



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 10, 2024 – 11:54 PM EST

PDB ID : 2QD9  
Title : P38 Alpha Map Kinase inhibitor based on heterobicyclic scaffolds  
Authors : Sack, J.S.  
Deposited on : 2007-06-20  
Resolution : 1.70 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](mailto: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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), 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

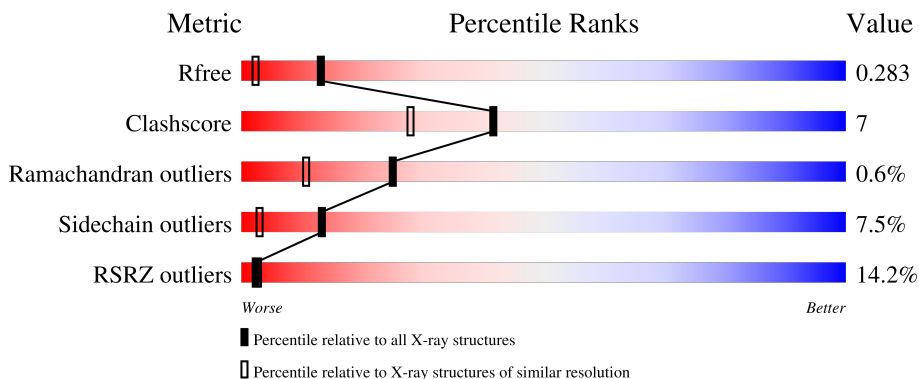
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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  $\geq 3$ , 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	366	

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 2850 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.

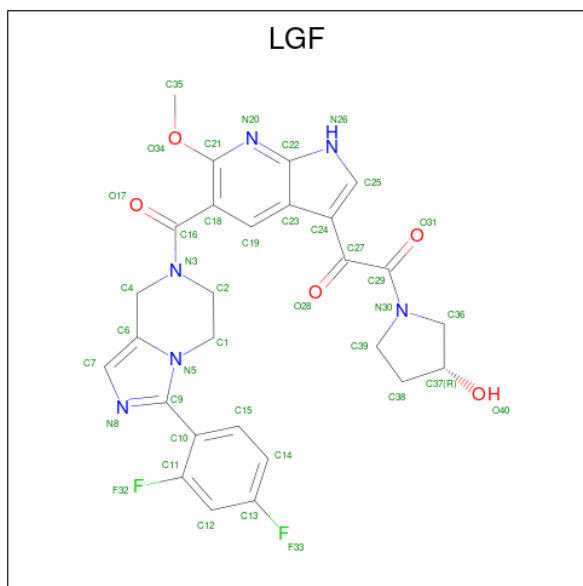
- Molecule 1 is a protein called Mitogen-activated protein kinase 14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	330	2671	1718	455	487	11	0	0	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	cloning artifact	UNP Q16539
A	-4	ALA	-	cloning artifact	UNP Q16539
A	-3	HIS	-	expression tag	UNP Q16539
A	-2	HIS	-	expression tag	UNP Q16539
A	-1	HIS	-	expression tag	UNP Q16539
A	0	HIS	-	expression tag	UNP Q16539
A	1	HIS	-	expression tag	UNP Q16539

- Molecule 2 is 1-[5-[[3-[2,4-bis(fluoranyl)phenyl]-6,8-dihydro-5 {H}-imidazo[1,5-a]pyrazin-7-yl]carbonyl]-6-methoxy-1 {H}-pyrrolo[2,3-b]pyridin-3-yl]-2-[(3 {R})-3-oxidanylpyrrolidin-1-yl]ethane-1,2-dione (three-letter code: LGF) (formula: C<sub>27</sub>H<sub>24</sub>F<sub>2</sub>N<sub>6</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	F	N	O		
2	A	1	40	27	2	6	5	0	0

