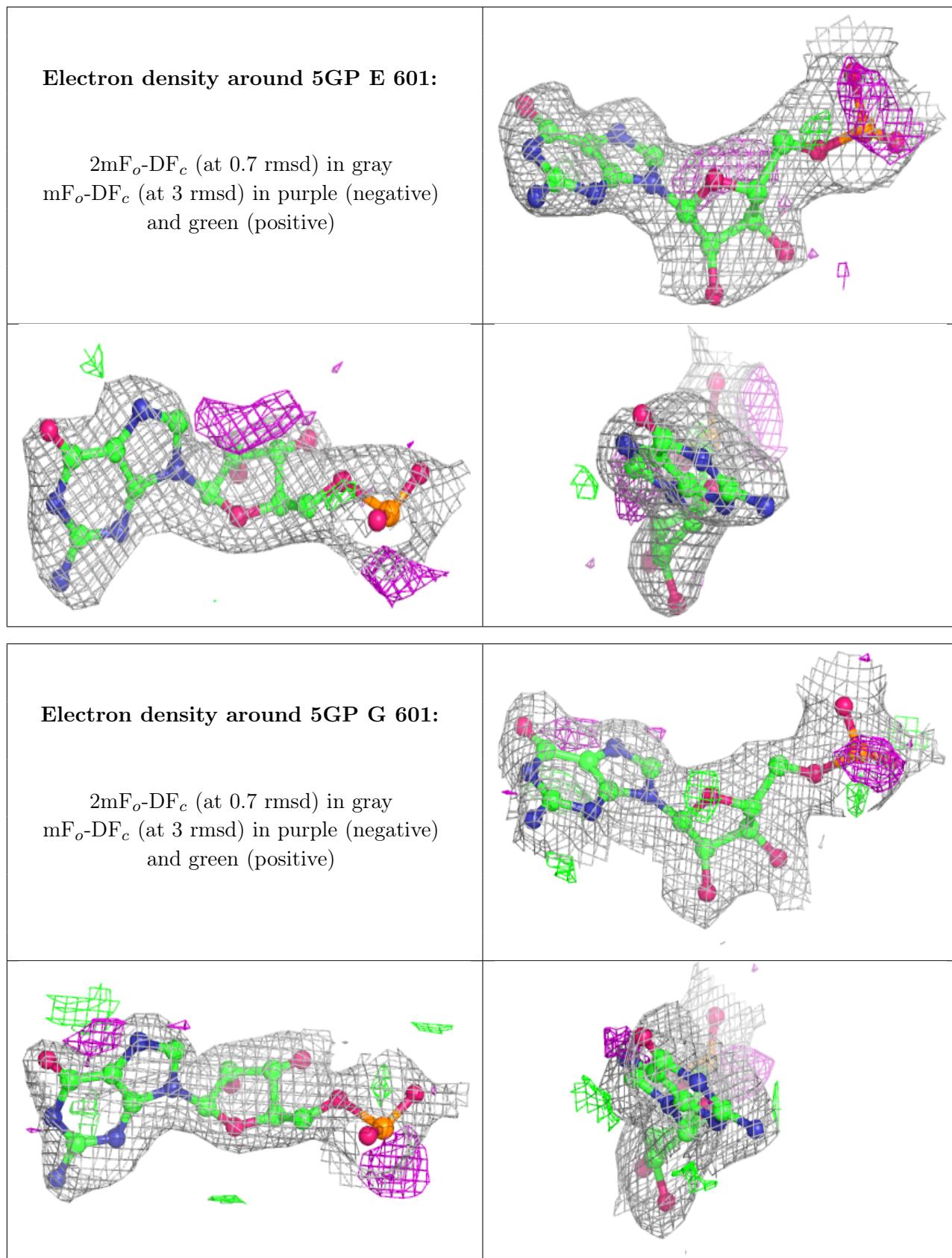
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

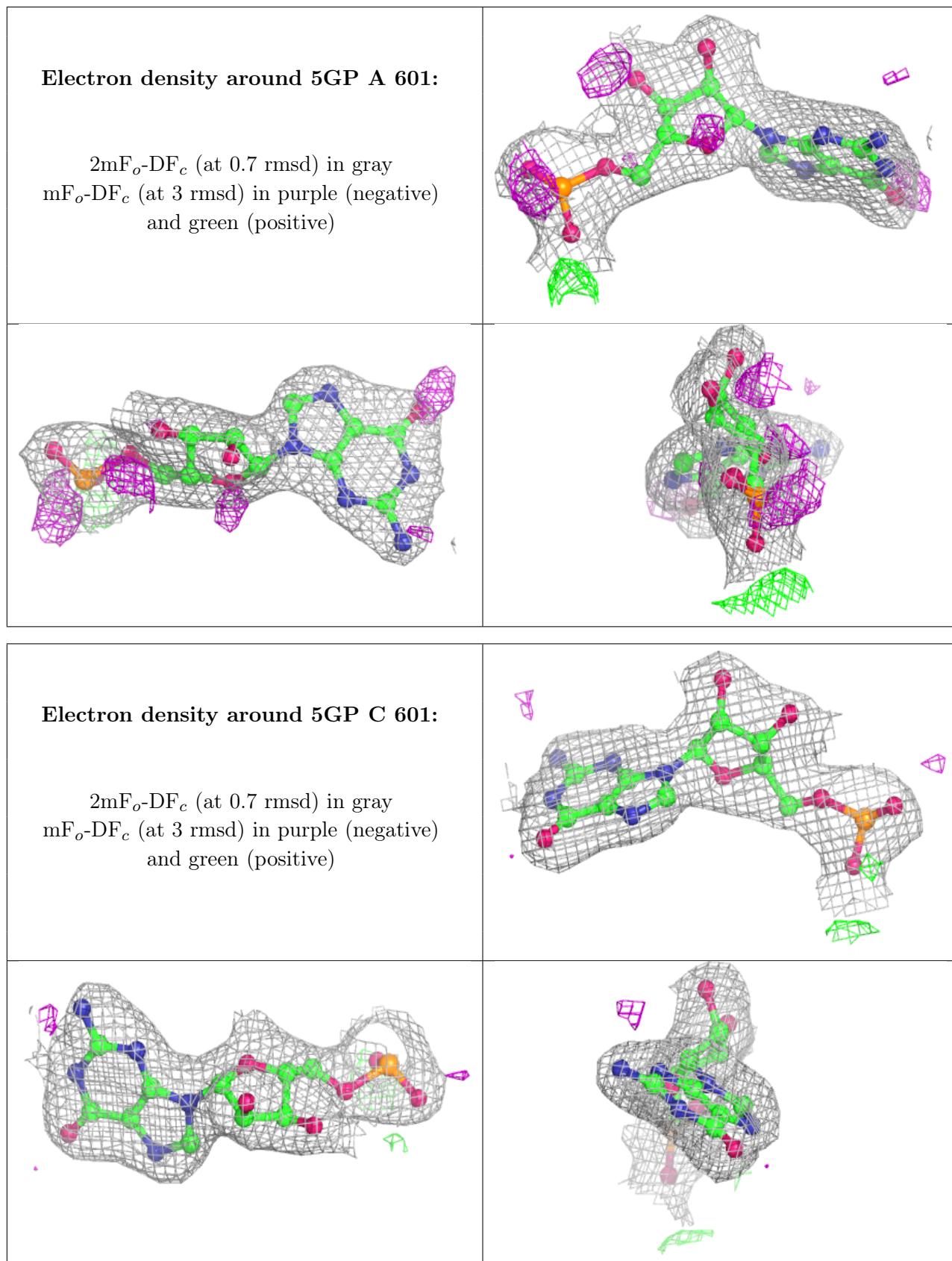
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	5GP	E	601	23/24	0.91	0.20	64,71,79,79	0
4	MN	H	201	1/1	0.92	0.30	100,100,100,100	0
4	MN	E	602	1/1	0.93	0.10	79,79,79,79	0
3	5GP	G	601	23/24	0.93	0.17	41,57,67,69	0
5	PO4	E	603	5/5	0.95	0.12	62,65,66,67	0
4	MN	A	602	1/1	0.96	0.23	67,67,67,67	0
3	5GP	A	601	23/24	0.96	0.14	41,45,49,52	0
5	PO4	G	603	5/5	0.96	0.13	48,49,60,63	0
4	MN	G	602	1/1	0.97	0.09	52,52,52,52	0
3	5GP	C	601	23/24	0.97	0.16	46,49,53,56	0
4	MN	C	602	1/1	0.98	0.16	51,51,51,51	0
5	PO4	A	603	5/5	0.98	0.15	43,44,52,56	0
5	PO4	C	603	5/5	0.98	0.13	41,45,52,52	0
4	MN	F	201	1/1	0.98	0.07	55,55,55,55	0
4	MN	D	201	1/1	0.98	0.15	48,48,48,48	0
4	MN	B	201	1/1	0.99	0.12	44,44,44,44	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.





6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.