



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 11:41 AM UTC

PDB ID : 4B8M / pdb_00004b8m
Title : Aurora B kinase in complex with VX-680
Authors : Sessa, F.; Villa, F.
Deposited on : 2012-08-28
Resolution : 1.85 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

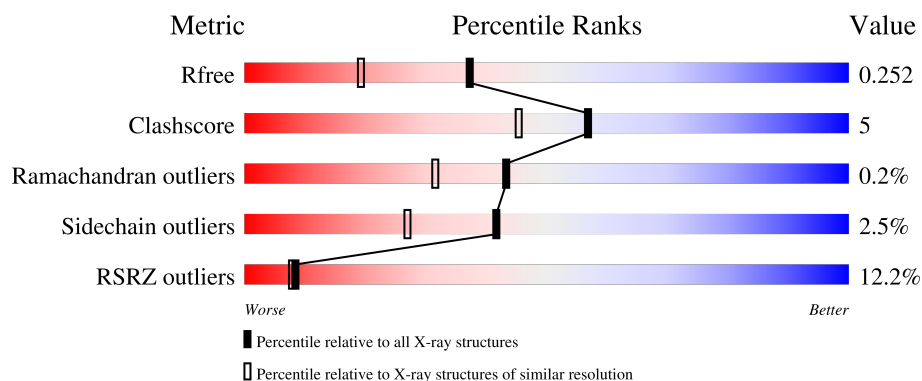
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	286	9% 83% 11% 5%
1	B	286	9% 87% 10%
2	C	44	11% 86% 7% 7%
2	D	44	48% 93% 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5407 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 AURORA KINASE B-A.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	271	Total	C	N	O	P	S	0	3	0
			2268	1456	405	393	1	13			
1	B	280	Total	C	N	O	P	S	0	7	0
			2365	1518	425	407	1	14			

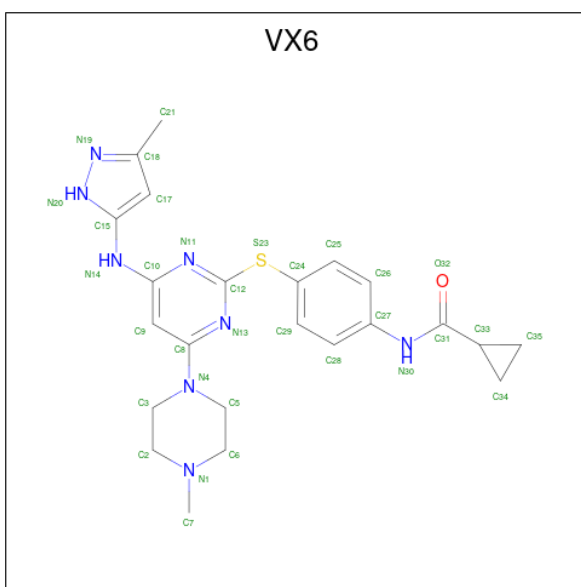
There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ALA	-	expression tag	UNP Q6DE08
A	362	ASP	-	expression tag	UNP Q6DE08
B	77	ALA	-	expression tag	UNP Q6DE08
B	362	ASP	-	expression tag	UNP Q6DE08

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	41	Total	C	N	O	S	0	2	0
			346	225	57	63	1			
2	D	43	Total	C	N	O	S	0	0	0
			351	225	58	67	1			

- Molecule 3 is CYCLOPROPANECARBOXYLIC ACID {4-[4-(4-METHYL-PIPERAZIN-1-YL)-6-(5-METHYL-2H-PYRAZOL-3-YLAMINO)-PYRIMIDIN-2-YLSULFANYL]-PHENYL}-AMIDE (CCD ID: VX6) (formula: C₂₃H₂₈N₈OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			33	23	8	1	1		
3	B	1	Total	C	N	O	S	0	0
			33	23	8	1	1		

- Molecule 4 is water.