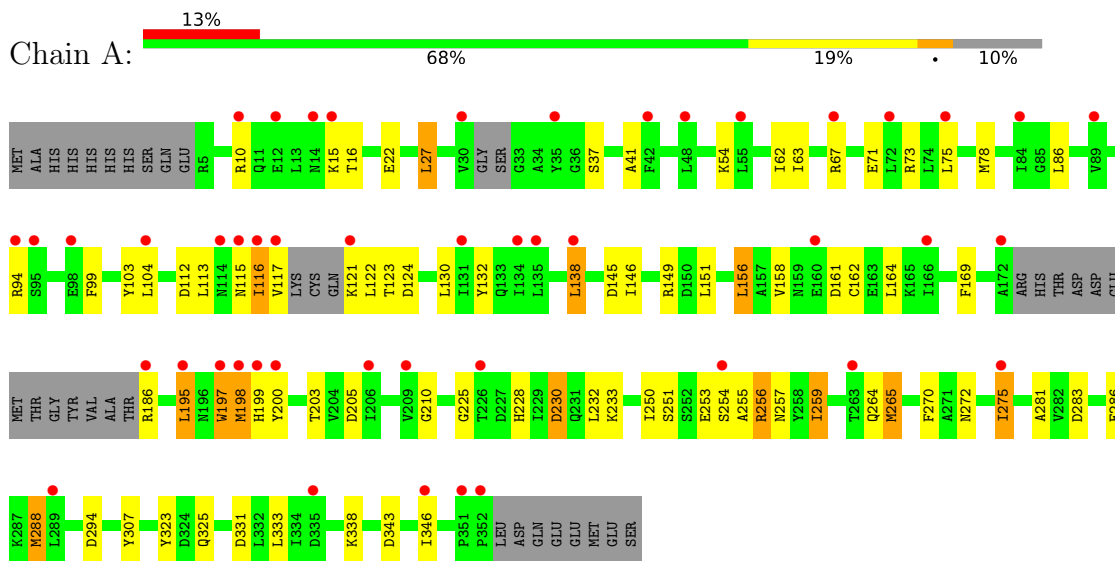
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	139	Total	O	0	0
			139	139		

### 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: Mitogen-activated protein kinase 14



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.65Å 74.36Å 78.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.07 – 1.70 27.07 – 1.70	Depositor EDS
% Data completeness (in resolution range)	97.1 (27.07-1.70) 97.1 (27.07-1.70)	Depositor EDS
$R_{merge}$	0.04	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.83 (at 1.71Å)	Xtrriage
Refinement program	REFMAC 5.1.19	Depositor
R, $R_{free}$	0.251 , 0.282 0.255 , 0.283	Depositor DCC
$R_{free}$ test set	2102 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	27.3	Xtrriage
Anisotropy	0.353	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 46.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	2850	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.22% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: LGF

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	1.07	5/2732 (0.2%)	1.12	12/3707 (0.3%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	162	CYS	CB-SG	-18.11	1.51	1.82
1	A	71	GLU	CD-OE2	7.94	1.34	1.25
1	A	288	MET	SD-CE	-7.08	1.38	1.77
1	A	71	GLU	CD-OE1	6.44	1.32	1.25
1	A	132	TYR	CE1-CZ	-5.21	1.31	1.38

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	156	LEU	CB-CG-CD2	-8.31	96.87	111.00
1	A	288	MET	CG-SD-CE	-7.64	87.97	100.20
1	A	124	ASP	CB-CG-OD2	7.14	124.72	118.30
1	A	138	LEU	CB-CG-CD1	6.55	122.13	111.00
1	A	164	LEU	CB-CG-CD1	-6.32	100.26	111.00
1	A	283	ASP	CB-CG-OD2	6.24	123.91	118.30
1	A	333	LEU	CA-CB-CG	-5.61	102.39	115.30
1	A	230	ASP	CB-CG-OD2	5.59	123.33	118.30
1	A	104	LEU	CB-CG-CD1	-5.36	101.89	111.00
1	A	294	ASP	CB-CG-OD2	5.24	123.02	118.30
1	A	73	ARG	NE-CZ-NH2	-5.17	117.72	120.30
1	A	331	ASP	CB-CG-OD2	5.04	122.83	118.30

There are no chirality outliers.

There are no planarity outliers.

## 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	2671	0	2673	38	0
2	A	40	0	23	0	0
3	A	139	0	0	5	0
All	All	2850	0	2696	38	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 7.

