



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:27 PM UTC

PDB ID : 6MFW / pdb_00006mfw
Title : Crystal structure of a 4-domain construct of LgrA in the substrate donation state
Authors : Reimer, J.M.; Eivaskhani, M.; Schmeing, T.M.
Deposited on : 2018-09-12
Resolution : 2.50 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

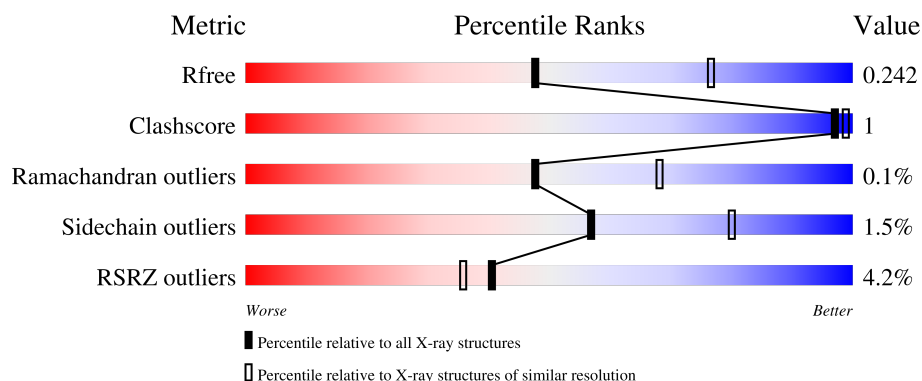
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	1210	4% 94% ..

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 19072 atoms, of which 9373 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.

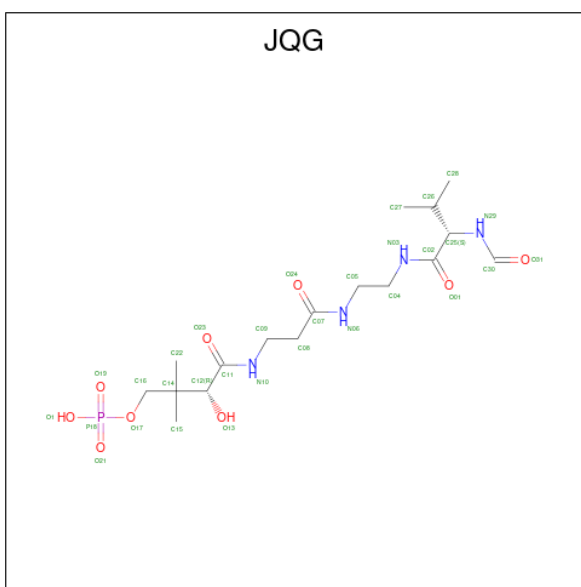
- Molecule 1 is a protein called Linear gramicidin synthase subunit A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1181	Total	C	H	N	O	S	0	0	0
			18710	6017	9299	1602	1752	40			

There are 13 discrepancies between the modelled and reference sequences:

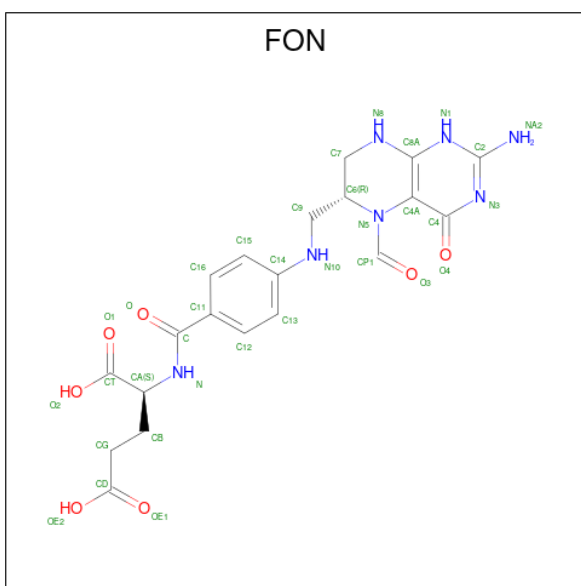
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP Q70LM7
A	0	ALA	-	expression tag	UNP Q70LM7
A	1	MET	-	expression tag	UNP Q70LM7
A	2	GLY	-	expression tag	UNP Q70LM7
A	1200	ALA	-	expression tag	UNP Q70LM7
A	1201	ALA	-	expression tag	UNP Q70LM7
A	1202	ALA	-	expression tag	UNP Q70LM7
A	1203	GLU	-	expression tag	UNP Q70LM7
A	1204	ASN	-	expression tag	UNP Q70LM7
A	1205	LEU	-	expression tag	UNP Q70LM7
A	1206	TYR	-	expression tag	UNP Q70LM7
A	1207	PHE	-	expression tag	UNP Q70LM7
A	1208	GLN	-	expression tag	UNP Q70LM7