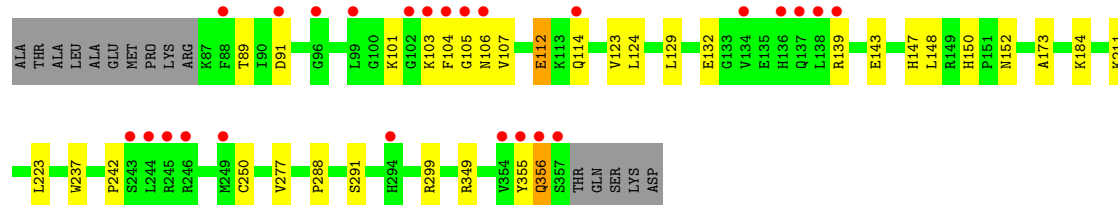
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	6	Total	O	0	0
			6	6		
4	B	5	Total	O	0	0
			5	5		

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.

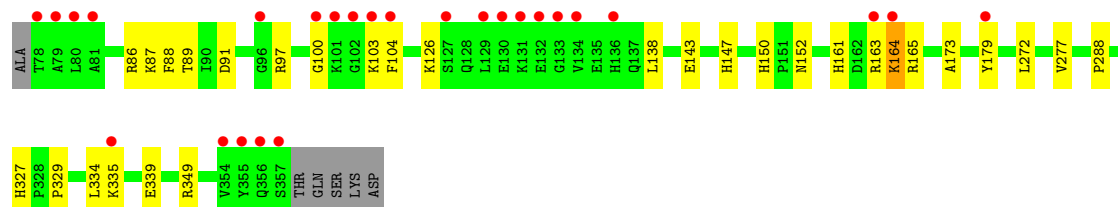
• Molecule 1: AURORA KINASE B-A

Chain A: 



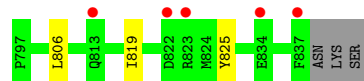
• Molecule 1: AURORA KINASE B-A

Chain B: 

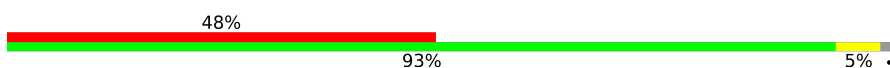


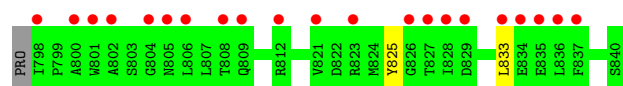
• Molecule 2: INNER CENTROMERE PROTEIN A

Chain C: 



• Molecule 2: INNER CENTROMERE PROTEIN A

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	45.79Å 67.26Å 116.75Å 90.00° 96.58° 90.00°	Depositor
Resolution (Å)	116.25 – 1.85 115.99 – 1.85	Depositor EDS
% Data completeness (in resolution range)	97.9 (116.25-1.85) 97.9 (115.99-1.85)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.04 (at 1.85Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.191 , 0.236 0.225 , 0.252	Depositor DCC
R_{free} test set	2977 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	18.4	Xtriage
Anisotropy	0.647	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 31.4	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	0.92	EDS
Total number of atoms	5407	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.37% 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: VX6, TPO

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	0.50	0/2327	0.78	2/3132 (0.1%)
1	B	0.51	0/2437	0.73	0/3278
2	C	0.46	0/361	0.82	0/490
2	D	0.45	0/359	0.77	0/485
All	All	0.50	0/5484	0.76	2/7385 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	291	SER	CA-C-N	5.06	124.72	119.56
1	A	291	SER	C-N-CA	5.06	124.72	119.56

