



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 27, 2022 – 03:05 pm BST

PDB ID : 2VGO  
Title : Crystal structure of Aurora B kinase in complex with Reversine inhibitor  
Authors : D'Alise, A.M.; Amabile, G.; Iovino, M.; Di Giorgio, F.P.; Bartiromo, M.; Sessa, F.; Villa, F.; Musacchio, A.; Cortese, R.  
Deposited on : 2007-11-15  
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 : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.31.2  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0267  
CCP4 : 7.1.010 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

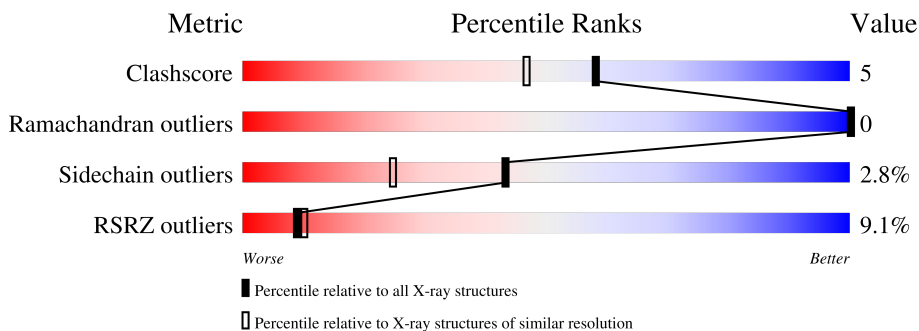
# 1 Overall quality at a glance

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))
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	284	 6% 84% 10% • 5%
1	B	284	 7% 88% 10% •
2	C	44	 9% 86% 5% • 7%
2	D	44	 36% 84% 14% •

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 5956 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.

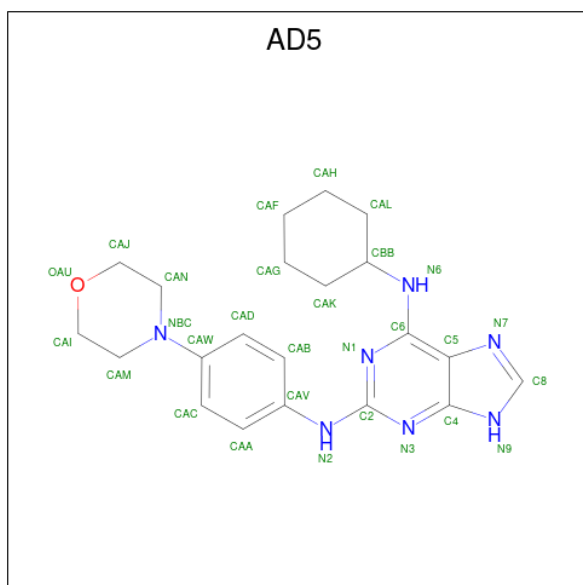
- Molecule 1 is a protein called SERINE/THREONINE-PROTEIN KINASE 12-A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	P				S
1	A	269	Total	C	N	O	P	S	0	2	0
			2258	1449	404	391	1	13			
1	B	278	Total	C	N	O	P	S	0	2	0
			2324	1488	418	403	1	14			

- Molecule 2 is a protein called INNER CENTROMERE PROTEIN A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	41	Total	C	N	O	S	0	1	0
			340	220	55	64	1			
2	D	43	Total	C	N	O	S	0	0	0
			350	225	58	66	1			

- Molecule 3 is N 6 -cyclohexyl-N 2 -(4-morpholin-4-ylphenyl)-9H-purine-2,6-diamine (three-letter code: AD5) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>7</sub>O).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			29	21	7	1		
3	B	1	Total	C	N	O	0	0
			29	21	7	1		

