



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:23 PM UTC

PDB ID : 7KSK / pdb_00007ksk
Title : Thiophenyl-Pyrazolourea Derivatives as Potent, Brian Penetrant, Orally Bioavailable, and Isoform-Selective JNK3 Inhibitors
Authors : Park, H.
Deposited on : 2020-11-23
Resolution : 1.84 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

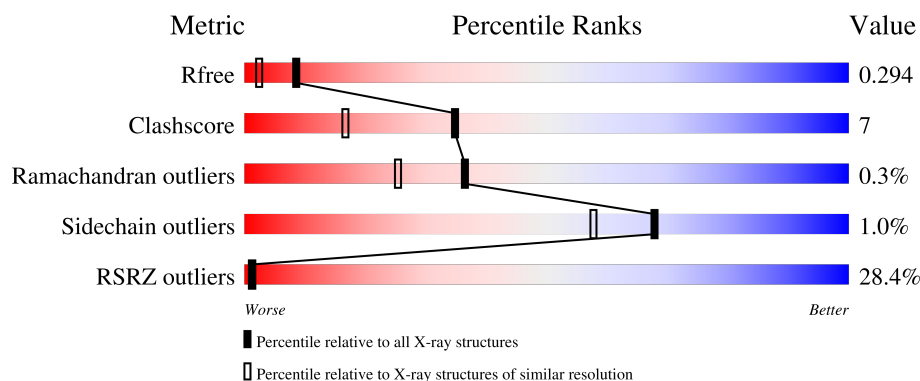
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.84 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	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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	464	20% 61% 10% 28%

2 Entry composition [i](#)

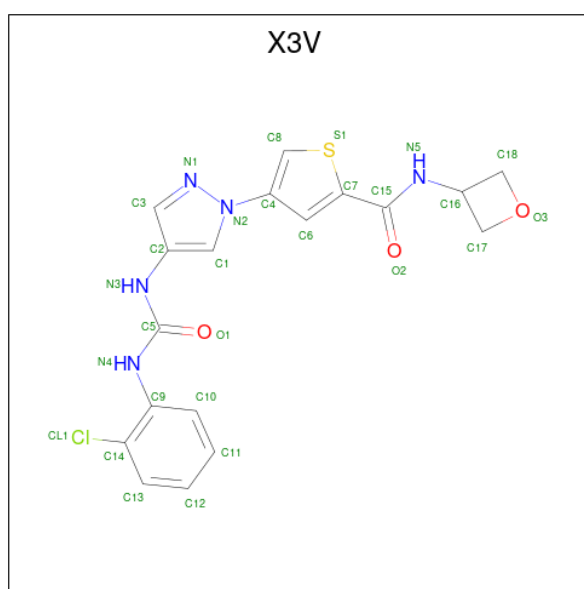
There are 3 unique types of molecules in this entry. The entry contains 5548 atoms, of which 2751 are hydrogens and 0 are deuteriums.

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 10.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	334	Total	C	H	N	O	S	0	0	0
			5451	1743	2735	461	491	21			

- Molecule 2 is 4-(4-[[[(2-chlorophenyl)carbamoyl]amino}-1H-pyrazol-1-yl]-N-(oxetan-3-yl)thiophene-2-carboxamide (CCD ID: X3V) (formula: C₁₈H₁₆ClN₅O₃S).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
2	A	1	Total	C	Cl	H	N	O	S	0	0
			44	18	1	16	5	3	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	53	Total 53 O	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	52.14Å 71.22Å 107.60Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.80 – 1.84 53.80 – 1.84	Depositor EDS
% Data completeness (in resolution range)	86.9 (53.80-1.84) 86.9 (53.80-1.84)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 1.83Å)	Xtriage
Refinement program	PHENIX DEV_3965	Depositor
R, R_{free}	0.247 , 0.290 0.256 , 0.294	Depositor DCC
R_{free} test set	1564 reflections (4.37%)	wwPDB-VP
Wilson B-factor (Å ²)	27.2	Xtriage
Anisotropy	0.832	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 26.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5548	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.56% 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: X3V