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	2268	0	2282	28	0
1	B	2365	0	2400	17	0
2	C	346	0	351	1	0
2	D	351	0	347	4	0
3	A	33	0	28	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	33	0	28	4	0
4	A	6	0	0	0	0
4	B	5	0	0	0	0
All	All	5407	0	5436	50	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 (50) 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:355:TYR:HA	1:A:356:GLN:HB2	1.18	1.11
1:A:355:TYR:HA	1:A:356:GLN:CB	1.85	1.06
1:B:173:ALA:H	3:B:1359:VX6:H20	1.05	0.93
1:A:211:LYS:HD3	1:A:242:PRO:HA	1.50	0.92
1:A:173:ALA:H	3:A:1359:VX6:H20	1.21	0.87
1:A:223:LEU:HD21	3:A:1359:VX6:H26	1.61	0.81
1:B:150:HIS:HD2	1:B:152:ASN:H	1.34	0.76
1:A:150:HIS:HD2	1:A:152:ASN:H	1.33	0.75
1:B:89:THR:HG22	1:B:91:ASP:H	1.54	0.73
1:A:355:TYR:CA	1:A:356:GLN:HB2	2.07	0.72
1:A:143:GLU:O	1:A:147:HIS:HD2	1.75	0.69
1:A:150:HIS:CD2	1:A:152:ASN:H	2.10	0.69
1:B:143:GLU:O	1:B:147:HIS:HD2	1.79	0.65
1:A:105:GLY:HA3	1:A:123:VAL:O	1.97	0.64
1:A:355:TYR:CA	1:A:356:GLN:CB	2.68	0.63
1:A:152:ASN:HD21	1:A:349:ARG:HH21	1.43	0.63
1:B:173:ALA:N	3:B:1359:VX6:H20	1.88	0.63
1:B:126:LYS:NZ	1:B:161:HIS:HD2	1.96	0.62
1:A:237:TRP:CD2	1:A:250:CYS:HB2	2.34	0.62
1:B:150:HIS:CD2	1:B:152:ASN:H	2.17	0.61
1:B:126:LYS:HZ3	1:B:161:HIS:HD2	1.48	0.61
1:A:112:GLU:HG2	2:D:825:TYR:OH	2.04	0.58
1:A:101:LYS:HA	1:A:106:ASN:OD1	2.03	0.58
1:A:89[B]:THR:HG22	1:A:91:ASP:H	1.69	0.57
1:A:152:ASN:ND2	1:A:349:ARG:HH21	2.03	0.56
1:A:277:VAL:HG13	1:A:288:PRO:HD2	1.87	0.56
1:A:355:TYR:CD2	1:A:356:GLN:HB3	2.42	0.54
1:B:335:LYS:O	1:B:339:GLU:HG2	2.11	0.50
1:B:164:LYS:HE2	1:B:165:ARG:NH2	2.28	0.49
1:A:124[B]:LEU:HB3	1:A:129:LEU:HD11	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ARG:CD	2:D:833:LEU:HB3	2.43	0.49
3:B:1359:VX6:H17	3:B:1359:VX6:C25	2.43	0.48
1:B:277:VAL:HG13	1:B:288:PRO:HD2	1.96	0.47
3:A:1359:VX6:H17	3:A:1359:VX6:N11	2.29	0.47
3:A:1359:VX6:N11	3:A:1359:VX6:C17	2.79	0.46
1:B:100:GLY:HA3	1:B:104:PHE:HB2	1.98	0.45
1:B:272[A]:LEU:HD21	1:B:334:LEU:HG	2.00	0.44
1:B:152:ASN:HD21	1:B:349:ARG:HH21	1.65	0.44
1:A:104:PHE:CE2	1:A:132:GLU:HG3	2.53	0.43
1:A:355:TYR:HA	1:A:356:GLN:HB3	1.90	0.42
3:B:1359:VX6:H17	3:B:1359:VX6:N11	2.34	0.42
1:B:327:HIS:CD2	1:B:329:PRO:HD2	2.55	0.42
1:A:237:TRP:CE3	1:A:250:CYS:HB2	2.55	0.42
1:B:88:PHE:HZ	2:C:825:TYR:HD1	1.67	0.42
1:B:86:ARG:HG2	1:B:87:LYS:N	2.35	0.41
1:A:139:ARG:HD2	2:D:833:LEU:HB3	2.02	0.41
1:A:107:VAL:HG21	3:A:1359:VX6:H28	2.03	0.40
1:A:139:ARG:HG3	2:D:833:LEU:HD13	2.02	0.40
1:A:173:ALA:N	3:A:1359:VX6:H20	2.03	0.40
3:A:1359:VX6:H9	3:A:1359:VX6:H32	1.87	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	271/286 (95%)	261 (96%)	9 (3%)	1 (0%)	30	17
1	B	284/286 (99%)	277 (98%)	7 (2%)	0	100	100
2	C	41/44 (93%)	39 (95%)	2 (5%)	0	100	100
2	D	41/44 (93%)	39 (95%)	2 (5%)	0	100	100
All	All	637/660 (96%)	616 (97%)	20 (3%)	1 (0%)	43	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	356	GLN

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	247/256 (96%)	241 (98%)	6 (2%)	43	28
1	B	258/256 (101%)	252 (98%)	6 (2%)	44	30
2	C	38/39 (97%)	36 (95%)	2 (5%)	20	7
2	D	38/39 (97%)	38 (100%)	0	100	100
All	All	581/590 (98%)	567 (98%)	14 (2%)	42	28