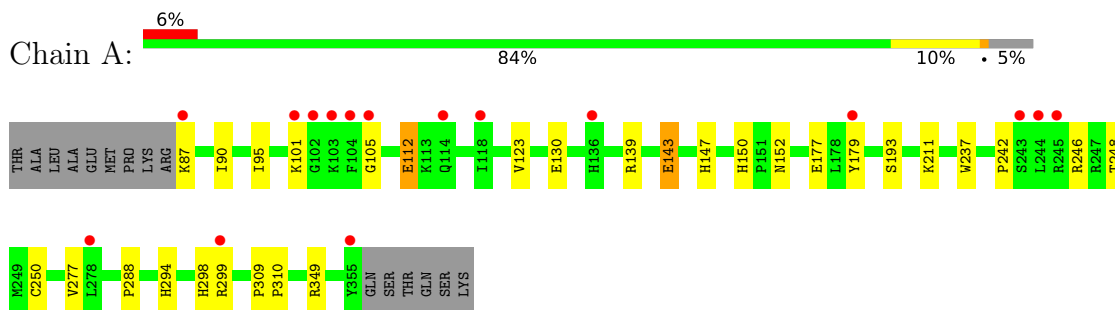
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	305	Total	O	0	0
			305	305		
4	B	261	Total	O	0	0
			261	261		
4	C	28	Total	O	0	0
			28	28		
4	D	32	Total	O	0	0
			32	32		

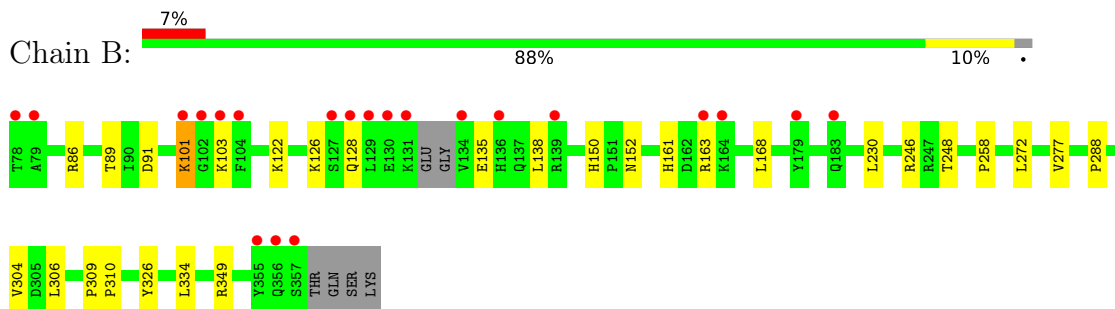
### 3 Residue-property plots [i](#)

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.

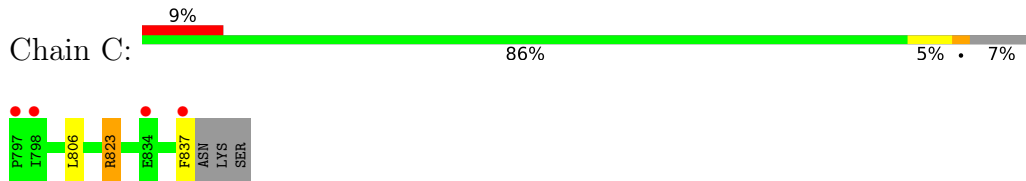
- Molecule 1: SERINE/THREONINE-PROTEIN KINASE 12-A



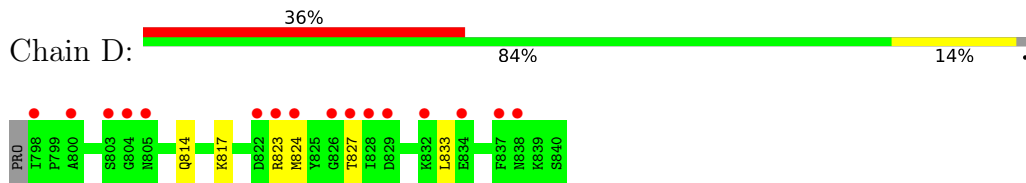
- Molecule 1: SERINE/THREONINE-PROTEIN KINASE 12-A



- Molecule 2: INNER CENTROMERE PROTEIN A



- Molecule 2: INNER CENTROMERE PROTEIN A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	45.74Å 67.60Å 116.63Å 90.00° 96.59° 90.00°	Depositor
Resolution (Å)	116.25 – 1.70 24.11 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.6 (116.25-1.70) 96.1 (24.11-1.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.74 (at 1.70Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, $R_{free}$	0.197 , 0.229 0.196 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	17.3	Xtriage
Anisotropy	0.857	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	5956	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: TPO, AD5