- Molecule 2 is (2 {R})- {N}-[3-[2-[(2 {S})-2-formamido-3-methyl-butanoyl]amino]ethylamino]-3-oxidanylidene-propyl]-3,3-dimethyl-2-oxidanyl-4-[oxidanyl-bis(oxidanylidene)-5-hydroxy]oxy-butanamide (CCD ID: JQG) (formula: C₁₇H₃₂N₄O₉P).



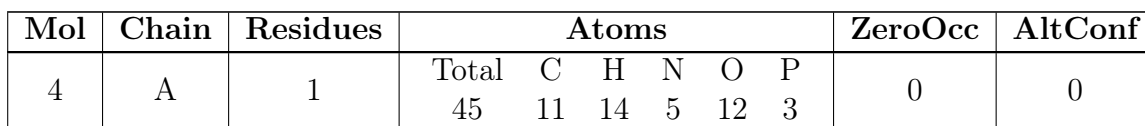
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			61	17	31	4	8	1		

- Molecule 3 is N-{[4-({[(6R)-2-amino-5-formyl-4-oxo-1,4,5,6,7,8-hexahydropteridin-6-yl]methyl}amino)phenyl]carbonyl}-L-glutamic acid (CCD ID: FON) (formula: $C_{20}H_{23}N_7O_7$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	H	N	O		
			55	20	21	7	7	0	0

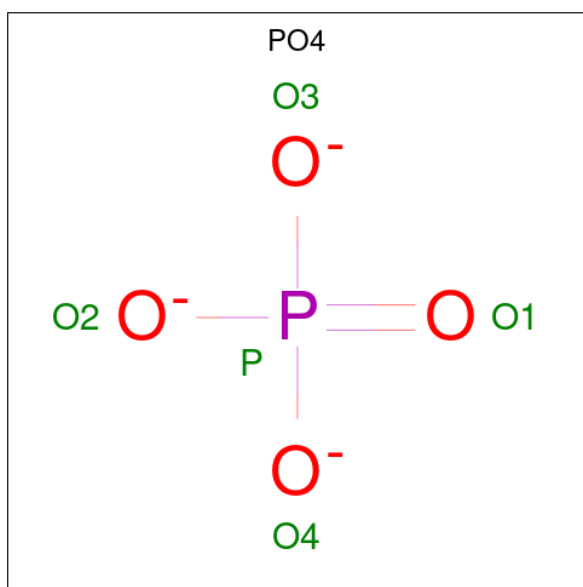
- Molecule 4 is DIPHOSPHOMETHYLPHOSPHONIC ACID ADENOSYL ESTER (CCD ID: APC) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



- [illegible]

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	H	N	O	0	0
			16	5	8	1	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Mg	0	0
			1	1		

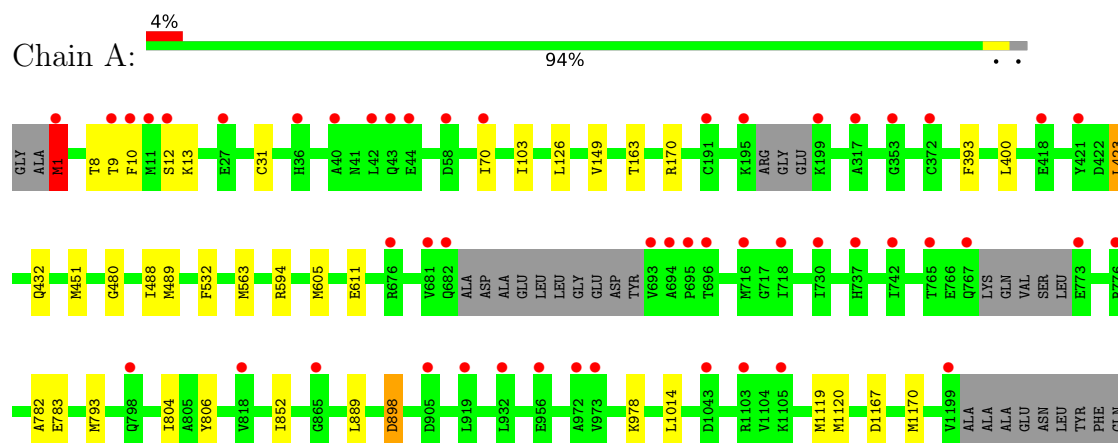
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	179	Total	O	0	0
			179	179		