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	LYS
1	A	112	GLU
1	A	114	GLN
1	A	148	LEU
1	A	184	LYS
1	A	299	ARG
1	B	97	ARG
1	B	103	LYS
1	B	138	LEU
1	B	163	ARG
1	B	164	LYS
1	B	179	TYR
2	C	806	LEU
2	C	819	ILE

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	136	HIS
1	A	147	HIS
1	A	150	HIS
1	A	152	ASN
1	A	330	GLN
1	B	147	HIS
1	B	150	HIS
1	B	152	ASN
1	B	161	HIS
1	B	298	HIS
1	B	327	HIS
2	D	809	GLN
2	D	813	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	A	248	1	8,10,11	0.68	0	10,14,16	1.06	0
1	TPO	B	248	1	8,10,11	0.63	0	10,14,16	1.02	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	A	248	1	-	0/9/11/13	-
1	TPO	B	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.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	VX6	B	1359	-	36,37,37	1.79	5 (13%)	48,52,52	1.86	9 (18%)
3	VX6	A	1359	-	36,37,37	1.79	6 (16%)	48,52,52	1.92	9 (18%)

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	VX6	B	1359	-	-	4/20/32/32	0/5/5/5
3	VX6	A	1359	-	-	0/20/32/32	0/5/5/5

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1359	VX6	N20-N19	-6.25	1.23	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1359	VX6	N20-N19	-6.15	1.23	1.36
3	A	1359	VX6	C17-C18	-4.12	1.33	1.40
3	B	1359	VX6	C17-C18	-4.11	1.33	1.40
3	B	1359	VX6	C17-C15	-4.00	1.33	1.38
3	A	1359	VX6	C17-C15	-3.91	1.33	1.38
3	A	1359	VX6	C27-N30	-3.44	1.34	1.41
3	B	1359	VX6	C27-N30	-3.26	1.35	1.41
3	A	1359	VX6	C10-N14	-2.72	1.34	1.40
3	B	1359	VX6	C10-N14	-2.70	1.34	1.40
3	A	1359	VX6	C8-N4	2.03	1.42	1.37

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1359	VX6	C12-N11-C10	7.06	121.73	115.15
3	B	1359	VX6	C12-N11-C10	6.81	121.49	115.15
3	A	1359	VX6	C12-N13-C8	5.33	121.16	115.50
3	B	1359	VX6	C12-N13-C8	5.17	120.99	115.50
3	A	1359	VX6	N13-C12-N11	-3.75	120.16	127.00
3	B	1359	VX6	N13-C12-N11	-3.60	120.44	127.00
3	B	1359	VX6	N14-C10-N11	3.52	121.85	113.33
3	A	1359	VX6	N14-C10-N11	3.33	121.40	113.33
3	B	1359	VX6	C10-C9-C8	3.27	119.26	116.64
3	B	1359	VX6	N13-C8-N4	3.19	120.59	116.56
3	A	1359	VX6	N13-C8-N4	3.03	120.38	116.56
3	A	1359	VX6	C10-C9-C8	3.02	119.06	116.64
3	B	1359	VX6	C5-N4-C3	2.84	117.96	111.57
3	A	1359	VX6	C5-N4-C3	2.73	117.72	111.57
3	B	1359	VX6	C9-C8-N13	-2.28	118.94	123.34
3	A	1359	VX6	C9-C8-N13	-2.25	119.00	123.34
3	B	1359	VX6	C9-C10-N11	-2.15	118.88	123.35
3	A	1359	VX6	C9-C10-N11	-2.15	118.89	123.35

There are no chirality outliers.