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	0.38	0/2308	0.54	0/3106
1	B	0.37	0/2374	0.52	0/3194
2	C	0.32	0/349	0.54	0/474
2	D	0.35	0/358	0.50	0/485
All	All	0.37	0/5389	0.53	0/7259

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	2258	0	2261	24	0
1	B	2324	0	2334	18	0
2	C	340	0	335	5	0
2	D	350	0	347	6	0
3	A	29	0	27	1	0
3	B	29	0	27	2	0
4	A	305	0	0	4	0
4	B	261	0	0	5	0
4	C	28	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	32	0	0	1	0
All	All	5956	0	5331	51	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 5.

All (51) 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)
2:C:823:ARG:HH11	2:C:823:ARG:HG3	0.94	1.09
1:A:112:GLU:HG3	4:A:2022:HOH:O	1.68	0.93
2:C:823:ARG:HG3	2:C:823:ARG:NH1	1.73	0.87
1:A:211:LYS:HD3	1:A:242:PRO:HA	1.58	0.86
1:A:150:HIS:HD2	1:A:152:ASN:H	1.23	0.84
3:B:1359:AD5:N1	3:B:1359:AD5:HAA	2.00	0.77
1:A:143:GLU:HG2	2:D:833:LEU:CD1	2.15	0.77
1:B:150:HIS:HD2	1:B:152:ASN:H	1.34	0.76
1:A:150:HIS:CD2	1:A:152:ASN:H	2.03	0.76
1:B:258:PRO:HG2	4:B:2233:HOH:O	1.86	0.74
1:A:87:LYS:HB3	4:A:2004:HOH:O	1.90	0.71
1:B:122:LYS:HE2	1:B:168:LEU:HD12	1.74	0.70
1:B:326:TYR:HA	4:B:2233:HOH:O	1.92	0.69
1:A:152:ASN:HD21	1:A:349:ARG:HH21	1.41	0.67
1:A:143:GLU:HG2	2:D:833:LEU:HD12	1.76	0.66
1:B:150:HIS:CD2	1:B:152:ASN:H	2.13	0.65
1:A:143:GLU:HA	1:A:143:GLU:OE1	1.97	0.65
3:A:1357:AD5:HAA	3:A:1357:AD5:N1	2.14	0.62
1:A:237:TRP:CD2	1:A:250:CYS:HB2	2.36	0.61
1:A:139:ARG:HG2	2:D:833:LEU:HD13	1.83	0.60
1:A:143:GLU:O	1:A:147:HIS:HD2	1.87	0.57
2:C:823:ARG:HH11	2:C:823:ARG:CG	1.88	0.55
1:A:193:SER:HB3	4:A:2133:HOH:O	2.05	0.55
1:A:152:ASN:ND2	1:A:349:ARG:HH21	2.04	0.54
2:D:817:LYS:HG3	4:D:2014:HOH:O	2.06	0.54
1:A:105:GLY:HA3	1:A:123:VAL:O	2.07	0.53
1:B:126:LYS:NZ	1:B:161:HIS:HD2	2.06	0.53
1:B:230:LEU:HD22	4:B:2106:HOH:O	2.10	0.51
1:B:272:LEU:HD21	1:B:334:LEU:HG	1.91	0.51
1:B:152:ASN:HD21	1:B:349:ARG:HH21	1.59	0.51
3:B:1359:AD5:N1	3:B:1359:AD5:CAA	2.64	0.50
2:C:823:ARG:NH1	2:C:823:ARG:CG	2.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:GLU:HB2	4:A:2030:HOH:O	2.11	0.50
1:B:89:THR:HG23	1:B:91:ASP:H	1.78	0.49
2:D:823:ARG:HA	2:D:827:THR:HG23	1.95	0.49
1:A:143:GLU:HG2	2:D:833:LEU:HD11	1.95	0.47
1:B:304:VAL:HG22	4:B:2233:HOH:O	2.14	0.47
1:A:277:VAL:HG13	1:A:288:PRO:HD2	1.99	0.45
1:A:90:ILE:HD11	1:A:95:ILE:HD11	2.00	0.44
1:B:126:LYS:HZ3	1:B:161:HIS:HD2	1.64	0.44
1:B:277:VAL:HG13	1:B:288:PRO:HD2	2.00	0.44
1:A:246:ARG:HD2	1:A:248:TPO:O2P	2.17	0.43
1:A:177[B]:GLU:OE1	1:A:179:TYR:HE2	2.00	0.43
1:B:101:LYS:O	1:B:101:LYS:HG2	2.18	0.43
1:A:143:GLU:O	1:A:147:HIS:CD2	2.70	0.43
1:B:306:LEU:HA	4:B:2186:HOH:O	2.17	0.43
1:B:309:PRO:HA	1:B:310:PRO:HD3	1.92	0.41
1:A:309:PRO:HA	1:A:310:PRO:HD3	1.87	0.41
1:A:150:HIS:HD2	1:A:152:ASN:N	2.03	0.41
1:B:246:ARG:HB3	1:B:248:TPO:O1P	2.21	0.40
1:B:135:GLU:HG3	2:C:837:PHE:CD2	2.57	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	268/284 (94%)	259 (97%)	9 (3%)	0	100	100
1	B	275/284 (97%)	266 (97%)	9 (3%)	0	100	100
2	C	40/44 (91%)	39 (98%)	1 (2%)	0	100	100
2	D	41/44 (93%)	38 (93%)	3 (7%)	0	100	100
All	All	624/656 (95%)	602 (96%)	22 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	244/255 (96%)	238 (98%)	6 (2%)	47	29
1	B	252/255 (99%)	246 (98%)	6 (2%)	49	31
2	C	37/39 (95%)	35 (95%)	2 (5%)	22	7
2	D	38/39 (97%)	36 (95%)	2 (5%)	22	7
All	All	571/588 (97%)	555 (97%)	16 (3%)	43	25