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: Linear gramicidin synthase subunit A



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	66.37Å 133.87Å 162.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	69.33 – 2.50 69.33 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.9 (69.33-2.50) 94.8 (69.33-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.05 (at 2.37Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.200 , 0.243 0.200 , 0.242	Depositor DCC
R_{free} test set	2000 reflections (3.31%)	wwPDB-VP
Wilson B-factor (Å ²)	40.8	Xtriage
Anisotropy	0.387	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	19072	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: JQG, MG, APC, PO4, FON

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	0.28	3/9619 (0.0%)	0.43	9/13059 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	594	ARG	C-O	-6.68	1.16	1.24
1	A	126	LEU	C-O	-6.13	1.17	1.24
1	A	70	ILE	C-O	-5.71	1.17	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	10	PHE	CA-C-N	7.14	130.80	120.38
1	A	10	PHE	C-N-CA	7.14	130.80	120.38
1	A	1	MET	CA-C-N	6.87	126.63	120.10
1	A	1	MET	C-N-CA	6.87	126.63	120.10
1	A	10	PHE	CA-C-O	-6.15	114.69	121.33
1	A	8	THR	CB-CA-C	-5.80	99.84	110.62
1	A	8	THR	CA-C-N	5.46	127.86	120.38
1	A	8	THR	C-N-CA	5.46	127.86	120.38
1	A	9	THR	CA-C-O	-5.11	115.11	120.63

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	9411	9299	9299	16	0
2	A	30	31	0	1	0
3	A	34	21	21	0	0
4	A	31	14	13	1	0
5	A	8	8	8	0	0
6	A	5	0	0	0	0
7	A	1	0	0	0	0
8	A	179	0	0	0	0
All	All	9699	9373	9341	17	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.

All (17) 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:978:LYS:HG3	1:A:1170:MET:HE1	1.81	0.63
1:A:898:ASP:OD1	1:A:898:ASP:N	2.35	0.60
1:A:793:MET:HE1	1:A:806:TYR:CG	2.39	0.56
4:A:1303:APC:H5'2	4:A:1303:APC:H8	1.88	0.56
1:A:1167:ASP:H	1:A:1170:MET:HE3	1.70	0.55
1:A:1167:ASP:OD1	1:A:1170:MET:HE2	2.08	0.54
1:A:480:GLY:HA3	1:A:489:MET:HE2	1.95	0.47
1:A:1:MET:HE3	1:A:1:MET:HB2	1.89	0.46
1:A:423:LEU:CB	1:A:451:MET:HE3	2.46	0.46
1:A:400:LEU:C	1:A:400:LEU:HD23	2.42	0.43
1:A:423:LEU:HB2	1:A:451:MET:HE3	2.02	0.42
1:A:782:ALA:C	1:A:783:GLU:HG2	2.44	0.42
1:A:1014:LEU:HG	1:A:1120:MET:HE1	2.03	0.41
1:A:978:LYS:CG	1:A:1170:MET:HE1	2.48	0.41
1:A:532:PHE:CD2	1:A:563:MET:HE3	2.56	0.41
1:A:605:MET:HE2	1:A:611:GLU:O	2.21	0.40
1:A:1119:MET:HE1	2:A:1301:JQG:C27	2.52	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	1173/1210 (97%)	1142 (97%)	30 (3%)	1 (0%)	48 68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	488	ILE

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	1013/1053 (96%)	998 (98%)	15 (2%)	57 80

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	12	SER
1	A	13	LYS
1	A	31	CYS
1	A	103	ILE
1	A	149	VAL
1	A	163	THR
1	A	170	ARG
1	A	393	PHE
1	A	423	LEU