All (4) torsion outliers are listed below:

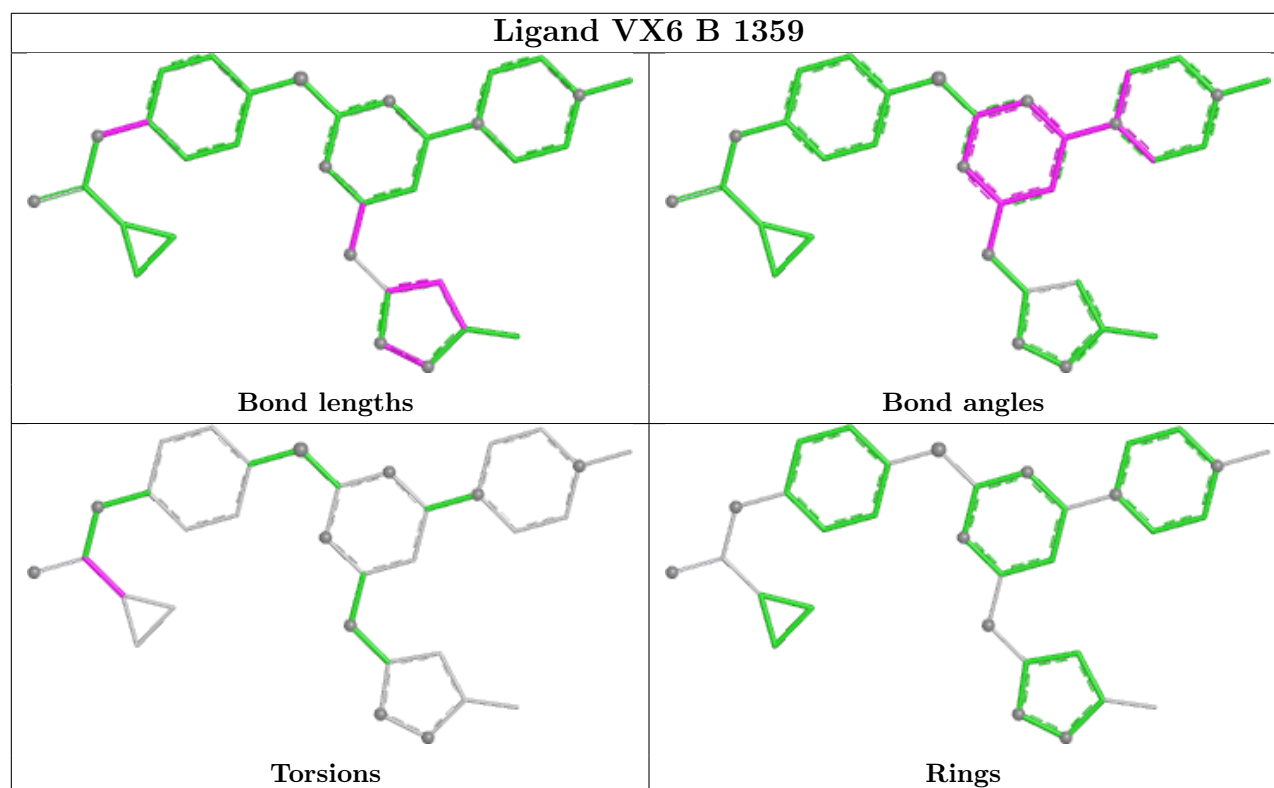
Mol	Chain	Res	Type	Atoms
3	B	1359	VX6	O32-C31-C33-C34
3	B	1359	VX6	O32-C31-C33-C35
3	B	1359	VX6	N30-C31-C33-C34
3	B	1359	VX6	N30-C31-C33-C35