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	0.65	4/2769 (0.1%)	0.75	3/3734 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	202	THR	C-O	-7.58	1.14	1.23
1	A	165	ARG	C-O	-6.29	1.16	1.24
1	A	97	ARG	N-CA	-5.41	1.42	1.46
1	A	97	ARG	CA-CB	5.29	1.56	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	68	LYS	CA-C-N	6.17	126.08	119.85
1	A	68	LYS	C-N-CA	6.17	126.08	119.85
1	A	69	PRO	N-CA-C	-5.68	102.36	111.38

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	2716	2735	2729	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	28	16	0	1	0
3	A	53	0	0	0	0
All	All	2797	2751	2729	41	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 (41) 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:88:ARG:HH21	1:A:147:GLU:HG3	1.61	0.65
1:A:253:MET:HG2	1:A:336:LEU:HD21	1.81	0.61
1:A:219:MET:HA	1:A:219:MET:HE2	1.83	0.60
1:A:250:GLY:HA2	1:A:339:MET:HE3	1.84	0.59
1:A:231:ALA:O	1:A:235:ILE:HG12	2.06	0.56
1:A:107:ARG:O	1:A:111:GLU:HG3	2.06	0.55
1:A:68:LYS:HE2	1:A:80:ALA:HB3	1.90	0.53
1:A:178:LYS:NZ	1:A:351:ASP:OD1	2.42	0.52
1:A:159:MET:HE2	1:A:161:LEU:HD21	1.90	0.52
1:A:230:ARG:HD3	1:A:234:VAL:HG11	1.91	0.52
1:A:111:GLU:O	1:A:115:MET:HG2	2.10	0.51
1:A:218:PHE:CZ	1:A:220:MET:HE2	2.45	0.51
1:A:165:ARG:HH11	1:A:165:ARG:HG3	1.76	0.51
1:A:97:ARG:HD3	1:A:140:GLN:OE1	2.12	0.49
1:A:220:MET:O	1:A:220:MET:HG3	2.13	0.48
1:A:360:ASN:OD1	1:A:360:ASN:C	2.55	0.48
1:A:68:LYS:N	1:A:68:LYS:HD3	2.29	0.48
1:A:250:GLY:CA	1:A:339:MET:HE3	2.43	0.48
1:A:53:VAL:O	1:A:53:VAL:HG13	2.14	0.48
1:A:296:ASN:OD1	1:A:296:ASN:C	2.56	0.48
1:A:220:MET:O	1:A:220:MET:CG	2.62	0.48
1:A:287:MET:HE1	1:A:298:VAL:HG12	1.94	0.47
1:A:77:ILE:HG12	1:A:78:VAL:N	2.29	0.47
1:A:46:ASN:O	1:A:62:LYS:HE3	2.15	0.46
1:A:240:TYR:C	1:A:240:TYR:CD1	2.94	0.46
1:A:121:LYS:O	1:A:204:LYS:NZ	2.47	0.46
1:A:136:LEU:C	1:A:136:LEU:HD13	2.41	0.46
1:A:121:LYS:HE3	1:A:367:GLU:OE1	2.15	0.45
1:A:235:ILE:HG12	1:A:235:ILE:H	1.62	0.45
1:A:115:MET:HE3	1:A:126:LEU:CG	2.47	0.45
1:A:121:LYS:NZ	1:A:367:GLU:OE2	2.44	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ARG:HD3	1:A:240:TYR:CD2	2.53	0.44
1:A:321:ASP:N	1:A:321:ASP:OD1	2.51	0.44
1:A:77:ILE:HG12	1:A:78:VAL:H	1.82	0.44
1:A:46:ASN:O	1:A:46:ASN:OD1	2.36	0.43
1:A:146:MET:HG2	2:A:1101:X3V:C11	2.49	0.42
1:A:115:MET:HE3	1:A:126:LEU:HD11	2.01	0.42
1:A:309:PHE:N	1:A:310:PRO:CD	2.82	0.42
1:A:120:HIS:HB2	1:A:179:HIS:CD2	2.55	0.41
1:A:102:GLN:OE1	1:A:385:HIS:O	2.38	0.41
1:A:313:PHE:CD2	1:A:336:LEU:HD13	2.55	0.41