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Mol	Chain	Res	Type
1	A	432	GLN
1	A	804	ILE
1	A	852	ILE
1	A	889	LEU
1	A	898	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	243	HIS
1	A	255	GLN
1	A	709	HIS
1	A	737	HIS
1	A	741	ASN
1	A	781	GLN
1	A	798	GLN
1	A	1075	HIS
1	A	1091	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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
3	FON	A	1302	-	34,36,36	4.16	12 (35%)	34,50,50	1.21	2 (5%)
2	JQG	A	1301	1	24,29,30	2.32	7 (29%)	30,38,41	1.08	1 (3%)
4	APC	A	1303	7	29,33,33	3.37	10 (34%)	44,52,52	1.89	10 (22%)
5	VAL	A	1304	-	6,7,7	1.04	1 (16%)	8,9,9	0.69	0
6	PO4	A	1305	-	4,4,4	0.90	0	6,6,6	0.45	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
2	JQG	A	1301	1	-	5/38/40/41	-
3	FON	A	1302	-	-	8/24/37/37	0/3/3/3
5	VAL	A	1304	-	-	2/8/8/8	-
4	APC	A	1303	7	-	6/19/38/38	0/3/3/3

All (30) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1302	FON	C4A-N5	11.57	1.56	1.38
3	A	1302	FON	C7-N8	-11.09	1.35	1.46
3	A	1302	FON	C8A-N8	10.84	1.43	1.32
4	A	1303	APC	PB-O3B	10.02	1.69	1.58
4	A	1303	APC	C3'-C4'	-8.23	1.32	1.53
4	A	1303	APC	O4'-C4'	7.82	1.62	1.45
3	A	1302	FON	C7-C6	-6.28	1.45	1.52
2	A	1301	JQG	C07-N06	5.66	1.46	1.33
4	A	1303	APC	C6-N6	5.45	1.48	1.34
2	A	1301	JQG	C02-N03	5.45	1.46	1.33
2	A	1301	JQG	C11-N10	5.35	1.46	1.33
3	A	1302	FON	C2-N1	5.19	1.50	1.37
3	A	1302	FON	CP1-N5	5.03	1.45	1.36
3	A	1302	FON	C8A-N1	4.98	1.44	1.37
3	A	1302	FON	C2-NA2	4.90	1.45	1.34
3	A	1302	FON	C4-N3	4.88	1.46	1.38
4	A	1303	APC	O4'-C1'	-4.60	1.31	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1302	FON	C-N	4.58	1.44	1.34
2	A	1301	JQG	C30-N29	3.96	1.46	1.33
4	A	1303	APC	PB-O2B	-3.03	1.49	1.56
4	A	1303	APC	PA-O1A	-2.73	1.45	1.51
4	A	1303	APC	O2'-C2'	-2.65	1.36	1.43
3	A	1302	FON	O4-C4	-2.64	1.18	1.23
2	A	1301	JQG	O23-C11	-2.53	1.18	1.23
4	A	1303	APC	O3'-C3'	2.51	1.49	1.43
4	A	1303	APC	C1'-N9	2.35	1.52	1.46
2	A	1301	JQG	O01-C02	-2.28	1.19	1.23
5	A	1304	VAL	OXT-C	-2.22	1.23	1.30
3	A	1302	FON	C14-N10	2.07	1.44	1.38
2	A	1301	JQG	O24-C07	-2.06	1.19	1.23

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1303	APC	N3-C2-N1	-4.97	121.06	128.58
4	A	1303	APC	C5-C4-N3	-4.83	120.06	126.72
4	A	1303	APC	N9-C8-N7	-3.82	108.52	113.94
4	A	1303	APC	N3-C4-N9	3.68	133.43	127.17
4	A	1303	APC	C2-N3-C4	3.63	120.70	111.83
4	A	1303	APC	C4-N9-C8	3.43	109.34	105.74
4	A	1303	APC	C5-N7-C8	3.26	108.58	103.45
4	A	1303	APC	C4-C5-N7	-3.09	107.05	110.58
3	A	1302	FON	O3-CP1-N5	-2.91	119.75	124.67
4	A	1303	APC	PB-O3B-PG	-2.86	122.21	132.45
2	A	1301	JQG	O31-C30-N29	-2.18	119.69	125.32
3	A	1302	FON	C16-C11-C12	2.16	121.32	118.57
4	A	1303	APC	C2-N1-C6	2.14	122.25	118.73