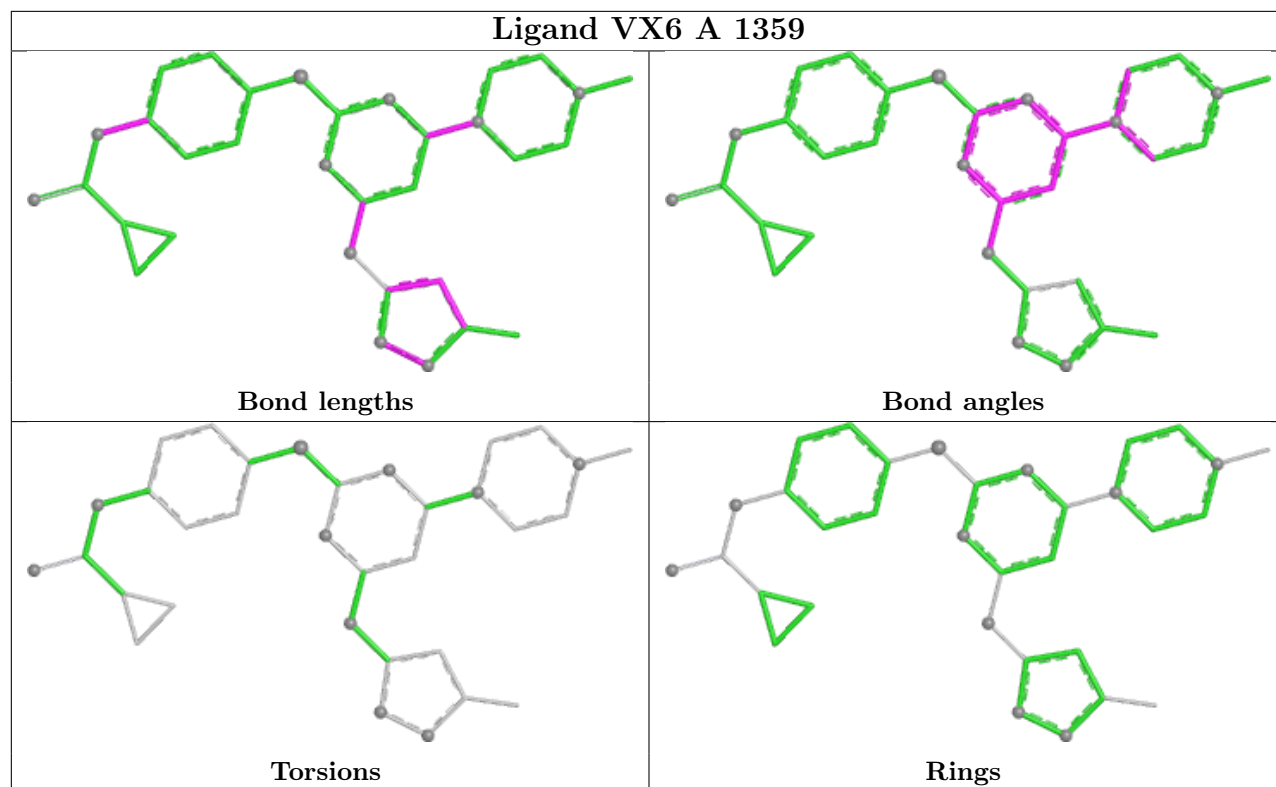
There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1359	VX6	4	0
3	A	1359	VX6	7	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	270/286 (94%)	0.40	25 (9%)	14 14	8, 18, 36, 43	3 (1%)
1	B	279/286 (97%)	0.39	26 (9%)	14 14	6, 18, 42, 49	7 (2%)
2	C	41/44 (93%)	1.26	5 (12%)	8 8	17, 27, 38, 40	2 (4%)
2	D	43/44 (97%)	2.05	21 (48%)	0 0	21, 39, 48, 50	0
All	All	633/660 (95%)	0.56	77 (12%)	8 8	6, 19, 42, 50	12 (1%)

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	837	PHE	5.1
1	B	357	SER	4.9
1	B	355	TYR	4.9
1	B	78	THR	4.8
1	B	104	PHE	4.8
1	A	243	SER	4.7
1	B	103	LYS	4.1
1	A	244	LEU	4.1
1	B	100	GLY	4.0
1	B	79	ALA	4.0
1	B	133	GLY	3.9
1	A	104	PHE	3.8
1	A	106	ASN	3.7
1	B	134	VAL	3.7
1	B	136	HIS	3.7
2	C	823[A]	ARG	3.7
1	A	103	LYS	3.7
1	A	105	GLY	3.5
1	A	136	HIS	3.3
1	B	102	GLY	3.3
1	A	356	GLN	3.2