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	317/464 (68%)	305 (96%)	11 (4%)	1 (0%)	36 25

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	218	PHE

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	304/416 (73%)	301 (99%)	3 (1%)	68 58

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	GLN
1	A	165	ARG
1	A	296	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	47	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	X3V	A	1101	-	24,31,31	2.81	8 (33%)	32,43,43	4.00	18 (56%)

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	X3V	A	1101	-	-	2/18/26/26	0/4/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1101	X3V	C10-C9	10.27	1.56	1.39
2	A	1101	X3V	C9-C14	-4.83	1.29	1.39
2	A	1101	X3V	C9-N4	2.84	1.47	1.41
2	A	1101	X3V	C16-N5	2.70	1.52	1.46
2	A	1101	X3V	N2-N1	2.68	1.42	1.37
2	A	1101	X3V	C2-N3	-2.46	1.33	1.41
2	A	1101	X3V	C3-N1	2.20	1.36	1.32
2	A	1101	X3V	C6-C4	2.00	1.45	1.42

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	X3V	C14-C9-N4	7.95	131.50	119.25
2	A	1101	X3V	C8-S1-C7	7.89	98.57	91.65
2	A	1101	X3V	C9-C14-CL1	-7.71	111.16	119.52
2	A	1101	X3V	C6-C7-S1	-7.41	104.13	111.02
2	A	1101	X3V	C2-C1-N2	7.37	109.83	104.95
2	A	1101	X3V	C13-C14-C9	6.11	130.10	121.48
2	A	1101	X3V	C6-C4-C8	-5.89	110.89	114.58
2	A	1101	X3V	C10-C9-C14	-5.49	110.56	117.89
2	A	1101	X3V	C8-C4-N2	4.08	126.56	122.72
2	A	1101	X3V	C7-C15-N5	3.82	123.51	116.86
2	A	1101	X3V	C4-N2-N1	3.37	125.28	120.35
2	A	1101	X3V	C17-O3-C18	-3.32	88.19	91.34
2	A	1101	X3V	C11-C12-C13	-2.89	116.68	120.24
2	A	1101	X3V	C3-N1-N2	2.62	106.37	103.81
2	A	1101	X3V	N4-C5-N3	2.55	119.74	114.22
2	A	1101	X3V	C10-C9-N4	-2.34	116.40	121.82
2	A	1101	X3V	O2-C15-C7	-2.33	116.38	120.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1101	X3V	C15-C7-S1	2.23	128.65	119.62

There are no chirality outliers.

All (2) torsion outliers are listed below:

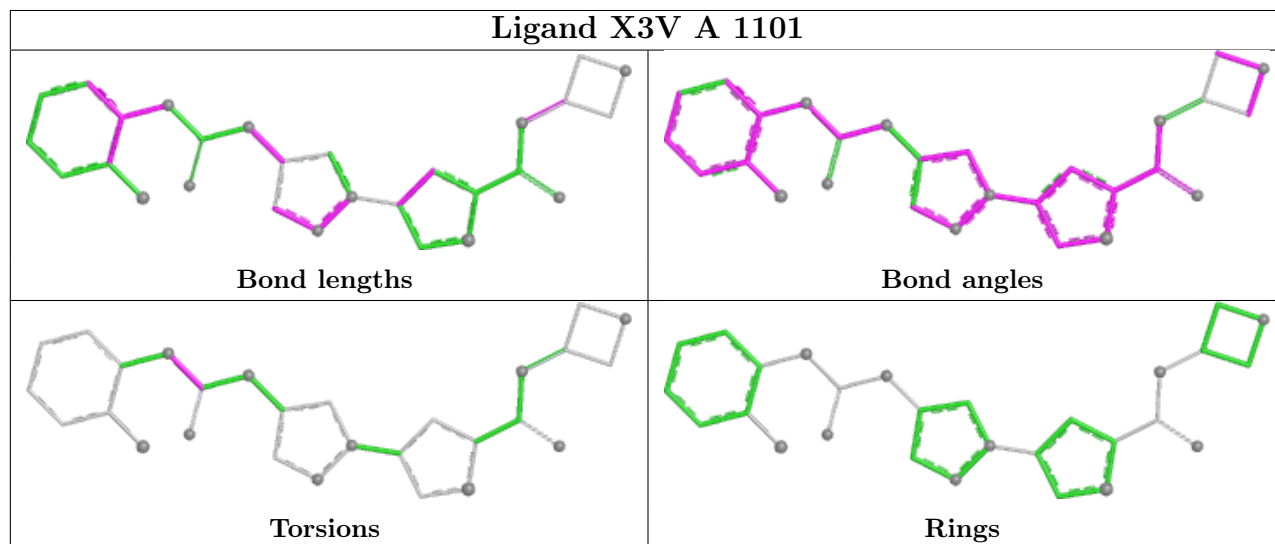
Mol	Chain	Res	Type	Atoms
2	A	1101	X3V	N3-C5-N4-C9
2	A	1101	X3V	O1-C5-N4-C9