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	1303	APC	PB-C3A-PA-O1A
4	A	1303	APC	C5'-O5'-PA-O1A
2	A	1301	JQG	N29-C25-C26-C27
2	A	1301	JQG	C02-C25-C26-C27
2	A	1301	JQG	C02-C25-C26-C28
2	A	1301	JQG	N29-C25-C26-C28
3	A	1302	FON	N-C-C11-C12

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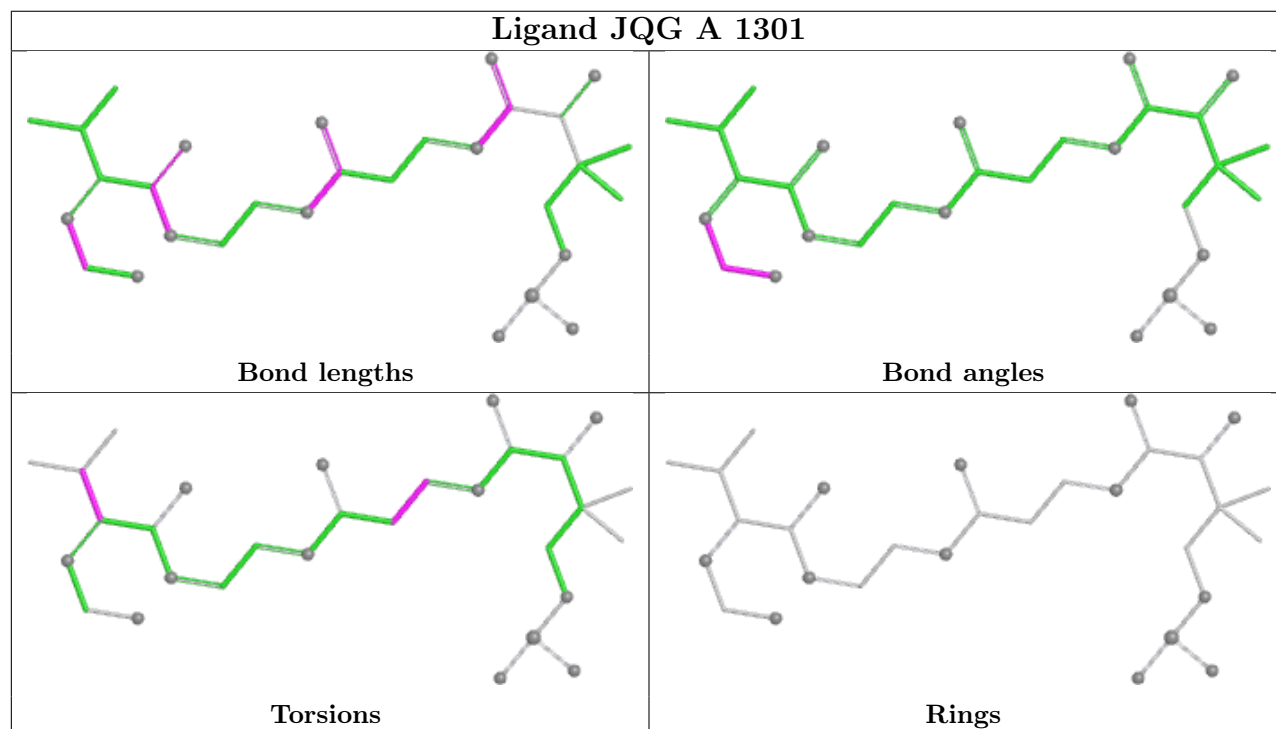
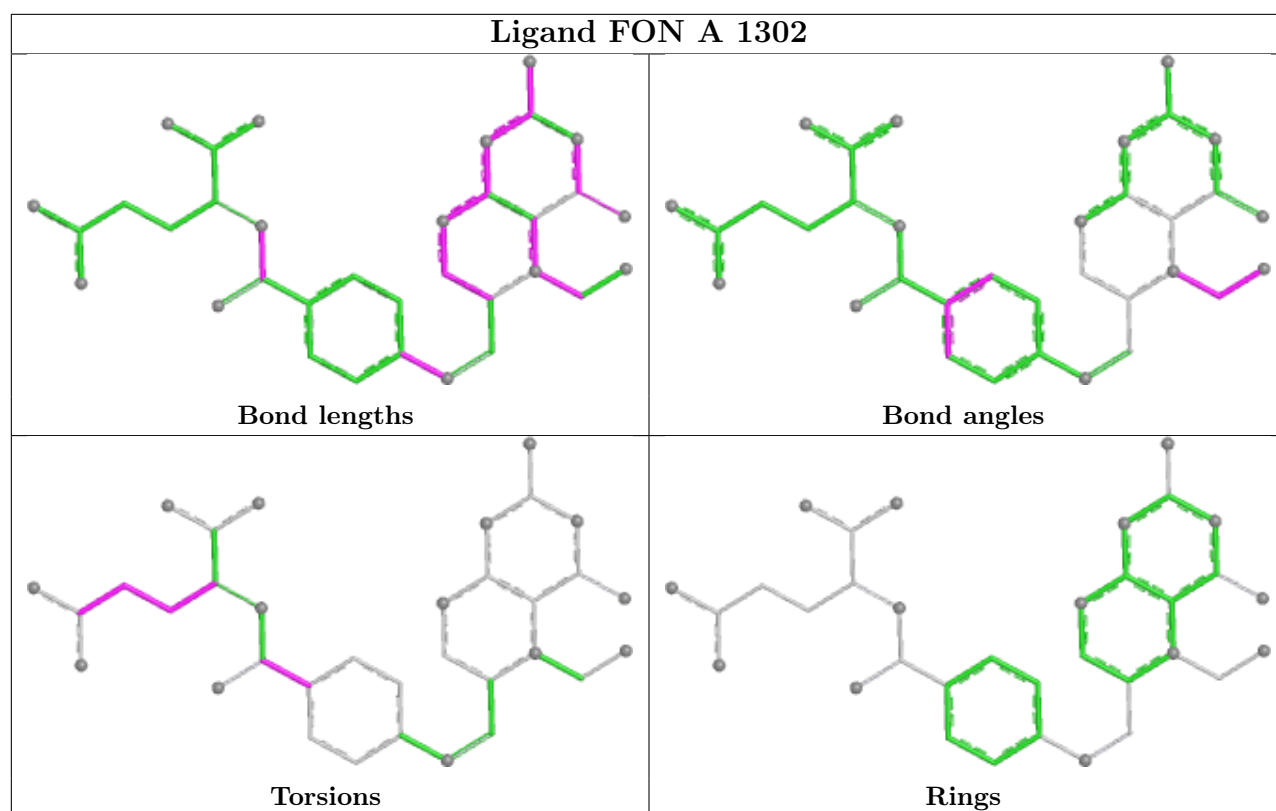
Mol	Chain	Res	Type	Atoms
3	A	1302	FON	O-C-C11-C12
5	A	1304	VAL	O-C-CA-CB
5	A	1304	VAL	OXT-C-CA-CB
3	A	1302	FON	N-C-C11-C16
3	A	1302	FON	O-C-C11-C16
4	A	1303	APC	PB-C3A-PA-O2A
4	A	1303	APC	PB-C3A-PA-O5'
2	A	1301	JQG	C07-C08-C09-N10
3	A	1302	FON	N-CA-CB-CG
3	A	1302	FON	CA-CB-CG-CD
3	A	1302	FON	OE1-CD-CG-CB
3	A	1302	FON	OE2-CD-CG-CB
4	A	1303	APC	C5'-O5'-PA-O2A
4	A	1303	APC	C5'-O5'-PA-C3A