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Mol	Chain	Res	Type	RSRZ
2	D	804	GLY	3.1
1	A	102	GLY	3.1
2	D	827	THR	3.0
1	B	101	LYS	3.0
2	C	834	GLU	3.0
1	A	357	SER	2.9
1	B	179	TYR	2.9
2	C	822	ASP	2.9
2	D	806	LEU	2.9
2	C	837	PHE	2.9
1	A	139	ARG	2.9
2	D	826	GLY	2.9
1	A	294	HIS	2.8
1	A	354	VAL	2.8
1	A	249	MET	2.8
2	D	805	ASN	2.7
2	D	800	ALA	2.7
1	B	131	LYS	2.7
1	B	129	LEU	2.7
2	D	798	ILE	2.7
2	D	823	ARG	2.6
2	D	809	GLN	2.6
2	D	828	ILE	2.6
2	D	835	GLU	2.6
1	A	134	VAL	2.6
1	B	127	SER	2.6
1	A	114	GLN	2.5
2	D	821	VAL	2.5
1	B	354	VAL	2.5
1	B	132	GLU	2.5
2	D	834	GLU	2.5
1	A	88	PHE	2.4
2	D	801	TRP	2.4
1	A	245	ARG	2.4
1	B	356	GLN	2.4
2	C	813	GLN	2.4
1	A	355	TYR	2.4
1	B	96	GLY	2.4
2	D	833	LEU	2.3
2	D	812	ARG	2.3
2	D	829	ASP	2.3
1	B	80	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
2	D	802	ALA	2.2
1	A	137	GLN	2.2
1	B	335	LYS	2.2
1	B	81	ALA	2.2
2	D	808	THR	2.2
1	A	91	ASP	2.2
1	A	246	ARG	2.1
1	A	99	LEU	2.1
1	A	96	GLY	2.1
1	B	164	LYS	2.0
1	A	138	LEU	2.0
2	D	836	LEU	2.0
1	B	163	ARG	2.0
1	B	130	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
1	TPO	A	248	11/12	0.96	0.08	21,23,24,24	0
1	TPO	B	248	11/12	0.98	0.06	17,17,19,20	0

6.3 Carbohydrates [i](#)

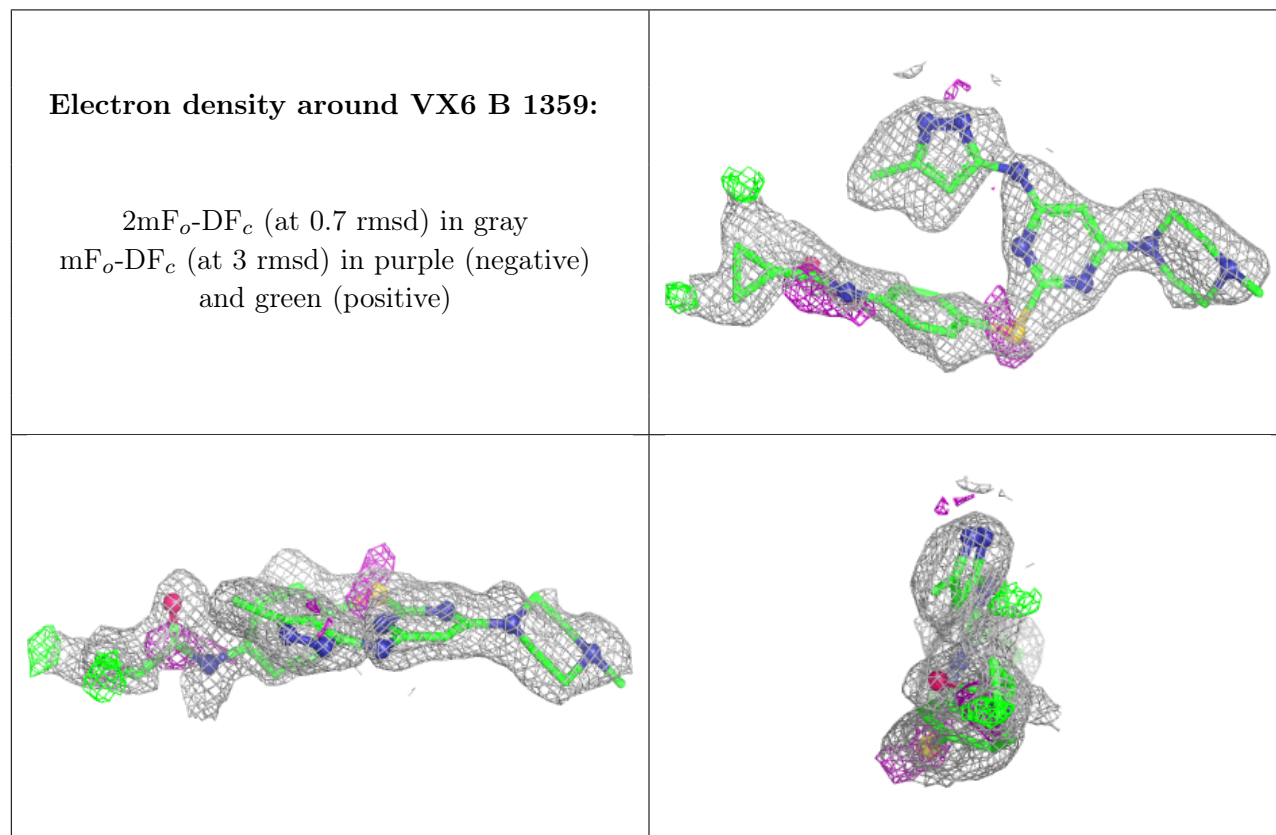
There are no oligosaccharides in this entry.