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	LYS
1	A	112	GLU
1	A	143	GLU
1	A	294	HIS
1	A	298	HIS
1	A	299	ARG
1	B	86	ARG
1	B	101	LYS
1	B	103	LYS
1	B	128	GLN
1	B	138	LEU
1	B	163	ARG
2	C	806	LEU
2	C	823	ARG
2	D	814	GLN
2	D	824	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	114	GLN

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Mol	Chain	Res	Type
1	A	115	ASN
1	A	128	GLN
1	A	136	HIS
1	A	147	HIS
1	A	150	HIS
1	A	152	ASN
1	B	128	GLN
1	B	137	GLN
1	B	147	HIS
1	B	150	HIS
1	B	152	ASN
1	B	161	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

2 non-standard protein/DNA/RNA residues are 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
1	TPO	B	248	1	8,10,11	0.68	0	10,14,16	0.97	0
1	TPO	A	248	1	8,10,11	0.75	0	10,14,16	0.95	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
1	TPO	B	248	1	-	0/9/11/13	-
1	TPO	A	248	1	-	0/9/11/13	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	248	TPO	1	0
1	A	248	TPO	1	0

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

2 ligands are 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
3	AD5	B	1359	-	29,33,33	1.33	6 (20%)	36,45,45	1.60	5 (13%)
3	AD5	A	1357	-	29,33,33	1.13	3 (10%)	36,45,45	1.56	3 (8%)

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	AD5	B	1359	-	-	7/12/28/28	0/5/5/5
3	AD5	A	1357	-	-	5/12/28/28	0/5/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1357	AD5	C5-C4	-2.69	1.33	1.40
3	B	1359	AD5	CAM-CAI	2.64	1.60	1.50
3	B	1359	AD5	C5-C4	-2.63	1.34	1.40
3	B	1359	AD5	CAN-CAJ	2.49	1.60	1.50
3	B	1359	AD5	CAN-NBC	2.24	1.50	1.46
3	A	1357	AD5	CAV-N2	-2.23	1.35	1.40
3	B	1359	AD5	CAV-N2	-2.15	1.36	1.40
3	B	1359	AD5	CAM-NBC	2.07	1.50	1.46
3	A	1357	AD5	CAN-NBC	2.01	1.49	1.46