All (38) 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:343:ASP:O	1:A:346:ILE:HG12	1.87	0.75
1:A:145:ASP:HB3	3:A:496:HOH:O	1.88	0.73
1:A:63:ILE:O	1:A:67:ARG:HG3	1.90	0.70
1:A:250:ILE:O	1:A:256:ARG:NH2	2.25	0.70
1:A:270:PHE:CD2	1:A:286:GLU:HG2	2.28	0.69
1:A:195:LEU:HB3	1:A:197:TRP:NE1	2.11	0.65
1:A:186:ARG:HH11	1:A:186:ARG:HB2	1.61	0.65
1:A:117:VAL:HG12	1:A:122:LEU:HD11	1.80	0.64
1:A:195:LEU:HB3	1:A:197:TRP:CD1	2.34	0.63
1:A:78:MET:HE2	1:A:146:ILE:HD13	1.83	0.61
1:A:253:GLU:O	1:A:257:ASN:HB2	2.03	0.57
1:A:195:LEU:HD23	1:A:232:LEU:HD22	1.87	0.57
1:A:255:ALA:O	1:A:259:ILE:HD12	2.06	0.55
1:A:272:ASN:O	1:A:275:ILE:HG13	2.07	0.54
1:A:78:MET:HG3	1:A:169:PHE:CZ	2.42	0.54
1:A:22:GLU:HG3	3:A:489:HOH:O	2.10	0.52
1:A:225:GLY:HA2	1:A:230:ASP:OD2	2.10	0.52
1:A:99:PHE:O	1:A:338:LYS:HE3	2.10	0.51
1:A:112:ASP:H	1:A:115:ASN:ND2	2.09	0.49
1:A:281:ALA:HB2	1:A:307:TYR:CE1	2.47	0.49
1:A:149:ARG:NH2	3:A:448:HOH:O	2.45	0.48
1:A:210:GLY:HA2	1:A:288:MET:HE3	1.95	0.48
1:A:186:ARG:HB2	1:A:186:ARG:NH1	2.26	0.48
1:A:186:ARG:NH1	3:A:494:HOH:O	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:SER:C	1:A:256:ARG:HH22	2.19	0.46
1:A:54:LYS:HE3	1:A:103:TYR:OH	2.17	0.44
1:A:113:LEU:HD11	1:A:130:LEU:HD13	1.98	0.44
1:A:27:LEU:HD22	1:A:41:ALA:HB2	2.00	0.43
1:A:198:MET:O	1:A:200:TYR:N	2.52	0.43
1:A:270:PHE:CG	1:A:286:GLU:HG2	2.54	0.43
1:A:186:ARG:NH1	1:A:186:ARG:CB	2.83	0.42
1:A:323:TYR:CE2	1:A:325:GLN:HG2	2.55	0.42
1:A:75:LEU:HB3	1:A:86:LEU:HG	2.01	0.41
1:A:265:MET:HG2	3:A:422:HOH:O	2.20	0.41
1:A:203:THR:C	1:A:205:ASP:N	2.71	0.41
1:A:151:LEU:HD11	1:A:156:LEU:HD21	2.02	0.41
1:A:116:ILE:HD13	1:A:158:VAL:HG11	2.04	0.40
1:A:78:MET:CE	1:A:146:ILE:HD13	2.48	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	322/366 (88%)	313 (97%)	7 (2%)	2 (1%)	25 11

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	199	HIS
1	A	197	TRP

### 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	293/325 (90%)	271 (92%)	22 (8%)	<b>13</b> <b>3</b>

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ARG
1	A	15	LYS
1	A	16	THR
1	A	27	LEU
1	A	37	SER
1	A	62	ILE
1	A	94	ARG
1	A	116	ILE
1	A	121	LYS
1	A	123	THR
1	A	138	LEU
1	A	161	ASP
1	A	195	LEU
1	A	198	MET
1	A	228	HIS
1	A	233	LYS
1	A	254	SER
1	A	256	ARG
1	A	259	ILE
1	A	264	GLN
1	A	265	MET
1	A	275	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	114	ASN
1	A	115	ASN

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Mol	Chain	Res	Type
1	A	126	HIS
1	A	202	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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	LGF	A	361	-	40,45,45	2.87	14 (35%)	50,67,67	2.13	16 (32%)

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	LGF	A	361	-	-	9/22/44/44	0/5/6/6

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	361	LGF	C18-C21	9.20	1.53	1.40
2	A	361	LGF	C24-C23	7.09	1.48	1.42
2	A	361	LGF	C16-N3	6.26	1.48	1.34
2	A	361	LGF	C7-N8	5.05	1.43	1.36
2	A	361	LGF	C23-C22	-4.61	1.30	1.43
2	A	361	LGF	C15-C10	3.47	1.45	1.40
2	A	361	LGF	C12-C11	3.35	1.43	1.37
2	A	361	LGF	C12-C13	-3.07	1.32	1.37
2	A	361	LGF	C9-N8	-2.99	1.29	1.34
2	A	361	LGF	C18-C16	2.96	1.55	1.50
2	A	361	LGF	C14-C13	2.86	1.42	1.37
2	A	361	LGF	C29-N30	2.82	1.39	1.34
2	A	361	LGF	C4-C6	-2.11	1.46	1.50
2	A	361	LGF	C21-N20	-2.05	1.25	1.30