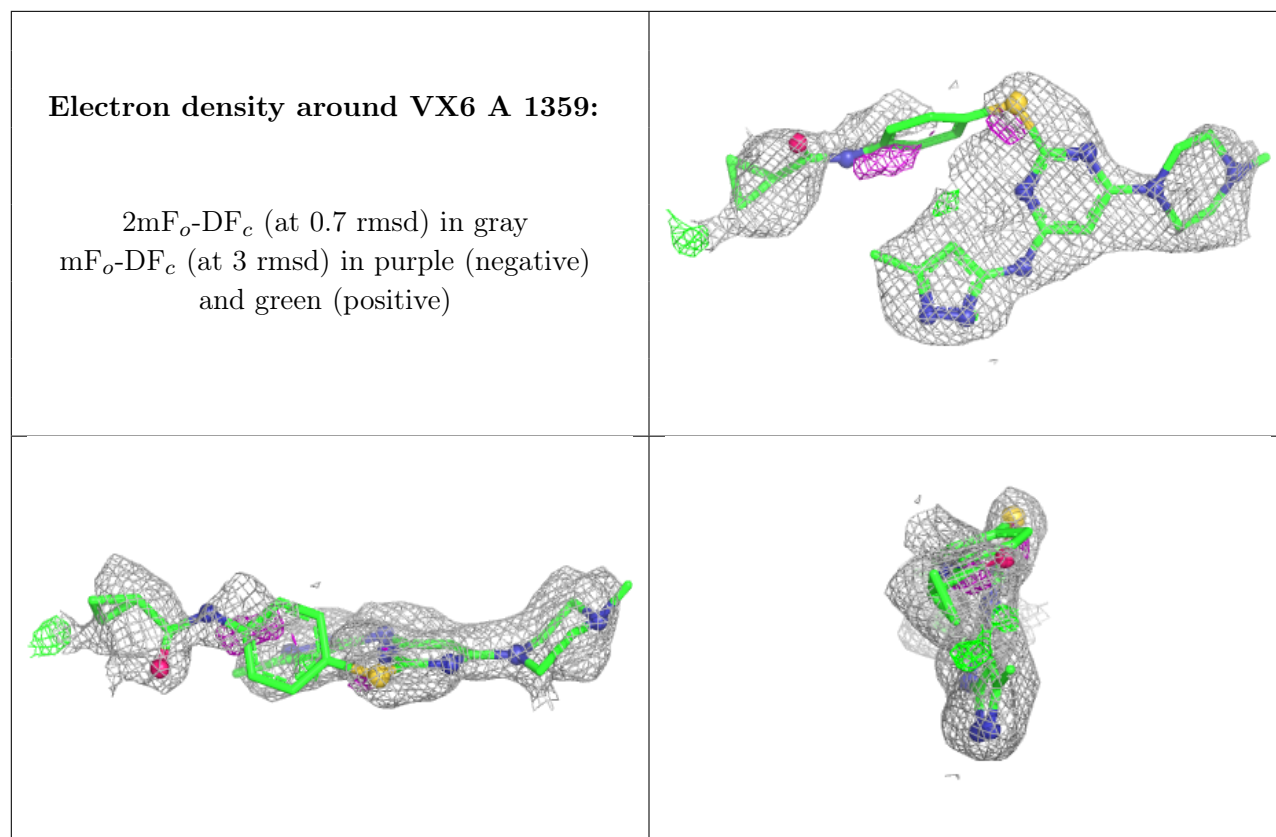
6.4 Ligands [i](#)

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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	VX6	B	1359	33/33	0.68	0.19	46,50,51,52	0
3	VX6	A	1359	33/33	0.69	0.21	49,53,54,54	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.