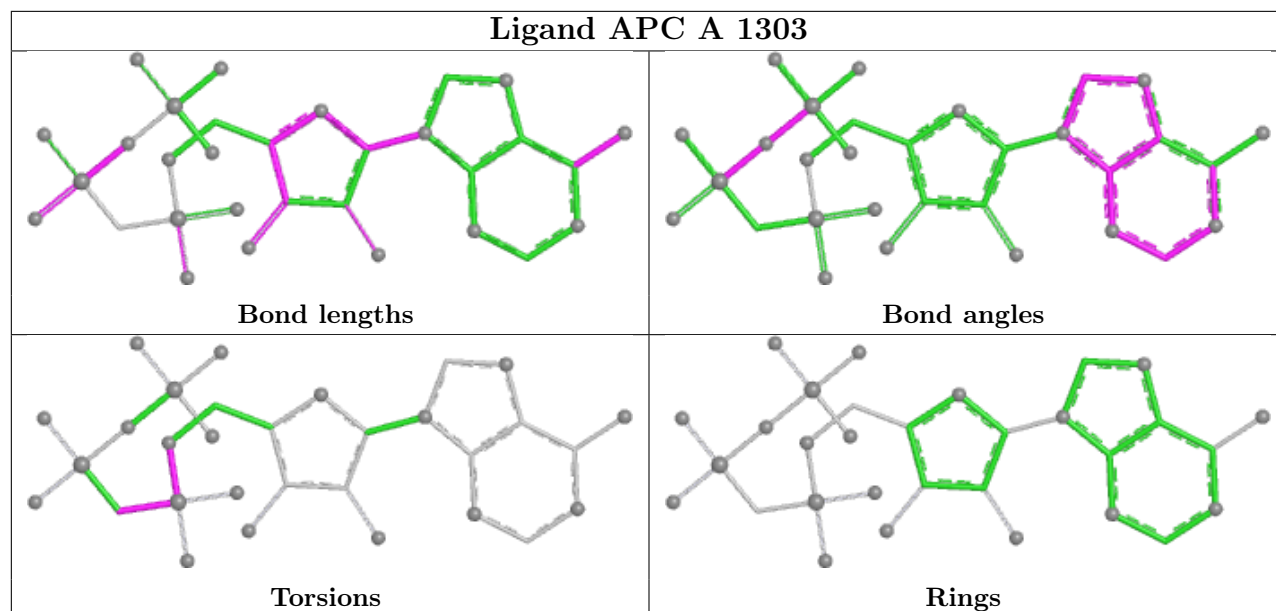
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1301	JQG	1	0
4	A	1303	APC	1	0