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	361	LGF	C15-C14-C13	5.80	124.36	118.36
2	A	361	LGF	C18-C19-C23	-4.71	112.14	120.86
2	A	361	LGF	C27-C29-N30	4.63	123.08	118.52
2	A	361	LGF	O31-C29-N30	-3.78	116.64	122.67
2	A	361	LGF	C14-C15-C10	-3.67	114.06	120.33
2	A	361	LGF	C18-C21-N20	-3.45	121.18	124.45
2	A	361	LGF	O17-C16-C18	3.34	126.79	120.06
2	A	361	LGF	C10-C9-N8	3.14	127.98	122.52
2	A	361	LGF	C2-N3-C16	-2.93	113.51	122.78
2	A	361	LGF	O17-C16-N3	-2.91	117.52	122.34
2	A	361	LGF	C11-C12-C13	-2.82	113.66	116.62
2	A	361	LGF	C39-C38-C37	-2.82	100.55	104.17
2	A	361	LGF	C4-N3-C2	2.35	122.56	115.57
2	A	361	LGF	O31-C29-C27	2.21	120.24	116.91
2	A	361	LGF	F32-C11-C12	-2.13	114.36	118.61
2	A	361	LGF	C15-C10-C11	2.06	119.07	116.10

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	361	LGF	O28-C27-C29-O31
2	A	361	LGF	O28-C27-C29-N30
2	A	361	LGF	C15-C10-C9-N8

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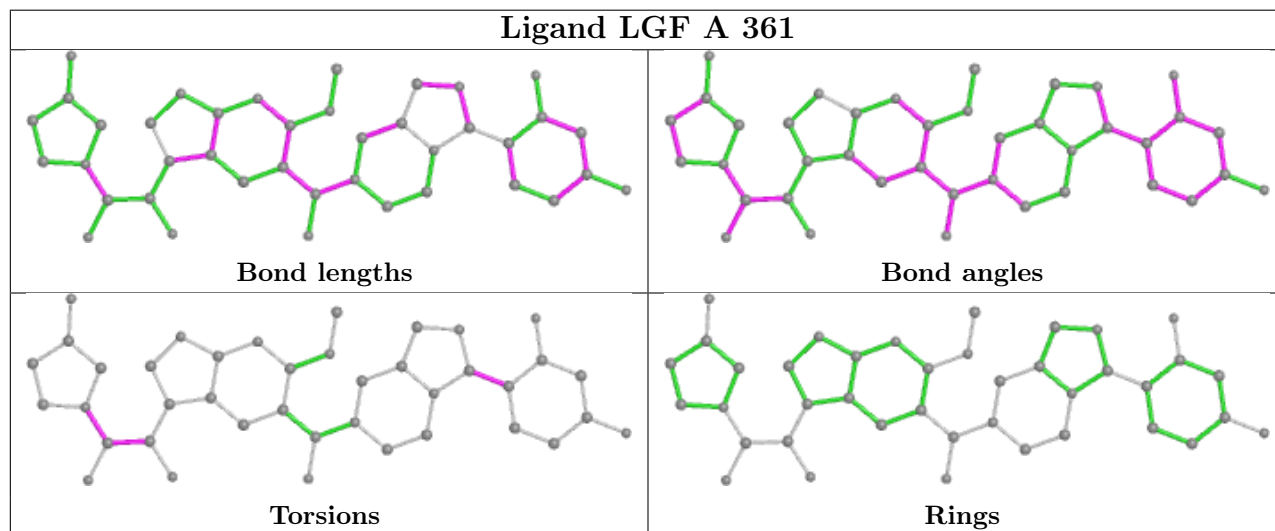
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Mol	Chain	Res	Type	Atoms
2	A	361	LGF	C27-C29-N30-C36
2	A	361	LGF	C27-C29-N30-C39
2	A	361	LGF	O31-C29-N30-C36
2	A	361	LGF	O31-C29-N30-C39
2	A	361	LGF	C11-C10-C9-N8
2	A	361	LGF	C24-C27-C29-O31

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

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	330/366 (90%)	0.79	47 (14%) <b>2</b> <b>3</b>	17, 33, 58, 79	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	199	HIS	8.5
1	A	352	PRO	7.5
1	A	197	TRP	5.0
1	A	198	MET	4.7
1	A	195	LEU	3.9
1	A	14	ASN	3.9
1	A	72	LEU	3.8
1	A	104	LEU	3.6
1	A	116	ILE	3.5
1	A	200	TYR	3.4
1	A	75	LEU	3.2
1	A	84	ILE	2.9
1	A	254	SER	2.8
1	A	12	GLU	2.8
1	A	115	ASN	2.8
1	A	55	LEU	2.7
1	A	114	ASN	2.7
1	A	263	THR	2.7
1	A	94	ARG	2.7
1	A	15	LYS	2.7
1	A	346	ILE	2.7
1	A	30	VAL	2.6
1	A	95	SER	2.6
1	A	335	ASP	2.6
1	A	131	ILE	2.6
1	A	275	ILE	2.5
1	A	289	LEU	2.5