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1101	X3V	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	334/464 (71%)	1.65	95 (28%) 1 1	31, 46, 83, 107	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	379	GLN	6.7
1	A	72	SER	6.3
1	A	76	GLY	5.9
1	A	224	VAL	5.7
1	A	380	LEU	5.5
1	A	364	ASP	4.8
1	A	114	LEU	4.8
1	A	222	PRO	4.5
1	A	365	PRO	4.3
1	A	367	GLU	4.2
1	A	53	VAL	4.1
1	A	220	MET	4.0
1	A	71	GLY	3.8
1	A	217	SER	3.8
1	A	382	GLU	3.8
1	A	321	ASP	3.7
1	A	68	LYS	3.7
1	A	115	MET	3.6
1	A	107	ARG	3.5
1	A	225	VAL	3.5
1	A	119	ASN	3.4
1	A	301	ARG	3.4
1	A	211	ALA	3.4
1	A	366	ALA	3.3
1	A	289	LYS	3.3
1	A	290	LEU	3.2
1	A	218	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	117	CYS	3.2
1	A	381	ASP	3.2
1	A	362	TRP	3.1
1	A	221	THR	3.1
1	A	305	ALA	3.1
1	A	303	LYS	3.1
1	A	297	TYR	3.1
1	A	267	ASP	3.1
1	A	319	PRO	3.1
1	A	70	ILE	3.0
1	A	399	MET	3.0
1	A	318	PHE	3.0
1	A	45	ASP	3.0
1	A	304	TYR	3.0
1	A	51	VAL	2.9
1	A	306	GLY	2.9
1	A	46	ASN	2.9
1	A	201	CYS	2.9
1	A	52	GLU	2.8
1	A	283	CYS	2.8
1	A	67	LEU	2.8
1	A	185	ILE	2.8
1	A	285	GLU	2.8
1	A	113	VAL	2.8
1	A	123	ILE	2.7
1	A	177	ILE	2.7
1	A	276	ILE	2.7
1	A	384	GLU	2.7
1	A	219	MET	2.6
1	A	369	GLU	2.6
1	A	294	VAL	2.6
1	A	385	HIS	2.6
1	A	307	LEU	2.6
1	A	65	GLN	2.5
1	A	183	ALA	2.5
1	A	268	TYR	2.5
1	A	311	LYS	2.4
1	A	383	ARG	2.4
1	A	112	LEU	2.3
1	A	312	LEU	2.3
1	A	280	GLY	2.3
1	A	361	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	398	VAL	2.3
1	A	210	LEU	2.3
1	A	400	ASN	2.3
1	A	269	ILE	2.3
1	A	57	THR	2.3
1	A	360	ASN	2.3
1	A	349	SER	2.3
1	A	79	CYS	2.3
1	A	296	ASN	2.3
1	A	240	TYR	2.2
1	A	77	ILE	2.2
1	A	92	ILE	2.2
1	A	257	VAL	2.2
1	A	116	LYS	2.2
1	A	291	GLN	2.2
1	A	55	ASP	2.2
1	A	104	HIS	2.2
1	A	126	LEU	2.2
1	A	235	ILE	2.1
1	A	329	ALA	2.1
1	A	58	PHE	2.1
1	A	106	LYS	2.1
1	A	300	ASN	2.1
1	A	118	VAL	2.0
1	A	161	LEU	2.0
1	A	359	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](#)