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1357	AD5	C2-N3-C4	4.70	120.61	115.28
3	A	1357	AD5	N3-C2-N1	-4.69	118.81	126.23
3	B	1359	AD5	N3-C2-N1	-4.58	118.99	126.23
3	B	1359	AD5	C2-N3-C4	4.47	120.35	115.28
3	A	1357	AD5	CAN-NBC-CAM	4.10	120.57	111.52
3	B	1359	AD5	CAN-NBC-CAM	3.63	119.53	111.52
3	B	1359	AD5	OAU-CAJ-CAN	-2.66	105.94	111.80
3	B	1359	AD5	CAV-N2-C2	-2.16	122.96	129.23

There are no chirality outliers.

All (12) torsion outliers are listed below:

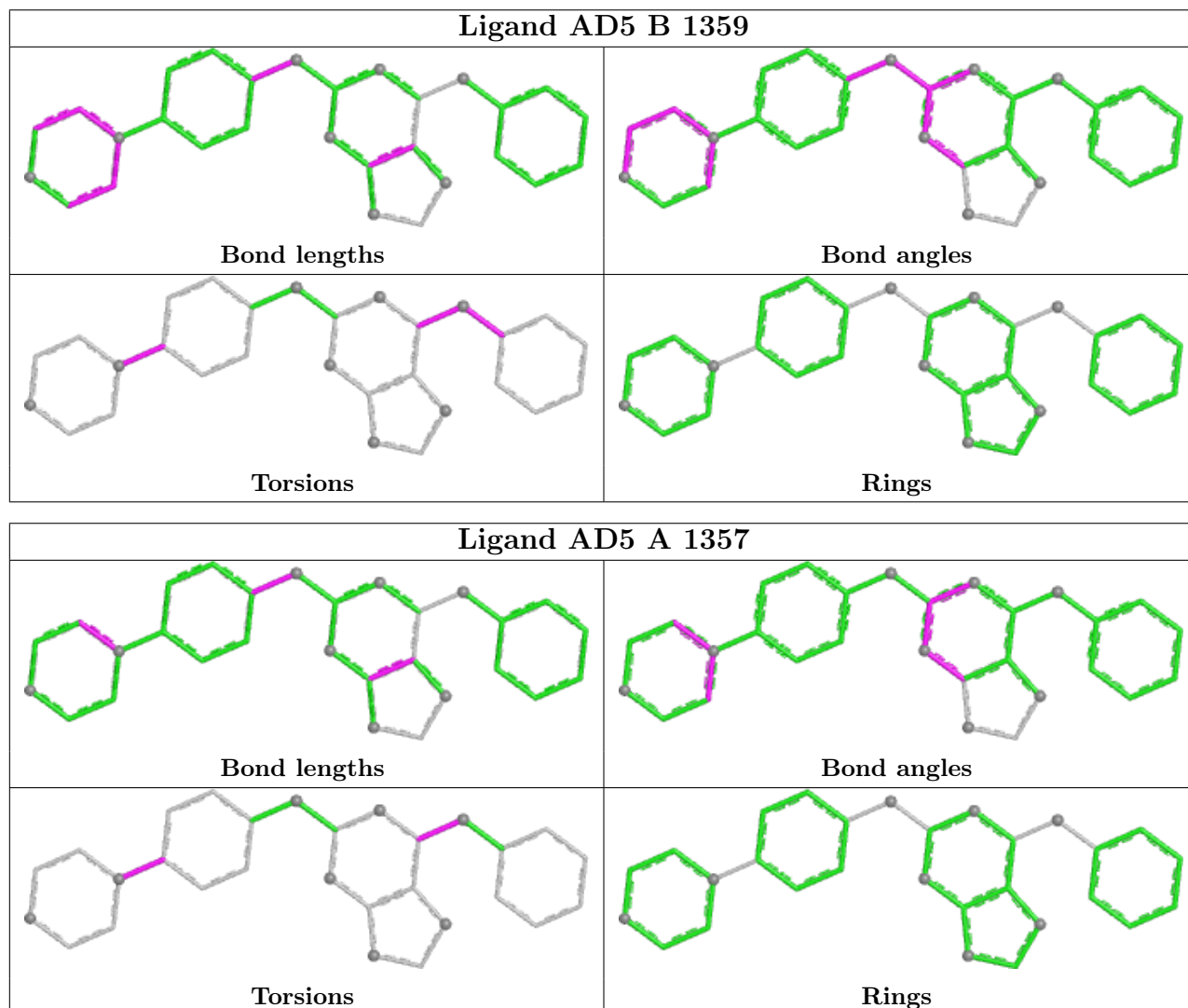
Mol	Chain	Res	Type	Atoms
3	A	1357	AD5	N1-C6-N6-CBB
3	A	1357	AD5	C5-C6-N6-CBB
3	B	1359	AD5	N1-C6-N6-CBB
3	B	1359	AD5	C5-C6-N6-CBB
3	B	1359	AD5	CAD-CAW-NBC-CAM
3	B	1359	AD5	CAD-CAW-NBC-CAN
3	B	1359	AD5	CAC-CAW-NBC-CAM
3	B	1359	AD5	CAC-CAW-NBC-CAN
3	B	1359	AD5	CAK-CBB-N6-C6
3	A	1357	AD5	CAC-CAW-NBC-CAN
3	A	1357	AD5	CAD-CAW-NBC-CAM
3	A	1357	AD5	CAC-CAW-NBC-CAM