*Continued on next page...*

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Mol	Chain	Res	Type	RSRZ
1	A	89	VAL	2.5
1	A	172	ALA	2.5
1	A	226	THR	2.5
1	A	166	ILE	2.4
1	A	48	LEU	2.3
1	A	121	LYS	2.3
1	A	117	VAL	2.3
1	A	67	ARG	2.2
1	A	160	GLU	2.2
1	A	135	LEU	2.2
1	A	134	ILE	2.2
1	A	351	PRO	2.2
1	A	10	ARG	2.2
1	A	98	GLU	2.1
1	A	138	LEU	2.1
1	A	206	ILE	2.1
1	A	35	TYR	2.0
1	A	42	PHE	2.0
1	A	186	ARG	2.0
1	A	209	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 monosaccharides in this entry.

## 6.4 Ligands [i](#)

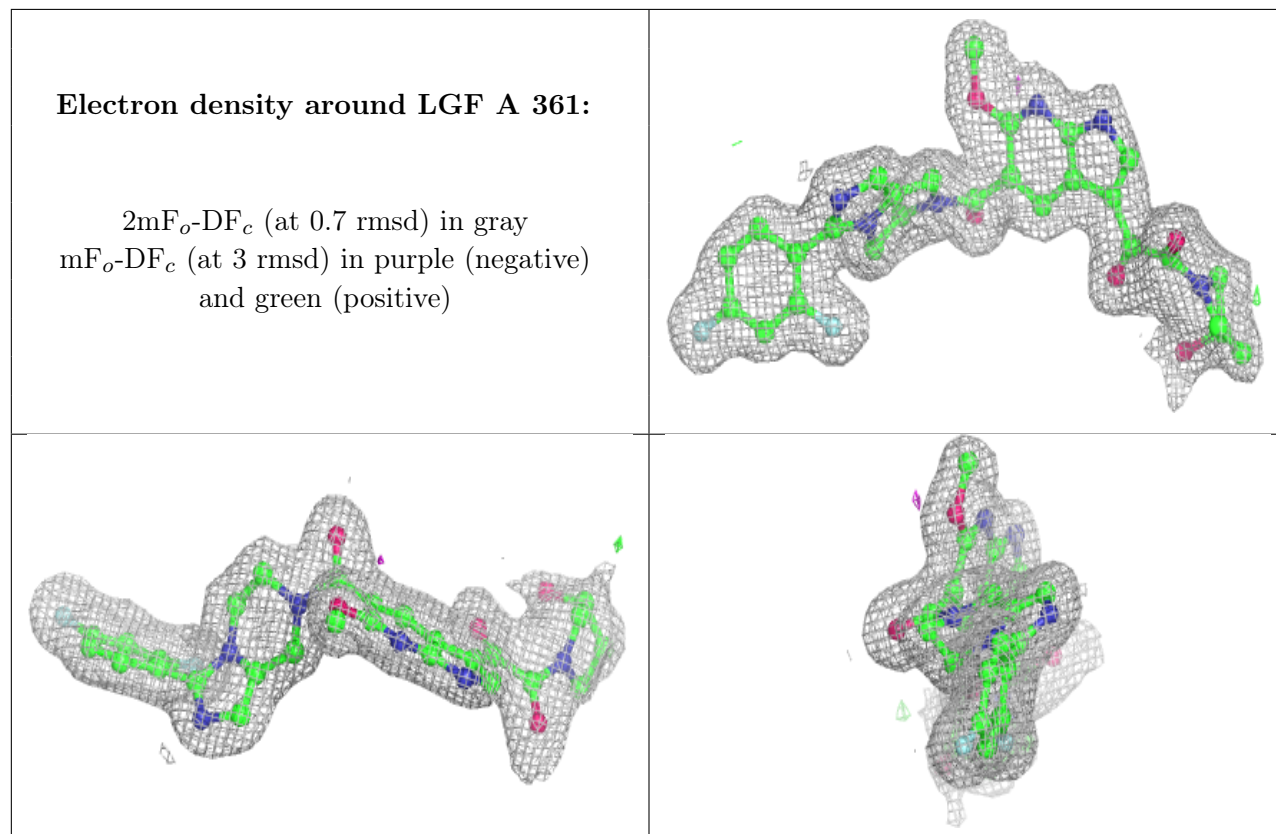
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	LGF	A	361	40/40	0.85	0.14	17,27,64,67	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.