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

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	A	1181/1210 (97%)	0.38	50 (4%)	40 36	34, 60, 91, 136	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	767	GLN	7.7
1	A	9	THR	7.4
1	A	43	GLN	6.0
1	A	696	THR	5.7
1	A	195	LYS	5.4
1	A	199	LYS	5.3
1	A	776	ARG	4.8
1	A	11	MET	4.2
1	A	10	PHE	4.2
1	A	372	CYS	3.8
1	A	919	LEU	3.8
1	A	1105	LYS	3.7
1	A	695	PRO	3.6
1	A	191	CYS	3.5
1	A	972	ALA	3.5
1	A	905	ASP	3.4
1	A	676	ARG	3.3
1	A	40	ALA	3.1
1	A	1043	ASP	3.1
1	A	693	VAL	3.1
1	A	1	MET	3.0
1	A	421	TYR	3.0
1	A	44	GLU	2.9
1	A	42	LEU	2.7
1	A	716	MET	2.7
1	A	718	ILE	2.6
1	A	973	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	317	ALA	2.6
1	A	765	THR	2.6
1	A	36	HIS	2.6
1	A	418	GLU	2.5
1	A	742	ILE	2.4
1	A	1103	ARG	2.3
1	A	865	GLY	2.3
1	A	730	ILE	2.3
1	A	1199	VAL	2.2
1	A	737	HIS	2.2
1	A	58	ASP	2.2
1	A	694	ALA	2.2
1	A	681	VAL	2.1
1	A	798	GLN	2.1
1	A	818	VAL	2.1
1	A	353	GLY	2.1
1	A	773	GLU	2.1
1	A	682	GLN	2.1
1	A	27	GLU	2.1
1	A	12	SER	2.1
1	A	932	LEU	2.0
1	A	956	GLU	2.0
1	A	70	ILE	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](#)