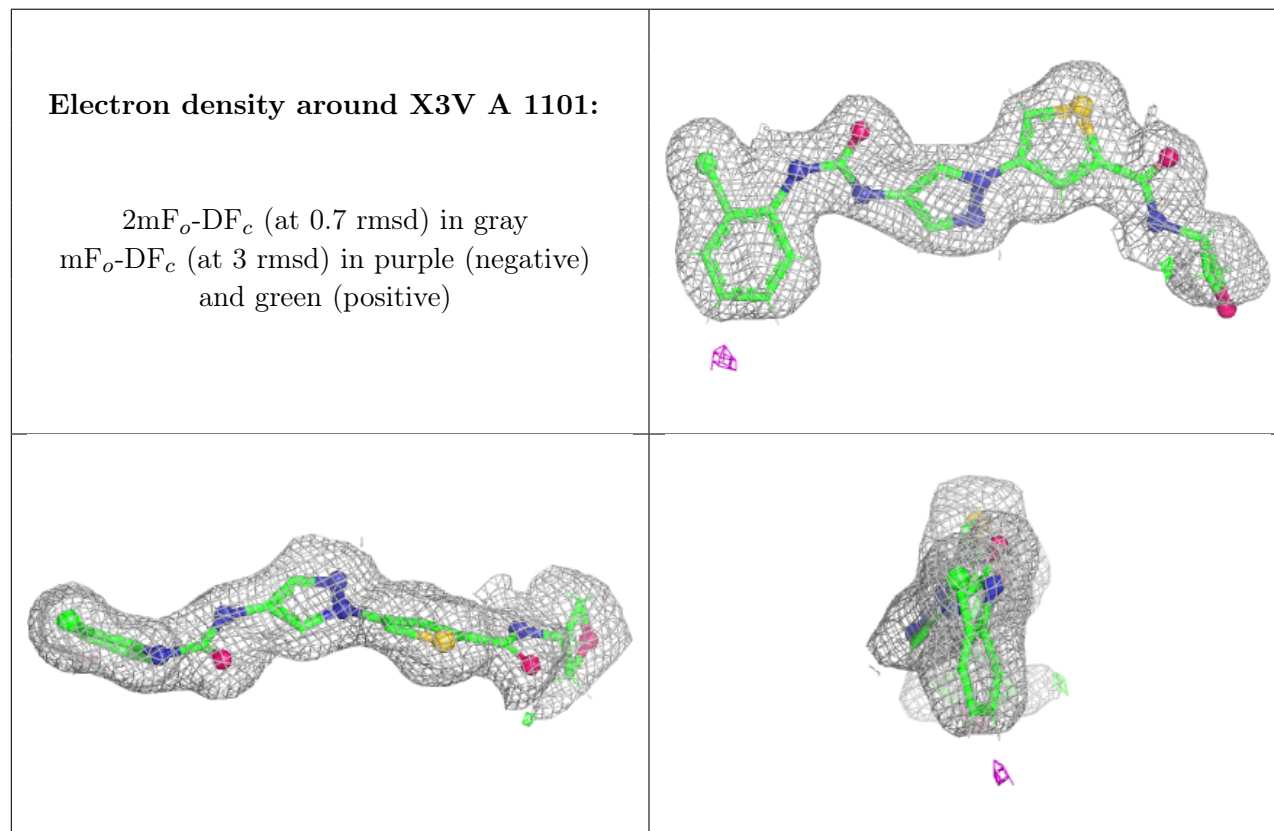
There are no oligosaccharides in this entry.

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.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	X3V	A	1101	28/28	0.92	0.11	27,36,58,65	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.