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1359	AD5	2	0
3	A	1357	AD5	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, 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	268/284 (94%)	0.51	16 (5%) 21 24	10, 17, 31, 39	0
1	B	277/284 (97%)	0.38	21 (7%) 13 16	10, 19, 37, 48	0
2	C	41/44 (93%)	0.69	4 (9%) 7 8	24, 27, 37, 40	0
2	D	43/44 (97%)	1.57	16 (37%) 0 0	21, 37, 42, 43	0
All	All	629/656 (95%)	0.54	57 (9%) 9 10	10, 20, 39, 48	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	104	PHE	7.2
1	A	244	LEU	6.9
1	A	103	LYS	5.4
1	B	136	HIS	5.2
1	A	243	SER	5.2
1	B	357	SER	4.7
1	B	163	ARG	4.5
1	A	102	GLY	4.3
2	D	804	GLY	4.3
1	A	104	PHE	4.1
2	D	827	THR	4.0
1	B	78	THR	3.9
1	A	355	TYR	3.8
2	D	803	SER	3.8
2	D	822	ASP	3.6
1	A	105	GLY	3.5
1	B	179	TYR	3.4
1	B	355	TYR	3.4
2	C	837	PHE	3.4
2	D	800	ALA	3.1
1	B	129	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	130	GLU	3.0
2	D	805	ASN	3.0
1	B	127	SER	3.0
2	C	834	GLU	3.0
2	D	823	ARG	2.9
1	A	114	GLN	2.9
1	B	134	VAL	2.9
1	B	183	GLN	2.8
1	B	128	GLN	2.8
1	B	79	ALA	2.8
1	A	136	HIS	2.7
1	A	278	LEU	2.6
2	D	837	PHE	2.6
1	B	164	LYS	2.6
2	D	798	ILE	2.6
2	D	834	GLU	2.5
1	A	87	LYS	2.5
2	D	828	ILE	2.5
2	D	838	ASN	2.4
1	A	101	LYS	2.4
2	D	832	LYS	2.4
1	B	139	ARG	2.3
1	A	299	ARG	2.3
1	B	131	LYS	2.3
1	B	102	GLY	2.2
1	B	103	LYS	2.2
1	B	101	LYS	2.2
1	A	245	ARG	2.2
1	B	356	GLN	2.2
2	C	798	ILE	2.2
2	D	826	GLY	2.2
2	C	797	PRO	2.1
1	A	118	ILE	2.1
2	D	824	MET	2.1
1	A	179	TYR	2.0
2	D	829	ASP	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains

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( $\text{\AA}^2$ )	Q<0.9
1	TPO	A	248	11/12	0.98	0.07	18,20,21,21	0
1	TPO	B	248	11/12	0.98	0.05	18,19,21,21	0