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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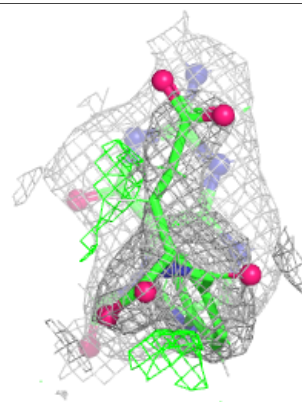
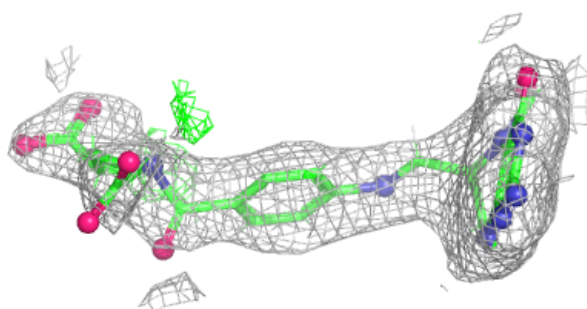
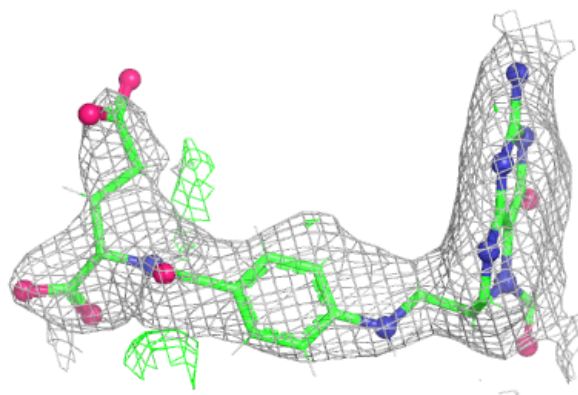
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	VAL	A	1304	8/8	0.82	0.25	43,62,67,74	0
3	FON	A	1302	34/34	0.85	0.13	50,72,105,105	0
6	PO4	A	1305	5/5	0.90	0.13	45,46,60,85	0
2	JQG	A	1301	30/31	0.92	0.12	39,67,99,102	0
4	APC	A	1303	31/31	0.94	0.08	26,43,61,67	0
7	MG	A	1306	1/1	0.98	0.08	36,36,36,36	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.

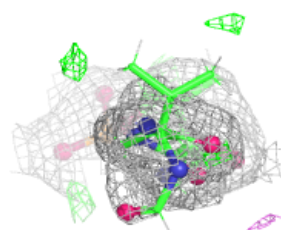
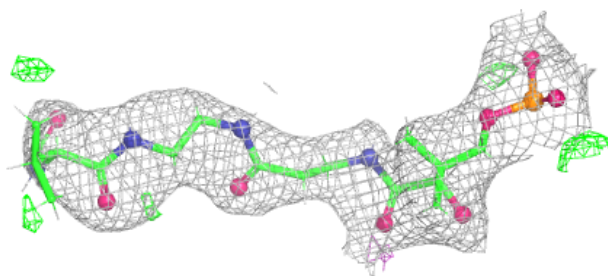
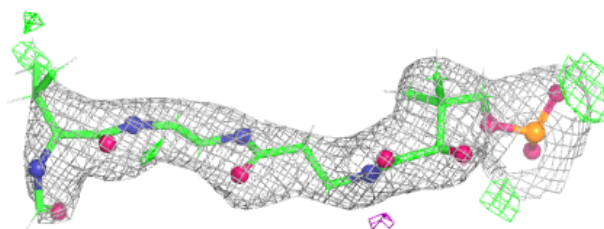
Electron density around FON A 1302:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

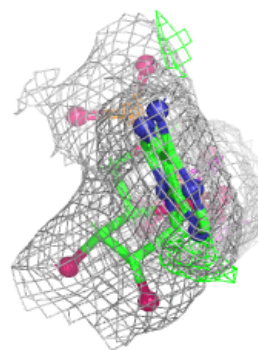
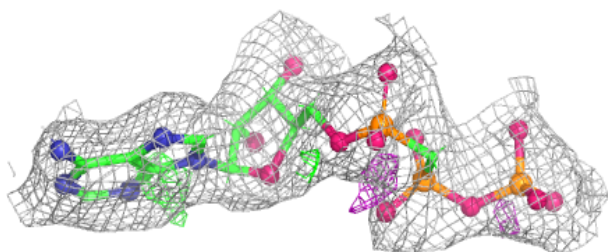
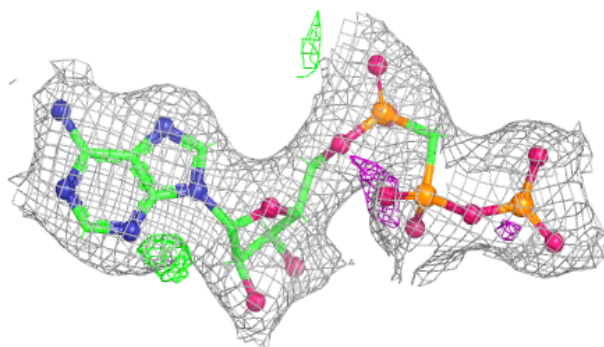


Electron density around JQG A 1301:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around APC A 1303:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.