### 6.3 Carbohydrates [i](#)

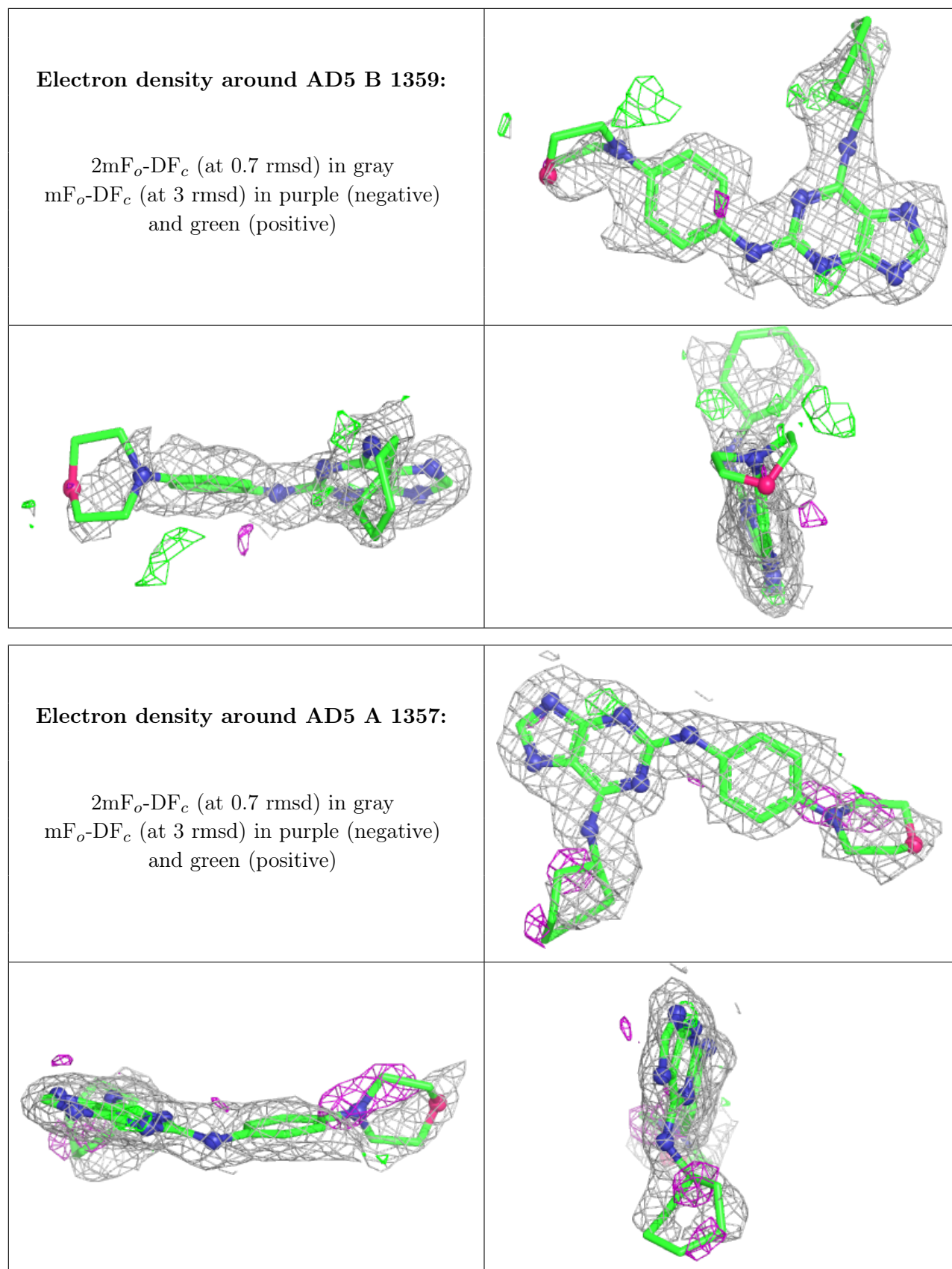
There are no monosaccharides in this entry.

### 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( $\text{\AA}^2$ )	Q<0.9
3	AD5	B	1359	29/29	0.57	0.28	48,49,52,52	0
3	AD5	A	1357	29/29	0.68	0.26	36,39,42,42	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.